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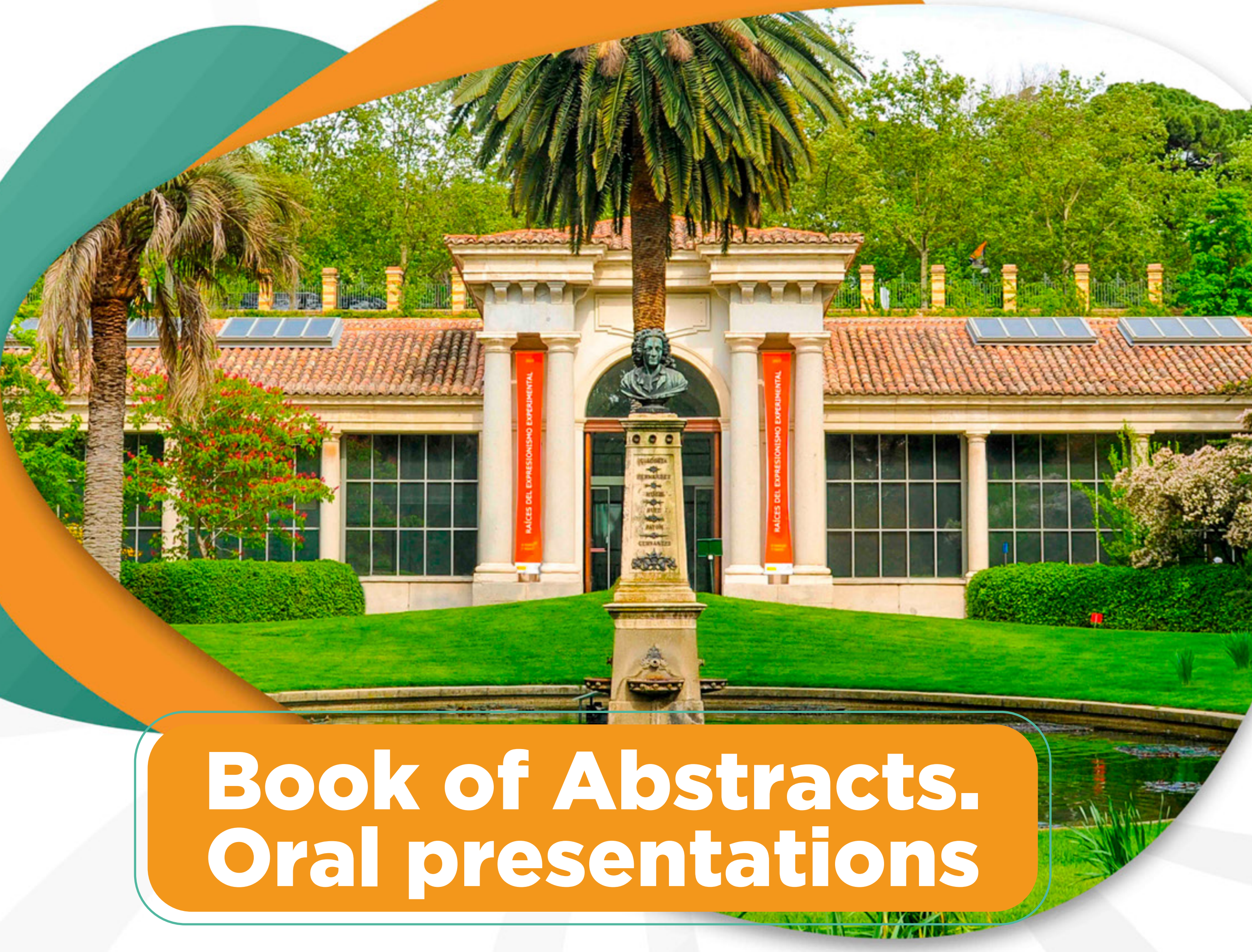

Book of Abstracts. Oral presentations

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INDEX BY SYMPOSIA

Invited Speakers

Why botany? Why now?

Sandra Knapp.

Natural History Museum, Cromwell Road, London SW7 5BD, United Kingdom

Abstract

Botany – broadly speaking, the study of algae, fungi, and plants – is a global enterprise. We depend upon the organisms for the very air we breathe, yet their survival, along with our own, is ever more in question. How should we come together to tackle this planetary emergency – the mutually reinforcing threats of climate change and biodiversity loss? Individual botanists, or individual botanical institutions, cannot tackle this alone. At this critical time in Earth's history, it is more important than ever to work together – across boundaries, institutions, and career stages – to effect change and affect our planetary future. The time for concentrating the power and influence in a few institutions is gone, and our strength lies in our diverse skills and complementary understandings of the natural world. Our goal must be to create a level playing field where all those studying algae, fungi, and plants can come together to share ideas and exchange knowledge, so we can together develop solutions both from nature but most importantly for nature. I will share some learnings from projects I have been fortunate enough to have been involved in and will bring new ideas for discussion. Today, at almost the quarter-point of this century, it is time for us to join efforts in better, more diverse, and more distributed ways to find solutions for Earth's problems so the algae, fungi, and plants upon which we all depend and that we all so love, have a secure future.

Unraveling diversity and evolution of lichens in the genomic era

H. Thorsten Lumbsch, Todd J. Widhelm, Felix Grewe

Collections, Conservation, and Research and Grainger Bioinformatics Center, The Field Museum, Chicago, USA

Abstract

Our understanding of the biology, evolution, and diversity of lichens has dramatically changed over the last decade. This symbiotic system has been shown to be complex. Several fungi can be involved in the symbiosis and recent studies suggest a diversity of photosynthetic partners shaped by phylogeny and ecology. In addition, bacteria and various groups of other fungi have been found to form part of the lichen holobiome. Whereas lichens were thought to be ancient organisms, molecular data suggest that the evolution of these organisms happened in parallel to land plants and there is no indication from molecular or well-preserved fossils that would support an ancient origin of the lichen symbiosis. The knowledge of the phylogeny of lichenized fungi has been revolutionized with genetic and genomic data that resulted in a classification that is dramatically different from the classifications inferred from phenotypical data. Potential reasons for the bewildering complexity of phenotypical data in lichens are discussed in the presentation.

Genomic data have also fundamentally changed our understanding of species delimitation and biogeography of lichens. In the pre-molecular era, it was assumed that ecology was the main driver shaping distri-

butional ranges with only very limited attempts to interpret observed patterns in a historical biogeographical framework. Molecular data showed that numerous species that were interpreted as having wide, inter-continental distributions belong to distinct clades, often not closely related to each other. As a consequence, historical biogeography has seen a revival in lichenology over the last decade. The genomic era is in its infancy in lichenology and some open questions will be highlighted that will be addressed with the growing number of genomic data becoming available

Tropical tree adaptation to fire regimes and infertile soils: key for ecosystem conservation

Kaoru Kitajima 1, Hiroki Sato2, Joseph Percival1, Tomohiro Nishigaki 3, Kaoru Oshima1, Ando Rakotomamonjy1, Zo Lalaina Razafiarison4

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Abstract

Fire is a key threat to the conservation of natural forests worldwide. In many tropical countries, especially in Africa, population increase and expansion of agricultural lands encroach the remaining frontier of pristine forests, many of which are on marginal lands that do not support sustainable agricultural production. This talk highlights the case in NW Madagascar, where we have established a 15-ha forest monitoring plot in a seasonally dry forest on infertile white sand within Ankarafantsika National Park. This forest supports a high diversity of plants and animals, including eight species of lemurs in mutualistic relationships with many tree species via frugivory-seed dispersal. The woody plant community of this forest has a high level of endemism, with dominance of evergreen species despite the prolonged dry season (April November). Fire has been a main driver of forest loss in the region, resulting in the highest rate of forest loss in Madagascar during the last three decades. During the last five years, the number and area burned increased rapidly within the national park border. We have conducted intensive analyses of ca. 3000 ha near the southern border of the park, where there were no fires until 2014. Large areas of primary forest burned in 2017, 2019, and 2021, partly due to a lack of fire adaptation in the tree community. The first burn makes a site susceptible to repeated burns, as dead woody materials above and below ground serve as fuel to support intense burns. After a few fire episodes, the dense closed-canopy forest turns into a barren desert. The fire vulnerability of the primary forest in Ankarafantsika is a testimony to the importance of paying attention to variations in fire adaptation within the tropical dry forest biome to design effective conservation strategies at the landscape level.

The science of plant conservation in a changing Mediterranean world

Thompson, John D

CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France

Abstract

The Mediterranean region and its climate are changing, perhaps faster than we realize. As scientists, a modern challenge is to identify how species, communities, and ecosystems respond to global change and to integrate information on the underlying processes into conservation management and recommendations for political decision. This knowledge is necessary to fulfill conservation objectives. This talk will focus on different elements of contemporary ecological and evolutionary dynamics of West Mediterranean endemic plant species whose distribution patterns cover all, or a small part of, a narrow belt from northern Morocco, though eastern Spain, to mediterranean France. This distribution is a recurrent pattern in the flora of the West Mediterranean. The often narrow latitudinal range of species with this distribution pattern contrasts with a wide longitudinal range. As a result, many species occur in areas subject to different representations of the Mediterranean climate, and very often in peripherally isolated populations at the limits of their distribution. Using examples of several species with this distribution pattern I will illustrate ongoing processes of adaptation in a changing Mediterranean climate and the issues associated with conserving species that show marked variability in the their ecological niche on different spatial scales, their spatial genetic structure, and variation in their floral biology at their distribution limits. I conclude with a message concerning how our knowledge of the history of the Mediterranean region improves not only our understanding of this variability but also the reasons and values for local efforts to conserve such species, often in areas where they are rare.

Cryptic disruptions of plant-animal mutualisms in the Anthropocene

Jordano, Pedro

Estación Biológica de Doñana, CSIC, and Dept. Plant Biology and Ecology, Univ. Sevilla, Spain

Abstract

Pairwise plant-animal mutualistic interactions build up into mega-diverse networks involving dozens of interacting species. These mutualisms among free-living species fundamentally consist of food provisioning by plants and, their counterpart, plant propagule (pollen, seeds) movement by the animals. They are based on interaction outcomes serviced by multiple species, so that studies focusing on pairwise interactions in isolation underestimate the levels of biodiversity required to maintain multifunctional networks. Loss of biodiversity in these assemblages entails losses of key functional services that may remain cryptic, i.e., their consequences undetected well after the loss. I explore study cases documenting the extinction of mutualistic interactions, and the loss of associated services that may occur well before the partner species become extinct. In addition, also how addition of interactions (e.g., by invading species) may deconstruct native interaction networks. The combination of direct and passive interaction sampling (e.g., direct census, camera traps) and last-generation sequencing (DNA barcoding) allow to identify species-specific contributions to these mutualisms and estimate both demographic and genetic outcomes of interactions. The functionality of most generalized mutualisms among free-living species relies on complementarity of effects across a high diversity of partners. Disruptions of these mutualisms by anthropogenic drivers may remain subtle and undetected despite being pervasive in many real world ecosystems. The loss of these interactions, frequently occurring well before their plant and animal partners go extinct, generates a type of extinction debt not adequately addressed when biodiversity loss is considered.

Evolution of floral disparity through integration of fossil and extant morphological diversity

Susana Magallón, Andrea M. López-Martínez, Maria von Balthazar, Jürg Schönenberger, Hervé Sauquet, Marion Chartier.

Abstract

Integration of molecular data, to provide a general phylogenetic framework, and morphological data, to allow incorporation of fossils, represents a cardinal approach to investigate evolution in deep time. We assembled a morphological matrix for 1201 extant species representing all angiosperm families, and 121 well-preserved fossil flowers, and in combination with a molecular database for extant species based on exemplar representation, used it to investigate methodological issues relating to integration of extant and fossil taxa in phylogenetic estimation; divergence time estimation in a full Total Evidence approach; and estimation of the theoretical floral morphospace. Phylogenetic analyses used different optimization criteria and kinds of data to estimate relationships, as well as uncertainty in fossil placements. We found that the joint use of molecular and morphological data in a parametric context allows to recover a phylogenetic framework in agreement with molecular estimates, and fossils associated to branches in agreement with assessments based on detailed morphological comparisons. Nevertheless, uncertainty associated to fossil placements is usually high. An attempt to estimate divergence times using morphological, molecular and temporal information indicates that, while available models to integrate extant and fossil species in the same diversification process represent significant advances, there are practical difficulties with fossils for which few characters can be scored, and in the free estimation of model parameters. The theoretical morphospace of floral structure was estimated through the construction of a pairwise distance matrix among extant and fossil species, estimation of disparity, and ordination techniques to reduce dimensionality. The area of the theoretical morphospace occupied by extant and fossil species was identified, as well as how morphospace occupation has changed through time and among groups. A decrease in morphospace occupation towards the present and canalization in the of morphospace occupation among derived clades are documented, in agreement with previous independent observations.

Integrating Plant Hydraulics and Ecological Processes Across Scales

Rafael Oliveira

Ph.D in Integrative Biology at the University of California, Berkeley. Professor at Plant Biology Department at University of Campinas, Campinas, Brazil

Abstract

Plant hydraulics is increasingly recognized as a central link between plant biology and fields such as community and ecosystem ecology, climatology, and earth-system science. Understanding the intricate interactions between plant hydraulics and ecological processes is essential for predicting plant responses to environmental changes and managing ecosystems effectively. In this talk, I will present an overview of recent findings that demonstrate how hydraulic traits can explain species distributions across various spatial scales and influence ecological processes such as growth, demography, community assembly, and carbon dynamics,

particularly in tropical ecosystems, which are crucial for global water and carbon cycles. Furthermore, I will discuss how plant hydraulics can offer a mechanistic explanation for vegetation resistance or vulnerability to predicted climate changes, and how this knowledge can be used to forecast future dynamics of species and communities in changing climatic conditions.

Evolution of woody plants on the tropical coasts inferred from a full set of mangrove genomes

Shi, Suhua

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Abstract

Genomic studies are now poised to explore whole communities of species. The ~70 species of woody plants that anchor the coastal ecosystems of the tropics, collectively referred to as mangroves, are particularly suited to this exploration. In this study, we de novo sequenced the whole genomes of 32 mangroves, which we combined with other sequences of 30 additional species, comprising almost all mangroves globally. These community-wide genomic data will be valuable for ecology, evolution and biodiversity research. While the data revealed 27 independent origins of mangroves, the total phylogeny shows only modest increases in species number, even in coastal areas of active speciation, suggesting that mangrove extinction is common. A possible explanation for common extinction is the frequent sea-level rises and falls documented in the geological record. Indeed, near-extinctions of species with extremely small population size (N) often happened during periods of rapid SLR, as revealed by the genome-wide heterozygosity of almost all mangroves. Reduction in N has possibly been further compounded by population fragmentation and the subsequent accumulation of deleterious mutations, thus pushing mangroves even closer to extinction. The impact of the next SLR will be exacerbated by human encroachment into these mangrove habitats. Finally, in addition to possible extinctions, this talk will also cover the opposite phenomenon, namely, the patterns speciation along the tropical coasts.

The phylogenetics of plant geography: past, present, and future

Donoghue, Michael J.

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Abstract

In decades past, vicariance/cladistic biogeographers emphasized the importance of discovering general biogeographic patterns and their underlying causes. Since then, however, most of the focus has been on inferring geographic movements using phylogenetic trees of individual clades. Another development has been the application of phylogenetic approaches to major biogeographic patterns of interest especially to ecologists. With the hope of revealing general patterns I have revisited and updated two papers that I published with colleagues in 2004 one on the latitudinal gradient in species richness and one on major disjunctions around the Northern Hemisphere. In both cases, I have carried out a systematic review of progress based on plant studies published

over the past twenty years. Although a number of hypotheses have been well supported over this time period, and others can now safely be set aside, there are still substantial gaps in our understanding, and a need for further coordination of efforts and methodological improvements. I will present the results of these studies while highlighting the value of syntheses that draw upon multiple primary analyses. These observations also highlight improvements that can be made in studying individual clades. To illustrate many of the central points I will make special reference to our ongoing studies of Viburnum biogeography

Delving into South African medicinal plant treasures

Nokwanda Makunga

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Abstract

South Africa has an incredible floral heritage that has a strong history of being important to local people for diverse range of ethno-cultural uses and those plants that are exploited for medicinal purposes have also encouraged entry of new natural products into global markets. There are thus unique opportunities that are presented by interfacing various biotechnologies to study medicinal plants of South Africa, more especially with the intention of generating socioeconomic benefits. This talk will touch on historical aspects linked to the exploitation of medicinal plant resources and define the importance of indigenous knowledge and medicinal plants when interfaced with biotechnology in relation to the bioeconomy strategy of South Africa. Using specific examples from medicinal plants that occur in the greater Cape Floristic Region, various studies are thus presented and summarized. The application of LC-MS-based metabolomics technologies has been useful as a qualitative tool, enabling fast detection and a reliable method of studying mesembrine alkaloids produced by Sceletium tortuosum (Aizoaceae). Microplant and callus cultures also accumulate a wide array of these alkaloids. By applying both non-targeted and targeted metabolomics, influence of varied microenvironments on the phytochemistry and cytotoxicity of Sutherlandia frutescens (Fabaceae) plants is evident. Proteomic analyses under stressed conditions provided new insights into the impacts of salinity and drought stress with respect to both central and specialized metabolism of S. frutescens. Combining microsatellite and chemometric analyses confirmed biogeographical-based genetic structure amongst populations of Dodonaea viscosa (Sapindaceae) and Aspalathus linearis (Fabaceae), pinpointing chemotype(s) that may fit domestication and industrialization for the production of phytopharmaceutics. These studies illustrate the exciting potential of medical plants of South Africa that still remain chemically under explored.

Distyly as a model for studying convergent evolution - insights from genomic studies

Tanja Slotte

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Abstract

Recent advances in sequencing technologies, in combination with powerful new simulation and analysis tools, have opened up a wealth of new possibilities to address classic evolutionary questions in non-model

systems. In this talk, I will highlight how we are harnessing this development to study the evolution of plant mating systems, with a focus on the evolution of a balanced floral polymorphism termed distyly.

Distyly is a floral polymorphism governed by a supergene, that has evolved convergently in multiple angiosperm lineages. Distyly promotes outcrossing and efficient pollen transfer via the presence of two floral morphs that differ reciprocally in the positions of their male and female sexual organs. These morph differences are usually coupled with a heteromorphic self-incompatibility system that reduces self- and intra-morph fertilization. Loss of distyly has also occurred very frequently, often in association with convergent evolution of floral selfing syndromes. Studying the evolution and loss of distyly therefore offers an opportunity to address classic questions on the genetic basis of convergent phenotypic evolution, supergene breakdown and the genomic consequences of selfing.

Here, I will present our work on these topics in Linum, a non-model plant system that is exceptionally well suited for this purpose. Harnessing new high-quality genome assemblies, we have identified and characterized the distyly supergene in Linum at the molecular level, tested theory on genetic causes of loss of distyly, and documented pervasive population genomic consequences of this shift. Genomic studies of distyly in Linum and other systems have revealed striking similarities in hemizygous genetic architectures and molecular evolution of independently evolved distyly supergenes and provided a foundation for further characterization of the genetic underpinnings and genomic consequences of convergent evolution and loss of distyly. This body of work demonstrates the power of genomic analyses in non-model systems to shed new light on classic evolutionary questions.

Biodiversity and ecosystem function in subtropical forest

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Abstract

In order to explore the relationship between biodiversity and ecosystem functioning such as primary productivity in forest ecosystem, a large manipulation experiment was established in subtropical China in 2009 and 2010. Based on the experiment platform, German, Swiss and Chinese scientists worked together and published more than 200 papers. The key findings are as follows. 1, After 8 years, 16-species mixtures had accumulated over twice the amount of carbon found in average monocultures and similar amounts as those of two commercial monocultures. Species richness effects were strongly associated with functional and phylogenetic diversity. 2, Effects of functional diversity (FD) values on productivity became larger than effects of community-weighted mean (CWM) values after 7 years of forest development and that the FD values also became more reliable predictors of productivity than the CWM values. In contrast to CWM, FD values consistently increased productivity across ten different species-pool subsets. 3, Tree species richness improved community stability by increasing asynchrony. That is, at higher species richness, interannual variation in productivity among tree species buffered the community against stress-related productivity declines. This effect was mediated by the diversity of species hydraulic traits regarding drought tolerance and stomatal control. 4, Effects of experimentally increased tree species richness were consistently positive for species richness and abundance of herbivores, predators and parasitoids. Richness effects decreased as trophic levels increased for species richness and abundance of all trophic groups. Multitrophic species richness and abundance of arthropods were important mediators of plant diversity effects on tree productivity. These long-term studies emphasize the importance of planting functionally diverse, mixed-species for the restoration and reforestation projects to improve ecosystem functioning, maintain multitrophic diversity and mitigate climate change.

Pollination ecotypes: niche-driven floral evolution below the species level

Steven D. Johnson

DST-NRF SARChI chair in Evolutionary Biology. Associate editor of Proceedings of the Royal Society B and Biological Journal of the Linnean Society.

Abstract:

Ecological niche shifts are a key driver of phenotypic divergence among populations and can also contribute to reproductive isolation. While patterns of historical ecological shifts and the associated trait-environment correlations are well-documented at the macroevolutionary level, the process is initiated below the species level, as shown originally by Turesson, Clausen and others in their seminal studies of edaphic and climate ecotypes in plants. Pollinators are critical for the establishment and persistence of populations of the majority of plant species, thereby forming part of their fundamental niche. Novel floral trait combinations allow plants to exploit particular pollinator niches in local habitats and evolve primarily through sexual selection due to their effect on plant mating success. Shifts in pollinator niches among plant populations lead to the formation of "pollination ecotypes". Work on pollination ecotypes has revealed that their origin is best explained by contemporaneous ecological gradients arising from the mosaic-like spatio-temporal distribution of pollinators. I discuss case studies on the evolution of pollination ecotypes and use these to identify a number of challenging practical and conceptual issues. These include the paucity of reliable natural history data, difficulty of knowing when ecotypes should be considered species, reconstructing the number and direction of intraspecific shifts, and distinguishing between extinctions and isolating barriers as explanations for phenotypic and genetic discontinuities among population clusters.

The Changing Face of Herbarium Collections

Pamela S. Soltis

Abstract

Herbaria have long provided the foundation for our understanding of plant diversity and distributions. Beyond their fundamental role in taxonomy, herbarium specimens, like other natural history collections, reflect a history of unanticipated uses. Although collected to document plant occurrences, the world's 400,000,000 herbarium specimens, spanning space and time, provide unparalleled resources for plant science and are indeed undergoing a renaissance in their use. Preserved plant tissues are reservoirs of genetic information that can be used to reconstruct the evolutionary history of plants. The resulting family tree provides a foundation for basic biology and for solving many societal problems, such as food security and the search for new medicines. Digitized herbarium specimens also offer new research opportunities, particularly in relation to climate change and conservation. These herbarium resources provide novel opportunities for mobilizing and integrating massive amounts of information from organismal biology, ecology, genetics, climatology, and other disciplines. As the number of online records continues to grow, these data provide excellent information on species distributions, changes in distributions over time, phenology, and a host of traits. Integration of information from specimen records with phylogenies, climate data, and other resources enables new questions to be addressed while also providing new perspectives on longstanding questions in ecology and evolutionary biology. Through a series of case studies, I will illustrate some of the many uses to which herbarium specimens and their digital data are currently being applied. These case studies link specimen data and related heterogeneous data sources and show how high-throughput molecular analysis and artificial intelligence can be applied to centuries-old herbarium specimens to address a range of evolutionary, ecological, and societal problems.

Exploring the underground: unraveling the complex interplay of biodiversity and disease in plant communities

Liesje Mommer

Wageningen University, Wageningen, the Netherlands

Abstract

Biodiversity loss is a significant driver of disease risk in ecosystems, yet the intricate relationships between diversity and disease remain poorly understood. This keynote lecture will delve into the knowledge frontiers of this field.

Traditionally, plant ecologists have explained diversity-disease relationships by distinguishing between host and non-host species. When biodiversity loss increases the density of hosts compared to non-hosts, disease risk increases, and vice versa. However, focusing on this host-non-host dichotomy overlooks the substantial variation in 'host quality'—a measure of a host's contribution to parasite fitness.

To illustrate this concept, I will present findings from a temperate grassland biodiversity experiment involving 16 plant species (forbs and grasses). Using Illumina MiSeq amplicon sequencing, we assessed the abundance of root-associated fungal pathogens in plant monocultures and four-species mixtures. Our study identified three major fungal pathogens with differing host ranges: Paraphoma chrysanthemicola, associated with forb species of the Asteraceae family; Slopeiomyces cylindrosporus, associated with grass species; and Rhizoctonia solani, affecting both forb and grass species. We discovered that plant community composition rather than plant species richness per se significantly influences pathogen relative abundance. The presence of specific high quality host species appeared key.

Another concept that may modify diversity-disease relationships belowground in the presence of arbuscular mycorrhizal fungi. These organisms are form symbiotic relationships with 80% of plant species and are known to enhance nutrient uptake in plants. I will present preliminary evidence that these mycorrhizal fungi modify plant-pathogen interactions in grassland systems.

Our findings highlight the intricate interplay between plant community properties, host-pathogen and host-symbiont interactions and their vital role for understanding the impacts on overall grassland productivity and ecosystem health. Be invited to journey underground to uncover the hidden dynamics of biodiversity and disease in plant communities.

Into the wild: addressing plant extinction through population reintroductions

Gallagher, Rachael V.

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Abstract

Over the last three decades, vast international resources have been committed to conservation seed banking, to great success. Seed bank collections have grown rapidly since the millennium and seeds and plant germplasm are now routinely stored to safeguard species against extinction. Yet seed banks were never intended to be a final stop along the road to recovery for plant species. Currently, when we do reintroduce or translocate plant populations, failure rates associated with their establishment can be unacceptably high. We also often do not know

where to situate new plant populations relative to their historical distributions, given immense changes in climate and land use. New science is therefore needed to improve and intensify the strategic reintroduction of plant populations to the landscape. In this talk, I will outline gaps in ecological and conservation knowledge that hamper current reintroduction success, explore solutions, and demonstrate how we might use emerging financial market mechanisms to fund initiatives that reduce plant extinction risk. I hope to inspire new thinking about how we can thoughtfully design initiatives that get more plant species out of the fridge and into the wild across the world.

Bringing ecophysiology closer to plants from extreme environments and diverse phylogenetic groups

Flexas Sans, Jaume

INAGEA - Universitat de les Illes Balears, Palma, Spain

Abstract

Plant (eco) physiology deals with the physiological responses of plants to environmental conditions. Within this definition, it should deal with any kind of plant and environment. However, perhaps because this discipline often requires the use of electronic devices and heavy equipment, most studies deal with a limited number of Angiosperms, especially crops. Studies are most often conducted under tropical, temperate and Mediterranean conditions, with scarce studies in more extreme environments such as high elevation mountains, hot and cold deserts.

Here I will show examples on how my research group has recently expanded along the land plant phylogeny and towards climatically extreme ecosystems. First, I will show how photosynthetic capacity changes along the land plant phylogeny, and its underlying physiological, anatomical and biochemical causes. Second, I will present some home-made, relatively portable techniques, for assessing the short-term tolerance of plant photosynthetic organs to dehydration, low and high temperature, and excess visible and UV-B radiation, and how the use of these devices is allowing us to test for the trade-off between photosynthetic capacity and abiotic stress tolerance across the entire land plant phylogeny and along the entire spectrum of Earth biomes.

Finally, I will focus on two specific studies in some extreme environments. In the first, I will show how well standardized, portable and commercially available ecophysiological tools allowed for a diagnose of different species physiological status without the need for a previous knowledge of each species optimal status along a Chinese transect, from the Xinjiang steppes through the Taklamakan desert to the Tibet Plateau. In the second, I will deal with the particular case of giant cushion Azorella species along the Chilean Andes Range, and discuss how its particular anatomy generates a very contrasted microclimate that may allow these species to establish and, perhaps, help them to facilitate other species.

The evolution of extant South American tropical Biomes

Jaramillo, Carlos

Smithsonian Tropical Research Institute, Panama

Abstract

When and why South American tropical biomes developed? Tropical vegetation had a complete turnover from non-angiosperm dominance at the onset of the Cretaceous to angiosperm dominance nowadays. Cretaceous tropical biomes do not have extant equivalents; lowland forests were dominated mainly by gym-

nosperms and ferns lacking a closed canopy. This structure was transformed following the Cretaceous Paleogene meteorite event. The extant lowland tropical rainforests first developed at the onset of the Cenozoic with a multistratified forest, an angiosperm-dominated closed canopy, and abundant legumes. Cenozoic rainforest diversity has increased during warmings and decreased during coolings. Tropical dry forests emerged at least by the late Eocene, whereas other drier Neotropical biomes are much younger.

Reimagining arid zone ecology in a changing world: is rainfall all that matters?

Austin, A.

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Abstract

While forests have received intense attention regarding their role in the global carbon cycle, the drier parts of the world, constituting over 40% of the terrestrial land surface, are often overlooked as unproductive and unresponsive to human-induced global change. In contrast to forest ecosystems, these arid regions present unique conditions, encompassing a matrix of climate, land use, and plant-soil interactions that suggest complex responses to changing environmental conditions, which we are only beginning to comprehend. Our research specifically focuses on understanding how alternative climatic controls, such as exposure to solar radiation, temperature, and the seasonality of rainfall, exert substantial impacts on carbon turnover and storage in arid land ecosystems. In contrast to a singular focus on rainfall as the primary determinant of ecosystem functioning in arid lands, our findings highlight the significant, positive effect of solar radiation exposure on carbon emissions and subsequent microbial turnover. By shedding light on these often-neglected arid land ecosystems and their specific controls, we may provide more predictive power for effective management and conservation amidst ongoing climate and land use changes.

Machine learning and new inference algorithms: expanding what is possible in evolutionary biology and phylogenetic analysis

Sanmartín, Isabel

Real Jardín Botánico, CSIC, Madrid, Spain

Abstract

Investigators across different fields of evolutionary biology are increasingly turning their attention to more integrative and complex inference models. This trend is fueled partly by the emergence of next generation sequencing technologies, scaling up the number of genes, individuals, and species sampled, and partly by the rapid expansion of biodiversity, climatic and biogeographic databases at the local, regional and community scales. This massive increase in the quantity of data available has opened up a range of new questions but also unexpected challenges that require the development of more sophisticated approaches to data modeling. For example, a standing challenge is how to hybridize lineage-based, individual-based, and gene-based models to adress all aspects of biodiversity loss (richness, abundance, genetic diversity) in order to explain the biotic impacts of climate change. The COVID-19 pandemic introduced the need for models that are computationally efficient and can analyze in a short time thousands of sequences differing only in a few nucleotides. Statistical models in evolutionary biology are typically built around stochastic parameters interconnected by rigid dependencies, but there is a growing demand for models that allow hidden, unobserved components. Moreover, some commonly employed models for evolutionary inference face challenges related to non-identifiability, where distinct model parameters induce the same probability distributions and are structurally or practically indistinguishable. Phylogenetic inference itself is classified as a non-polynomial time problem, meaning that the number of steps needed to solve a problem grows exponentially with the size of the problem. Here, I review some possible solutions and paths forward in relation to these challenges, including the advent of online Bayesian phylogenetics, the popularization of (deep) machine learning approaches, and the introduction of probabilistic programming languages that promise to speed up analyses and tackle more complex biological questions in fields as diverse as phylogenetics, epidemiology, community ecology and phylogeography.

What do we know about mutualism? A thirty-year retrospective on a very young field

Judith L. Bronstein

University of Arizona, Tucson, USA

Abstract

The study of mutualism (interspecific, mutually beneficial interactions) is a surprisingly young subfield of ecology and evolutionary biology. Building on centuries of natural history knowledge, it began to coalesce in the 1970s; key patterns and processes only started to attract intensive attention in the 1990s. I will start by briefly summarizing the best-understood mutualisms in which plants are involved, interactions that have fundamentally shaped plant biology: nutritional mutualisms (including symbioses with mycorrhizal fungi and Rhizobium bacteria), transportation mutualisms (biotic pollination and seed dispersal) and protection mutualisms (involving ants that attack herbivores). I will then offer a capsule history of the study of mutualism as a whole, focusing on its origins and subsequent development. I will highlight key research questions that have emerged in recent years, as well as some main findings to date from each of them. Finally, I will lay out questions likely to drive mutualism research in the coming years. My approach throughout is to highlight features uniting mutualisms that differ radically in natural history, as well as features that make mutualisms similar to and different from other types of interspecific interaction. We are only now beginning to recognize what we need to know about these critically important interactions to help secure the future of plants and the larger systems in which they occur. As a whole, it is a exciting time for this very young field.

Diploidization, Polyploidy, and the Evolution of Plant Diversity

Barker, Michael S.

Department of Ecology & Evolutionary Biology University of Arizona

Abstract

Polyploidy, or whole-genome duplication, is widely recognized as an important force in the evolution of plants. Ancient genome duplications have driven the re-organization of plant genomes and nearly ⅓ of contemporary flowering plants are of recent polyploid origin. Despite the recognition that polyploidy has been important across plant evolution, there are still many unresolved issues surrounding polyploidy and its role in evolution. Among these issues is reconciling the apparent success of ancient polyploid species with observations that contemporary polyploids have much lower net diversification rates than their diploid relatives. Here, I present new analyses of polyploidy across the plant phylogeny and explore the impact of species tree topology on WGD inferences. Using these new inferences, I will present phylogenetic simulations that explore the legacy of ancient WGDs with different diversification dynamics of polyploid and diploid species. We find that multiple rounds of polyploidy occur in the ancestry of lineages when diploid species have higher net diversification rates than polyploid species. This occurs in simulations using arbitrary rates as well as those using parameters derived from empirical analyses. Using empirical estimates of diploid and polyploid diversification rates from plants and estimates of the rate of polyploid speciation from diploids, our simulations indicate an average of 3.5 rounds of WGD in flowering plant species.This is consistent with observations from phylogenomic studies and suggests that the results of many independent lines of research, from empirical estimates of diversification rates to inferences of WGDs, broadly agree with each other and are likely generally accurate. Our simulations also indicate that the rate of diploidization is an important driver of the evolutionary dynamics of polyploidy and may explain variation in the numbers of ancient WGDs inferred in different lineages of eukaryotes. Overall, our simulations reconcile the seemingly contradictory observations of low polyploid diversification rates with the repeated rounds of WGDs that have been inferred throughout the evolutionary history of flowering plants.

One third backwards! The varied ways plants have already changed in response to climate change and the implications for plant communities and conservation.

Moles, Angela

Evolution & Ecology Research Centre, UNSW Sydney, NSW 2052, AUSTRALIA

Abstract

Plant species are already responding to climate change by undergoing rapid evolution, altering their phenology, and undergoing remarkably rapid shifts in distribution. I will review current understanding of these changes, highlighting the fact that different species are changing in different ways and at different rates, and that not all of the responses are as we would expect. Most strikingly, a third of species seem to be shifting their distributions downhill or toward the equator rather than shifting to cooler areas. This variation in species responses to climate change means that broad change in plant communities seems inevitable. I will finish by discussing implications of all this change for conservation.

State of the World's Plants and Fungi

Alexandre Antonelli

Director of Science at the Royal Botanic Gardens, Kew, UK. Professor of Biodiversity and Systematic at the University of Gothenburg, Sweden, and Visiting Professor at the University of Oxford.

Abstract

The race is on to scientifically describe the world's plants and fungi, so we can better understand, protect, and sustainably use biodiversity. But how do we accelerate scientific research and conservation, while strength-

ening local capacity and equity? These are questions at the heart of Kew's State of the World's Plants and Fungi reports, which bring together global scientific expertise, large data sets and practical experiences to synthesise current knowledge on plants and fungi. In this talk I will provide a short overview of the themes published so far and then take a deep dive into the latest report focused on how our communities could collectively work to fill in the most critical knowledge gaps – through innovative and sometimes unexpected approaches.

Save the male! Reflections on sex and gender in flowers and flowering plants

Pannell, John R.[1]

Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland

Abstract

Plant sexual reproduction involves strategic decisions in the context of variation in sex and gender. These decisions include who to mate with and how often (the mating system), whether and when to mate as a male or a female partner, and how much resource to allocate to each sexual function (the sex allocation). All these decisions may be subject to tradeoffs and will often reflect only a partial resolution to genetic and sexual conflicts. The wonderful diversity of flowers illustrates the numerous ways in which conflict resolution has been achieved. In this presentation, I will address the complexity of mating systems and sex allocation, especially with a view to the benefits and costs of being male. How does selection on the mating system interact with selection on sex allocation? How well do we understand the costs and benefits of being both male and female? Can we satisfactorily address Charles Darwin;s difficulty in understanding why hermaphrodite plants should ever have been rendered dioecious? To what extent can current theory explain the distribution of combined versus separate sexes among individuals in a population? Can the same theory also help to explain why female flowers are so rarer than male flowers on plants with bisexual flowers, whereas females are so much more likely than males to co-occur with hermaphrodites in a population? To address these questions, I will reflect on variation in sex and gender in plants, drawing upon: insights gained from observations of plant and floral sex ratios; evidence of sexual selection in wild and experimental populations; observations of rapid transitions between combined and separate sexes under experimental evolution; the association between mating pair identity and sex allocation strategies; and the phylogenetic distributions of reproductive and other traits.

Morphological and genomic consistency for 20 million years

Elizabeth A. Kellogg

Robert E. King Distinguished Investigator at the Donald Danforth Plant Science Center in St. Louis, Missouri. Member of the National Academy of Sciences of the U.S. and is an Académica (Fellow) of the Academia Nacional de Ciencias, Argentina.

Abstract

Nearly one fifth of the world's land area is inhabited by wild grasses of a single clade, the tribe Andropogoneae, which originated about 20 million years ago in the early Miocene. A cultivated member of this same tribe, maize, now replaces wild grasses in many areas, dominating the landscape and the world's economy. The tribe is characterized by spikelets borne in pairs, with the spikelet pair as the dispersal unit. Thanks to this type of dispersal unit, the tribe spread throughout the Old World, diversifying into more than 1000 species. Much later and coincident with the well-documented global grassland expansion, members of the tribe arrived in the Americas as the result of several independent dispersal events. Aerodynamic properties of the spikelet pairs are consistent with long-distance dispersal by wind for most, but not all, species. We have generated de novo genome sequences for about 40% of the 1200 species in the tribe using a combination of long-read and short-read sequencing. The 33 new long-read genomes are high qaulity as shown by several measures of completeness and contingity. Genome alignments indicate collinearity of genomes, with the ancestral haploid number and architecture of 10 chromosomes being preserved even through polyploidization events. We have developed data and tools to improve annotation of the maize genome, inferred the chromosomal evolution of maize, investigated amplification of transposable elements, and begun to identify conserved regulatory sequences. Together these resources can enhance breeding for environmental change in the crops and illuminate the history of wild species.

Beyond regional flora's: what do we know about the ecology and evolution of the African flora?

Muasya, Muthama

University of Cape Town, Cape Town, South Africa

Abstract

Studies on the diversity of African plants have lagged. Efforts to document the floral wealth have spanned nearly two centuries, with oldest treatments in Flora Capensis dating back to 1860s, but the tropical regions of the continent have only been more recently studied, and knowledge gaps remain. Overwhelmingly, there is good coverage in documenting species occurrence and taxonomy, and indepth studies have focused on crops and other economically important taxa. Ecological and evolutionary studies have sought to explain the origin and processes maintaining the distinctive assemblages, in part driven by questions on the origin of hominins and other iconic fauna. The continent has a rich diversity of vascular plants, with over 65,000 species, distributed in five major vegetation types (lowland forests, savannas, temperate, montane and alpine, and desert). Africa was covered in lowland forests at about 60 million years ago, gradually opening into savannas since the Eocene, and fragmented further by the uplifting and volcanism during the mid Miocene. Africa position, straddling the equator and its earlier emergence of open habitats, drove origin of earliest savanna lineages, in particular C4 graminoids and associated fauna, which dispersed into other continents as open habitats evolved. The temperate (Cape) flora, together with the montane and alpine flora, have assembled more recently, seeded from the savanna and other temperate floras, though the directionality of dispersal between oceanic and sky islands is contentious. Most intriguing is the assembly of the arid flora, where there is evidence for both antiquity and recent origin, and hypotheses on an African arid corridor persists. Heterogeneity in topography, soils and climate, together with fire and biotic interactions, drives the wide species riches and functional diversity. With a focus on the Cenozoic, the current knowledge and gaps on the ecology and evolution of African flora will be interrogated.

Evolution and development of iridescent petals

Glover, Beverly J.

University of Cambridge, UK

Abstract

The enormous diversity of flower colour is largely the result of modifications to and combinations of chemical pigments. But some plants also use physics to modify the colour of their flowers. In this talk I will describe the way that diffractions gratings, formed from folds of the epidermal cuticle, can produce structural colour in flowers. I will summarise our recent work analysing the distribution and diversity of this trait in the angiosperms, its function in pollinator attraction and the developmental programmes underlying the formation of floral iridescence.

Symposia Session 1 Monday

S.1 MERGING EVOLUTIONARY APPROACHES WITH ETHNOBOTANICAL KNOWLEDGE. SESSION 1

S.1.1 The potential of phylogenies to safeguard human well-being

Rafael Molina-Venegas[1,2]

1 Department of Ecology, Faculty of Science, Universidad Autónoma de Madrid, Spain. 2 Biodiversity and Global Change Research Center, Universidad Autónoma de Madrid, Spain.

The idea that conserving evolutionary history is more efficient than species-based approaches for capturing biodiversity benefits to people has remained largely theoretical since the early 1990s. These benefits may not necessarily be currently known or realized benefits but 'option values', that is, benefits that are yet to be discovered or demanded by future generations, which hampers assessing the long-standing hypothesis that preserving the main branches of the Tree of Life (i.e., high levels of phylogenetic diversity) would help to safeguard human well-being. However, it is reasonable to assert that known benefits today were at one point in human history unknown future options. Hence, proving that current benefits of biodiversity (i.e., the 'option values' of past generations) are to a great extent provided by subsets of taxa that encapsulate high levels of phylogenetic diversity could serve as a proof of concept on the relationship between evolutionary history and future options. Adhering to this reasoning, some recent studies have begun to yield empirical evidence supporting the theoretical background, thus opening an exciting avenue of research to further investigate the complex relationship between biodiversity and human well-being.

S.1.2 The hot node analysis incompletely explains the position of phylogenetic structure in taxon samples

Darío Atienza-Barthelemy[1], Manuel J. Macía[1,2], Rafael Molina-Venegas[2,3]

1 Department of Biology (Botany), Faculty of Science, Universidad Autónoma de Madrid, Spain. 2 Biodiversity and Global Change Research Center, Universidad Autónoma de Madrid, Spain. 3 Department of Ecology, Faculty of Science, Universidad Autónoma de Madrid, Spain.

Advances in phylogenetics have provided a revolutionary way to address ethnobotanical data, generally based on calculating the phylogenetic structure of a set of medicinal plants, and identifying the clades showing significant overabundance of such plants (i.e., hot nodes). However, this emerging discipline is in need for more quantitative evidence, and the common assumption that hot nodes represent the main clades responsible for phylogenetic structure remains to be tested. Here, we use the most extended metrics on the field and a comprehensive database (1,803 medicinal species) to calculate the phylogenetic structure of the medicinal plants of Ecuador. Specifically, we (1) conduct the analyses on both species- and genus-level phylogenies to assess the influence of the phylogenetic grain, and (2) evaluate whether hot nodes can tackle the position of phylogenetic structure using a jack-knifing procedure to identify clades significantly influencing phylogenetic distance-based metrics. Phylogenetic structure was found to be strongly dependent on taxonomic level and the identified hot nodes incompletely matched those with a significant contribution to phylogenetic structure metrics. Significant information may be missed whenever the influence of the taxonomic level is not evaluated, and the position of phylogenetic structure cannot be fully tackled by the hot nodes. We suggest combining different phylogenetic grains and methods to identify highly influencing clades before drawing any conclusion that may misguide the search for plants with bioactive potential.

S.1.3 A new phylogenetic analysis pipeline to support the identification and the prioritisation of plants with medicinal potential

Giovanni Zecca[1,2], Elisa Toini[1,2], Massimo Labra[1,2], Fabrizio Grassi[1,2]

1 Department of Biotechnology and Biosciences, University of Milano-Bicocca, Milan, Italy. 2 NBFC, National Biodiversity Future Center, Palermo, Italy.

Recent studies have proposed that phylogenetic methods can be effective tools for exploiting the untapped potential of medicinal plants. Under the assumption that medicinal properties tend to be phylogenetically clustered, phylogenies can be used to narrow down the relevant species for bioprospecting, increase the discovery rate and reduce the time and costs involved. Nonetheless, some restrictions exist. By integrating ethnobotanical knowledge with phylogenetic methods, it has often been necessary to group plants into macro-categories of therapeutic effects, limiting the potential of the approach. In many studies "hot nodes" corresponding to lineages overrepresented in medicinal taxa were identified. However, as larger phylogenies and databases become available, the possibility of huge lineages being identified by "hot nodes" is also likely to increase, once again posing a prioritization problem. To tackle these issues, we propose a new analysis pipeline, mixing existing and new developed methods. Briefly, our workflow is as follows: 1) using selected databases that integrate traditional medicine data with growing molecular information, species linked to specific diseases or specific biological effects are obtained; 2) different methods to estimate the phylogenetic clustering of taxa are applied using a reference phylogeny; 3); where a phylogenetic signal has emerged, "hot nodes" are repeatedly estimated to assess their robustness; 4) in case of large lineages subtended by stable "hot nodes", a (relative) probability of being linked to the disease or biological effect of interest is calculated for each taxa; 5) results are summarised and graphically displayed to combine different information. To test our pipeline data related to 10 diseases and 10 biological effects were obtained from two different public databases and were analysed together with a published phylogeny including ~ 30,000 species. Our results show the effectiveness of the approach suggesting that it will be useful in the bioprospecting of new potential medicinal plants.

S.1.4 Exploring ethnobotanical knowledge dynamics across time scales: the contribution of phylogenetic comparative methods

Irene Teixidor-Toneu[1,2*], Anneleen Kool[2], Simon J. Greenhill[3,4], Karoline Kjesrud[5], Jade J. Sandstedt[2], Fiona M. Jordan[6]

1 Mediterranean Institute for Biodiversity and Ecology, French National Research Institute for Sustainable Development, Marseille, France. 2 Natural History Museum, University of Oslo, Oslo, Norway. 3 Australian National University College of Arts and Social Sciences, ARC Centre of Excellence for the Dynamics of Language, Canberra, Australia. 4 Department of Linguistic and Cultural Evolution, Max-Planck-Institut fur Menschheitsgeschichte, Jena, Germany. 5 Museum of Cultural History, University of Oslo, Oslo, Norway. 6 Department of Anthropology and Archaeology, University of Bristol, Bristol, UK.

Knowledge of plants is dynamic and can change at rapid time scales. Grasping past human-plant relations is largely concomitant to having historical and archaeological evidence. Yet, apart from major crops, this is uncommon for most social-ecological systems and time periods. This presentation outlines a multi-disciplinary triangulation method that combines inferences of ancestral plant uses by a cultural evolutionary approach with historical, linguistic, and archaeobotanical evidence (Teixidor-Toneu et al 2021). Phylogenetic comparative methods that use linguistic phylogenies representing people's historical relations are applied to ethnobotanical data. Results fill gaps of evidence and link data sources for the study of past human-plant relations. The triangulation method is illustrated by taking the Nordic countries as a case study, as extensive historical collections of various plant use records are very limited until the 1700s and there is also limited direct evidence of plant use from archaeological contexts. A language tree models the population history of the Nordic region and allows to computationally infer ancestral plant uses from recent ethnographic data. We evidence a wealth of Viking-age plant uses, especially for medicine and food. All plants for which ancestral uses were inferred by phylogenetic comparative methods had vernacular names with shared North Germanic word roots, confirming the past knowledge and importance of these species. We inferred the ancestral use of a diversity of species (such as *Angelica archangelica* or *Juniperus communis*) and uses (wild foods, beer, and mead brewing) whose cultural history had been overlooked in botanical or archaeological studies. This multi-disciplinary triangulation method evidences that while most plant use knowledge may quickly arise and fade through time, some human-plant relations persist through centuries shaping both culture and the environment.

S.1.5 INDIGENOMICS: Linking indigenous knowledge with metabolomics to assess the chemical traits underpinning human-plant interactions

Rodrigo Cámara-Leret[1], Luiz L. Saldanha[1], Kim Castro[1], Juan C. Copete[1], Lauren Raz[2], Uldarico Matapí[3]

1 Department of Systematic & Evolutionary Botany, University of Zurich. 2 Universidad Nacional de Colombia, Instituto de Ciencias Naturales, Bogotá, Colombia. 3 Independent researcher, Bogotá, Colombia.

INDIGENOMICS is a Swiss National Science Foundation Starting Grant (2023-2028) that aims to integrate Indigenous ways of knowing with science to address a long-standing question about the chemical traits that underpin human-plant interactions. Co-developed with the Indigenous Matapí of the Colombian Amazon, we are testing hypotheses that link Matapí and western ecological knowledge to better understand how plant chemistry influences the use, management, and conservation of Amazonian forests. Coupling metabolomics and Indigenous knowledge, we unravel the phytochemical space used by Indigenous communities to predict how much chemodiversity may vanish as global change accelerates across Amazonia. Supporting Indigenous elders and their apprentices, *INDIGENOMICS* boosts indigenous-led research to preserve the endangered knowledge of the Matapí— thus strengthening Indigenous contributions to science while creating opportunities that reinforce cultural heritage.

S.1.6 Botanicultural macroevolution? Theory and tools for investigating cross-cultural uses of plants

Fiona M. Jordan[1], Julie Hawkins[2], Jamie Thompson[3]

1. Anthropology & Archaeology, University of Bristol, UK. 2 Ecology & Evolutionary Biology, University of Reading, UK. 3 Life Sciences, University of Bath, UK.

Evolutionary approaches to human culture and language are now commonplace in anthropology, including the use of comparative phylogenetic methods to understand cultural macroevolution. Using linguistic phylogenies to model human population history, it is possible to infer the dynamics of change in ethnographic, archaeological, material, linguistic and cognitive phenomena. Ancestral features of cultural groups can be estimated, and both transformational sequences of change as well as coevolutionary hypotheses about culture and environment can be robustly tested while accounting for historical autocorrelation between populations. Language families spanning the globe and human lifeways are now represented by computationally inferred language phylogenies, and the maturity of the field has accelerated with large-scale cross-cultural databases and data collection surveys. To further promote ethnobotanical research in this arena, we present a selection of key studies that investigate botanical resource use. Our recent study of Polynesian medicinal plant traditions explores the roles for adaptation and ancestral knowledge in plant-based healthcare at pre-historic timescales. We test the extent to which (a) the new floristic environments encountered, (b) cultural ancestry or (c) geographic proximity predict the composition of ethnopharmacopoeias in seven Oceanic ethnolinguistic groups. This small study highlights the need for large-scale ethnobotanic databases in order to progress future work, while highlighting the challenges of collating and synthesising traditional ecological knowledge in ways that are sensitive to the CARE principles of indigenous data management.

S.2 THE ANGIOSPERM REPRODUCTIVE SPECTRUM FROM FLOWERS TO SEEDS. SESSION 1

S.2.1 The eFLOWER project: what have we done, where are we, and where are we heading now?

Hervé Sauquet[1,2,3], Andrea M. López-Martínez[4], Maria von Balthazar[5], Marion Chartier[5], Julian Herting[1], Santiago Ramírez-Barahona[4], Susana Magallón[4], Jürg Schönenberger[5]

1 Botanic Gardens of Sydney, Mount Annan, Australia. 2 University of New South Wales, Sydney, Australia. 3 University of Sydney, Sydney, Australia. 4 Universidad Nacional Autónoma de México, Ciudad de México, Mexico. 5 University of Vienna, Vienna, Austria.

The eFLOWER project started thirteen years ago as a long-term initiative to address key questions on the early evolution and diversification of angiosperm flowers. A central part of eFLOWER has been the development and continuous curation and expansion of a collaborative database named PROTEUS allowing to record floral traits at the species level while documenting the explicit source of each data point. Here we review the diverse contributions that eFLOWER has brought so far to our understanding of floral evolution, reflect upon the questions and challenges encountered along the way, and outline future directions. An important milestone was reached seven years ago with the publication of a new model for the ancestral flower of all angiosperms, based on ancestral state reconstructions using a dataset of 792 species sampled from most families. Despite uncertainty remaining for some traits, this new model proved effective in questioning long-term assumptions and opening new research opportunities on floral evolution. Interestingly, this model appears to be robust to new analyses of a recently published, expanded dataset of 1201 species sampled from all families, but some results continue to be highly sensitive to methodological approaches and models of character evolution. Another significant milestone has been the development and evaluation of angiosperm-wide 'phyloscan' approaches to assess the phylogenetic position of fossil flowers using these datasets of floral traits. While these methods appear to provide a powerful new tool to systematically assess fossil flowers, they have also revealed high uncertainty in the placement of many taxa, reflecting the limits of the number of preserved, standardised characters that may be recorded from fossil flowers. Lastly, we present briefly some recent new avenues linked with this project, including new ideas on the origin of pollination and evidence on early angiosperm diversification from morphospace analyses of floral disparity.

S.2.2 Evolution of fruits and seeds of Solanaceae, from extinct to extant diversity

Rocio Deanna[1,2]

1 Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC), Córdoba, Argentina. 2 Department of Ecology and Evolutionary Biology, University of Colorado at Boulder, Boulder, USA. rociodeanna@gmail.com

The placement of extinct taxa on phylogenies relies on scoring informative morphological characters, which can be difficult given the fragmentary nature of the fossil record. Although detailed studies of Solanaceae fossils remain few, the family exhibits wide variation in seed and fruit traits to use in estimating fossil placement from morphological data. Therefore, we reviewed a total of 106 seed and seven fruit fossils of Solanaceae, including two recently published South American species that are the oldest records in the family. We scored 28 traits, including 11 continuous and 17 discrete, for all the fossils gathered and almost 400 extant taxa, sampling at least one species per genus. We then performed a cluster analysis to morphologically compare these fossil seeds to extant Solanaceae, along with a phylogenetic analysis including all the morphological traits and 10 DNA regions in order to infer the phylogenetic placement of the fossils. We also reconstructed the ancestral states of the most conspicuous morphological traits over a molecular phylogenetic tree to finally compare the morphological evolution inferred with the placement of the fossils. The clusters found in the statistical analysis were congruent with the phylogenetic placement of the fossils in all the species, except by some fossil seeds. According to the morphological reconstructions, traits that have been acquired only once in the family were the most informative to place the fossils, like the finger-like appendages in the fruiting calyx of the fruit fossil *Lycianthoides calycina* placed in the chili pepper clade. Converged traits (e.g., inflated fruiting calyx) were less informative but the combination of fruiting calyx traits was sufficient to place the *Physalis* fruit fossils. Continuous traits were highly informative, especially in the placement of the fossil seeds. These results lay the foundation for new total evidence dating analysis for the entire family.

S.2.3 The evolution of embryo size in angiosperms seeds

Filip Vandelook[1,2], Angelino Carta[3]

1 Meise Botanic Garden, Meise, Belgium. 2 Katholieke Universiteit Leuven, Leuven, Belgium. 3 University of Pisa, Pisa, Italy.

Seeds are the main dispersal and propagation units of angiosperms, and they are very diverse in their external and internal features. When dispersed, seeds consist of an embryo, the next generation of a plant, surrounded by the seed and/or fruit coat and by an alternative storage tissue (endosperm or perisperm) in case the nutritive reserves are not stored in the cotyledons. Examining the relative allocation of seed reserves by quantifying the relative embryo size at dispersal (i.e., size of the embryo relative to the seed, ES) across angiosperms, sets the basis to track the evolutionary history of this key reproductive trait related to germination timing and offspring survival. We used macroevolutionary approaches to estimate adaptive shifts of ES in the entire angiosperm radiation. We also evaluated how tempo (i.e., evolutionary rates) and mode (i.e., evolutionary process) of ES evolution changed through time and the role of paleo-temperatures on ES evolutionary rates. Early angiosperms typically had a low ES, which is still reflected in contemporary magnoliids and ANA-grade species. The analysis of major shifts in ES throughout angiosperm evolution revealed that these shifts occurred after 145 Myr and were predominantly associated with the formation of the main angiosperm lineages. Comparison of a series of paleo-inspired models showed that tempo and mode of ES evolution altered from a very dynamic ES evolution early in angiosperm history towards a more static evolution driven by stronger stabilizing selection. Finally, a consistent trend for a slowdown in rates of ES evolution during periods of climate warming was found. Fast evolutionary rates under cold climates are consistent with the macroecological observation that rates of phenotypic evolution are higher at high latitudes. This study provides crucial new insights in seed trait evolution, which contribute to understanding the diversification of reproductive strategies in angiosperms.

S.2.4 Are flower and fruit colors associated with environment? Exploring global ecogeographic patterns in flower and fruit colors

Agnes S. Dellinger[1], Leah Meier[2], Stacey D. Smith[2], Miranda Sinnott-Armstrong[2,3]

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Flowers and fruits are central to plant reproduction because they facilitate gene dispersal through pollen or seeds, respectively. In species engaging in biotic interactions during reproduction (i.e., with pollinators and dispersers), flower and fruit coloration are important as visually attractive cues. Different groups of pollinators (i.e., bees, birds, bats) and dispersers (i.e., birds, monkeys, lizards) differ in their sensory abilities, which might drive color evolution in flowers and fruits. The abiotic environment may also be an important selective factor on coloration. For instance, the synthesis of anthocyanin pigments (most reds, pinks, and blacks) is triggered by cold temperatures and UV-B radiation. Although flowers and fruits originate from the same organ and constitute a continuous developmental sequence, we currently lack understanding of whether flower and fruit traits are correlated in space. If flower and fruit colors show similar spatial patterns, those patterns may be influenced strongly by similar abiotic factors. If, however, flower and fruit color are decoupled, then they likely result from different selective agents (either abiotic or biotic). To address this gap, we collated a dataset of 2800+ species from 51 clades with animal-pollinated flowers and animal-dispersed fruits and scored flower and fruit colors into eight categories. We combined the color data with GBIF occurrence records for these species and found striking differences in the geographic distribution of flower and fruit colors. Overall, fruit color diversity is higher in the tropics, but flower color diversity is not. Red and pink in both flowers and fruits are more prevalent at high northern latitudes, which suggests that a common selective agent may drive the evolution of red/pink under those environmental conditions. Aside from red/pink, flower and fruit colors and color diversity are decoupled across the globe, indicating different importance of abiotic and biotic selective agents.

S.2.5 The emergence of a floral economic spectrum and its association with the leaf economic spectrum

Lars Götzenberger[1,2], Marketa Applova[1,2], Anna E-Vojtko[1]

1 Institute of Botany of the Czech Academy of Sciences, Trebon, Czech Republic. 2 Department of Botany, University of South Bohemia, Budweis, Czech Republic.

Understanding resource allocation strategies in plants is crucial for unraveling ecological and evolutionary dynamics. The traditional fast-slow continuum is a well-established framework that has primarily been explored through vegetative above and below-ground traits of leaves and roots. Recent propositions suggest the existence of a floral economic spectrum (FES) that parallels leaf traits, in particular with regard to area and mass-related traits, as well as longevity of individual organs. In a survey of herbs across a wide range of plant families, we confirm the expected negative correlation between specific leaf area (SLA) and leaf dry matter content (LDMC) but also demonstrate a similar relationship in flowers, i.e., a negative correlation between specific floral area (SFA) and floral dry matter content (FDMC). Across organs, the analogous traits are positively associated, i.e., FDMC correlates positively with LDMC, and SLA with SFA. In addition, with data from a greenhouse experiment of 8 species, we show that these relationships also hold within species, and are influenced by water availability. Our findings show that flowers and leaves, though serving very different functions, are constrained at least to some degree with respect to their morphology and structure. The often-assumed independent evolution of floral characters depends much on what traits are considered, and the same can be said about the previously reported independent dimension of floral traits in the space of plant form and function.

S.2.6 The seed germination spectrum of Mediterranean plants

Diana María Cruz Tejada[1], Eduardo Fernández Pascual[2], Efisio Mattana[3], Angelino Carta[1]

1 University of Pisa, Pisa, Italy. 2 IMIB Biodiversity Research Institute (University of Oviedo – CSIC - Principality of Asturias), University of Oviedo, Mieres, Spain. 3 Royal Botanic Gardens, Kew, Wakehurst, UK.

The understanding of seed biology of wild plant species is fundamental to address ecological, evolutionary, and biogeographical questions, as well as to the success of seed-based conservation and restoration actions. Despite recent attempts to synthesise seed germination knowledge across major temperate biomes, most assumptions about the germination ecology of Mediterranean plants are based on individual species or local studies, missing an integrated view of germination patterns for the whole Mediterranean Basin biodiversity hotspot. Here, we performed a binomial phylogenetically informed Bayesian meta-analysis, considering ca. 7,000 germination tests of ca. 400 species characteristic of EUNIS Mediterranean habitats (European habitat classification system) from laboratory experiments conducted across the Mediterranean Basin. We estimated the effect on germination proportions of five environmental cues, including mean incubation temperature, temperature regime, light, and dormancy-breaking treatments for typical Mediterranean plants (i.e., species that only occur in lowland habitats of the Mediterranean Basin) and generalist plants (i.e., distribution wider than the Mediterranean Basin). Overall, typical Mediterranean species exhibit a cold-cued germination response, a positive effect of scarification, and are insensitive to light and alternating temperatures, in accordance with previously described germination syndromes for the area. Generalist species are also stimulated by cool temperatures but show positive effects of alternating temperatures, light, and cold stratification. Our results suggest that specific germination responses could vary according to species macroclimatic constraints (typical vs. generalist species) and secondarily local habitat conditions. Indeed, we found consistent patterns across different habitats (forests, scrublands, and grasslands) with few exceptions, including anthropogenic habitats, in which opportunistic germination strategies were found. Finally, whilst phylogenetically related species exhibit similar germination responses, our results also suggest a functional convergence of the seed germination patterns across Mediterranean species. Our integrative methodological approach emphasised the significance of utilising extensive datasets to formally test eco-evolutionary and biogeographical research questions.

S.3 APOCYNACEAE - ON THE WAY TO A MODEL FAMILY

S.3.1 Phylogenomic analysis of Apocynaceae based on the Apoc836 probe set: toward resolution of recalcitrant nodes

Chelsea R. Smith[1,2], Shannon C. K. Straub[3], Tatyana Livshultz[1,2]

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The broad outline of Apocynaceae phylogeny, divided into three subfamilies (Periplocoideae, Secamonoideae, Asclepiadoideae) and two informal grades: rauvolfioids (11 tribes) and apocynoids (9 tribes) has been stable since the earliest single gene plastid analyses: a paraphyletic rauvolfioid grade subtending a monophyletic APSA clade (apocynoids, Periplocoideae, Secamonoideae, Ascelpiadoideae). Accumulation of data, culminating in the first phylogenomic analysis of the family (Antonelli, et al. 2021) has highlighted areas of continued topological uncertainty including relationships within the APSA clade, specifically the positions of Periplocoideae and Rhabdadenieae, and an earlier radiation that includes the rauvolfioid tribes Melodineae, Hunterieae, Amsonieae, and Alyxieae. We revisited Apocynaceae phylogenomics with expanded sampling of taxa and loci (Apoc836; Straub, et al. 2020). We constructed trees using summary coalescent and concatenation methods and conducted sensitivity analyses to evaluate the robustness of our topologies to sampling and analytical decisions. An intriguing outcome of these analyses is the frequent placement of Periplocoideae as sister to the well-established clade of Baisseeae, Secamonoideae, and Asclepiadoideae, harkening back to the abandoned Asclepiadaceae (comprised of Periplocoideae, Secamonoideae, and Asclepiadoideae) and re-opening questions about homology of pollen aggregation, translators, and coronas in these taxa. This topology is sensitive to both sampling and analytical choices, and we conclude that the weighted ASTRAL analysis most accurately represents remaining uncertainty. This new Apocynaceae species tree suggests a revised classification for the family at the subfamily and tribal levels.

References: Antonelli, A., et al. (2021). Settling a family feud: a high-level phylogenomic framework for the Gentianales based on 353 nuclear genes and partial plastomes. https://doi.org/10.1002/ajb2.1697. Straub, S. C. K., Boutte, J., Fishbein, M., & Livshultz, T. (2020). Enabling evolutionary studies at multiple scales in Apocynaceae through Hyb-Seq. Applications in Plant Sciences, e11400. https://doi.org/10.1002/aps3.11400.

S.3.2 Biome lability and substrate conservatism fuelled plant evolution in xeric ecosystems

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The expansion of arid environments following the Eocene-Oligocene climate transition is thought to have promoted increased species diversification rates across several plant lineages. In this study, we use the Apocynaceae as a model to assess whether a combination of biotic (e.g., lifespan and dispersal traits) and abiotic (e.g., climate and soil) predictors favoured diversification during the expansion of dry biomes. To accomplish this, we reconstructed a comprehensive time-calibrated phylogenetic tree for Apocynaceae using the Angiosperms353 bait set to establish a backbone. Subsequently, we merged all Apocynaceae species with sequence data (for ITS, *trnL-F*, and *rps16*) available on GenBank. Finally, distribution and trait data were compiled to test three hypotheses: [H1] Biome shifts between Apocynaceae species primarily occur from rainforest to savanna, whereas transitions between tropical and temperate environments are rare; [H2] Diversification in Apocynaceae was driven by "key synnovation" involving anemochory, presence of pollinia and climbing habit; and [H3] High speciation rates favoured the diversification of Apocynaceae lineages adapted to xeric environments. Our study suggests that lineages in more xeric environments exhibit higher speciation rates as they adapt to new, harsher conditions. These findings suggest that substrate, rather than biome, might be the primary factor regulating evolutionary rates in plants adapted to dry ecosystems.

S.3.3 Marsdenieae (Apocynaceae – Asclepiadoideae) – phylogenetic analysis clarifies generic concept and unveils abundant parallelisms

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S.3.4 Biogeography and multiple origins of Indian open-flowered Ceropegia

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The open-flowered type of *Ceropegia*, formerly *Brachystelma* is a rare and elusive group of plants in India. They occupy the relatively dry habitats of peninsular India which is influenced by the highly seasonal monsoonal climate. The diversity of *Brachystelma* is about 35 species in peninsular India. Molecular phylogeny reveals that within the radiation of *Ceropegia* (tubular-flowered species). *Brachystelma* has evolved at least three times from closed tubular-flowered. In this study, I examine the distribution of the Indian open-flowered lineages based on the most up-to-date and comprehensive sampling of the genus. The diversity of the genus is linked to open grassland in the Eastern Ghat region of India. Using climatic niche modelling, I discuss the climatic requirements which might have led to the diversity of the open-flowered genotypes. Furthermore, using transcriptomic approaches, I examine the genes responsible for the shift from tubular flowers to open type flowers. I also discuss preliminary data on pollinators of Indian open-flowered genera of *Ceropegia*.

A densely sampled molecular phylogeny of the pantropical, predominantly forest-dwelling tribe Marsdenieae, including almost a quarter of the ca. 740 species shows that the tribe is divided in two large clades, with two genera *Rhyssolobium* (southern Africa) and *Sicyocarpus* (Madagascar) placed outside of both clades. The first of the two large clades has a native distribution exclusively in Asia and the Pacific area. The type genus of the tribe, *Marsdenia* R.Br., is sister to all remaining genera of this clade, and comprises ca. 10 species. This clade harbours two species-rich radiations, *Leichhardtia* (ca. 80 species) in the Pacific realm and the *Hoya*-alliance (>300 species). The second large clade shows a cosmopolitan distribution with several small Asian lineages as sisters to some larger genera of African-Asian distribution, as well as the New World genus *Ruehssia* (ca. 130 species). As far as known, all larger clades comprise species adapted to various types of pollinators (small and larger flies, bees, butterflies, moths), forcing highly similar floral structures. For the *Hoya*-alliance, we present a densely sampled phylogeny obtained using target enrichment and including ca. 80 % of the known diversity of *Hoya* and *Dischidia*, all taxa of *Oreosparte* (3 species) and *Papuahoya* (3 species). *Dischidia*, *Oreosparte* and *Papuahoya* are confirmed as monophyletic, but *Hoya* is paraphyletic, with a smaller clade sister to *Papuahoya* and a larger clade (*Hoya* s.s.) sister to *Dischidia* + *Oreosparte*. Within *Hoya* s.s., some clades are characterised by uniform flower morphologies while others, including the main radiation of species in New Guinea, independently developed a large range of flower morphologies. The largest molecular and morphological diversity of *Hoya* s.s. is found in Borneo. Our results will contribute towards a modern, stable classification of the *Hoya*-alliance, and studies on its origin and and diversification.

S.3.5 Tackling tough taxonomy: genomic, morphological, and ecological approaches to Asclepias (Apocynaceae) in North America

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Rapid diversification may present taxonomic challenges resulting from the gradual nature of speciation. Processes including incomplete fixation of ancestral polymorphisms and partial establishment of reproductive barriers permitting gene flow after speciation result in conflicting information about species boundaries and phylogeny. The rapid diversification of >130 species of American *Asclepias* provides a good system to demonstrate that integration of genomic data, population genetics, ecological modeling, and traditional approaches can resolve longstanding taxonomic challenges. We present two case studies. The "dwarf milkweed" clade has been variously treated as 1-4 species (*A. eastwoodiana, A. ruthiae, A. sanjuanensis, A. uncialis*) distributed across semiarid western North America. Populations exhibit limited morphological variation, largely in the shape and vestiture of leaves. Previous research supported recognition of four species based on population genetics and ecological niche modeling. We support this taxonomy with a plastome phylogeny and newly discovered floral differences and resolve the phylogeny of the four species using sequence data from >2000 nuclear genes. In the second example we address circumscription of *A. hirtella* and *A. longifolia*. Populations of these taxa are found in the eastern United States, with coastal populations assigned to *A. longifolia* and interior populations to *A. hirtella* (or *A. longifolia* subsp. *hirtella*). In the western Gulf Coast (Texas and Louisiana) populations are morphologically intermediate and have been commonly assigned to *A. longifolia*, which they most resemble. Using population genomic data from >1400 SNP loci and a plastome phylogeny, we found evidence for two largely discrete gene pools. However, the western Gulf Coast populations belong to the interior *A. hirtella*, not the coastal *A. longifolia*, and we present supporting morphological evidence for this circumscription. These case studies pave the way for achieving deeper understanding of evolutionary and biogeographic history of *Asclepias*.

S.3.6 Citizen science and its impact on systematics and natural history of Apocynaceae of Mexico

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By 2003, humanity had created the equivalent of 5 exabytes of information. Today, this information is generated in 2 days. Although most of it is entertainment, some of it has allowed us to benefit and connect the daily life of citizens and scientists. Social networks have enabled a proximity between science and society, but citizen science platforms have created a very productive link, an example of which is INaturalist. In Mexico, INaturalist integrates more than 3000 photos daily, many of them exotic or cultivated organisms, but others of great importance for the information they contain. This has contributed to aspects such as systematics, biogeography, plant-animal interactions, biological invasions and, of course, the relationship between people and scientists. One of the plant families that has benefited from these platforms is the Apocynaceae. This is one of the most diverse families in the world, with more than 5000 species, and in Mexico there are about 500 species, making it the 12th most diverse family in the country. Since 2018, the INaturalist database has been managed as the "Apocynaceae of Mexico" project. The project includes about 60,000 photos, the presence of 4 specialists in the group and a curation of more than 80 %. As a result, the distribution of many taxa has been adjusted. Over 400 species have been documented, including some with flowers and fruits. The documentation includes the presence of five species that have not been collected in over 30 years, the discovery of five new species, and the identification of invasive species within natural areas. Likewise, floral visitors and potential pollinators have been documented, many of them unknown to the country. Proper utilization and management of this information will enhance the comprehension of the biology and systematics of the organisms under investigation.

S.4 BIOGEOGRAPHY AND DIVERSIFICATION OF INTERCONTINENTAL TROPICAL PLANT DIVERSITY. SESSION 1

S.4.1 The biogeography of tropical plants with megafaunal fruits

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Plants with megafaunal fruits (>4 cm) have relied on dispersal by megafauna and other large-bodied vertebrates (> 40 kg) throughout their million-year evolutionary history. How megafruit plants have persisted in contemporary ecosystems after the Pleistocene extinction of most megafauna - especially in the Neotropics, Madagascar, and Australasia - remains an evolutionary enigma. By integrating global data on traits, seed dispersal interactions, phylogenies, and geographical occurrences for >1500 megafruit plants, we show that many megafruit species (613 species, 40%) interact with contemporary dispersers, including humans, megafauna (e.g., elephants), secondary dispersers (e.g., rodents), or water, providing an explanation for their persistence. These megafruit species often have large geographical range sizes, strongly contrasting the 128 (up to 300) megafruit species that are currently threatened with extinction, suffer from small range sizes, and lack suitable co-occurring dispersers, primarily on (isolated) tropical islands in the Australasia, IndoMalay and Madagascar regions. Our results illustrate how the Pleistocene extinctions and ongoing defaunation limit seed dispersal of many tropical plant populations with megafaunal fruit, but humans may have replaced megafaunal dispersal functions for s subset of taxa.

S.4.2 The spatio-temporal co-diversification of frugivores and three vertebrate-dispersed tropical plant families

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Fleshy-fruited plants and their fruit-eating and seed-dispersing animals (frugivores) have originated millions of years ago, but it remains unclear when and where their mutualistic interactions evolved, and whether this led to co-diversification and co-adaptation of frugivory-related traits. Here, we hypothesize that shifts in diversification and trait evolution rates of tropical, fleshy-fruited plant lineages coincided with the evolution of frugivorous vertebrate lineages and their traits, as a result of co-evolutionary selective pressures from interacting partners. To test this hypothesis, we focus on three pantropical keystone plant families comprising >6,200 species with vertebrate-dispersed fruits: custard apples (Annonaceae), palms (Arecaceae) and mulberries and figs (Moraceae). We align their evolution with that of their primary seed dispersers based on data from extant and Late Quaternary mammals and birds (~ 5,200 species). Because fruit and seed size are constrained by frugivore gape widths and body sizes, with the largest fruits depending on dispersal by the largest animals, we also collected information on fruit and/or seed sizes and body sizes/gape widths/diet. We integrated these data in a phylogenetic framework and used comparative methods to identify the origin and biogeography of major frugivore lineages and their food plants. Using diversification and trait evolution models, we showed that several plant and frugivore lineages co-diversified in the Cenozoic (i.e., last 66 million years), with increased rates of diversification coinciding with increases in fruit and body size evolution. These findings suggest that reciprocal adaptations in frugivory-related morphological traits between plants and frugivores have influenced their mutualistic-dependent co-diversification across the tropical realms, explaining high contemporary diversity and 'trait matching' in tropical rainforests.

S.4.3 Climatic niche and functional shifts after Neotropics colonization drive diversification in the amphi-pacific genus Dendropanax

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Dendropanax is a species-rich genera of Araliaceae and a classic example of the Asian-Neotropical disjunction or amphi-pacific tropical disjunction. Previous biogeographic reconstructions of the genus point to an East Asian origin and posterior colonization of the Neotropics, with higher diversity in the Neotropical clade. Here we investigated the role of climatic niche evolution and colonization events in the diversification of the functionally and climatically heterogeneous genus *Dendropanax*. We used Hyb-Seq phylogenomics on 237 Araliaceae species to obtain time-calibrated nuclear and plastid phylogenies used to perform biogeographic analyses, diversification models, and climatic niche and functional trait reconstructions (habit, leaf type, dimorphism, and area, stipule and trichome presence) for *Dendropanax* and phylogenetically close genera. Curated databases were used to estimate current and ancestral climatic niches (6,496 occurrences) and leaf areas (910 measurements) using a novel probabilistic approach that considers niche heterogeneity. Diversification in *Dendropanax* followed a temperature-based model with a decrease of diversification towards the present. After an Asian origin, successive colonizations of Central and South America preceded climatic niche expansions and shifts towards warmer and drier climates coupled with an increase in leaf area and variability and associated with the persistence of high diversification rates in the Neotropical *Dendropanax* clade in comparison with the Asian *Dendropanax* clade. Given that the evolution of leaf area followed the colonization of the Neotropics, we believe that this trait could be associated with the adaptation to the climatic conditions in the colonized area. Our results support the relevance of colonization events, climatic niche evolution and functional trait shifts to explain phylogenetic diversification in the intercontinental tropical *Dendropanax*.

S.4.4 Phylogenetic insights into the origins of tropical rainforest hyperdiversity: Big Data versus model groups

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Rainforests occur across the tropics and are consistently the most biodiverse biome on Earth. Despite centuries of scientific interest, the eco-evolutionary drivers of rainforest hyperdiversity remain elusive. That said, it seems clear that explanations have to be sought in deep time, involving dynamics of diversification, migration and adaptation over tens to hundreds of millions of years. Phylogenetic trees can provide a unique window on those deep-time dynamics, but are notoriously hard to obtain at the scale needed to unpick rainforest hyperdiversity. Robust and well-sampled phylogenetic trees tend to be only available for small "model groups" that may or may not be representative for the assembly of rainforest biotas. Meanwhile, "Big Data" approaches investigating major groups as a whole (e.g. seed plants) consistently suffer from limited, patchy and biased phylogenetic data. Similar trade-offs exist for the geographic and ecological data needed to assign species to biomes, a prerequisite for investigating biome assembly over time. Here, we discuss recent efforts to understand the evolutionary assembly of rainforest hyperdiversity using both "Big Data" and "model group" approaches, comparing their findings and highlighting the specific challenges, pros and cons of each approach. Specifically, we report our recent findings based on phylogenetic, geographic and biome association datasets for all seed plants (Spermatophyta), contrasting them with focused studies mostly from the palm family (Arecaceae), a well-established model group for tropical plant ecology and evolution.

S.4.5 Reconciling deep and recent time to unravel global tropical rain forest diversification dynamics at unrivaled levels of precision

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The evolution and processes leading to the remarkable biodiversity contained within tropical rain forests (TRF) have been subject to research for decades. Traditionally, at a macroevolutionary scale, two predominant contrasting hypotheses are generally debated, the museum hypothesis, where low extinction rates lead to a constant diversification and a steady increase of diversity through time, and the cradle hypothesis, where increased speciation rates lead to rapid bursts of diversity. To date, most studies were based on regional or limited global taxonomic sampling spanning either recent or deep time scales. These studies suggested a more nuanced view with a mixed or neutral model of high species turnover, implying both elevated speciation and extinction rates in TRF. Here, we reconcile deep and recent time scales to test these hypotheses by generating for the first time a global near complete species level dated phylogenetic tree of the major TRF family Annonaceae Juss. (ca. 2000 out of 2450 species). Using this framework, we tested both hypotheses using different macroevolutionary methods and statistics. We shall present the major results obtained from these analyses and implications for our understanding of TRF evolution through time at global scales. Our study marks a significant advancement in understanding TRF evolution, by presenting the first comprehensive species-level phylogenetic tree of one of the oldest rain forest angiosperm families on a global scale.

S.4.6 The biogeography and evolution of derived woodiness in tropical and sub-tropical angiosperms

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The repeated evolution of woodiness in herbaceous lineages has long been perceived as defining feature of island floras, in particular in the Tropics and sub-Tropics ("insular woodiness"). However, scattered evidence indicated comparable transitions of herbaceous lineages towards woody growth on continents, for instance on tropical mountains ("derived woodiness"). Here, we contrast recent results on the evolution of insular woodiness with a novel dataset on derived woodiness on continents. We identified numerous independent transitions towards woodiness in 57 eudicot angiosperm families, resulting in more than 6,500 recent derived woody species. We found more transitions and derived woody species on continents than on islands but derived woodiness on islands was more common when accounting for total angiosperm richness (on average 0.77% of the total flora on continents vs 1.85% on islands). Furthermore, we identified four global continental centers of derived woodiness, mostly in the Tropics and sub-Tropics: The Andes, South Africa, parts of Australia and New Zealand ("Australasia "), and the Old-World dry belt. Our results reveal the re-evolution of woodiness in herbaceous lineages as widespread phenomenon on island and on continents driven globally by environmental conditions, albeit with important regional and systematic idiosyncrasies.

S.5 ADVANCES IN SEED CONSERVATION OF WILD SPECIES. SESSION 1

S.5.1 Status of European seed Conservation of Wild Plants in Seed banks

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Conserving orthodox seeds of wild plants through seed banking (at 15% RH and -20°C) has become a valuable tool in safeguarding threatened populations and species, supporting conservation interventions such as plant translocations, but also in conserving genetic resources for plant breeding and food security. Despite over 90% of the European flora is likely to possess bankable seeds, there is no general assessment of how many taxa are secured in seed banks, where the gaps are and whether the countries met the objectives of global conservation initiatives such as the GSPC (i.e., target 8: 75% of threatened plants conserved ex situ). Within the framework of the COST Action ConservePlants (CA18201), a European-wide survey on seed bank collections was launched to gain an overview over the current state of ex situ conservation of wild plant taxa in seed banks across Europe. After a challenging process of taxonomic harmonization, we identified over 13,000 taxa conserved in 109 institutions from 29 countries across Europe and the

Middle East. We mapped the taxonomic names and the original provenance of seed lots against the respective national red lists to identify the coverage met by each country concerning the GSPC target 8. We reveal gaps in species conservation and point out future directions on how to meet global conservation targets. Our study demonstrates the importance of collaborative approach for seed banking to support safeguarding threatened plants across Europe but also highlights that its potential has not at all been fully exploited yet.

S.5.2 Research Progress on in vitro preservation of Wild Plants in China

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Both in situ and ex situ conservation are complementary and synergistic approaches that are essential for the protection of wild plants and their biodiversity. As a major national scientific infrastructure, the Southwest China Germplasm Bank of Wild Species has established a wild plant germplasm resource bank that includes a seed bank, plant tissue culture bank, DNA bank, animal germplasm bank, and microbial germplasm bank. The plant tissue culture bank is mainly based on the theory and methods of tissue culture to carry out species conservation, in order to achieve long-term conservation of "exceptional" species with low yield, poor quality, recalcitrance, and cannot be directly sown. Explants are obtained through field collection or exchange, and then cultured through various methods such as protocorn type, short branch cutting type, clustered shoots proliferation type, or organ type. Finally, strategies such as normal temperature or low temperature restriction are used to achieve in vitro preservation of germplasm resources. The use of in vitro conservation methods allows wild plant germplasm resources to obtain regenerability, repeatability, and sustainability in research and utilization, which is a major characteristic that distinguishes in vitro preservation from other ex situ conservation methods and provides new strategies to make up for the shortcomings of in situ and other ex situ conservation methods. The staff of the Southwest China Germplasm Bank of Wild Species has made certain progress in large-scale in vitro preservation of wild plants through years of accumulation. As of the end of 2023, the plant tissue culture bank has preserved in vitro culture materials of more than 1,100 species and 27,100 samples, with orchid species accounting for over 60%. It has preserved one-third of the species and 55% of the genera of wild orchids in China, as well as other rare and endangered plants.

S.5.3 Spectrometry and machine learning technologies to aid conservation of native dry forest seeds

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Seed-based conservation plays a critical role in the conservation, enrichment, and restoration of degraded environments. Climate change and agricultural pressure has enhanced the vulnerability to desertification of tropical dry forests. Plant biodiversity conservation is urgent, mainly in populations located in climate change threatening hotspots. Traditional stored seed quality assessment relies on destructive tests to evaluate viability, germination, and moisture content. These usually take more time and seeds than is convenient for restoration actions. Quick and accurate non-destructive methods allow efficient decision making in all native seed conservation activities, from harvest to storage, and also in seed-based restoration actions. Spectrometry allied to machine learning can be an effective method for evaluating the quality of native forest seeds, while maintaining the usually small bulk of stored seeds. Thus, we aimed to develop an easy and non-destructive method for evaluating stored seeds physiological quality and moisture content using a portable Vis-NIR spectrometer and a machine learning algorithm model. Stored and fresh seeds of different populations of two dry forest Fabaceae were individually evaluated for germination, moisture content and spectral data using a portable spectrometer. External and internal validation of the model were carried out by dividing the data into training (70%) and testing (30%) stages, using 10x cross-validation. The spectral data were processed using Weka 3.8.6 software. The discriminative algorithms applied were Support Vector Machine, Multilayer

Perceptron, Random Forest and J48. For germination, the seeds were classified as YES (germinated) and NO (not germinated). Multilayer Perceptron algorithm obtained the best results for water content evaluation, with calibration and prediction correlation coefficients above 0.70. Random Forest and J48 algorithms showed best performances for seed germination classification. Although the algorithms were efficient in seed quality classification, increasing the number of sampled seeds may improve their prediction accuracy and aid seed-based conservation activities.

S.5.4 Capturing representative genetic diversity in quality conservation germplasm collections

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Seed banking of wild plants is a cost-effective conservation tool that allows for genetically representative germplasm collections to be stored for extensive periods of time. Such collections are becoming increasingly more important particularly for species where anthropogenic activities are contributing towards local extinction and population decline, leading to a loss of genetic diversity and adaptive capacity. Seed collecting aimed at capturing genetic diversity across the range of wide-spread species can be daunting specially in parts of the world where resources are limited, and such germplasm collections are only now being initiated. Here we use a range of genomic datasets to provide guidelines for building representative conservation germplasm collections. Progeny datasets for multiple species that we obtained from seed collected across multiple sites and multiple maternal lines allowed us to explore how different collecting strategies (numbers of seed, families, and sites) capture genetic diversity. The results from this empirical data were encouraging indicating that a.) small quality collections can capture a large proportion of allelic variation and b.) we can use population genomic data to strategize seed collections to maximise genetic diversity. We apply the outcomes from the progeny analysis to multiple extensive population genomic datasets available through the Restore and Renew program and discuss guidelines for capturing various representative levels of allelic variation. Finally, based on these progeny data sets and other results from our teams' extensive work in taxonomy, conservation and restoration genomics, we prompt seed collectors and seed bank managers to maintain maternal lines during the life of the collection as this maximises the value and utility of these precious germplasm collections.

S.6 NEW FRONTIERS IN PLANT PHYLOGENOMICS. SESSION 1

S.6.1 New Views on Fern Phylogenetics. Updates from the GoFlag Targeted Enrichment Probe Set

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Ferns are the second largest group of vascular land plants, with ca. 10,000, species, and they are critical components of Earth's biodiversity – ferns can be found in nearly every type of ecosystem and habitat, from desert to rainforest. Ferns also occupy a pivotal evolutionary position as sister to the megadiverse seed plants, and they are thus the critical outgroup needed to understand the evolution of key seed plant features. Fern phylogenetics as a field has evolved considerably since the 1990s, when the first rbcL-based phylogenetic analyses of ferns were completed. Fern phylogenetics has presented researchers with a number of challenges, including the deep evolutionary history of the group and their propensity to undergo hybridization and whole genome duplication. We present a phylogenomic approach to fern evolution, using the most highly resolved nuclear dataset to date (targeting 408 loci), and with highly targeted taxonomic sampling (including nearly all fern families and genera). This dataset allows us to explore a range of outstanding questions in fern phylogenetics, including resolving recalcitrant nodes, and comparing results between our nuclear based trees and other recent large-scale fern phylogenies based on chloroplast loci.

S.6.2 Completing the Angiosperm Tree of Life

William J. Baker[1], the PAFTOL Community

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The tree of life is the fundamental biological roadmap for navigating the evolution and properties of life on Earth, and yet remains largely unknown. Even angiosperms are fraught with data gaps, despite their critical role in sustaining terrestrial life. Since 2016, the Plant & Fungal Trees of Life (PAFTOL) project at the Royal Botanic Gardens, Kew has targeted this knowledge gap in angiosperms by leveraging biological collections with novel genomic tools at unprecedented scale. Here, we describe our efforts to complete the angiosperm tree of life for all genera. Key achievements include: **(1)** the creation of Angiosperms353, an innovative, open-access, target sequence capture toolkit for tree of life research on any flowering plant; **(2)** the assembly of Angiosperms353 sequence data for 8,336 (61%) of the 13,600 genera of flowering plants, amounting to over 1.5 billion base pairs in total; **(3)** a tree of life containing all 7,514 genera of flowering plants sequenced to date, integrating novel data for over 8,000 samples, with data sourced from collaborators and public resources; **(4)** the *Kew Tree of Life Explorer* (https://treeoflife.kew.org/) launched in February 2021, an open data portal through which our tree of life and all data are made publicly available, with release 3.0 (April 2023) containing data for 10,377 samples; **(5)** a collaborative network of >300 individuals worldwide driving numerous projects using Angiosperms353 data; **(6)** outreach activities communicating the science of PAFTOL to the public. A wealth of primary research has also arisen from our data ranging from species-level studies, through to big picture analyses exploring the rise of the angiosperms. As the project approaches its goal of sampling all angiosperm genera, we welcome collaboration from all corners of the community and encourage anyone with interests in working with us on data generation, sharing or utilisation to get in touch.

S.6.3 Angiosperms353 Version 2: improving gene recovery and locus length for universal single copy genes in flowering plants

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Angiosperms353 has gained popularity both as informative single copy genes and universal probes for cost-effective target capture in high-throughput sequencing. With data from over 10,000 species and 60% of extant genera now represented in the Kew Tree of Life Explorer (treeoflife.kew.org), Angiosperms353 has become an important tool for phylogenetics and population genetics studies. However, several shortcomings of the original gene targets and associated probe sequences have led to poorer than average recovery of sequences in certain angiosperm groups. We seek to improve Angiosperms353 probes by using expanded resources of high-quality genome references in angiosperms and data generated by the Plant and Fungal Tree of Life (PAFTOL) project at RBG-Kew and the Genomes of Australian Plants (GAP) project at RBG-Victoria. For Angiosperms353v2, we expanded the targeted sequence of each gene to include coding regions not captured in the first version. We also improved the regions covered in Angiosperms353v1 by using kmediods clustering to select represented sequences at a per-exon level. We describe the in-silico testing of Angiosperms353v2 and associated resources, including curated clade-specific target files for use in gene recovery workflows. Our new probe design is intended to continue the success of Angiosperms353 with improved recovery and increased gene sequence length, thus enhancing future phylogenetic inference.

S.6.4 Integrative phylogenomics of the model tropical rain forest family Annonaceae: from herbaria to global scale diversity dynamics

Thomas L.P. Couvreur[1]; Carlos Rodrigues-Vaz[1,2]; Vincent R.C. Soulé[1]; Laura Holzmeyer[1]; Francis J. Nge[1]; Serafin J. R. Streiff[1], Annonaceae Global Phylogenetics Consortium[3]

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Annonaceae is a major pantropical family with 2450 known species mainly occurring in rain forests worldwide. Based on decades of taxonomic research and resource generation, Annonaceae provide an excellent model-clade to understand the evolution of hyperdiverse tropical rain forests. We present ongoing integrative research combining phylogenomics, evolution and ecology of Annonaceae. Using a custom Annonaceae baiting kit, we sequenced hundreds of nuclear genes for over 85% of its diversity worldwide (> 2000 species). Over 75% of species were sequenced from herbarium specimens, the oldest dating from 1785. In parallel, we produced a massive morphological dataset documenting functional diversity, generated precise species-level distribution based on herbarium specimens documenting spatial diversity, and finally, used innovative near infrared scanning (NIRs) to estimate species specific spectra documenting chemical diversity. Most relationships were well resolved producing one of the first ever near-complete robust species level phylogenetic hypotheses of a major tropical rain forest plant family. The results mainly confirmed past systematic studies in Annonaceae, but also produced some surprises. By integrating these large-scale datasets with a robust dated phylogenetic tree at the species level, we present preliminary results about global rain forest diversification. Finally, we discuss the advantages and challenges of leading a large-scale project on a model clade, and how herbaria are (and will be) central to tackling numerous questions about rain forest evolution.

S.6.5 A phylogenomic analysis of Salsoloideae (Amaranthaceae). An example of extreme paralogy and discordance

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Caroxyloneae and Salsoleae constitute a species-rich lineage of Amaranthaceae containing around 40 genera and 300–400 species, including the largely polyphyletic *Salsola*. Members of this lineage are primarily distributed in the steppes and deserts of Eurasia, northern and southern Africa. It includes leaf- and stem-succulent halophytic, xerohalophytic, xerophytic, and ruderal plants, where C_4 photosynthesis is prominent. Generic boundaries in Caroxyloneae and Salsoleae have been historically a matter of long-standing debates, with numerous transfers, reinstatements, or newly established genera in recent years. To date, phylogenetic analyses of the tribe have been based on a limited number of DNA regions, leaving most phylogenetic relationships unclear in an already highly taxonomic challenging group. To build a comprehensive backbone phylogeny of the group to clarify generic boundaries and investigate patterns of C_4 photosynthesis, we used 483 putative single-copy loci from a custom target enrichment bait set and sampled 175 spp. from 36 genera from Caroxyloneae and Salsoleae. We recovered many paralogs for all species, including many pseudo-gene copies. These paralogs were spread across all Chenopods II, with several species even having gene copies as far as nested within Polycnemoideae (one of the other subfamilies in Amaranthaceae). This extreme paralog pattern largely halted the ability to infer orthologs using tree-based methods because the many duplications found in the gene trees resulted in mainly small orthologs, which ultimately resulted in a phylogeny with massive discordance and low to no support for most nodes. Here, we explore the challenges and strategies for overcoming the issue of rampant paralogy to attempt to build a backbone of Caroxyloneae and Salsoleae.

S.6.6 Applying the phylogenomics package Captus to polyploid, contaminated, and degraded samples

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Our recently developed software package, Captus (available at https://github.com/edgardomortiz/Captus), greatly simplifies processing high-throughput sequencing data into alignments ready for phylogenetic analyses. Captus can remove paralogs from these alignments for use in traditional species tree estimation methods or include the complete set of recovered paralogs for use in more recent methods such as ASTRAL-Pro. Even though Captus normally searches for previously known sets of orthologs (e.g., Angiosperms353, BUSCO lineage databases) it can also be used to discover new putative homologs across the samples analyzed, making it possible to extract phylogenetically informative loci from any group of organisms. Besides recovering accurately and rapidly a greater number of more complete loci across more samples, Captus is also capable of dealing with several common issues that arise in current phylogenomics practice. We show that the accuracy of recovery helps minimizing the methodological sources of conflict between gene trees and the species tree revealing clear patterns of reticulation or hybridization. Captus facilitates the combination of sequence data from samples of varying quality (i.e., silica-preserved, herbarium), different data types (i.e., target capture, high and low depth whole genome sequencing, and RNA-Seq), and pre-assembled genomes and transcriptomes to build a single phylogenomic dataset for analysis. Captus can also be used to identify outlier samples containing an excess of paralogs due to polyploidy or potentially contamination. Captus can be used to remove phylogenetically distant contaminants from a sample. Finally, we show an additional feature of Captus, an easy-to-use workflow to find putative homologs and design baits for target enrichment and how we used it to create a set of baits to capture 989 protein coding genes (854 single-copy and 135 associated with morphological traits of interest) as well as 177 non-coding regions for the family Cucurbitaceae.

S.7 MECHANISMS AND CONSEQUENCES OF DISPERSAL IN LAND PLANTS: TOWARDS A MORE UNIVERSAL UNDERSTANDING. SESSION 1

S.7.1 Seed dispersal mismatches under global change: what can we apply to the rest of terrestrial plants?

Irene Mendoza[1]

1 Estación Biológica de Doñana (CSIC), Sevilla, Spain

Seed dispersal implies the movement of a seed at a certain distance from the maternal plant, which favours propagation towards new environments. Many Spermatophyta rely on animals for seed dispersal, especially those with fleshy fruits which offer a nutritious award for the disperser. The unprecedented environmental change produced by human activities (including climate and land-use changes) is not only reducing biodiversity in terms of the number of species, but it is also changing the probabilities of interactions among plants and their dispersers. Seed dispersal by avian species necessarily implies that the phenology of birds and fruit production matches in time. Whereas we have evidence that species are already changing their geographic distribution ranges and their life cycles' timing (e.g., bird migration, fruiting time) as a consequence of climate change, we still have a knowledge gap in understanding whether these changes will result in mismatches among interacting species. Network analytical advances and new technologies applied to biodiversity monitoring have paved the road to undertake this challenging objective. In this presentation, I focus on these specific questions 1) What phenological changes are currently taking place in Southern Spain as a consequence of global change? 2) Are these phenological shifts resulting in a mismatch between the phenology of birds and fleshy-fruited plants? 3) How can we forecast phenological mismatches? For answering these questions, I use methods from classical field monitoring and new technologies such as digital images from phenocams or unmanned aerial vehicles that have barely been applied to research on ecological interactions, combined with cutting-edge analytical tools including network analyses and forecasting modeling. These methods and conceptual advances can be easily extended to other terrestrial plants and will help understanding the ultimate consequences for ecosystem functioning and biodiversity conservation of seed dispersal mismatches induced by global change.

S.7.2 How can dispersal by endozoochory by waterbirds influence the genetic structure of a dry-fruited wetland plant?

M. Angeles Ortiz[1], Raul Sanchez[2], Iciar Jim[2], Karin Tremetsberger[3], Casper van Leeuwen[4], Adam Lovas-Kiss[5], Andrew J. Green[2].

1 Dpto. Biología Vegetal y Ecología, Universidad de Sevilla, Spain 2 Dept of Wetland Ecology, Doñana Biological Station EBD-CSIC, Sevilla, Spain. 3 Institut für Botanik, Universität für Bodenkultur Wien, Wien, Austria 4 Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands 5 Wetland Ecology Research Group, Centre for Ecological Research, Danube Research Inst., Debrecen, Hungary

One of the main challenges when reconstructing the evolutionary history of a plant species is the lack of information about its dispersal mechanisms. These mechanisms shape the distribution of plants, favoring long-distance dispersal events or confining them to much more restricted areas. Some species exhibit obvious dispersal syndromes, like plants with fleshy fruits. However, plants without clear modifications in their fruits or seeds promote controversy regarding whether they have a specialized dispersal system, fall passively near the mother plant, or depend on random events to colonize new habitats. A specific case involves dry-fruited plants in wetlands, traditionally assumed to have hydrochorous dispersal due to their distribution in or near water-bodies. Recent studies have shown that aquatic birds can disperse dry-fruited plants through endozoochory, after feeding on the plants or in the seed bank, egesting viable seeds in their faeces. But how does this type of dispersal affect the genetic structure of plants? Does it promote long-distance dispersal along migratory flyways, and/or connectivity between nearby wetlands?

We will test the dispersal processes shaping the population structure and gene flow in Eleocharis palustris (Cyperaceae). This species inhabits wetland borders and temporarily flooded areas, being native to the Northern Hemisphere. Endozoochory of this species has been recorded for many different waterbird species. Morphological and ploidy level studies have been conducted to characterize its variability. To delve into this topic, population genomics was investigated applying GBS (genotyping by sequencing) in 188 plants from 20 populations in seven European countries. Finally, the relationship between the migratory flyways and the population networks will be discussed, as well as the role of their ecological niche. The understanding of how endozoochory can shape the distribution of a species could be key to management and conservation policies for native taxa.

S.7.3 Autorotating diaspores of flowering plants: an inspiring strategy in wind dispersal

Drisya V.V.[1], C. Pramod[1,2], A.K. Pradeep[2], T.P. Suresh[3]

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Plants are excellent source of inspiration for design innovation as they are already figured out what works to spread over the planet and provide numerous examples of stable design and specialized functionality that are worth to study (Pandolfi & Izzo, 2013). One amazing demonstration of 'intelligent' behavior of plants for wind dispersal is the production of autorotating diaspores. Dispersal units, such as fruits, seeds, and other structures which constantly rotate in the air during dispersal basically due to aerodynamic forces for moving away from the parent plant to establish the progeny as an independent sapling are known as autorotating diaspores. Based on the morphology and type of rotation during the fall, three types of autorotating diaspores are identified: autogyros, rolling autogyros, and helicopters (Augspurger, 1986). In a study conducted on the winged diaspores of the flowering plants of South India, a total of about 120 species (55 autogyros, 24 helicopters, 41 rolling autogyros) were recorded, which produce autorotating diaspores with well-defined morphological adaptations. Macromorphological, micromorphological, developmental, anatomical, flight behavioural, and aerodynamic studies of a subset of diaspores from each category show that each of them varies in its origin, pattern of development, and configuration of the wings, which account for the variation in the overall morphology and eventually the dispersal potential. The autorotating diaspores of the flowering plants of South India display a variety of morphology and design for the efficient mechanism of dispersal, also effective as natural inspiration for design innovation. The present paper aims to provide a better understanding of the morphology, geometry, underlying mechanisms of flight, specificity of the direction of rotation, and biomimetic application of the autorotating diaspores of flowering plants of south India.

S.7.4 Linking pollen limitation and seed dispersal effectiveness

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Seed production and dispersal are crucial ecological processes impacting plant demography, species distributions, and community assembly. Plant-animal interactions commonly mediate both seed production and seed dispersal, but current research often examines pollination and seed dispersal separately, which hinders our understanding of how pollination services affect downstream dispersal services. To fill this gap, we propose a conceptual framework exploring how pollen limitation can impact the effectiveness of seed dispersal for endozoochorous and myrmecochorous plant species. We summarize the quantitative and qualitative effects of pollen limitation on plant reproduction and use Optimal Foraging Theory to predict its impact on the foraging behavior of seed dispersers. In doing so, we offer a new framework that poses numerous hypotheses and empirical tests to investigate links between pollen limitation and seed dispersal effectiveness and, consequently, post-dispersal ecological processes occurring at different levels of biological organization. Finally, considering the importance of pollination and seed dispersal outcomes to plant eco-evolutionary dynamics, our framework opens new avenues for future studies exploring the current and future functioning of these key interactions, both deeply threaten by human landscape modification and ongoing climatic changes.

S.33.3 How can dispersal by endozoochory by waterbirds influence the genetic structure of a dry-fruited wetland plant?

M. Ángeles Ortiz[1], Raul Sanchez[2], Iciar Jiménez[2], Karin Tremetsberger[3], Casper van Leeuwen[4], Adam Lovas-Kiss[5], Andrew J. Green[2]

1 Departamento de Biología Vegetal y Ecología, Universidad de Sevilla, Spain. 2 Dept. of Wetland Ecology, Doñana Biological Station -CSIC, Sevilla, Spain. 3 Institut für Botanik, Universität für Bodenkultur Wien, Wien, Austria. 4 Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands. 5 Wetland Ecology Research Group, Centre for Ecological Research, Danube Research Inst., Debrecen, Hungary

One of the main challenges when reconstructing the evolutionary history of a plant species is the lack of information about its dispersal mechanisms. These mechanisms shape the distribution of plants, favoring long-distance dispersal events or confining them to much more restricted areas. Some species exhibit obvious dispersal syndromes, like plants with fleshy fruits. However, plants without clear modifications in their fruits or seeds promote controversy regarding whether they have a specialized dispersal system, fall passively near the mother plant, or depend on random events to colonize new habitats. A specific case involves dry-fruited plants in wetlands, traditionally assumed to have hydrochorous dispersal due to their distribution in or near waterbodies. Recent studies have shown that aquatic birds can disperse dry-fruited plants through endozoochory, after feeding on the plants or in the seed bank, egesting viable seeds in their faeces. But how does this type of dispersal affect the genetic structure of plants? Does it promote long-distance dispersal along migratory flyways, and/or connectivity between nearby wetlands? We test the dispersal processes shaping the population structure and gene flow in *Eleocharis palustris* (Cyperaceae). This species inhabits wetland borders and temporarily flooded areas, being native to the Northern Hemisphere. Endozoochory of this species has been recorded for many different waterbird species. Morphological and ploidy level studies have been conducted to characterize its variability. To delve into this topic, population genomics was investigated applying GBS (genotyping by sequencing) in 188 plants from 20 populations in seven European countries. Finally, the relationship between the migratory flyways and the population networks will be discussed, as well as the role of their ecological niche. The understanding of how endozoochory can shape the distribution of a species could be key to management and conservation policies for native taxa.

S.7.5 Pollen dispersal in flowering plants. Importance of pollinators from single visits to regional patterns

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Pollen dispersal in flowering plant species results from the joint action of the pollinators at each plant population. These dispersal agents determine the mating patterns between plants and ultimately the genetic composition of the populations as well as their degree of genetic isolation. Here, results from a series of studies will be introduced to highlight the importance of pollinators for the genetic dispersal of flowering plants at different scales. At the level of individual plants, a study demonstrates how pollinators can widely differ in their capacity of transporting pollen of different genetic diversity and origin. At the population level, a study is used to evidence the role of these animals in generating contemporary patterns of pollen flow between plants. At the regional level, a study performed on several plant species demonstrates how pollinator diversity correlates with the genetic diversity and connectivity of plant populations. Taken together, these studies demonstrate that addressing the mechanisms of pollen flow is essential to explain the genetic patterns found within and between plant populations that ultimately provide insights into plant evolution.

S.8 SAPINDALES: UNDERSTANDING ANGIOSPERM EVOLUTION BY INTEGRATION ACROSS DATA, SPACE AND TIME

S.8.1 Hybrid Capture resolves the phylogeny of the pantropically distributed Zanthoxylum (Rutaceae) and reveals an Old World origin

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With about 225 species, *Zanthoxylum* L. is the second most species rich genus in Rutaceae. It is the only genus with a pantropical distribution. Economically, it is used in several Asian countries as traditional medicine and spice. In the past *Zanthoxylum* was divided into two genera, the temperate *Zanthoxylum* sensu strictu (s.s.) and the (sub)tropical *Fagara*, due to the large differences in flower morphology: heterochlamydeous in *Fagara* and homochlamydeous in *Zanthoxylum* s.s. This genus is much under studied and previous phylogenetic studies using Sanger sequencing did not resolve the relationships sufficiently. In this study, we use Hybrid Capture with a specially designed bait set for *Zanthoxylum* to sequence 347 putative single-copy genes. The taxon sampling has been largely improved as compared to previous studies and I present preliminary results based on 371 specimens representing 133 species from all continents and major island groups. Our preliminary results reveal similar tree topology as the previous studies while providing more details to the backbone of the phylogeny. The phylogenetic tree consists of four main clades: **a)** African/Malagasy clade, **b)** *Z. asiaticum* clade - a clade consisting widespread species occurring in (sub)tropical Asia and Africa as well as Madagascar, **c)** Asian/Pacific clade and **d)** American clade, which also includes the temperate Asian species. The merging of *Fagara* and *Zanthoxylum* is supported by our results and the homochlamydeous flowers of *Zanthoxylum* s.s. are likely derived from heterochlamydeous flowers. Several of the morphologically defined sections within *Zanthoxylum* are not monophyletic. In this presentation, we **(1)** introduce the framework of this project; **(2)** present preliminary results and **(3)** the ongoing progress of the study.

S.8.2 Systematics and morphological diversity of the cashew family (Anacardiaceae)

Susan K. Pell[1], John D. Mitchell[2]

1 United States Botanic Garden, Washington, USA. 2 The New York Botanical Garden, New York, USA

Anacardiaceae is an ecologically and economically important plant family of about 800 species in more than 80 genera worldwide. Most well-known for its commercial crops, cashew (Anacardium occidentale), mango (Mangifera indica), and pistachio (Pistacia vera), and its many contact dermatitis-causing species (e.g., poison ivy and oak; Toxicodendron spp.), the family includes many other regionally important taxa and exhibits substantial morphological diversity. Anacardiaceae is particularly diverse in leaf architecture, flower and fruit morphology, and pollination and dispersal syndromes. Fruit diversity is the primary reason 30 of the genera are monotypic and that so many genera are recognized in the family. Recently published Sapindales phylogenies and newly discovered Anacardiaceae fossils have shed new light on the evolution of structural diversity in the family. This presentation provides an overview of the noteworthy morphological diversity of Anacardiaceae in the context of systematics and paleobotany. Several newly recognized taxa, including newly published and yet-to-be published genera, are discussed.

S.8.3 Meliaceae (mahogany family): model group for a better understanding of tropical angiosperm evolution?

Alexandra N. Muellner-Riehl[1,2], Meliaceae Taxonomic Expert Network

1 Leipzig University, Leipzig, Germany. 2 German Centre for Integrative Biodiversity Research, Halle-Jena-Leipzig, Leipzig, Germany

Meliaceae comprises woody plants widely distributed throughout the tropics and subtropics, extending into temperate zones. With over 740 species in 58 genera, they constitute a medium-sized family in Sapindales. The Indo-Malesian region is the geographic centre of diversity. Africa-Madagascar is almost as diverse as Indo-Malesia, followed by Australasia. Only eight genera are present in the Neotropics, but they are as diverse as the Africa-Malagasy region as for the number of species. Comparing geological evidence with the fossil record as well as biogeographic studies, there is indication that the nowadays pantropically distributed family has made use of three routes to acquire its current distribution: land connections (i) between Eurasia and North America, (ii) between North America and South America, and (iii) dispersal paths between Africa and South America that have existed since the proposed evolutionary origin of modern Meliaceae (Cretaceous). Although important new insights into Meliaceae evolution have been gained during the past two decades, there are also still open questions. A careful revision of the entire fossil record of Meliaceae will be an important step into a more comprehensive understanding of the biogeographic history of this family, which may serve as a prime example for understanding the evolution of rainforest (and related) taxa on a global scale. A more or less completely sampled species-level phylogeny, accompanied by molecular clock dating making use of the rich fossil record, complemented by biogeographic reconstructions (incl. the investigation of niche evolution), will only be achievable by a scientific community effort, bringing together researchers from different disciplines, who have a keen interest in Meliaceae evolution. The vision of this longer-term research agenda will be to establish this—also economically very important—family as a model group for a better understanding of angiosperm evolution.

S.8.4 The evolution of Meliaceae: systematics, genome duplications and implications for taxonomy

Monika M. Iskander[1], Elizabeth M. Joyce[2]

1 Rhenish Friedrich Wilhelm University of Bonn, Germany. 2 Ludwig Maximilian University of Munich, Germany

Meliaceae is a widespread angiosperm family of c. 740 species in 58 genera, mainly comprising tropical and subtropical trees. Given its distribution and diversity, Meliaceae is considered a useful lineage for understanding the evolution of tropical forests; however, our understanding of the family's evolution and infra-familial relationships remain unclear. Here, we present the first genus-complete phylogenies for the family, generated with Angiosperms353 and chloroplast loci, and including 139 taxa with good geographic representation. In the nuclear trees, many relationships were retrieved with maximum support (PP=1, BS=100) and suggest that some genera are non-monophyletic and should be recircumscribed, while some relationships remained poorly supported or conflicted with the topology of the chloroplast phylogeny, particularly in the Melioideae. Analysis and placement of paralogs suggest that this poor resolution is likely caused by a history of hybridisation and genome duplication events. Our results indicate that this may confound our ability to reconstruct relationships in bifurcating trees, raising interesting questions about how we might classify tribes and genera within the family.

S.8.5 Phylogeny of Galipeeae (Rutaceae, Sapindales), a group of the Citrus family. with insights of critical morphological traits.

Milton Groppo[1], Jacquelyn Ann Kallunki[2], Carla P. Bruniera[3], José Rubens Pirani[1], Carolina Ferreira[1], Paola de Lima Ferreira[4]

1 University of São Paulo, Brazil. 2 New York Botanical Garden, USA. 3 Federal University of São Paulo, Brazil. 4 Aarhus University, Denmark

Tribe Galipeeae (Rutaceae, Subfamily Zanthoxyloideae) is the largest group of Rutaceae in the Neotropical Region, with 33 genera and c. 181 species. The tribe is composed of two subtribes, Galipeeae (28 genera and c.130 species) and Pilocarpinae (5 genera, 51 species). Subtribe Galipeinae is different from Pilocarpinae by the possession of zygomorphic flowers (v. actinomorphic flowers in Pilocarpinae) and by the constant presence of staminodes (v. all fertile stamens in Pilocarpinae.) A phylogenetic analysis was conducted to test the monophyly of Galipeeae and its two subtribes. A total of 120 terminals, representing 24 genera and 80 species of both subtribes were sampled. Species of Balfourodendron, Choisya, Helietta, Hortia, and Plethadenia, all from genera traditionally not included in Galipeeae were also used; Zanthoxylum, a phylogenetically distant genus was used as outgroup in all analyses. Molecular data included four regions, two from the cpDNA (trnL-trnF and rps-16) and two nuclear (ITS1 and ITS2) analyses. Parsimony and Bayesian analysis was conducted. Results showed all Galipeeae grouped in a strongly supported clade (Bootstrap Percentages BP-100% BP, Posterior Probabilities PP = 1); Subtribes Galipeeae and Pilocarpinae appear as sisters, both clades with strong support. Balfourodendron and Helietta appear as part of the Pilocarpinae and Hortia along with the Galipeinae. Critical morphological characteristics such as zygomorphic flowers, presence of staminodes, embryo and fruit characteristics are discussed in the light of the new produced phylogeny.

S.9 TOWARDS INTEGRATIVE TAXONOMY. THEORY AND PRACTICE. SESSION 1

S.9.1 Integrated Taxonomy

R.W. Scotland[1]

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Tropical plants are in the most urgent need of taxonomic revision as the majority of tropical genera have never been monographed, that is they have not been the subject of detailed study across their entire geographical range. To complete the inventory of tropical flowering plants phylogenetics and monophyly are important but need to be integrated with nomenclature, description, morphology, geography, literature, interpretation of specimens, plant collectors and protologues. In the absence of this integration the inventory of tropical plants remains partial and problematic to tackle the biodiversity crisis.

S.9.2 Taxonomic updates to Caribbean Pitcairnia (Bromeliaceae) based on genomic, morphological, and ecological data

Natalia Ruiz-Vargas[1], Roberta Mason-Gamer[1]

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Pitcairnia is the second largest genus in the family Bromeliaceae, distributed from Mexico to northern Argentina, and the only one with presence in Africa. There are approximately 15 species reported for the Caribbean islands, most of which are island endemics; one species, *Pitcairnia angustifolia*, has wider distribution. Among the islands, Ayiti (Hispaniola), shared by the Dominican Republic and Haiti, stands out with six proposed species, while most of the islands have one. Using a target Sequence Capture approach with the Bromeliad 1776 baits set we analyze the relationships within the Caribbean group and found 1) that current species delimitation does not match the molecular data, and 2) that species diversity has been overestimated, likely because of high phenotypic plasticity in the group. We analyzed morphological characters in the group to understand differences between taxa and intraspecific variation. Ecological factors that influence morphological variations and promote or inhibit isolation are also analyzed.

S.9.3 Carex sect. Fecundae: a boreotemperate-origin adaptative radiation in the Neotropics

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Carex, a member of the Cyperaceae family, stands as a megadiverse genus encompassing over 2000 recognized species, primarily thriving within the boreal and temperate zones of the northern hemisphere. Despite this, certain lineages of Carex have successfully ventured into the tropical zones of the southern hemisphere on multiple occasions. Notably, *Carex* sect. *Fecundae* emerges as one such lineage, displaying a distribution entirely within the Neotropics, predominantly within high-altitude forests and grasslands spanning from Central Mexico to Northern Argentina. Comprising more than 30 species, *Carex* sect. *Fecundae* stands as one of the broadest lineages within *Carex*. It boasts perhaps the most intricate inflorescence patterns among its counterparts. However, akin to numerous Neotropical plant groups, the understanding of sect. *Fecundae* remains significantly limited. Only three treatments of this section exist to date, none of which are comprehensive. Our research addresses this gap through a comprehensive taxonomic revision of *Carex* sect. *Fecundae*, reviewing more than 1000 specimens and statistically testing more than 100 characters. We established morphometric boundaries for species within the section by selecting the most distinguishing characters, such as inflorescence conformation, utricle, glumes, and achene dimensions. Furthermore, we undertook the first complete molecular phylogeny of the section, employing HybSeq to unravel the evolutionary relationships within *Carex* sect. *Fecundae*. Our combined analysis of morphological and molecular data led to the discovery of 18 previously overlooked species within the section. Additionally, we dated the recent origin of this section to approximately 5.77 Mya, affirming the rapid adaptive radiation witnessed within *Carex* sect. *Fecundae*. Through biogeographical analysis, we inferred the most recent common ancestor of the section between the Neotropical and South American Transition Zones. This origin was followed by two independent rapid radiations—one in Mexico and the other in South America—further elucidating its evolutionary history.

S.9.4 Heuristics, species, and the analysis of systematic data - or why morphology is still king

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The rise of molecular phylogenetics and "integrative taxonomy" have led to a sense that disagreements about the fundamental nature of the species category are no longer an issue in contemporary systematics. The implicit consensus is that increases in the volume, type, and precision of data and methods available to contemporary researchers will automatically lead to more accurate and consistent species delimitations, without the need for a widely accepted definition of what species are and how they should be identified and used in biological research. The chief challenge to this triumphalist view of 'integrative taxonomy' remains the heterogenous nature of speciation. Since speciation proceeds over extended periods of time and through different processes, it results in the inconsistent manifestation of different 'contingent properties' for its recognition, depending on the taxa in question. Simply combining multiple forms of data or methods under an 'integrative approach' cannot automatically overcome this fundamental obstacle because of the continued lack of an overarching theoretical framework for species delimitation and how to treat incongruence between different types of Systematic data. Deciding what properties to assess, how to do so, and which to prioritise in the event of incongruence remains an unresolved issue, requiring a theoretical framework within which to make those decisions. In this talk, I explore how treating species as a "heuristic" can provide the basis of just such a framework. Species delimitation inherently involves the use of heuristics – through the study of representative specimens, the use of selected diagnostic characters, and strategic sampling of "tree space". Meanwhile, species themselves are routinely used in a heuristic manner to investigate broader patterns of biodiversity and the processes underpinning them. Acknowledging these aspects of systematic research can therefore inform both operational ways of accurately and consistently delimiting species, and theoretical ideas about their nature.

S.9.5 Challenges in defining genera: the limits of integrative taxonomy in the Funariaceae (Bryophyta)

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Traditionally, morphology played a pivotal role in shaping bryophyte taxonomy until the advent of the molecular phylogenetic revolution, substantially impacting their systematics. The integration of morphology and sequence data, while occasionally feasible, often remains elusive in select groups, likely due to the constrained morphospace of their anatomy and the prevalence of homoplasy. Here, we delve into the transformative influence of molecular investigations on classical generic concepts within the moss family Funariaceae. Despite the general conservation of moss sporophyte architecture driven by selective pressures for efficient spore dispersion, the Funariaceae exhibit an exceptionally diverse sporophytic generation. Historically, generic assignment relied on specific trait combinations, resulting in the recognition of 17 genera, including three specious ones—*Funaria*, *Entosthodon*, and *Physcomitrium*—and 14 paucispecific genera. Many of the latter were established to reflect intuitively unique morphological variations, typified by single or very few species, such as for *Physcomitrella*, harboring the model taxon *P. patens*. However, a series of molecular phylogenetic studies at different scales has substantially reshaped the taxonomic landscape within the Funariaceae. These investigations have unveiled novel insights: For example, most highly reduced sporophyte morphologies reflect a recurrent syndrome within the family, lacking predictive value of systematic affinities. Secondly, certain taxa arise from hybridization events, exhibiting combinations of morphological traits that may or may not align with the progenitor species. Additionally, what seemed like a coherent lineage, *Entosthodon*, reveals itself as two separate groups (*Entosthodon* s.s. and *Physcomitrellopsis*) diverging 30 mya. While proposing a novel generic synopsis consolidating the family's diversity into seven genera was feasible, achieving a complete integration between morphology and molecular systematics remains a partially realized goal. The refinement of Funariaceae taxonomy remains an ongoing challenge, prompting future inquiries to uncover overlooked synapomorphies that complement the evolutionary narratives elucidated by molecular data.

S.9.6 Modern taxonomic revisions: example of our approach in the big pantropical genus Solanum (Solanaceae)

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Agriculture has benefited from the large morphological diversity found within the large genus *Solanum* through the exploitation of tubers (potatoes) and fruits (tomatoes, eggplants, and several minor crops). We present an overview of how taxonomic work on *Solanum* has developed over the past decades, highlighting what tools and approaches have been useful at different stages and how "integrative taxonomy" has helped our work. Our main aim is to provide a classification framework for the megadiverse and agriculturally important genus to be used across research fields, including taxonomically authoritative molecular phylogenies, updated list of accepted species names and synonyms, and morphological descriptions of all species. In our view, phylogenies are important but the main core of our work is around morphology, nomenclature and field work as molecular sequence data (including full reference genomes) are being published more widely by non-taxonomists. We are passionate to expand the number of taxonomic specialists working in the genus across different parts of the world, and to provide interactive and visual identification tools that enable botanists to identify *Solanum* species with higher confidence. Our taxonomic expertise enables us to collaborate with evolutionary developmental biologists and genomics experts to understand the genetic control of distinct morphologies in the group and our understanding of evolution across *Solanum*. Core part of this work is using our database of taxonomically verified herbarium specimens from across >400 herbaria to characterise species and traits in ecological and geographical space to better understand their biology and function.

S.10 FLORAL SPECIALIZATION AND THE GENERALISED NATURE OF POLLINATION INTERACTIONS. SESSION 1

S.10.1 Flowers on an adaptive plateau: which floral traits mediate specialization in buzz-pollinated Melastomataceae?

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While the ecology and evolution of plant-pollinator interactions has often been studied through the comparison of closely-related species differing in functional pollinator groups (e.g., bees and birds), many plant lineages exhibit a single pre-dominant pollination strategy. Buzz-pollination is one such strategy, where, in the case of the plant family Melastomataceae, more than 5000 species are adapted to pollination by bees capable of producing specialized vibrations on flowers. While many buzz-pollinated flowers across angiosperms converge into a single main phenotype ('*Solanum*-type' flowers), Melastomataceae exhibit highly diverse flowers differing in color and scent profiles, corolla shapes, sizes, and the architecture and biomechanics of stamens. To date, we know comparatively little about how unbalanced patterns of flower diversity and uniformity arise across plant lineages, and how they play out in communities of co-flowering species. In this talk, we introduce patterns of macroevolutionary diversity of Melastomataceae flowers, and present new results on how flower traits may contribute to pollination niche partitioning and specialization despite substantial overlap in buzzing bee pollinators among closely-related, co-flowering Melastomataceae species. We compare trait and pollinator data across selected Melastomataceae communities from the South-Eastern USA, Ecuador and Brazil, covering a broad range of floral phenotypes and phylogenetic diversity of the group. By analyzing the links between buzz-pollination niche specialization, flower traits commonly considered important in pollinator attraction (scent, color, reward) and pollen transfer (flower-pollinator fit), we aim at better resolving the processes underlying the evolution of floral diversity within pollination strategies.

S.10.2 Pollinator shifts, floral evolution, and geographic range evolution in the genetic divergence of three Aeschynanthus species

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How do plants evolve under a geographic mosaic of pollinators? The Grant-Stebbins model predicts that local adaptation to different pollinators may drive ecological speciation. We test this hypothesis in the SE Asian genus *Aeschynanthus*, whose 160 species mostly overlap with their putative pollinators, nectar-specialist sunbirds. A conspicuous exception is *A. acuminatus*, a species widespread across mainland East Asia that also occurs in Taiwan, beyond the range of sunbirds. In Taiwan, *A. acuminatus* is exclusively pollinated by a mixed group of generalist passerines. Less is known about its pollination in mainland Asia, where both sunbirds and generalist passerines are available. In this study, we investigate the roles of pollinator shifts and range expansions in the genetic divergence of *A. acuminatus* from its closest relatives, *A. moningeriae* and *A. pedunculatus*. Pollinator observations of *A. acuminatus* across its range showed varied degrees of visitation by both sunbirds and generalist passerines on mainland Asia. In contrast, its closest relatives are both exclusively pollinated by sunbirds. Genome-wide SNP analysis revealed a mainland origin in *A. acuminatus*, preceding its range expansion to Taiwan. The sunbird specialists have independent origins: *A. moningeriae* is nested within *A. acuminatus* and *A. pedunculatus* is reciprocally monophyletic. The origin of *A. acuminatus* was thus likely on the mainland, coincident with a shift from specialized sunbird pollination to a more generalized pollination system that facilitated its colonization of Taiwan. *A. moningeriae* represents a localized reversal to sunbird specialization on Hainan. The evolutionary history of *A. acuminatus* and its closest relatives was not consistent with the classic Grant-Stebbins model. Instead, our research exemplifies how multiple transitions between generalized and specialized pollination systems can influence the genetic divergence and range dynamics, and the potential for speciation.

S.10.3 Pollination niche partitioning promotes coexistence of specialists in a Neotropical plant community

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Neotropical habitats harbor over 40% of the world's angiosperm diversity including several plant families with specialized pollination systems such as the Orchidaceae, Malpighiaceae, and the Plantaginaceae. The Malpighiaceae is considered one of the most common elements of the Neotropical Flora and is known for its specialized pollination system involving the production of floral oils (i.e., lipids) which are harvested by solitary, oil-collecting bees and used for larval provisioning or nest construction. Comprising 1,300 species, the Malpighiaceae has its center of diversity in South America, where the family is thought to have originated 65 Mya. Among South American biomes, the Brazilian Cerrado, a seasonally dry savannah-like vegetation considered one of the World's Biodiversity Hotspots for angiosperms, is especially rich in Malpighiaceae species. But how do these specialists coexist and persist successfully in sympatry if competition for pollination services and risk for hybridization (i.e., via interspecific pollen transfer) among close relatives is expected to be high? Here, we explore the niche ecology of 33 sympatric Malpighiaceae species, focusing on potential temporal, spatial, behavioral, and morphological partitioning mechanisms. Among other factors, we show the importance of temporal niche partitioning in phenology promoting the Malpighiaceae species richness that characterizes the Cerrado vegetation throughout its geographic range. We discuss the relevance of the emergent patterns observed in this system to improve our understanding of niche and community ecology in other Neotropical plant communities where specialized pollination is also widespread.

S.10.4 Chemical divergence in floral scents of two Magnolia species from the Colombian Andean region

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Floral scents serve as chemical signals to attract pollinators and thus play an essential role in the reproductive strategies of angiosperms. In Magnoliaceae, floral scents were identified as primary attractants for floral visitors. This study explores the chemical composition of floral scents in two Colombian endemics species, *Magnolia jardinensis* and *M. yarumalensis*, from the Andean cloud forests. Through scent collection by dynamic headspace methods, followed by Gas Chromatography-Mass Spectrometry (GC-MS) analysis, we identified distinct volatile compounds from flowers in their staminate and pistillate stages, in both the species. *Magnolia jardinensis* exhibited seven compounds, while *M. yarumalensis* displayed a more complex profile with sixteen compounds. Notably, five compounds were shared between the male and female floral stages of *M. yarumalensis*, reinforcing the notion of specialized pollination systems. The chemical divergence between these two *Magnolia* species aligns with previously observed differences in floral visitors and phenological patterns. *Magnolia yarumalensis* attracts beetles of the Staphylinidae family, while *M. jardinensis* attracts beetles of the *Cyclocephala* genus (Family Scarabaeidae). This work holds significance for conservation efforts. The specialized pollination systems observed in these *Magnolia* species highlight the vulnerability of these ecosystems to disruptions, underscoring the need for targeted conservation measures to safeguard the intricate relationships between *Magnolia* trees and their pollinators.

S.10.5 Sapromimesis as a pollination strategy – floral mimicry of the necrobiome

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Some flowers use false advertisements to deceptively attract pollinators. Mimetic resemblance to other organisms or their by-products can result in pollinators cognitively misclassifying the flowers, as evident by behavior such as mating attempts or egg-laying. Floral mimicry of decomposing substrates, frequently termed "oviposition-site mimicry," presents a particularly challenging study system. Current studies on flowers mimicking decomposing substrates (e.g. carrion, fermentation, dung) show intriguing patterns of convergence of floral scents, color, and texture. However, we do not yet fully understand the cues utilized by foraging and/or gravid saprophagous insects which pollinate sapromimetic flowers. Examining floral phenotype convergence in sapromimetic species may help elucidate crucial cues used by these insects. Traditional views of mimicry suggest that increased phenotypic overlap of the mimic with a specific model should increase mimic fitness. But in sapromimesis, it is frequently unclear whether the flower imitates a general set of cues used by saprophagous insects or more specialized imitation of a particular model, such as a species of fermenting fruit. I present ongoing research for two sapromimetic species – *Asimina triloba* (Annonaceae) and *Symplocarpus foetidus* (Araceae) – occurring in the same habitats of northeastern USA. Yeasty-smelling maroon flowers of *A. triloba* overlap chemically with odors of a range of fermenting environmental substrates and attract a range of fermentation-seeking Diptera. Fetid, carrion-smelling inflorescences of *S. foetidus* chemically overlap with both carrion and fermenting substrates, potentially attracting a broader range of saprophagous insects. We highlight convergent floral characteristics between these species as well as potentially important differences. We present substrate chemical data for locally-occurring potential models. Finally, we identify insect taxa attracted to flowers of both species, and to carrion and fermentation baits placed near blooming plants. This investigation helps elucidate boundaries and potential overlap between substrate properties and attracted insect communities within a close geographic area.

S.10.6 Future distribution of Iranian Salvia and its pollinators using ecological niche modeling and molecular data

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Climate change and anthropogenic drivers are widely considered as the most important threat to biodiversity. Pollinators play an important role in ecosystem regulation. Phenological mismatches between plant-pollinator interactions can threat at population or species level depend on the degree of specialization. Taken into account these adverse effect and limited time for conservation, providing maps of species distribution are required to identify where vulnerable species are at risk of decline or even extinction specially for plants depend on pollinators for reproduction. *Salvia*, the largest genus in Lamiaceae, includes approximately 1000 species in the world with around 200 species in southwestern Asia distribution. More than 80 percent of the species are characterized by special pollination system known as lever mechanism. Salvia species in southwest of Asia are melittophilous, pollinated by insects, mostly bees. (Apis mellifera, Bombus sp and Xyclocopa sp.). Iran with 72 species of *Salvia* in which 19 of them are endemic is one of the main center of Salvia diversity in southwestern Asia, we focused on Iranain *Salvia* and relevant pollinators to realize how the ongoing climate change can effect on Salvia distribution in future using ecological niche modeling. We used the current and the future models to realize whether the niche shift in plants and pollinators are at the same rate in 4 stamen type of Iranian *Salvia*. Our analysis showed that Salvia species with smaller floral size (4-9 mm) in lower latitude reduce their suitable area in future more than Salvia with larger flowers. Also, small flowers have lower niche overlap with their relevant pollinators. We integrated molecular data with ecological information in aspect of phylogenetic diversity, which shows those species in lower latitudes have higher phylogenetic diversity.

S.11 ASSESSING THE INTERPLAY BETWEEN GENETIC AND NON-GENETIC MECHANISMS CONTRIBUTING TO PHENOTYPIC VARIATION AND ADAPTATION OVER TIME

S.11.1 Cumulative reinforcement of plasticity: non-genetic transgenerational effects in stable vs. unstable environmental conditions

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Non-genetic heritable variances in phenotype, within and across populations, play a crucial role in facilitating adaptation in non-mobile organisms like plants. They regulate the expression of traits in response to shifts in the environment. In addition to within-generation plasticity (short-term modifications occurring within an individual's lifetime), plasticity can be inherited across generations, manifesting as non-genetic effects shaped by the conditions in which parental plants developed (transgenerational plasticity). The extent to which these non-genetic effects accumulate in stable environmental conditions and how rapidly they revert when conditions change remains unclear. In a three-generation experiment with wild radish, we maintained different cohorts in either consistent or varied environmental conditions, with respect to the conditions experienced by parental generations, with or without herbivory by caterpillars. Results revealed a robust plastic response marked by phenotypic adaptation, specifically an increase in plant defenses characterized by two traits—trichome abundance and glucosinolate production. As expected, conditions experienced during a plant's lifetime induce a strong plastic response within an organism's life cycle. However, our findings also demonstrate that transgenerational plasticity cumulatively reinforces lifetime plasticity, particularly for individuals whose all previous parental generations were grown in the same conditions. This cumulative effect causes phenotypes of a given genotype to diverge when exposed for several generations to either stressed or benign conditions, resulting in increased non-genetic phenotypic divergence across populations grown for several generations in different environments. Contrarily, in more unstable environments, where conditions varied across parental generations, we observed increased phenotypic differences among individuals growing in the same conditions. This suggests the presence of mechanisms supporting bet-hedging effects—enhanced trait diversity to potentially bolster population resilience. These results highlight important and previously unexplored effects with implications for ecological theories beyond species adaptation.

S.11.2 Phenotypic diversity generated by transgenerational plasticity and transposable elements enhances population functioning

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The observed positive effect of diversity on ecosystem functioning, explained by mechanisms of trait diversity, has rarely been assessed within populations. However intraspecific phenotypic variability should theoretically cause similar biodiversity effects. Intraspecific trait variation could stem both from underlying genetic diversity and non-genetic mechanisms such as plasticity in response to environmental cues. This plasticity can potentially last multiple generations and can derive, for example, from epigenetic modifications or mobilization of transposable elements. Using *Arabidopsis thaliana* as a proof-of-concept model, our work has been on unravelling the effect of phenotypic diversity generated by 1) heritable plasticity and 2) transposable elements on coexistence, population productivity, and resistance to stress, as well as on comparing their magnitude with the effect of genetic diversity. Across two glasshouse experiments, three different types of *Arabidopsis thaliana* populations were established: one type with differing levels of genetic diversity, another one with a different mixture of individuals that differed in their *ONSEN* retrotransposon insertions, and a last one, genetically uniform but with varying diversity levels of the parental environments (parents grown in the same or different environments). In all populations, we tested whether the increasing diversity increased the phenotypic diversity of populations and enhanced their functioning under different conditions. As expected, both heritable plasticity and transposable elements created differentiation in ecologically important traits connected to different axes of the plant 'economics' spectrum. Such increased phenotypic diversity ameliorated the negative effect of competition between coexisting individuals and enhanced population productivity and stress resistance; and interestingly, by a similar magnitude as genetic diversity did. Our results highlight the ecological relevance of unexplored sources of phenotypic variability because as other sources of biodiversity, they could similarly affect ecosystem and population functioning.

S.11.3 Intraspecific trait variability within and across generations: implications for coexistence and stability

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To comprehend the responses of ecosystems to global change, unraveling the dynamics of biological diversity and ecosystem function over time is imperative. A key pursuit in this context is deciphering the factors fostering coexistence and resilience to environmental shifts within communities and populations. Ecologists have debated various mechanisms modulating local biodiversity effects on ecosystem properties although effects within populations remain largely unexplored. Ecological mechanisms act initially on individuals, scaling up to communities and ecosystems, shaping and being shaped by Intraspecific Trait Variability (ITV). These variations stem from diverse sources: genetic (attributed to DNA differences) or non-genetic (e.g., epigenetic mechanisms without DNA sequence modifications). Genetic diversity is believed to empower populations to adapt to changing environmental conditions by providing a broader array of phenotypes from which the fittest can be selected. Concurrently, the ability of an organism to adjust trait expression in response to the environment (i.e., phenotypic plasticity) can be also heritable. Plasticity, in fact, does not allow only short-term responses within an individual's lifetime (within-generation plasticity) but also cause inherited differences across generations (transgenerational plasticity). The relative impact of genetic versus non-genetic heritable mechanisms, encompassing their temporal extents and responsiveness to different environmental drivers, remains largely unknown. Questions persist regarding the cumulative nature of non-genetic effects in stable environmental conditions across generations and the reversibility of induced differences when environmental conditions shift. Addressing these issues necessitates researchers to develop new approaches to evaluate how genetic diversity and non-genetic inheritance diversity intersect with population stability over time. Additionally, outlining experimental approaches to tackle these questions is crucial. This contribution seeks to synthesize ideas and perspectives aimed at understanding the interplay between genetic and non-genetic effects on short- and long-term phenotypic variation within species. It explores how these effects influence coexistence and ecological stability of growing conditions and traits.

S.11.5 Epigenetics and transgenerational plasticity in the face of climate change: a matter of reproductive mode?

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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, a phenomenon known as transgenerational plasticity. Specifically, the extent and ecological implications of this heritability are known to potentially differ between sexual and clonal reproductive modes. However, the impact of environmentally induced epigenetic changes on transgenerational plasticity across these reproductive modes remains poorly understood. Here, we assessed the adaptive potential of woodland strawberry (*Fragaria vesca*), a widely distributed herb with both clonal and sexual reproductive capabilities, in the face of projected environmental conditions expected by the end of the 21st century. These conditions included a temperature rise of 4 °C, an atmospheric CO_2 concentration twice that of the present (800 ppm), and periodic drought periods. We quantified ecologically relevant phenotypic traits and examined whole-genome DNA methylation patterns in both parental individuals and their clonal and sexual offspring. We found evidence for transgenerational plasticity induced by the parental environment, with a stronger overall effect observed in the clonal offspring compared to the sexual offspring. These results suggest that transgenerational plasticity via DNA methylation could potentially facilitate plant adaptation to future environmental conditions, particularly in clonal species.

S.11.6 Epigenetic memory of climate change associated stress in forest trees

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Memory is the acquisition, retention and transmission of information guiding future action. The imprinting of memory in plants mostly happens by altering its epigenetic signature through DNA methylation, which has been shown to contribute to both short-term phenotypic plasticity and the longer-term adaptive capacity. In our large research project MEMBRA, we are studying epigenetic changes and transgenerational memory because of climate change-associated stress in key forest tree species present. Different abiotic (i.e., drought, frost, elevated CO2) and biotic stresses (i.e., insect infestation and different diseases) have been selected based on our data showing that they alter important traits, such as growth, within UK forests. Leaf DNA from selected trees exposed to stress has been extracted and subjected to Whole Genome Bisulfite Sequencing (WGBS). A custom bioinformatic pipeline was established to call differentially methylated points (DMPs) and regions (DMRs) and to associate the differential stresses to the methylome. Our long-term aim is to integrate the capacity of tree species to develop memory into the spectrum of tree form and function and test its influence on forest resilience. Memory will be used as a plant functional trait to help select the most resilient forests and populations to be targeted as a source of seeds for afforestation programme. Therefore, MEMBRA is concerned with the implications of establishing long-term memory of stress as a key characteristic of trees that can fundamentally change climate resilience strategies. Through this multidisciplinary project working with artists, ethicists and policy experts, we are providing a paradigm shift in our understanding of the adaptation capacity of forests to the unprecedented rapid global-change-driven environmental shifts.

S.12 METAL HYPERACCUMULATORS: NEW ADVANCES ON A BOTANICAL CURIOSITY. SESSION 1

S.12.1 Trace element hyperaccumulator plant traits: a call for trait data collection

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Hyperaccumulator plants exhibit extreme ecophysiological characteristics, which make them valuable for conservation and suited for phytoremediation. Understanding their ecological strategies might help identify the species and functions to be fostered in phytoremediation, restoration, and conservation projects for metalliferous sites. Here, we identified the hyperaccumulator species in the worldwide plant trait database TRY and cross-referenced these trait syndromes associated with the ability of plants to concentrate metals. We collected three traits (leaf area (LA), specific leaf area (SLA), and leaf dry matter content (LDMC)) on all available species on TRY (n= 4523), from which 20 were identified on the global hyperaccumulator database. This allows us to link trace element hyperaccumulation with broader plant ecological strategies, such as competitive, stress-tolerant, and ruderal strategies (CSR) or resource acquisition ones. With these primary data, hyperaccumulators seem to have smaller leaves and poor competitive ability compared to non-hyperaccumulator species. Contrary to expectations, we found no indication of hyperaccumulators being more resource-conservative on the leaf economics spectrum. However, these data remain fragmentary as only 2.7% of hyperaccumulators have their traits published in the TRY database. We thus proceed to a systematic review to retrieve around 40 additional new hyperaccumulator species present on TRY and call for an international collaborative sampling effort to measure traits in more hyperaccumulator species. The recent development of trait-based models to construct plant communities providing optimal ecosystem services (*e.g.,* phytoremediation, restoration)[3] requires further research to identify predictable trait-service relationships. This research provides a first synthesis of the research advancement on hyperaccumulator traits, as well as a first synthesis analysis of their strategies at a global scale.

S.12.2 Functional syndromes of hyper-accumulating species: recent advances and perspectives

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Data bases of plant traits are now available at the global scale, and functional axes of variation among plants are well defined. Here, we present the synthesis of two recent studies revealing the position of herbaceous metallophyte species along these functional axes, with a special focus on hyper-accumulators. These studies covered the major kinds of metalliferous ecosystems either spontaneous or anthropogenic and in diverse biogeographical regions: Cu-rich environments including the "copper hills" in central Africa; Zn-Pb-Cd rich calamine substrates and Ni-Co-Cr rich serpentinic substrates in Western Europe. Shoot and root functional traits have been characterized following standardized protocols for 348 species present in 30 metalliferous communities, as well as leaf metal concentration and soil biogeochemical properties. In all cases metallophyte species exhibited small size like many species growing on other harsh substrates, some being among the shortest plants worldwide. This confirms a constant impact of metal-stress on plant stature. Additionally, an important variability regarding the leaf resource economics axis related to soil resource acquisition was found. Metallophyte communities are composed by a mix of conservative species (slow resource acquisition, long-lasting leaves) together with acquisitive species (fast resource acquisition and growth, short-lasting leaves). Remarkably, hyper-accumulating species were found among the most acquisitive species in the metalliferous communities studied. These results offer new perspectives regarding the evolution of metal-accumulation in plants. Fast-growing species maintain high soil resource acquisition on harmful substrates, leading to an important inflow of metals into their leaves. This may represent a first step towards hyper-accumulation if specific physiological adaptations are selected afterwards. Future studies should test the genericity of these results, by focusing on woody species present in some serpentinic regions. Additionally, the importance of the collaboration with mutualistic *fungi* (another functional axis related to both soil resources acquisition and plant-metal relationships) for hyper-accumulating species should be specified.

S.12.3 Addressing the diversity of the mechanisms involved in metal hyperaccumulation in plants

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The extraordinary ability to accumulate and tolerate tremendous amounts of metals such as nickel, zinc, or manganese in their leaves has been observed in about 700 plant species belonging to more than 50 families. For many years, these metal hyperaccumulator species have attracted the attention of scientists interested in understanding the evolution of this complex and peculiar trait. In the context of the decarbonization of energy, metal hyperaccumulators appear as an opportunity to develop phytotechnologies aimed at limiting the metal pollution associated with to the growing demand for metals. However, our knowledge of the molecular mechanisms involved in metal hyperaccumulation, which is key to the development of these technologies, is still very limited. To extend our knowledge of the diversity of hyperaccumulator species, we participated in a global effort to identify new hyperaccumulator species using the X-ray fluorescence technology focusing on the flora of the neotropical region. Our herbarium and field studies revealed the first example of a zinc hyperaccumulator from the Amazonas region, as well as new nickel hyperaccumulators originating from Cuba. The identification of nickel hyperaccumulators and closely related non-hyperaccumulator species from different families has opened the possibility to perform comparative cross-species transcriptomic studies to identify orthologous genes whose expression is linked to nickel hyperaccumulation. Among candidate genes, our analyses revealed that the high expression in leaves of metal transporters of the IREG/ferroportin family is a highly conserved mechanism involved in nickel hyperaccumulation across distant plant species. We are now developing the multi-metal hyperaccumulator *Noccaea caerulescens* of the Brassicaceae family as a genetic model to validate and study the role of candidate genes in metal hyperaccumulation.

S.12.4 Deciphering the physiological and biochemical mechanisms of thallium hyperaccumulation in Biscutella laevigata

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Thallium (Tl) is a relatively rare element, but highly toxic for all living organisms already at low concentrations. Some plant however evolved Tl hyperaccumulation and the most extreme Tl hyperaccumulator is *Biscutella laevigata* capable of attaining >32,000 µg Tl g^{-1} in its leaves. Interestingly, only some ecotypes have the ability to hyperaccumulate Tl when growing on Tl-rich soils. The study aims at understanding the Tl handling mechanisms, tolerance and distribution in two ecotypes of *B. laevigata* using synchrotron-based X-ray fluorescence microscopy. Two *B. laeavigata* accessions were used in this study coming from: Les Malines (France, Tl-hyperaccumulator) and Feltre (Italy, non-accumulator). Both accessions were grown in aeroponics for two months and were subjected to three Tl treatments: 0 (control), 5 and 30 µM. The two accessions showed morphological differences in terms of leaves shapes and trichome distribution, with Les Malines having deeply lobate leaves and scarce trichomes compared to Feltre with almost entire leaves and dense trichomes. Overall, Les Malines accession showed greater Tl tolerance and accumulation, compared to Feltre, which did not survive in the 30 µM Tl treatment. Feltre accession accumulated 125 µg Tl g^{-1} in old leaves (at 5 µM), whereas Les Malines accession had 1750 and 24,130 µg Tl g^{-1} in old leaves (at 5 and 30 µM respectively). The distribution of Tl was similar in the two accessions. The synchrotron µXRF analysis revealed that Tl is localised in the vacuoles of epidermal cells, especially in trichome basal cells. Thallium also occurs in solid crystalline deposits (3–5 µm in size, ~40 wt% Tl) that are mainly found in guard cells of stomata and in foliar margins. Other studies need to be carried out including more accessions, and including transcriptomics to yield information on the genes and genetic pathways linked to the phenotypic variation in Tl hyperaccumulation.

S.12.5 Synchrotron elemental imaging for elucidating nickel distribution in hyperaccumulators tropical plant species from New Caledonia

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Following the discovery of hyperaccumulation syndrome, numerous species were discovered, of which Ni-hyperaccumulators are by far the most numerous. Over 400 plant species are currently known to be nickel hyperaccumulators, and about a quarter of this diversity is found in New Caledonia. The extremely high Ni concentrations found in hyperaccumulator species raise the question of how plants can survive with such high metal content in their cells, and how does plant diversity translate into Ni-location strategy within the plant. At particular, the exact localization of metal within the leaf is of central significance because it might interfere with metabolic process such as photosynthesis. In this talk, we present our current knowledge of Ni distribution in hyperaccumulators tropical plant species from New Caledonia, based on synchrotron elemental imaging. We then make of focus on Ni-enriched laticifer in the model species *Pycnandra acuminata* to bridge the gap between the structure and function of laticifers in metal accumulation. The extraordinarily high nickel concentrations in this species function as an effective natural tracer for both synchrotron-based X-ray fluorescence microtomography and phase contrast microtomography, allowing non-destructive probing of the structure and the physiological functioning of this unique duct system. Using fresh plant samples, we combined analysis with these techniques to visualize intact laticifers in vivo for the first time and further, to provide unprecedented insights in the distribution and structure of laticifers throughout the plant, from roots to leaves. Considering that laticifers extend from root-to-shoot, our study elicits the hypothesis that the laticifers network constitute an independent ion transport system, which would establish a new paradigm in long distance transport in plants.

S.12.6 How to achieve a selenium-rich lifestyle in the barren Australian outback

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Selenium (Se) is formed in supernovae and is a rare component in most soils. Nevertheless, many organisms including *Homo sapiens* need selenium to produce selenocysteine (SeCys), also referred to as the 21st amino acid, required for synthesis of so-called selenoproteins. In contrast, land-plants lost the need for selenium, likely due to a decreased bioavailability of Se over the last couple of million years. Interestingly, some plants have developed a selenophile lifestyle regardless, growing on selenium-rich soil toxic to most plants. Some of these plants such as *Neptunia amplexicaulis* hyperaccumulate selenium up to 1.3% of their dry mass. These high tissue Se levels normally cause severe oxidative stress and dysfunctional proteins due to inadvertent incorporation of SeCys *en lieu* of cysteine. The latter is caused by the chemical similarity of selenium to sulfur, leading to the production of various organic selenium compounds through the sulfur transport- and assimilation pathway, including SeCys and Selenomethionine. However, in the dry and saline Australian outback, *Neptunia amplexicaulis* manages to grow well on toxic soil and accumulate extreme concentrations of selenium in the plant tissue. Its sister-species *Neptunia heliophile* has also developed an increased tolerance to selenium, but rather excludes Se from its tissue instead of accumulating it. Our work aims to determine what mechanisms are necessary for the extreme lifestyles of *N. amplexicaulis* and *N. heliophila* and especially how to accumulate and tolerate high tissue selenium levels. This investigation involves the analysis of recently sequenced genomes of *N. amplexicaulis* and *N. gracilis* as well as full-length transcriptomics. Furthermore, this work involves the development of transformation protocols for *N. amplexicaulis* to get direct evidence of gene involvement in Se hyperaccumulation. The research outcomes could help improve crop Se content and thereby ameliorate the currently widespread Se-deficiency in various human populations.

S.13 SYSTEMATICS, PHYLOGENETICS, BIOGEOGRAPHY AND EVOLUTION OF MELASTOMATACEAE

S.13.1 A phylogenomic analysis of Melastomataceae: congruence and incongruence across genomes

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Melastomataceae is a megadiverse family, harboring almost 6000 species and distributed worldwide, mostly in the tropics. The monophyly of the family has been supported based on morphological and anatomical data through the last century. However, the advent of molecular phylogenies has helped to clarify the identification of new major clades within the family. Additionally, molecular phylogenies have also proven a challenging task to uncover relationships among major clades when using only a few sets of plastid and nuclear regions. The use of phylogenomic datasets in the family using target sequencing and plastome data has been shown to be a promising tool for obtaining robust phylogenetic relationships within this family. However, thus far phylogenomic studies have been focused on a limited taxon sampling and presented weakly supported nodes. Here we aimed to reconstruct a phylogenetic tree for Melastomataceae comprising 21 out of 23 tribes and almost 80 percent of the generic diversity. For this we relied on a Hyb-Seq approach, joining efforts from nuclear target sequencing and plastid genome skimming datasets. We reconstructed plastid, mitochondrial, and nuclear phylogenies using concatenated and coalescent approaches. While we recover fairly robust phylogenies and tribal composition congruent with previous analyses, the relationships and support recovered at some of the deeper nodes vary across genomes and analytical methods. We discuss sources of phylogenetic conflicts between approaches and genetic compartments. We suggest that incongruences are linked to deep/ancient events of introgression/duplication/reticulate processes of evolution.

S.13.2 Pollination syndromes and pollinator shifts can be explained by climatic and elevational gradients

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Pollination syndromes are defined as suites of floral traits, which have evolved repeatedly across angiosperms in adaptation to distinct functional pollinator groups. The large, pantropically distributed family Melastomataceae is dominated by buzz-bee pollination (95.5%), where pollen is released from tubular, poricidal anthers through vibrations. In seven (of 23) tribes, shifts to other syndromes have occurred. These shifts can be found in the New- and Old-World and have been shown to be correlated with increasing altitude in the Neotropics. We recorded 44 functional floral traits across 411 species, spanning the whole family. We used machine learning algorithms (random forest – RF) to identify pollination syndromes for species with documented pollinators and employed these trained models to predict pollinators for species without observations. We combined the results from the RF analyses with climatic and distribution data (elevation) to test if climatic variables and altitudinal gradients correlate with specific pollination syndromes and certain traits. Finally, we investigated if the same mechanisms apply for the New- and Old-World. Our results indicate strong support for four well differentiated pollination syndromes within Melastomataceae: "buzz-bee", "nectar-foraging vertebrate", "food-body-foraging vertebrate", and "generalist". Pollination syndromes in Melastomataceae can be discriminated by six system specific floral traits of which reward type and pollen release mechanism are the two most important traits. Climatic variables and altitude explain 67% of the variation found in Melastomataceae, with altitude having a particularly strong impact. Shifts away from the ancestral "buzz-bee" syndromes, which can be found along the whole elevational gradient but declines towards the top of the mountain, start to appear at about 1500m (except for the "generalist" syndrome – start at about 400m and goes up to 1800m). Also, shifts to the "nectar-foraging vertebrate" and "food-body-foraging vertebrate" syndrome are associated with cooler Temperatures. These patterns can be found in the New- and Old-World.

S.13.3 Bridging evolutionary gaps: utilizing public and newly generated target capture data for the placement of some enigmatic old world

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The strategic amalgamation of public and newly generated target capture data, utilizing the universal Angiosperms353 probe set and group-specific probe sets (e.g., Melastomataceae) and Sanger data have emerged as a potent strategies in phylogenetic studies. Through this synergistic integration, our aim is to unravel the evolutionary mysteries surrounding taxa that have never been sampled or placed in a phylogenetic context, to enrich our understanding of biodiversity and the tree of life. In recent years, efforts have been made to resolve phylogenetic relationships among OW Melastomataceae taxa. However, several enigmatic taxa, including *Dionychastrum schliebenii*, *Dissotis leonensis*, *Dissotis splendens*, *Feliciadamia stenocarpa*, *Medinilla mirabilis* and *Kendrickia walkeri*, persist as unplaced and/or unsampled in current taxonomic revisions and phylogenetic studies. With recent field collections of these taxa and the utilization of public and newly generated target capture data, our goal is to phylogenetically place all the aforementioned taxa. The resulting phylogenetic placement, complemented by morphology and anatomy, provides a clearer systematic picture and enhances our understanding of the evolution of Melastomataceae at large.

S.13.4 Phylogenomics of the Merianieae (Melastomataceae) bring new perspectives for its systematics, biogeography and macroevolution

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The tribe Merianieae (Melastomataceae) is a group of trees, lianas and herbs distributed in the American tropics. It contains ca. 288 species within 7 genera. The tribe is distributed in both lowland and highland rainforests, from southern Mexico and Central America, the Greater Antilles to the Central Andes, and eastwards to the Atlantic rain forest. We present the most up-to-date phylogenetic reconstruction of the tribe based on phylogenomic sequence data, including 184 species (ca. 64%) and hundreds of nuclear loci. We used different phylogenetic reconstruction approaches including paralogy resolution steps, and secondary calibration to date the tree. Phylogenetic results are consistent with previous studies based on Sanger sequence data, but phylogenetic placement of some clades (*Adelobotrys*, *Macrocentrum*, *Salpinga*) remains problematic. Indeed, we recovered many gene tree conflicts at both deep and shallow nodes in the Merianieae phylogeny and relate them to reticulate processes of evolution, possibly linked to introgression and rapid radiations. *Macrocentrum* is not monophyletic and recovered in three clades. *Meriania* likewise is not monophyletic, because one group (*Adelbertia*) is more closely related to *Adelobotrys*, and *Axinaea* is embedded within the remaining *Meriania*. *Graffenrieda* and *Centronia* form a well-supported clade. The group seems to have originated in the Guiana Shield, but most of the diversity is in the Andes, as a result of two distinct radiations (one in *Graffenrieda* and one in *Meriania*). Secondary radiations also occurred in the Guayana Shield and the Atlantic Forest. We discuss the impact of the Andes in generating the diversity and the biogeographic history of the clade.

S.13.5 A synopsis of the genus Sonerila Roxb. (Melastomataceae: Sonerileae) in India

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Sonerila Roxb., a taxonomically complex genus in the family Melastomataceae, comprises approximately 180 taxa, and as one of the largest groups in Asia, it is distributed mainly across Sri Lanka, India, Nepal, Bhutan, South China, Taiwan, Indo-China and the Malay Archipelago. The genus is represented by caulescent and acaulescent herbaceous plants of shady habitats. It is easily recognized by its generally trimerous flowers, mostly uniparous (scorpioid) cymes, and 3-locular, inferior ovary. *Sonerila* is the largest genus in the tribe Sonerileae in India, with 49 species and one variety, including a substantial percentage of endemics. The Western Ghats region indeed stands out as a hotspot for *Sonerila* with 43 species and one variety, an astonishing 86% of which are exclusive to this particular biogeographic zone. This remarkable richness of species serves as a clear indication of adaptive radiation and explosive evolution within the genus making it an intriguing subject of study in the realm of Melastomataceae systematics and evolution. The present study highlights the diversity of *Sonerila* in India with a revisionary account including key for the identification, detailed descriptions, notes on infraspecific variations, geographical distribution, and conservation status assessment. Six species were found new to science. Nomenclatural issues relevant to the taxonomic study were also resolved, resulting in subsequent synonymy, reinstatement of names, and typifications.

S.13.6 Neotropical depauperons: from neglected small genera to strategically placed clades in Melastomataceae phylogenetic trees

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Asymmetric patterns in species richness are a notable feature across different lineages and geographic regions. While some lineages are rich, diverse, and widely distributed, the "depauperons" are phylogenetically isolated, with only one or a few narrowly distributed species. Recent phylogenetic studies of Melastomataceae resulted in a new classification with both megadiverse lineages, such as tribes Miconieae (1900 species), Sonerileae (1100) and Melastomateae (820) and groups with few species, such as Lithobieae (1), Rupestreeae (2), Stanmarkieae (4), and Eriocnemeae (7) in the Neotropics, and Dinophoreae (8) and Feliciadameae (1) in Africa. These depauperon tribes have been very recently described, with their taxa traditionally placed in bigger tribes, even though they presented features uncommon for those groups or even the whole family. Three of these groups are restricted to Eastern South America: Lithobieae grows on rock crevices, and is sister to Pantropical Henrietteae+Astronieae (250 spp); Rupestreae grows in "campos rupestres", and is nested in Pantropical Melastomataeae+Dinophoreae+Rhexieae (850); Eriocnemeae's 3 genera grow in rainforest, iron ore outcrops, and montane vegetation, and are sister to Neotropical Miconieae (1900). The recognition and inclusion of these depauperons in phylogenetic analyses is critical to the study of biogeography, character evolution and ecology of their speciose sister groups. The different patterns found for depauperons and their relatives may be explained by different speciation/extinction rates, but also by other traits. Overall, the species in these groups have limited dispersal ability, dependency on water for dispersal, and restricted niches. Climatic niche spaces of the depauperons are limited but included within the niche space of the sister tribes. The threat level for them can be exacerbated by climate change, mainly due to their inability to spread over long distances, restricted niches and increased habitat fragmentation. Future conservational actions should prioritize these unique taxa in Melastomataceae, especially under a phylogenetic diversity perspective.

S.14 A CONTINENTAL SCALE CONSORTIUM APPROACH TO BUILDING GENOMICS CAPACITY AND RESOURCES: GENOMICS FOR AUSTRALIAN PLANTS. SESSION 1

S.14.1 A consortium approach to building the Australian Angiosperm Tree of Life.

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The Genomics for Australian Plants (GAP) Initiative, catalysed by Bioplatforms Australia in partnership with researchers from the Australian State and National Herbaria and Botanic Gardens, aims to develop genomics resources to enhance our understanding of the evolution of the Australian flora and support its conservation. GAP Phylogenomics, one of three GAP projects, has the long-term goal of resolving the Australian Angiosperm (flowering plant) Tree of Life (AAToL) to species level. To date, this inclusive project has brought together over 70 Australian researchers and herbarium staff and partnered with the global Plant and Fungal Trees of Life project (PAFTOL) to complete AAToL Stage 1 – a phylogenetic tree including at least one species exemplar of nearly 95% of Australian native angiosperm genera sequenced for a common set of hundreds of nuclear markers (using the Angiosperms353 target capture baits). From the outset, data quality and reusability have been a priority, ensured through mandating rigorous documentation of comprehensive sample metadata (e.g. identity, voucher, Nagoya compliance, etc.). We show, through discussion of its successes and challenges, the value of a multi-institutional consortium approach and the enablers such as well-curated collections and national collaborative research infrastructure, leading to substantial increase in capacity and delivery of biodiversity knowledge outcomes. Future directions for the AAToL project will be discussed.

S.14.2 Cross-platform and containerised phylogenomics-bioinformatics pipelines for sequence capture data: hybpiper-nf and paragone-nf

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The phylogenomics activity of the Genomics for Australian Plants consortium uses target capture / enrichment data. Early in the process, a phylogenomics-bioinformatics working group was established to evaluate options for the consortium's technical approach ranging from the desired sequencing depth across assembly to the phylogenetic analysis itself. In terms of the analysis pipeline, paralogy was identified as a key concern because phylogenetic analyses were going to be conducted both at the scale of all angiosperms and in selected genera and plant families known to be characterised by ancestral genome duplication events. We adapted the well-established HybPiper software for sequence assembly and paralog discovery, and a collection of previously published scripts for the inference of ortholog groups from gene tree topologies. We iteratively built an integrated workflow in which the HybPiper outputs were provided in a format directly usable for ortholog inference, discovered and fixed bugs, and added alternative options for several steps such as assembly, alignments, and gene tree inference. The resulting pipelines have been published as two Nextflow scripts with a Singularity container providing all dependencies to allow easy installation independent of platform, hybpiper-nf and paragone-nf, and recently also as Python packages that can be installed with conda. We discuss the history of their development, the principles behind the analyses, and important options available to the user.

S.14.3 Phylogenomics, continental biogeography and climate-dependent diversification of Australian Chamelaucieae (Myrtaceae)

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The Myrtaceae tribe Chamelaucieae is a diverse tribe predominantly distributed across Australia with over 660 species across 34 genera. The phylogenetic backbone of this tribe was previously unresolved based on studies utilising Sanger sequencing data. Here, we present an updated well-resolved phylogeny of the tribe as part of the GAP Stage 2 initiative, utilising over 400 nuclear single-copy loci (angio353 and Ozbaits). Ten out of the 11 subtribes with 33 out of the 34 genera are represented in our study. We dated the phylogeny using secondary calibrations and looked at biogeographic disjunctions across different Australian biogeographic regions using BioGeoBEARS. We also tested for environmental-dependent diversification using RPANDA. Findings from our biogeographic analyses indicate a mixture of vicariance and dispersal events across different simulated climatic scenarios (e.g., aridification of Australia since the Miocene). Biogeographic results and speciation decline detected from our phylogeny coinciding with the Eocene–Oligocene extinction event (33 Mya) will also be discussed.

S.14.4 Acacia phylogenomics using the Angiosperms353 target capture bait set

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Acacia – Australia's largest genus of flowering plants – was selected for a Genomics for Australian Plants (GAP)-supported phylogenomic analysis using the Angiosperms353 target capture bait set. While Sanger amplicon sequencing datasets have previously been compiled for approximately 50% of Acacia species, those datasets comprised fewer than 10 markers and lacked phylogenetic resolution in certain parts of the tree, demonstrating the need for a deeper phylogenomic-based sampling of the Acacia genome in order to resolve the phylogeny with greater support. In this talk, results are presented of an initial phylogenomic analysis of around 10% of the total number of Australian Acacia species, sequenced for the Angiosperms353 target capture baits and representing all major evolutionary lineages of Acacia that had previously been discovered in molecular phylogenies and morphological classifications. Initial phylogenetic analyses, including appropriate mimosoid legume outgroups and using several analytical approaches, have revealed congruence in the major clades that were previously discovered, such as the Pulchelloidea clade, which unites morphologically disparate taxa from several traditional sections in Acacia. When compared to the topologies found in previous molecular phylogenetic studies, the overall phylogenomics-based topology is somewhat different, which may be due to increased phylogenetic resolution of the markers or differences in the targeted sampling of species in particular parts of the tree. Some novel clades, including a sister clade to the majority of Acacia species, are recovered in our analyses. Due to the level of support for relationships, in combination with the very high success rates for sequencing of silica-dried and older herbarium samples, the Angiosperms353 bait set shows great potential as the basis for a larger-scale study of Acacia species, with the ultimate aim of generating a new formal classification of the genus.

S.14.5 Using sequence capture to look beyond floral symplesiomorphies and classify two new genera in the Australian Rutaceae (Sapindales)

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Taxonomists have relied heavily on floral characters to group taxa and assess relationships, despite the adaptive significance of these characters and their correlation with pollination modes. Even if the taxonomist, wary of misinterpreting homology, chooses to account for the instability of floral characters, there may not be sufficient morphological characters outside of these to make useful inferences. This is especially problematic in groups with numerous instances of separate floral specialisation, where interpreting which characters are symplesiomorphic is difficult. The *Eriostemon* group (Sapindales: Rutaceae) includes 16 genera and ~209 species that almost all occur naturally in Australia (with ~12 spp. in 3 genera outside of Australia). The group is most diverse in the south-east and south-west of Australia where species most commonly occur in eucalypt-dominated woodlands and forests, but are also found in rainforests, savanna, coastal and montane heathlands, semi-arid scrub and desert shrubland. Morphologically, members of the group vary in habit, leaf phyllotaxy, fruit type and, most notably, floral characters. Pollination syndromes vary between and within genera, with a predominant contrast between flowers that are borne upright with spreading, open petals and flowers that are pendent and tubular or aggregated into inflorescences surrounded by large or colourful bracts. This diversity has resulted in taxonomic legacy of large genera with unspecialised, open petalled flowers, and small or monotypic genera with more complex flowers. We present results from a phylogenomic study of the *Eriostemon* group based on target capture sequencing using the Angiosperms353 kit. Our results reveal the extent to which the genus *Philotheca* (54 spp.) is polyphyletic and highlight how the current classification of that genus is based on symplesiomorphic floral characters. They provide new insight into shifts in pollination modes across the group and support the recognition of two new genera, separated from *Philotheca*.

S.15 EVOLUTIONARY ECOLOGY OF PLANTS. SESSION 1

S.15.1 Pre-dispersal seed predation as a selective force on plant mating system and reproductive traits

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Not only mutualistic plant–pollinator interactions but also antagonistic plant–herbivore interactions can be a selective force on sex allocation in angiosperms. The present talk addresses how predispersal seed predation affects the reproductive success and floral gender of andromonoecious herbs on a natural snowmelt gradient. The developing fruits of an alpine herb (*Peucedanum multivittatum*: Apiaceae) were intensively predated by a specialist lepidopteran larvae (*Phaulernis fulviguttella*: Epermeniidae) in the early-snowmelt habitat, where flowering occurred from mid to late July. In the late-snowmelt habitat, where flowering occurred after early August, seed predation was negligible because the oviposition of the predator moths was concentrated in early summer. The moths tended to oviposit on umbels with more perfect flowers and taller stems, whereas the number of male flowers was independent of their oviposition preference. Plants having male-biased umbels and short floral stems were prevalent in the early-flowering population, where plants suffered from intensive predation damage. The proportion of perfect flowers increased in the later flowering populations. The contribution of perfect flowers to intact fruit production was small when flowering occurred early in the season, and it consistently increased with the lateness of flowering period along the snowmelt gradient. Fitness measurements in the early-flowering population revealed that the production of many perfect flowers resulted in lower female fitness due to intensive seed predation. In contrast, male fitness as a pollen donor increased with total flower production irrespective of the composition of perfect and male flowers. Taken together, the greater production of male flowers at the expense of perfect flowers is advantageous under intensive predation pressure owing to the mitigation of predation damage with keeping the siring success. These results revealed that predispersal seed predation acts as a selective force that promotes male-biased sex allocation in andromonoecious plants.

S.15.2 Constraints on the evolution of floral lifespan in a mixed-mating biennial

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Angiosperms display a brilliant diversity of floral forms, with striking variation in color, size, and scent, and morphology, including elaborate or specialized structures offering protection or rewards. Floral longevity, the length of time a flower remains open and functional, shows similarly impressive variation across species, ranging from a day or less to over a month, but by comparison has been largely overlooked. Consequently, even though floral longevity should strongly influence fitness by setting a critical time limit on opportunities for each flower to export and receive pollen, we lack a firm understanding of the forces that shape, maintain, and constrain variation in floral longevity. In fact, we even lack basic studies on the heritability of this trait in wild species. *Sabatia angularis* (Gentianaceae) is a mixed-mating biennial with remarkable intraspecific variation in maximum floral longevity, ranging from plants that produce flowers lasting only 5 days to those with flowers that can last over 20 days within a single population. I present data from a combination of field and greenhouse studies that characterize factors maintaining or constraining this variation, highlighting the importance of heritability, trade-offs, functional and ecological constraints, and plasticity.

S.15.3 The conflict between ant protection and buzz-pollination mutualisms across angiosperm evolution

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Mutualistic interactions involve varying degrees of conflicts, including the interference between different types of mutualism. One common interference occurs between protective ants and pollinators in plants bearing extrafloral nectaries (EFNs). While patrolling the plant, ants can reduce herbivory but also repel pollinators, especially bees. Since this conflict can affect plant reproductive performance, it might be selectively disadvantageous for plants to have both traits associated with ant defense and specialized bee pollination. Although conflicts in mutualisms have been extensively studied on the ecological scale, the evolutionary consequences of traits mediating interactions have not been considered. We hypothesize that there is a negative evolutionary correlation between traits mediating plant protection by ants and exclusive pollination by bees as in buzz pollinated plants. For that, we used a phylogenetic comparative approach, mapping all angiosperms reported to bear EFN associated with ant attendance and poricidal anthers associated with buzz pollination in an angiosperm tree comprising ca. 8,000 genera. We found that EFNs occur in 755 genera while poricidal anthers occurs in 544. However, only 45 plant genera have both traits. Moreover, we found a negative evolutionary correlation between EFNs and poricidal anthers, supporting our hypothesis that the interference of one mutualism in another can affect the evolutionary trajectory of the traits driving these interactions. This result means plants protected by ants are less likely to be involved in buzz pollination, or vice-versa, throughout angiosperm diversification. Altogether, our results evidenced that protective and pollination mutualisms may exert a reciprocal selective force that reduces the likelihood of the simultaneous occurrence of both ants and bee partners across angiosperm evolution. This emphasizes that we studies focused on the evolution of mutualistic traits should consider the joint effect of simultaneous mutualistic interactions instead of evaluating the traits related to different mutualisms separately.

S.15.4 Convergence in carnivorous pitcher plants reveals a mechanism for composite trait evolution

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Complex, composite traits involve multiple components that, only when combined, gain a new synergistic function. Thus, how they evolve remains a puzzle -- what Darwin referred to as a 'special diffulty' in the Origin of Species. I present the results of multi-disciplinary study (Chomicki et al., 2024) that combined field experiments in the field and in the lab, microscopy, chemical analyses and laser Doppler vibrometry with comparative phylogenetic analyses to show that two carnivorous *Nepenthes* pitcher plant species independently evolved similar adaptations in three distinct traits to acquire a new, composite trapping mechanism. Phylogenetic comparative analyses suggest that this new trait arose convergently via 'spontaneous coincidence' of the required trait combination, rather than directional selection in the component traits. Our results indicate a new mechanism for composite trait evolution and highlight the importance of stochastic phenotypic variation as a facilitator of evolutionary novelty. References: G Chomicki, G Burin, L Busta, J Gozdzik, R Jetter, B Mortimer, U Bauer (2024) Convergence in carnivorous pitcher plants reveals a mechanism for composite trait evolution. *Science* (In press).

S.15.5 Lower mate availability and leakier self-incompatibility in Argentina anserina populations with small effective population size

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Achieving reproductive success in self-incompatible (SI) populations can be difficult. Flowers must receive enough pollen to produce seeds, and that pollen must be genetically compatible. The lack of available mates can reduce population-level reproductive fitness, have negative impacts on population growth, and increase extinction risk. The effects of low mate availability are exacerbated in small populations, which often harbor fewer S-alleles. So, even with substantial pollination, reproduction may fail. The breakdown of SI systems, however, may rescue population declines. Evaluating mate availability across populations can help us to understand the factors and conditions leading to mate limitation. We tested the predictions that populations with small effective population size have reduced mate availability and exhibit signatures of a breakdown in their SI mechanism. Additionally, we evaluated mechanisms at the pollen-pistil interface that contribute to the failure of outcrossed flowers and success of self-pollinated flowers. We performed self and outcross pollinations in 13 populations of *Argentina anserina* with known genomic estimates of effective population size to estimate mate availability and the SI index, and used fluorescence microscopy to enumerate pollen deposition, germination, and tube extension. Results show that genetically depauperate populations have reduced mate availability but not a lower SI index. Unsuccessful outcrosses did not receive fewer pollen grains or have lower pollen germination than successful ones. Barriers to outcross fertilization occurred in the style, specifically pollen tubes were arrested at the S-allele recognition site. Pistils from self-crosses showed that a higher proportion of self-pollen grains extend tubes past the location of the SI mechanism in the style in effectively smaller populations. However, this does not necessarily result in seed production. Results highlight strong mate limitation in genetically small populations of *A. anserina* and suggest that leaky-SI in small populations may represent early stages of a breakdown in SI.

S.15.6 Fire-stimulated flowering: the effect of fire on pollination success in Mediterranean geophytes

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Fire-stimulated flowering is a widely recognized strategy in fire-prone ecosystems, such as Mediterranean ecosystems. Species with this strategy flower more profusely in postfire conditions than in absence of fire. We hypothesize that higher flowering density and less competition for pollinators could improve pollination success of plants that flower quickly after fire. We studied geophytes in Southern Spain and compared flowering in recently-burned areas with flowering in adjacent unburned areas. We performed pollinator censuses, estimated pollen grain deposition on the stigmas and counted fruit and seed production. We found that pollination rates and pollinator composition changed in burned areas compared to unburned areas. Individuals in burned areas showed higher pollen deposition on their stigmas and fruit and seed production was also higher in burned areas.

S.16 BOTANICAL CONTRIBUTIONS FROM THE BIODIVERSITY HERITAGE LIBRARY

S.16.1 Data for botany: unlocking the world of plants in the Biodiversity Heritage Library

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The Biodiversity Heritage Library (BHL) is the world's largest open access digital library for biodiversity literature and archives. Headquartered at Smithsonian Libraries and Archives (SLA), BHL is a global consortium of research institutions working together to build and maintain a critical piece of biodiversity data infrastructure. Created in 2006 as a direct response to the needs of the taxonomic community for access to early literature, BHL provides free access to over 61 million pages of biodiversity content from the 15th-21st centuries. BHL provides a global community with ready access to a vast body of botanical literature. BHL works with the biodiversity community to develop tools and services to facilitate greater access, interoperability, and reuse of content and data. Through taxonomic intelligence tools developed by Global Names Architecture, BHL has indexed more than 230 million instances of taxonomic names throughout its collection, allowing researchers to locate publications about specific taxa. BHL also works to bring historical literature into the modern network of scholarly research by retroactively assigning DOIs (digital object identifiers) and making this historical content more discoverable and trackable. Biodiversity databases such as the Catalogue of Life, International Plant Names Index, Tropicos, World Register of Marine Species, iNaturalist, and more rely on literature housed in BHL. To make this data FAIR (findable, accessible, interoperable, and reusable), BHL and its partners are working on a data pipeline to transform textual content into actionable data that can be deposited into data aggregators such as the Global Biodiversity Information Facility (GBIF). This paper provides an overview of BHL's botanical content.

S.16.2 BHL Australia: unlocking the foundation of Australia's botanical knowledge

Nicole Kearney [1]

1 Biodiversity Heritage Library, Australia

The Australian node of the Biodiversity Heritage Library (BHL) began operation in 2010 with just one organisation, Museums Victoria. Since then, it has grown considerably. BHL Australia is now a national consortium with over 50 organisations contributing content to BHL. These organisations include all of Australia's state museums and herbaria, as well as universities, government agencies, royal societies, field naturalist clubs and natural history publishers. Together these organisations have made over 550,000 pages of Australia's biodiversity heritage freely accessible online. This paper focuses on the botanic knowledge contained within the BHL Australia collection, showcasing highlights from the 1600s through to the current year. It also celebrate the close relationship between BHL and the Australian botanical community. BHL Australia's active digitisation operation prioritises requests, which are received regularly from researchers, librarians, artists, educators, and policy makers. These have resulted in the rapid digitisation of historic literature essential to botanists, such as those studying the impact of Australia's devastating 2020 bushfires on endangered species. Finally, this paper presents BHL Australia's leading role in BHL's global efforts to bring the historic literature into the modern linked network of scholarly research. At the onset of the COVID-19 pandemic, BHL Australia pivoted from digitising historic literature to generating historic article data, mobilising both volunteers and staff to make the contents of our historic journals searchable. Since then, we've worked closely with the publishers of botanical journals (in Australia and around the world) to assign DOIs (Digital Object Identifiers) to their back issues. Many have elected to have BHL assign DOIs to their current issues as well. These DOIs are now appearing seamlessly in new publications, taxonomic databases, social media, and Wikipedia, providing instant, permanent, and persistent open access to the primary literature, the foundation of our knowledge of biodiversity.

S.16.3 Amplifying the contribution of women to botany: an analysis of plant genera that were named after women

Carmen Ulloa Ulloa[1], Sabine von Mering[2], Lauren Gardiner[3], Sandra Knapp[4], Heather Lindon[5], Siobhan Leachman[6], Sarah Vincent[4], Maria S. Vorontsova[5]

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There are several thousand flowering plant genera named for people of all sorts, but those named for men outnumber -by more than 10 to 1- those named for women. In mid-2021, a discussion on social media led to the formation of the multidisciplinary international working group to answer a simple question: how many plant genera honor women? More than two years of mostly virtual interaction, and additional research questions, resulted in the compilation of a new open dataset of 728 flowering plant genera honoring women or female beings (mythological). Some 36% honor mythological beings, and Medusa had six genera named after her, more than any real woman! We verified all these genera by examining original literature (the majority of which are freely available on the Biodiversity Heritage Library), and have categorized the honorees by profession, status or relationship to the describer. As part of the project, we created or updated Wikidata items for each of these women and genera; we worked closely with IPNI, Tropicos® and BHL receiving and providing feedback and data. Our motivation for the development of this dataset was not only to highlight names of plant genera that honor women, but also to enrich and bridge this information with data that would allow the names, roles, and lives of these women – many with fascinating stories –, to be shared more widely with others, both researchers and data sources like Wikidata. Amplification of the contributions of women to botany through multiple means will enable the community to better recognize and celebrate the role of this particular marginalized group in the history and development of science, their contributions to art, and natural history collections.

S.16.4 Right on Kew: BHL at the Royal Botanic Gardens

David Iggulden[1]

1 Royal Botanic Gardens, Kew, London, UK

17 years on from its official formation, the Biodiversity Heritage Library's role continues to evolve, further increasing its relevance and demonstrating the collaborative resiliency of the consortium overall. BHL's global partnership of natural history, botanical and national libraries work together to develop the library and digitise their collections and make them freely available in BHL. As of November 2023, BHL has a total of 42 partners consisting of 19 Members and 23 Affiliates. As a Founder Member of the original project, the Royal Botanic Gardens, Kew has been a key member from the outset and is well placed to support the next stages of the resource's development. Kew's involvement with BHL provides an interesting case study overall, which illustrates how the BHL directly supports botanical research both within the organisation and across the globe. BHL provides an invaluable resource for work on plant nomenclature at Kew and has been a key partner in recent projects within both the Library and Archives and Economic Botany collections. BHL data is also being used to support the development of open science tools for taxonomy. It is for these reasons, plus the ongoing use by taxonomists that Kew continues to view BHL as essential to its mission to understand and protect plants and fungi for the well-being of people and the future of all life on earth.

S.16.6 Matching herbarium specimens with Mary Vaux Walcott watercolor paintings using machine learning and detective work

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Mary Vaux Walcott's five-volume collection of illustrations and descriptions, "North American wildflowers", was published between the years 1925 and 1929. All of the volumes, which include over 400 watercolor prints, have been fully digitized and made available through the Biodiversity Heritage Library (https://doi.org/10.5962/bhl.title.67774). Many of the illustrations were based on plant specimens collected by Walcott herself or other botanists from the Smithsonian Institution, and specimen labels on their preserved herbaria sheets include written notations that reference this connection. One example is US:1087120 (http://n2t.net/ark:/65665/3fd0d532a-72a3-4818-9dbe-904d72272759), which has a notation that it was "Painted by Mrs. Walcott", and closely matches Plate 44 of Volume 1 (https://www.biodiversitylibrary.org/page/42602857). In this project, we used digitized specimen data to explore candidate matching specimens, machine learning OCR and LLM validation tools from the VoucherVision project (https://github.com/Gene-Weaver/VoucherVision) to transcribe and clean specimen labels, and computer vision tools from LeafMachine2 (https://github.com/Gene-Weaver/LeafMachine2) to isolate morphological and phenotypic traits for comparison. With confident pairs of illustrations and specimens, we investigate the possibility of using the Biodiversity Heritage Library's extensive collection of botanical illustrations to extract valuable phenotypic and morphological data.

S.17 ACROSS LAND AND WATER: UNDERSTANDING PLANT GENE FLOW AT A LANDSCAPE SCALE. SESSION 1

S.17.1 Landscape effects on the spatial distribution of genetic lineages in a widespread, generalist herb

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The majority of landscape genetic studies to this day has focused on animals, often mammals of high conservation interest. The studies conducted in plants have found a significant to no effect of landscape features on the genetic structuring of the respective species. Previously, no differentiation was found between populations of the generalist, widespread herb *Veronica chamaedrys* (Plantaginaceae) growing in grasslands under different management regimes. We suspect however that grassland management changes on too short timescales to affect the species and that factors inhibiting or facilitating gene flow may reveal themselves at larger geographic scales. We sampled populations along a 500 km transect from the German North Sea coast to the central German xeric zone at the lee of the Harz mountains. At each location we characterized the surrounding vegetation via Ellenberg values. Moisture and soil reaction numbers showed the strongest geographic trends with the steepest change occurring at the southern margin of the Harz mountains. We expect these marked changes to be recognizable in genotyping-by-sequencing data. The species turned out to be much rarer in the north German plain than anticipated. This could be either due to a historical lack of suitable habitat as the region used to be characterized by extensive wetlands or due to a recent extinction of populations as a result of agricultural intensification. Yet, semi-natural and natural habitats were sampled preferentially. Should populations north of the central uplands prove not to show signs of isolation, it could indicate a buffering function of gardens and public green spaces as *V. chamaedrys* can be frequently found in parks and mature lawns.

S.17.2 Systematics and long-distance dispersal of family Urticaceae

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Urticaceae consists of approximately 54 genera with more than 2000 species and is widely distributed in tropical regions but less common in temperate regions, with by far the largest concentration of genera and species in tropical Asia. This family has important economic and medicinal value, a full understanding of relationships within this family would help to understand how these ecological assemblages evolved, and also to detect potential new sources of medicinal compounds. However, the infra-familial classification of Urticaceae has been controversial for more than one century, and relationships within it remain poorly known. In this talk, I introduce some of my studies on the systematics of Urticaceae in the last 10 years based on different molecular markers and research methods. In addition, I present an in-depth study of the biogeography of Urticaceae Integrated multiple lines of evidence including phylogenetic, molecular-dating, biogeographical, ecological, seed biology and oceanographic data, we found that Urticaceae originated in Eurasia ~69 Ma, followed by ≥92 LDD events between landmasses. Under experimental conditions, it was demonstrated that seeds of many Urticaceae floated for >220 days, and remained viable after ten months in seawater, long enough for most detected LDD events, according to oceanographic current modeling. Ecological trait analyses indicated that preferences for disturbed habitats might facilitate LDD. Nearly half of all LDD events involved dioecious taxa, so population establishment in dioecious Urticaceae requires multiple seeds, or for occasional selfing to be possible. This work clearly shows that seawater LDD played an important role in shaping the geographic distributions of Urticaceae, providing empirical evidence for Darwin's transoceanic dispersal hypothesis.

S.17.3 Tropical Montane Cloud Forest at risk: the importance of unprotected forest areas for tree genetic diversity and connectvity

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Magnolias are representative tree species of the Tropical Montane Cloud Forest (TMCF) in Mexico, which is one of the most endangered ecosystems due to anthropogenic habitat degradation and climate change. *Magnolia schiedeana* is a vulnerable and restricted endemic TMCF species, occurring in forest fragments in the Sierra Madre Oriental. We sampled remnant populations across the species range to investigate spatial patterns of genetic diversity and gene flow by genotyping polymorphic microsatellite loci. Our data showed a strong spatial structure, which matches the patchy geographic distribution of *M. schiedeana*. Contemporary migration rates between these genetic clusters are very low. Levels of genetic diversity were low in small populations relative to large populations, and no evidence of inbreeding was found. Landscape genetic analysis revealed that geographic isolation was the main factor shaping genetic differentiation, not slope or environmental variation. Urgent conservation actions are needed as most of the cloud forests in which large and genetically diverse *M. schiedeana* populations persist are not under federal protection, and which currently experience selective logging. Restoring landscape connectivity should be a priority to reduce risks of inbreeding and genetic drift as populations become smaller and geographically isolated.

S.17.4 Genetic diversity of grassland plants at adaptive and neutral loci - two actors on the stage of landscape change

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Over the past century, changes in land use have significantly reduced the extent of semi-natural grasslands, threatening the functional connectivity, i.e., exchange of genes through pollen and seed dispersal, among populations of plants characteristic of these valuable habitats. Although growing evidence suggests that landscape features can influence gene flow among isolated plant populations, the role of historical land use legacies in shaping the relationship between current landscape characteristics and gene flow in perennial grassland plants remains unclear. Notably, studies often focus solely on genetic diversity at neutral loci (not under natural selection), overlooking genetic diversity at adaptive loci (under natural selection) crucial for plant adaptability to changing conditions. We studied the impact of landscape characteristics on the functional connectivity of 32 populations of the grassland plant *Primula veris* in two historically semi-natural grassland-dominated landscapes in Western Estonia. Nowadays, one landscape remains grassland-dominated, while forests and agricultural fields prevail in the other. We examined genetic diversity at both neutral and adaptive loci and structure of these populations. We also assessed the role of landscape characteristics on gene flow at neutral loci. The relative permeability of different landscape elements for gene exchange depended on landscape context, likely reflecting opposite land use trajectories in these landscapes. Furthermore, the outcome was also affected by different gene flow indices, indicating their context-dependency. Notably, genetic diversity at neutral and adaptive loci showed different results to landscape context. Conclusively, applying connectivity measures based on findings from a landscape setting reflecting only one type of land use trajectory should be avoided. Interpretation of gene flow measures for long-lived plant species should also be approached with caution due to potential delays in their response to landscape changes. Lastly, the correlation between genetic diversity at neutral and adaptive loci is not consistent, warning against using one to estimate the other.

S.17.5 Applying genomics and metabolomics to elucidate evolution in the homoploid complex of Baccharis L. in Chile

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The genus *Baccharis* L. (Asteraceae-Astereae) in Chile is supposed to form a homoploid complex containing about 21 taxa and 33 described hybrids based on morphological and ecological evidence. In this study, we investigated evolutionary processes within this complex using genomic and metabolomic approaches with *Baccharis linearis* (Ruiz et Pavón) Pers., *B. macraei* Hook. et Arn., *B. vernalis* F.H. Hellwig and their putative hybrid *B.* x *intermedia* DC. in Central Chile. The sampling covered selected populations ranging from La Serena in the north to Concepción in the south. Next generation sequencing (ddRad/Illumina) and untargeted metabolomics (LC-qTOF) was performed using silicagel-dried material. The initial hypothesis on the hybrid nature of *B. intermedia* was corroborated by genomic and chemical evidence. Within the morphologically intermediate hybrid, a combination of genetic markers from both parents could be detected. The hybrid shows a significantly higher heterozygosity than both parental taxa. Moreover, metabolomics analyses revealed that *B. intermedia* has a mixed chemotype and combines the chemistry of the parental species. Both parents exhibit a north-south genetic differentiation that goes in parallel with their chemistry. This pattern is also found in the hybrid pointing to its polytopic origin. There is evidence for gene flow between the hybrid and the parental species, albeit at a low level, allowing independent evolution of the hybrid taxon. Time and history of the taxa involved are discussed in the light of ecology vegetation history.

S.17.6 Employing landscape genetics to forecast climate-driven habitat changes for high-mountain plant endemics in the Canary Islands

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Climate change poses a significant threat to endemic and native flora, particularly those inhabiting upper vegetation zones. While the impact of climate change on continental alpine ecosystems has been extensively studied, little progress has been made in understanding high mountain ocean ecosystems. Using a combination of species distribution models and landscape genetic methods, our study focuses on species inhabiting high mountain ecosystems in the Canary Islands. In this context, we aim to 1) characterize genetically different populations, 2) estimate interpopulation gene flow and functional connectivity, 3) determine the current and forecasting future habitat suitability, and, finally, 4) assess the impact of climate change on these plant species. Like alpine regions, we expect that species within the upper vegetation zones of the Canary Islands are vulnerable to population declines due to climate change, especially those with restricted distribution and short-distance dispersal, such as the Teide violet. Ultimately, our research aims to develop enhanced conservation strategies for the endemic and native flora of the Canary Islands.

S.18 INVENTORYING THE PLANT DIVERSITY OF THE EURO-MEDITERRANEAN AREA: INTEGRATING TAXONOMIC PROGRESS INTO DYNAMIC WEB CHECKLISTS AND ELECTRONIC FLORAS

S.18.1 How to classify apomictic polyploid complexes - challenges and perspectives

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Apomixis, the reproduction via asexually formed seeds, avoids cycles of meiosis and fertilization. Apomictic lineages appear scattered in the phylogenies of plants, and often comprise widespread and abundant taxa, which makes them highly relevant for biodiversity research. Apomixis poses a problem for species concepts and delimitation, because the popular biological species concept is per definition not applicable. Alternative species concepts, like the phylogenetic species concepts, cluster species concepts, evolutionary and ecological species concepts are theoretically applicable, but pose in theory and practice still many problems. A major conceptual problem is the predominant hybrid origin of many apomictic plants, which violates assumptions of tree-like diversification patterns, but also blur boundaries between clusters and lineages in the other classical concepts. Genetic clustering and vertical lineage formation remain weak without the homogenizing effects of sexuality. Pluralistic approaches for species delimitation are nowadays preferred for taxonomic decisions, i.e., case-by-case applications of concepts based on combinations and multiple datasets. Apomictic lineages might be included under one species name, as it often applied to autopolyploids. In allopolyploid complexes the sexual progenitors can be normally classified on species level, but the vast majority of ill-defined asexual lineages could be lumped under a cluster concept or named just as nothotaxa. The formal designation of hybrids is possible according to the Code if at least one parental taxon is known, which applies to most young apomictic complexes. This strategy would avoid swamping databases, floras and checklists with hundreds of species names for ill-defined taxa. Only few obligate long-term apomictic lineages exist in plants, without knowledge of progenitors. Such cases may deserve a classification as species (agamospecies). Application of genomic data and artificial intelligence tools will improve the classification process and help to delimit taxa as comparative units that can be handled in databases, floras, and checklists.

S.18.2 Assessing local and national floristic diversity through the Portal to the Flora of Italy

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Approximately two decades ago, the Working Group for Floristics, Systematics and Evolution of the Italian Botanical Society initiated a collaborative project to develop a checklist of the Italian vascular flora. The first project output was a book, published in 2005, followed by a significant update in 2018. Another update is scheduled for release in early 2024. The project triggered two crucial requirements: the digital storage and publication of floristic records, and the dissemination of the checklist through an online information system. Consequently, the collaborative floristic project "Wikiplantbase" (http://bot.biologia.unipi.it/wpb/italia) was launched in 2013, and in 2018 the online "Portal to the flora of Italy" (https://dryades.units.it/floritaly/index.php) was introduced to the scientific community. These two online tools operate in tandem, ensuring continuous updates and interoperability. They thus constitute a unified system, serving as a robust and reliable reference for the nomenclature, taxonomy, and distribution of the Italian vascular flora. Additional resources are slated to be incorporated into the system. These include a database storing protologues, type localities and other pertinent information about type designations for accepted plant names described in Italy, and the "Chrobase.it" database (http://bot.biologia.unipi.it/chrobase/index.php), focusing on chromosome numbers. Furthermore, the "The Italian flora of human interest" database (https://www.optima-bot.org/index.php/en/projects/8-category-en-gb/217-the-italian-cwr-whp-database) will contribute to the expanding repository. An ongoing effort involves establishing interoperability between this system and external initiatives, such as the "World Flora Online" (https://www.worldfloraonline.org/), "Plant of the World Online" (https://powo.science.kew.org/), and the "Euro+Med Plantbase" (https://europlusmed.org/). This integrated approach aims to create a more comprehensive and interconnected resource for sharing and accessing a wide spectrum of botanical data.

S.18.3 Designing a comprehensive online and print flora from scratch – the Flora of Greece project

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By starting from scratch, the Flora of Greece project represents a significant initiative aimed at constructing a thorough and annotated catalogue of the country's rich plant diversity, with both online and print components. Launched in 2010 and concluding three years later, in 2013, the "Vascular plants of Greece: An annotated checklist" (VPG) is the first comprehensive inventory of the flora of Greece more than a century after Eugen von Halácsy, finalized the most recent complete Flora of the country in its political borders. Since 2017, the project utilizes an advanced web tool (EDIT Platform for Cybertaxonomy) to facilitate easy access and navigation through extensive collection of taxonomic information. Users can access the electronic version of the VPG through the Flora of Greece website (https://portal.cybertaxonomy.org/flora-greece). The web checklist evolves dynamically, undergoing systematic and regular revisions to incorporate emerging scientific knowledge. The 1st version of the "Flora of Greece web" was published in May 2017 and the current, 5th version, summarizes all published information to the end of November 2023. This ambitious project stands as a collaborative achievement, based on the expertise of numerous scientists, aiming to the construction of a comprehensive database, currently comprising 5960 species and 2015 subspecies (6850 taxa). Looking ahead to 2024, the Flora of Greece project is poised to release an updated version. The project adheres to the nomenclatural adaptation via the APG IV, ensuring consistency with contemporary botanical standards. This new iteration, to be published in both online and print formats, will feature expanded content including additional descriptions and distribution maps. This ongoing commitment to floristic exploration and documentation underscores the project's enduring impact on the understanding and conservation of Greece's rich plant diversity.

S.18.4 Euro+Med PlantBase - how to integrate taxonomic knowledge and provide plant diversity data at a continental level

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Euro+Med PlantBase (E+M), a long-term project founded in the year 2000, has developed into a well-known standard resource for information on systematics, nomenclature and distribution of vascular plants and bryophytes in Europe and the Mediterranean region. At present, E+M contains more than 45,000 taxa, over 150,000 scientific names, nearly 150,000 common names in more than 40 languages, and ca. 380,000 source-referenced distribution records. The data are open access and can be retrieved through the Euro+Med Data Portal (https://europlusmed.org/), online in its present form since 2020. E+M provides a permanently updated taxonomic backbone and a dynamic checklist for native and alien plants in Europe, the Caucasus, the circum-Mediterranean countries and the Macaronesian archipelagos. Distribution is given for areas which correspond to all countries and most larger islands of the region. E+M is currently maintained by an informal consortium of participating European institutions, with the secretariat at the Botanic Garden Berlin since 2004. The editorial team of E+M continuously updates the systematic treatments of the checklist and adds new or corrects existing records. Initially based on *Flora Europaea* and integrating information from all taxonomic and floristic literature sources from the area, E+M is the most comprehensive resource on accumulated historical and actual floristic data at country level of the Euro-Mediterranean region. It keeps track of the newest publications in plant systematics and evolution, nomenclature and floristics, thus ensuring that the database is up to date in every respect. At present, approximately 200 taxa a year are added which are described as new to science from the E+M area. E+M also contributes taxonomic and distribution data to the World Flora Online (WFO) and links to other major online resources, thereby serving as a gateway to European and Mediterranean flora portals.

Symposia Session 2

S.19 BIOGEOGRAPHY AND DIVERSIFICATION OF INTERCONTINENTAL TROPICAL PLANT DIVERSITY. SESSION 2

S.19.1 Origin and biogeographical history of the Piper (Piperaceae)

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Target enrichment for Piperaceae, including all five genera, produced a well-supported maximum likelihood tree in which there was a good support for (*Verhuellia* ((*Manekia* + *Zippelia*) + (*Piper* + *Peperomia*))). Originating in South America in the Late Cretaceous, *Piper* then dispersed during the middle Eocene climatic optimum (ca. 40 Mya, when tropical species reached higher latitudes) to southern Africa and the Pacific islands first, followed by New Guinea, Southeast Asia and the Philippines. During the Oligocene the genus radiated in Southeast Asia and reached East Asia, India, Sri Lanka and Australia and re-colonised Africa. The New Caledonian and Vanuatuan species are sister to the New Guinean and Philippine taxa rather than the Pacific species. Once *Piper* left South America it exhibited a great number of intercontinental dispersals throughout its subsequent evolutionary history.

S.19.2 Biogeography of Indian Persea group (Lauraceae) - filling the gaps in the global phylogeny

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We investigated the phylogeny and biogeography of the basal angiosperm group Persea (Lauraceae) that comprises eight accepted genera i.e., 1) *Alseodaphne* 2) *Alseodaphnopsis* 3) *Apollonias* 4) *Dehaasia* 5) *Machilus* 6) *Nothaphoebe* 7) *Persea* and 8) *Phoebe*. In India, Persea group is distributed in low-elevation evergreen forests to broad leaved temperate forests of Himalayas and mid-elevation evergreen forests of Western Ghats, south India. We aim to understand the biogeographic origins of the *Persea* group and to decipher the times and modes of evolution in the Indian subcontinent compared to the Asian region. Two nuclear and one chloroplast gene marker are sequenced for *ca.* 100 samples collected across Northeast region and Western Ghats of India. We mapped the sequences of Indian *Persea* group in global dataset. Phylogenetic relationships were reconstructed using maximum likelihood and Bayesian inference methods. Divergence time estimated using BEAST 2.4.8. and Ancestral geographical ranges performed using BIOGEOBEARS. The *Persea* group has diverged around ~55.3 Mya (95% highest posterior density (HPD): 41.4 – 69.9 Mya) in China. We expect the probable divergence time of *Persea* group in India is early-mid Eocene. Also, molecular study shows the *Apollonias arnottii*, single known species of the genus globally, has to be shifted to the genus *Phoebe*. Phylogenetic tree we developed also supports the *Persea* group is not monophyletic. The *Persea* group requires in-depth taxonomic study of flower and fruit collections to resolve all the clades of different genera globally. This is the first attempt to understand the phylogenetic relationship and historical biogeography Indian Persea group in the global phylogeny.

S.19.3 Time calibrated phylogeny of Cunoniaceae reveals the biogeographical history of the Andean genus Weinmannia

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Cunoniaceae, mostly distributed in the Southern hemisphere, comprises 27 genera and c. 335 species. The highest diversity can be found in New Caledonia and South America. Also, diversity is concentrated in the genus *Weinmannia* (c. 80 species), which is dominant in cloud and montane forests along the Andes. Other ten to fifteen *Weinmannia* species are scattered throughout the Americas in the Atlantic Forest (South Brazil), the Guyana shield, Central America, Mexico, and the Caribbean islands. Our main objective is to reveal the phylogeographic history and diversification patterns of the group. We used a relaxed molecular clock, based on DNA sequences of three plastid markers *trnK-matK*, *trnL-trnF*, and *rps3-rpl16*, and twelve fossil calibrations, with an extended sampling across the Rosid lineages. We found the Cunonieae tribe (*Cunonia*, *Pancheria*, *Pterophylla* and *Weinmannia*) diverging during the late Eocene (~39.6 Ma), and the estimated age of *Weinmannia* (~34 Ma), correspond with the age of the Eocene-Oligocene Transition (33.9 Ma). This transition was characterized by the first formation of the Antarctic ice sheet and the isolation of the Gondwanan groups caused by the opening of the Drake Passage between South America and Antarctica, and the Tasman Seaway between Australia and Antarctica. Such continental rearrangement explains the current distribution of the taxa in the tribe. The most basal species of *Weinmannia* are in the Mascarenes Islands and Chile, while the central and northern Andean species show a recent evolutionary radiation estimated to have occurred ~5.5 Ma, which is consistent with the two major pulses of Andean uplift during the Miocene and Pliocene at c.12–6 Ma and ca. 4.5 Mya. Our results support the idea that continental drift and orogeny played a crucial role in determining the distribution and diversification of *Weinmannia*.

S.19.4 Unlocking Parablechnum from the field to the lab: a Hyb-Seq approach to unravel the global disjunction of a young fern genus

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Parablechnum is the most speciose genus of the fern family Blechnaceae, particularly represented in vulnerable habitats such as tropical montane cloud forests. Its 68 species exhibit a Gondwanan distribution, predominantly spread across two major centers of diversity —one in the Neotropics and the other in Australasia—; additionally, there are only three African species found in Southern Africa, Madagascar, and the Mascarene archipelago. Reconstructing the evolutionary history of these ferns has been hampered by their singular circumstances. Recent studies show that the genus is undergoing a rapid diversification that obscures its backbone phylogeny and hence the explanation of its current disjunct distribution. The taxonomy of the genus is still poorly understood as several species groups need further attention to be adequately circumscribed. Additionally, phenomena such as hybridization and cryptic speciation seem frequent in the genus, making it difficult to complete the phylogenetic approach. Combining the specimens from two recent field campaigns with herbarium material, we are attempting to improve the quality and quantity of molecular data. Our approach aims to reach a more detailed phylogenetic resolution via Hyb-Seq using the GoFlag probe set. Our preliminary results show a complex evolutionary history of a dynamic group shaped by long-distance dispersal events and ongoing diversifications. Guided by these results we are undertaking a comprehensive taxonomic reevaluation of the whole genus with the perspective of completing a global monograph.

S.19.5 Exploring evolutionary transitions across biomes in Zornia J.F.Gmel. (Leguminosae: Papilionoideae)

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The genus *Zornia* J.F.Gmel is the second most speciose representative of the Adesmia clade (Leguminosae: Papilionoideae), with ca. 80 species. *Zornia* is the only genus within the clade with a global distribution, mainly occurring in tropical and subtropical regions of the world. A previous phylogeny for *Zornia* revealed that most species diverged in Brazil ca. 8–10 mya, and suggested a single transoceanic dispersal event from the Americas to the Old World ca. 5 mya. Here, we augment the previous phylogeny with new sampling from Central America, Asia, Africa and Oceania. We aimed to investigate evolutionary patterns of distribution in *Zornia* and answer biogeographic questions related to ancestral range estimation and evolutionary transitions between biomes. Our results suggest that *Zornia*originated in the dry forest in Northeast Brazil. From there, the evolutionary path of the genus continued to the savannas of the Americas, where 40% of the present species occur. Lineages then adapted to the high elevation grassland in South America and Central America. The genus dispersed to the hight elevation grassland in Africa and then to the savannas in India and Australia. Our study shows the transoceanic dispersal occurred in *Zornia*, as previously it was not clear if this dispersal occurred from America to Africa or Australia first. We also clarify how the evolutionary transitions between biomes occurred in the genus, which is important to understand the dynamics of adaptation particularly to dry environments where *Zornia* mostly occurs.

S.19.6 Historical biogeography and niche evolution of Lecythidaceae in the American tropics

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Lecythidaceae (Ericales) is a pantropical family of woody plants of ca. 278 tree species with three subfamilies: *Foetidioideae* (Madagascar), *Planchonioideae* (Asia and Africa), and *Lecythidoideae* (ca. 232 species) restricted to the Neotropics. This family is within the 20 most-species rich families of trees in the lowland Amazon forests, providing important ecological services such as carbon sequestration and food resources for pollinators and seed dispersers. The global center of species richness and ecological importance is in the Amazon basin and Guiana Shield, where most Lecythidaceae research has been focused. However, there are genera occurring in the Andean and Chocó Biogeographic regions where several knowledge gaps lie. Despite multiple studies having been performed for Lecythidaceae, there are still incongruences among hypotheses about the evolution of this family. To infer the geographic history of Lecythidaceae in the Neotropics, and identify areas of importance for its diversification, we performed a Maximum Likelihood analysis in IQ-TREE, based on nuclear markers targeted by the Angio353 probes in 94 species, and an ancestral range reconstruction, using a dispersal-extinction-cladogenesis model (DEC) in BioGeoBEARS. According to our results, there is a high uncertainty about the ancestral area for the Neotropical clade. However, the Southeastern Amazonia was reconstructed as the most probable ancestral area for the zygomorphic-flowering clade, originated in the Paleogene (~34 Mya), while Central America and the Chocó were recovered as the most plausible ancestral area for the actinomorphic-flowering clade (originated ~37 Mya). Since most of the species included in this reconstruction occur in the Amazon basin and given the complexity of wetland habitats and their association with the Andean uplift that most likely had an important role in the evolution of Amazonian Lecythidaceae, increasing sampling from the InterAndean Valleys and Chocó will allow us to better understand the niche evolution and diversification history of this family.

S.20 CONTRASTING DIVERSITY PATTERNS, BIOGEOGRAPHY, AND CONSERVATION ISSUES IN NORTHERN AND SOUTHERN HEATHERS (ERICEAE, ERICACEAE)

S.20.1 Heath species help reconstruct the biogeographic role of the Strait of Gibraltar

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The Strait of Gibraltar is characterised by the diversity and uniqueness of its terrestrial flora. The floristic similarity between both sides of the Strait, together with the existence of some discontinuities, illustrates its biogeographical importance as a dispersal bridge/barrier. On the other hand, the Strait of Gibraltar has acted as a biogeographical refuge for flora from the Pleistocene glaciations. Many plant species found on both sides of the Strait are associated with sandy, very acidic and infertile soils. These include the heather *Calluna vulgaris* and *Erica australis*, characteristic species of the Mediterranean heathland or *herriza*. The Strait was an important glacial refuge for these species, followed by a post-glacial expansion along the western Iberian Peninsula. However, the Guadalquivir valley, dominated by clayey, non-acidic, fertile soils, would represent an edaphic barrier to the northward expansion of these acidophilic species. How did they overcome it? The phylogeographic analyses of these two heathland species were reviewed, and the geological and geomorphological literature of the Strait of Gibraltar region was examined. For both species, a certain genetic discontinuity is observed between the European area of the Strait and those of the rest of the Iberian Peninsula. In contrast, there is a striking genetic link between the W Iberian Peninsula and the African part of the Strait. Assuming a sea-level drop of about 140 m, the topography of the Strait of Gibraltar and the continental shelf of the Gulf of Cadiz, as well as the tectonic nature of their substrates, we suggest the existence of a glacial corridor between the African side of the Strait and the Portuguese Algarve. Confirmation of this Tingitano-Algarvian corridor using NGS approaches will help to clarify the role of the Strait of Gibraltar as a bridge or dispersal barrier in the geographical distribution of plants.

S.20.2 Phylogenetics, biogeography and phenotypic variation of four species of heathers (Erica L., Ericaceae) with contrasting distributions

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Erica tetralix, *E. ciliaris*, *E. mackayana* and *E. andevalensis* form a robust clade within the heathers (*Erica* L.) of the northern hemisphere. They share a number of traits such as their low size, the pluricellular glandular trichomes, and their ecological niche of permanently wet conditions. However, they cover different geographic areas, ranging from the widespread North Atlantic *E. tetralix*, to the narrowly endemic *E. andevalensis* of South western Iberia. Moreover, hybridisation occurs in northern areas between *E. tetralix* and *E. ciliaris* or *E. mackayana*, but not in overlapping southern populations. Here we present a dataset of over 400 plants obtained from the distribution range of the four species. Most samples have been analysed by means of genetic analyses using SNPs (nextRAD sequencing). Furthermore, we conducted measurements on an array of morphological traits, encompassing macro and micromorphological traits, including reproductive and vegetative characters. In this talk, we present the first results on the biogeography, phylogenetic relationships and morphological variation at the species, population and individual level including i) The biogeography of *E. mackayana*, which shows a clear pattern of recent multiple introduction events for the Irish populations from northern Spain, ii) both genetics and morphology support the species taxonomic level of *E. andevalensis*, and iii) the hybrids of *E. tetralix* and *E. mackayana* or *E. ciliaris* are intermediate in their morphology and genotype, and are produced only in certain regions. Results from this model group can aid in the interpretation of evolutionary and biogeographic patterns such as the northern recolonization by plants from southern refuges after the ice age.

S.20.3 Phylogenetic diversity and conservation prioritisation of Erica (Ericaceae)

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Estimates of the numbers of vascular plant species currently under threat of extinction are shockingly high, with the highest extinction rates reported for narrow-range, woody plants, especially in Mediterranean climate and tropical biodiversity hotspots. The genus *Erica* is a prime example: of the around 850 species, all shrubs or small trees, a large proportion are narrowly endemic to localities within the Cape Floristic Region of South Africa. Just under 200 are known to be threatened and a further 100 are 'Data Deficient'. We need to target conservation work as well as research to fill the most problematic knowledge gaps. This can be especially challenging in large genera such as *Erica* with numerous threatened species that are more or less closely related. One approach involves combining knowledge of phylogenetic diversity with that of IUCN threat status to identify the most evolutionarily distinct and globally endangered (EDGE) species. We present an expanded and improved phylogenetic hypothesis for *Erica* (representing 67% of described species diversity) and combine this with available threat and distribution data of species to assess which species and geographic areas should be targeted for conservation effort to maximise preservation of phylogenetic diversity. This analysis delivers priority lists of phylogenetically diverse taxa - threatened, or data deficient - and of areas. Priority lists can be cross-referenced to existing living and seed banked ex situ collections and used to target new and updated threat assessments and conservation action.

S.20.4 Pollinator shifts and budding speciation in the Cape Floristic Region's heathers

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Of the roughly 900 species of *Erica* worldwide, 690 (75%) occur in the Cape Floristic Region. This taxonomic diversity is accompanied by an impressive array of floral phenotypes corresponding to different modes of pollination, including wind, bird, bee, fly, and even rodent pollination. We focused on a clade with evidence of multiple shifts between bee and sunbird pollination syndromes and used genome-wide data to improve on previous estimates of the clade's phylogeny. This provided a much clearer picture of the group's evolutionary history; however, the picture is still by no means clear. What we can say is that the group's diversification happened very rapidly and is certainly still ongoing. Intriguingly, budding speciation – which is when one species gives rise to a new species without itself changing at all – appears to be a common occurrence and is often accompanied by a shift from bird to bee pollination. The prevalent paradigm of speciation by bifurcation might therefore be a poor model of what really happened during the group's spectacular diversification.

S.20.5 Systematics and evolution of the true blueberries (Vaccinium sect. Cyanococcus, Ericaceae)

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The true blueberries (Vaccinium sect. Cyanococcus) constitute a clade of about nine to 24 species in temperate North America. This group served as a model system during the Modern Synthesis for examining the origins, prevalence, and diversification of polyploidy in nature, and remains intensively studied because of its economic importance as a food crop. Nonetheless, its taxonomy and evolutionary history is still uncertain, particularly regarding the relative importance of allo- versus autopolyploidy in the evolution of the group, the extent to which levels of ploidy concord with species boundaries, and the utility of the morphological characters traditionally used for delimiting taxa. To address these knowledge gaps, we have collected over 750 silica-gel-dried leaf samples from natural populations with herbarium vouchers and photographs, nearly 500 of which have been analyzed with flow cytometry to estimate ploidy. A robust diploid phylogenetic estimate has been generated for 36 samples of known ploidy with a target-enrichment phylogenomic approach. To this diploid framework we have added polyploids in several ways to test their evolutionary origins. We found a strong correlation of leaf and stem stomata size and density with ploidy across the clade. With the knowledge gained from these studies, we have examined thousands of herbarium specimens from key U.S. herbaria to begin the process of a comprehensive taxonomic revision that will uniquely include expansive species descriptions, specimens cited, and distribution maps. Progress indicates that the revision will vary substantially from prior work, e.g., it includes the taxonomic resolution of two polyploid species to which names have been extensively misapplied, the resurrection of a localized polyploid endemic currently buried in synonymy, and the discovery of two diploids with unique morphology and localized geographic distribution that may represent undescribed species. We also discovered a morphological means to discern "rabbit-eye" blueberry cultivars that have escaped from cultivation.

S.20.6 Hybridisation and the debated species boundries in Rhododendron subgenus Pentanthera

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Rhododendron (Ericaceae) is one of the largest genera of woody plants with 1156 species. The genus has been divided into five subgenera, of which *R.* subg. *Pentanthera* G. Don comprises a group of highly ornamental species, with interesting distribution, indigenous to North America, Japan, China, and the Caucasus regions. The species (17 species) assigned to *R.* section *Pentanthera* are commonly known as Azaleas. The section has highly debated taxonomy and unresolved phylogeny. We here used the GBS techniques to assess the species boundaries using the population and phylogenomic approaches. Our initial results suggest that there is frequent admixture among different species of *R.* section *Penanthera*. The initial phylogenomic results also support reticulation in the tree backbone of the section.

S.21 NEW FRONTIERS IN PLANT PHYLOGENOMICS. SESSION 2

S.21.1 Darwin Tree of Life, towards reference genomes of an entire flora

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The Darwin Tree of Life project has the ambitious goal of producing reference quality genomes of all eukaryotic species in Britian and Ireland. Within this broader goal, the botanical aim is to collect 1900 species of land plant from Britain and Ireland and produce reference genomes from over half of these species by the end of 2024. In building such a large scale reference genome resource, considerable attention has been given to standard operating procedures and protocols. This involves work undertaken by Genome Acquisition Laboratories (GALs) at the Royal Botanic Garden Edinburgh and the Royal Botanic Gardens Kew and includes developing target species lists, defining and adhering to comprehensive meta-data standards, collection of plants directly snap frozen on dry-ice or liquid nitrogen in the field, and then using DNA barcoding to check species identify, and undertaking genome size estimates with flow-cytometry to guide sequencing efforts. High quality plant tissues are then submitted to the Wellcome Sanger institute for DNA extractions and genome sequencing using a combination of PacBio Hifi sequencing for the main assembly and scaffolding with HiC. In this presentation we give an overview of botanical progress on the Darwin Tree of Life project, summarising achievements (including the successful sequencing of the 90 gb mistletoe genome) and also the challenges including the multitude of difficulties that arise when from working with diverse tissues sources and often very small amounts of starting material.

S.21.2 Towards a better understanding of the genomics of tropical forests: a case study from Singapore

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S.21.3 What can we do with a continental phylogenetic tree?

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Australia, the world's smallest continent has a globally significant flora comprising over 2,100 genera and 21,000 native species of flowering plants, of which over 90% are endemic. The Genomics for Australian Plants (GAP) Initiative, catalysed by Bioplatforms Australia in partnership with researchers from the Australian State and National Herbaria and Botanic Gardens, aims to develop genomics resources to enhance our understanding of the evolution of this unique flora and support its conservation. GAP Phylogenomics, one of three GAP activity streams, has the long-term goal of resolving the Australian Angiosperm Tree of Life (AAToL) to species level. To date, this inclusive project has brought together over 70 Australian researchers and herbarium staff and partnered with the global Plant and Fungal Trees of Life project (PAFTOL) to complete AAToL Stage 1 – reconstructing a phylogenetic tree including at least one species exemplar of nearly 95% of Australian native angiosperm genera sequenced for a common set of hundreds of nuclear markers (using the Angiosperms353 target capture baits). However, because sampling is strongly biased due to being geographically constrained, the range of applications of this continental tree in evolutionary biology is limited

Approximately half of Singapore's native plant diversity resides in a small, 1.64 km² patch of rainforest in Bukit Timah Nature Reserve (BTNR). Between 2019 to 2022, we collected and vouchered a total of 882 angiosperm species from BTNR. Illumina shotgun short-read sequencing was carried out for each species to obtain a minimum of 30Gb of data, followed by genome assembly and gene prediction. For the first stage of the project, we focused our analysis on 499 good quality genomes. A set of 1,000 conserved single-copy genes were used to generate a high-resolution phylogeny of the BTNR species, illustrating that when compared with APG IV, there were differences in the position of Santalales and the relationships within the families in Malpighiales and some orders in the malvids and fabids. Gene predictions allowed us also to study ancestral whole genome duplication events, to look for evidence of introgression and to chart the proteomic diversity present in BTNR.

S.21.4 Angiosperm evolution and biogeography across the floristically diverse Canary Islands archipelago

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A fundamental characteristic of biodiversity is its uneven distribution across the Tree of Life. A prominent example of this is the flora of the Canary Islands, which comprises many spectacular species-rich radiations and dozens of depauperate, single-species lineages. Addressing why some lineages have diversified, whilst others have not, requires phylogenomic datasets, which can provide unparalleled insight into the dynamics governing diversity unevenness. For example, time-calibrated phylogenetic trees can be used to estimate dynamic biogeographic processes (such as rates of speciation, extinction, and colonisation), allowing us to infer the drivers of radiations and depauperate lineages alike. However, a community-wide phylogenetic dataset for the Canarian flora that would allow for such analyses is lacking. Here, we present a time-calibrated molecular phylogeny including over 800 species of native Canary Islands flowering plants (~60 % of the native flora), constructed using hybrid capture-based target enrichment of the angiosperm-wide 353 bait set. We sequenced the majority of species and lineages that make up the native angiosperm flora of the archipelago and, to estimate the colonisation and branching times of the Canarian lineages, integrated the sequences into a broader, time-calibrated angiosperm phylogeny based on the same angiosperm-353 gene set. Crucially, to provide an estimate of colonisation times, we also sampled the closest mainland relatives of each lineage. We also present an estimated number of independent colonisation events for all native angiosperm genera of the archipelago, inferred from the phylogenetics literature, and refined using our phylogenetic data. From the temporal information contained within the molecular phylogeny, we generate a novel reconstruction of the biogeographic history and temporal diversity dynamics of angiosperms in the Canary Islands. By combining biogeography, ecology, and evolution, our analyses present novel insights into the factors underlying the community dynamics of the near-complete flora of a large, floristically diverse oceanic archipelago.

S.21.5 Phylogenetic analyses of entire regional flora using Angiosperms353 sequences data

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Accurate knowledge of the phylogenetic relationships among the species composing the regional biota is crucial to understand how species were assembled and how much phylogenetic diversity they represent. However, phylogenetic information available for local species communities is still limited because of the poor resolution and uncomplete sampling of the tree-of-life at the species-level. Here, we demonstrate the feasibility of using Angiosperms353 target-enrichment and high-throughput genome sequencing on both fresh and historic DNA to estimate phylogenetic relationships among all species composing the regional flora of the Swiss plateau. The analysis of over 1300 species provides a more resolved and complete tree than available synthetic or plastid-based phylogenies, especially within complex families (e.g. Cyperaceae, Orobanchaceae, Poaceae). This new genomic reference for swiss plants points to several disagreements with the current plant classification and provides a new framework to assess the evolutionary dynamics of a complete regional flora. Our results bring new insights into the consequences of habitat conversion on phylogenetic diversity and the identification of areas that should be prioritized for long-term conservation strategies.

S.22 GLOBAL MYRTACEAE SYSTEMATICS: PURE AND APPLIED PERSPECTIVES FOR MANAGING AND CONSERVING THE EARTH'S PLANT DIVERSITY

S.22.1 Fruit evolution in Eugenia (Myrteae, Myrtaceae), with taxonomic implications in one of the world's largest tree genera

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Tropical forest habitats are characterized by the prevalence of plants bearing fleshy fruits dispersed by animals. In South America, the genus *Eugenia* stands out, with a high number of species and serving as a significant year-round producer of fleshy fruits. The evolution of fleshy fruits is considered a potential key innovation in the hyper-diversification of subtribe Myrteae and the large genus *Eugenia*. Our investigation focused on the hypothesis that variation in fleshy fruit traits within *Eugenia* is closely linked to infrageneric lineages. We aimed to determine if specific species groups display distinct patterns of fruit traits and whether these traits have evolved to enhance reproductive success by either attracting specific dispersers or reducing seed predation. Results revealed substantial variability in *Eugenia* fruit traits, with discernible trends within infrageneric groups. The predominant exocarp colour in sampled *Eugenia* fruits were dark purple and red, contrasting with a higher probability of ancestral colours being yellow. Ripened exocarp colour is relatively strongly associated with taxonomic sections, suggesting potential common ancestry. Larger-fruited species are rarer and concentrated in early diverging clades within *Eugenia*, offering a potentially informative taxonomic feature for these groups. The number of seeds, a labile trait within *Eugenia*, was commonly recorded as one, but early diverging clade species tend to produce fruits containing more than one seed. Pulp ratio exhibited a stronger association with taxonomic sections, suggesting that species from more recently diverging clades invest less energy in pulp production and instead allocate more resource to seed size. Our findings suggest that variation in fleshy fruit traits in *Eugenia* can help define infrageneric lineages. Specific groups of *Eugenia* species display unique patterns of fruit traits, and our evidence suggests that these traits may have evolved to maximize reproductive success by either attracting specific dispersers or minimizing seed predation.

S.22.2 The relationship between environment and reproductive traits in the clove genus (Syzygium-Myrtaceae)

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Syzygium (Myrtaceae), is one of the most diverse tree genera globally, encompassing economically significant species such as clove, lilly pilly, and water apple. Its natural habitat spans Southeast Asia, Southern Asia, Australia, and the Pacific, with most species falling within *Syzygium* subgenus *Syzygium*. Despite its economic importance, the taxonomic complexity of the genus, coupled with limited knowledge about its evolution and ecology, poses challenges to downstream activities such as conservation. Our study focuses on a representative sample of *Syzygium* subgenus *Syzygium*, leveraging reproductive traits, geolocation data, and climate information. Our aim is to identify the key environmental variables influencing floral and fruit diversity within the genus. Considering the relationships among biotic and abiotic factors, we explore these variables within a phylogenetic context to discern patterns independent of and influenced by the environment. Our investigation recorded 12 continuous and 13 discontinuous traits related to flowers and fruits from the sample species. To analyse climate variation, we extracted 19 CHELSA bioclimatic variables for all GBIF *Syzygium* occurrences. Mixed PCA plots were constructed to independently assess trait and environmental Principal Components. To understand the evolution of each trait cluster, we compared Brownian Motion and Ornstein-Uhlenbeck models of evolution based on a pruned version of the most comprehensive available phylogenetic hypothesis. Phylogenetic linear modelling was employed to observe the interplay between the environment and the main axes of trait variation while considering the evolutionary relationships between species. Our results highlight temperature, precipitation, and seasonality as the primary independent climatic drivers influencing Syzygium distribution. We found that flower/fruit size contributes more to morphological variation than any other biotic traits examined. Weak correlations were identified between flower/fruit size, inflorescence architecture, fruit colour, and climate. All biotic traits better fit the Ornstein-Uhlenbeck model suggesting that these characteristics are evolving under natural selection rather than randomly.

S.22.3 A review of eucalypt research from the last decade (2014-2024)

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Much progress has been made in the phylogenetic analysis of the eucalypts (*Angophora*, *Corymbia*, and *Eucalyptus*). This presentation aims to summarise the progress and now controversies that have occured in eucalypt generic classification since the previous International Botanical Congress in 2017. Two large-scale phylogenies of the group have been published and a new genus, *Blakella*, has been proposed to deal with the paraphyly of *Corymbia*. The eucalypt fossil record and our current understanding of the biogeography will be discussed. New species have been described from most Australian states, while other research suggests that some eucalypt species should be lumped. A new edition of the eucalypt identification key Euclid was published in 2019 but ways of creating new editions are now limited. Ways to solve this problem are discussed.

S.22.4 Exploring the timing of environmental shifts in response to trait evolution: a case study in Myrteae (Myrtaceae)

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The widespread convergence of plant traits in certain environments indicate that generalities exist for how plants diversify in space. However, because evolution and environments are dynamic, not all species are fully adapted to their environment at all times. A consequence of this is that infrequent trait-environment combinations – that is, plant traits that appear in environments where they may not be optimal—is also a common feature in nature. The presence of these infrequent combinations can be harnessed to test timing of trait evolution in relation to environmental shifts. Specifically, when analyzed in a phylogenetic context they might help indicate whether traits evolve prior to (as in exaptations) or after (as in adaptation) an environmental shift. Here, we demonstrate this in the context of leaf traits and biome shifts in Myrteae (Myrtaceae). We use a subset of 221 species with dry leaf mass/area (LMA g/cm^2) data measured from herbarium specimens and trait evolution analyses in a recently generated phylogeny for the group. Biome type and LMA appear correlated, with low LMA lineages being more common in closed-canopy biomes. Low LMA in closed-canopy biomes is recovered as the most likely root state in the group. Transition rates from this state to low LMA in open-canopy biomes are practically zero, meaning that the only route to transition to open-canopy biomes is by evolving high LMA first. Similarly, to transition from open-canopy back to closed-canopy, lineages have to evolve low LMA before a shift. These preliminary results support the idea that trait evolution precedes and may facilitate environmental shifts, at least for this trait and set of species.

S.22.5 Assembling the genome of rātā Moehau and applications for other New Zealand Metrosideros (Myrtaceae)

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The 12 *Metrosideros* (Myrtaceae) native to the New Zealand archipelago are facing a growing number of threats, particularly since the arrival of the pathogen myrtle rust (*Austropuccinia psidii*) in 2017. Despite their iconic status (e.g. Pōhutukawa *M. excelsa* known as the New Zealand Christmas tree) we have surprisingly little genetic data to help us understand how diversity is partitioned across the landscape for most species. One of the most threatened species is rātā Moehau (*M. bartlettii*), a critically endangered tree found only in the far north of New Zealand. At the last count only 14 trees were found in the wild. In conjunction with the iwi (tribe) Ngāti Kuri we have assembled a genome of rātā Moehau. This assembled genome forms the basis of multiple studies in the genus, e.g. resequencing almost the entire wild population of rātā Moehau, plus representatives of additional closely related species. At the same time, we are using the assembled genome to develop new low copy genetic markers and are gathering a dataset of as many New Zealand *Metrosideros* species as we can to sequence using amplicon sequencing. The end goal is an understanding of how the genetic diversity of each New Zealand *Metrosideros* species is distributed in space, with a particular focus on modelled refugia in the face of climate change and projected myrtle rust spread, to help prioritise conservation effort.

S.22.6 Digital approaches in taxonomy: surfacing datasets from herbarium specimens and images to treat a species complex in Myrcia (Myrtaceae)

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Herbaria are the most important source of information for taxonomic work. Facilities and technologies available today, such as digitisation of collections and herbarium DNA sequencing, can help accelerate taxonomic decisions. Species complexes are a major factor preventing a better understanding of plant diversity in the tropics. In this context, we employed a multi-source pipeline to address limits among taxa of the *Myrcia neoobscura* species complex (Myrtaceae) using herbarium specimens. We collected morphometric traits from high-resolution images and analysed them with a clustering analysis, resulting in twelve morphological groups. We subsequently tested these groups with phylogenomics using molecular data obtained from herbarium specimens. Congruence between morphology and phylogenomics was observed in the following: *Myrcia marliereana*, *M. neoobscura*, and *M. neoriedeliana*, as currently circumscribed, represent two entities each, and *M. excoriata* can be split in three entities. We also investigated species geographic distributions and phenological patterns using herbarium specimens and their labels. The two species today recognised under *M. neoriedeliana* and *M. neoobscura* differ in flower seasonality, while two of the taxa currently under *M. excoriata* differ in both geographic distribution and flowering phenophase. The final species delimited in this work are morphologically diagnosable and geographically structured, and most of them are monophyletic according to the obtained phylogenetic reconstruction. The successful results of this work are based on the high-quality data obtained from museum specimens, and other herbarium-based investigations of species complexes are encouraged to accelerate the much-needed taxonomic resolutions in the tropics.

S.23 INTEGRATING CONSERVATION BIOLOGY AND SOCIETY ENGAGEMENT TO ENHANCE PROTECTION OF AT RISK FLORA. SESSION 1

S.23.1 A survey of flora and habitat diversity in three cultural heritage sites of central and southern Italy

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Several scientific studies highlight that cultural heritage sites, e.g., monuments and sacred sites, often represent refuge sites for local flora and fauna and can constitute important ecological corridors and biodiversity hot spots. Hence, protected cultural heritage sites can play a key role in biodiversity conservation at the global scale, especially for those situated in environments modified by anthropogenic activities. To ensure adequate management of these sites to enhance and conserve biodiversity, in-depth knowledge of the flora, vegetation and the nature-man relationship are essential elements to consider. This research aims to provide the first characterization and analysis of the flora and habitats of three Italian sites of the Cultural Route of the Council of Europe "Aeneas' route". This research is also aimed at increasing citizens' awareness of the importance of maintaining biodiversity and analyzing the relationships between natural and historical characteristics of these important contexts in southern Italy. Currently, field surveys are being conducted in the following sites: 1) The archaeological Park of Cuma is a site of great archaeological and cultural importance, with areas of great naturalistic and conservation interest. Here, 160ca different taxa and two interesting forest communities formed by previous plantations now naturalized were founded. 2) Sanctuary of Sol Indiges, Torvaianica; to date, the site is rich in taxa (more than 180 species), with species of conservation interest (e.g., orchids) and high biodiversity and community patterns. 3) The archaeological area of Portus presents a high naturalistic, landscape, historical and cultural interest. Here, more than 160 different wild and cultivated taxa, and different vegetation patterns -including wetland and riparian - were found. Here, preliminary data useful for the next characterization, valorization, and conservation of the flora and vegetation of the above-listed sites are provided. The application of results includes the site management implementation and the planning of conservation actions.

S.23.2 Rare and endemic plant conservation: insights from the East Mediterranean experience

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The Mediterranean Basin is considered to be one of the most biodiverse regions in the world and an important site of floral exchange and active plant speciation. Lebanon, a micro-hotspot for plant biodiversity in the Mediterranean Basin is characterized by the coexistence of plants with diverse biogeographical origins and a large number of narrow endemic taxa. It clearly exhibits differentiated center of endemism. Topographical relief and sharp climatic contrasts within a small geographical area may have driven micro-evolutionary diversification processes of newly evolved species while water availability was critical for the long-term persistence of ancient lineages in refuge areas of smoother topography. As natural habitats continue to be lost and degraded, many plant species are becoming increasingly threatened especially endemic plant species that are usually more vulnerable to anthropogenic threats and natural changes. Therefore, they hold a higher extinction risk. The preservation of these species is a major concern on a worldwide context. Our research group has carried out for the last few years an interdisciplinary, integrated approach to the conservation of threatened plants of the Lebanese flora and to ecosystem restoration. Investigations on plant distribution, systematic relationships, autoecology, genetic structure, and some plant-animal species interactions were conducted in order to plan conservation activities. My talk will focus on Lebanese endemic Irises. Four of the 7 Iris studied are classified as “Endangered” and 2 as “Critically Endangered”. Knowing what taxonomic units need to be preserved and how unique they are is a prerequisite to any conservation action. Since rescue from possible extinction could be performed through the reinforcement of populations, defining species and differentiating *taxa* is crucial in order to define conservation units. For this purpose, molecular and cytogenetic studies were conducted, targeting different species in need of *in-situ* and *ex-situ* conservation.

S.23.3 Ecology and conservation of cliff-plant communities under increasing climatic and human pressures

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Cliffs are home to a large diversity of endemic and endangered plant species and millennial-old trees that are currently facing increasing threats from climate change and recreational climbing. In recent years, rock climbing has become very popular, with annual increases of 15-20% in the number of climbers. Rock climbing is known to damage plant communities and other organisms such as birds, lizards or snails. However, the origin of the climbing impact remain largely unknown. Climbing impact sometimes compels conservation managers to make insecure or even inappropriate decisions within a framework of growing conflicts among stakeholders. But the climbing community has expressed its willingness to contribute to cliff preservation, with various climbing associations focused on promoting sustainable climbing. We carried out a study investigating the origin of the climbing effects on cliff flora involving the local community. In primal and unaltered cliffs of El Potrero Chico (Mexico), we installed new climbing routes to unravel whether the greatest climbing impact is produced in an initial phase due to the installation (opening) of the route or rather due to increasing climbing frequency. Local climbers actively contributed to create the new routes and posteriorly climbed them simulating the post-opening climbing effect. We found that the opening of the climbing route produced the greatest negative impact on cliff flora, and also promoted the loss of individuals from the surroundings of the route. However, successive post-opening climbing have little effects on cliff flora. These findings clearly evidence the need to consider existing cliff vegetation before developing new climbing routes, and that managers should focus on this rather than closing existing climbing areas. Given the high complexity of study cliff ecosystems, promoting awareness on its biodiversity and protection needs to the local community will contribute to its preservation.

S.23.4 Local involvement for endemic floristic species conservation: case study of the Kirindy forest Morondava - Madagascar

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This study focuses on the crucial role played be the local community in safeguarding the endemic floristic species within the Kirindy Forest in Morondava, Madagascar, where several tree species face the imminent threat of extinction. Various stakeholders are actively combating deforestation and endeavoring to enhance the protection of unique species such as Dalbergia sp., Commiphora sp., Givotia madagascaraiensis, Cordyla madagascariensis, and Diospyros sp. The primary aim of this research is to evaluate and promote community engagement in the conservation of these distinctive botanical treasures. The methodology involves data collection through surveys and interviews with both the local population and managers, focusing on the utilization of these species. Additionally, in-depth interviews and field observations are employed to gather insights into the knowledge, attitudes, and practices of the local community, identifying traditional wisdom and indigenous practices related to biodiversity. The study results encompass a comprehensive assessment of the local population's knowledge and attitudes toward conserving endemic floristic species, proposing solutions for ensuring the sustainability of these species, and exploring traditional practices conducive to preservation. The outcomes will contribute to formulating recommendations for tailored awareness programs targeted at the local community. Furthermore, the study will underscore the implications and commitments of the local population in the conservation and protection of the floristic biodiversity of the Kirindy Forest, emphasizing the development of sustainable strategies for safeguarding their natural heritage.

S.23.5 Conservation strategies for large old trees to promote natural forest restoration and climate-change mitigation

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Primary forests, including old-growth forests, have a prominent role in biodiversity conservation. Furthermore, they represent a consistent repository of carbon in tree biomass and soil, making them critical regulators of the carbon cycle. Their ecological integrity strengthens their climate-change mitigation potential by fostering ecosystem stability as a C sink. Old trees are the most charismatic element of old-growth forests, harbouring large quantities of the overall biomass and contributing to forest biodiversity with unique arrays of microhabitats. We present the unique traits characterizing multi-century beech trees in a network of old-growth forests in the UNESCO Site 1133. We describe how traits change along environmental gradients and quantify their contribution to the forest carbon stock and sequestration, as well as the quantity and quality of biodiversity-hosting microhabitats. Tree-ring cores collected along the whole trees served to quantify tree conservation status in terms of response to climate change in the last decades. Old trees features were compared with data on exceptional tree distribution throughout managed landscapes gathered in a citizen science project promoted within the National Geographic-funded project "Old But Gold: Restoring old-growth forests to build effective climate-change mitigating landscapes". Comparing natural and managed forests will help quantify the potential of human-altered landscapes to host old trees and the contribution of natural forest restoration to climate mitigation and biodiversity conservation.

S.23.6 Pampa Singular: integrative conservation on subtropical grasslands of South America

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The Pampas is one of South America's major grassland ecosystems, extending from northern Argentina to Uruguay and southern Brazil. In addition to natural grasslands, rocky outcrops, coastal vegetation, swampy areas, savannas, and small patches of dry forests increase landscape heterogeneity and are home to a remarkable diversity of plant species, of which c. 5% are endemic to the Pampas. Cattle grazing was the dominant economic activity in the area until the late 20th century, and the natural grasslands were used in a more sustainable manner. However, the growth of agriculture, silviculture, and mining throughout the Pampas in recent decades has resulted in significant habitat loss and accelerated habitat fragmentation. Pampa Singular is an integrative project that focuses on understanding biodiversity in the Pampas, as well as the conservation of unique landscapes and rare plant species. We produced endemic flora species inventories and searched for crop wild relatives from the Pampas. Furthermore, science outreach initiatives were designed to raise awareness in the local population and to promote science and conservation for future generations. Most plant species endemic to the Pampas have never been assessed for their conservation status (extinction risk) and many lack sufficient data to be assessed. We used the Rapid Least Concern method to identify species that were not threatened and focused our efforts on likely threatened species. We mapped the most diverse areas for endemic species and for crop wild relatives, comparing historic and current species distributions taking into account land conversion to economic uses.

S.24 THE IMPACT GENOME SIZE AND CHROMOSOME EVOLUTION ON THE ARCHITECTURE OF THE GENOME

S.24.1 Challenges and lessons learnt from a giant plant genome: the European mistletoe (Viscum album L.)

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The European mistletoe (*Viscum album*) is an obligate hemiparasitic plant from the Santalaceae family. Although it is a well known plant for its many uses and traditions, evolutionary and genomic studies on mistletoe are rare due to its haploid genome size, which can vary from 85 Gbp up to 105 Gbp (more than 30 human genomes). This makes mistletoes one of the eudicot genera with the largest genomes. We have sequenced, assembled and curated the *Viscum album* genome to generate the largest high-quality, chromosome-level genome published to date. Moreover, here we present preliminary results not only on the genome assembly data but on the analysis of the repetitive fraction of the genome, including TE distribution as well as telomere and centromere repeat analyses. Our efforts are resulting in the first in-depth insights on a giant genome structure, which represents an invaluable resource for studies on the evolutionary processes underlying the evolution of genome obesity.

S.24.2 Interactions between cytogenetic diversity and habit - insights from neotropical orchids

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The relationship between cytogenetic and ecological data is a classical hypothesis. Recently, this subject was poorly analyzed within an evolutionary framework using phylogenetic comparative methods (PCM). To address this gap, we investigated the association between cytogenetic data and habitat using the subfamily Epidendroideae (Orchidaceae) as a model through PCM. The chromosome number (CN) and genome size (GS) data were organized into an online database (http://orchidcountsdb.epizy.com/) and a new phylogenetic tree was constructed based on four markers encompassing 1,754 species. Habit information was surveyed for all species with cytogenetic data. The CN varied 24x and presented a low phylogenetic signal (λ=0.53), while GS varied 119x and presented a high phylogenetic signal (λ=0.95). The mode and tempo of evolution suggest that both CN and GS show punctual evolution (κ=0.34), with long branches contributing more to the evolution of both characters (δ=3.00). When analyzing each tribe individually, Cymbidieae stands out as an interesting exception. This tribe shows adaptive radiation for CN and GS (κ = 0 and 0 / δ = 0.46 and 0.31, respectively), and CN presents a high phylogenetic signal (λ=0.89). The OU evolutionary model, suggesting a response to stabilizing selection, was considered the best model for CN in the subfamily and in individual tribes as well, while BM was the best for GS. Once again, the exception is Cymbidieae, which had EB as the best model for both characters, reinforcing the suggestion of adaptive radiation. Based on these results, GS is more suitable for performing macroecological analysis, while PCM using CN will function as an ordinary test. Considering GS, small GS is associated with an epiphytic habitat (p=0.00067). In conclusion, GS is associated with habit at higher taxonomical levels, such as subfamily, while CN, is associated with ecological traits, it should be true at lower taxonomic level.

S.24.3 The impact of repetitive DNA in the evolution of fern genomes

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Genomic architecture in ferns stands out significantly from that of other plant lineages. Ferns exhibit a unique response to whole genome multiplication (WGM), deviating from the typical diploidization pattern observed in angiosperms. Instead, ferns tend to accumulate chromosomes and trigger the silencing of newly acquired gene copies following WGM. Consequently, ferns display higher mean chromosome numbers (n=61) compared to angiosperms (n=17). Nevertheless, while average fern genome sizes (1C=12.11 Gbp) are larger when compared to angiosperms (1C=5.13 Gbp), the underlying mechanisms responsible for such differences remain unclear. Certainly, the contribution of repetitive DNA in driving shifts in genome size is well studied in angiosperms, but needs to be further explored in ferns. This study seeks to address this knowledge gap by conducting a comprehensive comparative analysis to identify and quantify the main types of repetitive DNA sequences in 50 fern species. The sampling covers a genome size range varying over 222-fold (0.72–160.4 Gbp), including the largest eukaryote genome recently discovered in the fern *Tmesipteris oblanceolata* (1C=160.4 Gbp). The central focus of this research is to enhance our understanding of the genomic processes contributing to the unique characteristics observed in fern genomes, shedding light on the broader evolutionary implications for plant genome size. The composition of the repetitive DNA fraction of the genome for each species has been identified and quantified through low-coverage genome skimming sequence data analysed with the RepeatExplorer2 pipeline. Overall, our results show that fern genomes have a more heterogenous genome landscape than angiosperms and, unlike them, they show a positive correlation of repetitive elements with genome size. Future studies will focus on identifying the particular role of specific families of repeats that are enriched or depleted in fern genomes, while diving deeper into the relationship between the accumulation of chromosomes and its implication on genome composition.

S.24.4 The Crocus Chronicles: Decoding the Triploid Puzzle of Clonal Saffron Crocus

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Saffron crocus (*Crocus sativus* L.), a sterile triploid (2n = 3x = 24), is a clonally propagated crop grown for the production of saffron, the highest priced spice of the world. The evolutionary origin of the triploid *C. sativus* was largely unknown, but debated since the early 20th century. Recent cytogenetic and comparative next-generation sequencing approaches pointed to ancient Greece as a point of origin for saffron and concluded that *C. sativus* is an autotriploid species solely derived from heterogeneous diploid cytotypes of *C. cartwrightianus* (Schmidt et al. 2019, Nemati et al. 2019, reviewed in Kazemi-Shahandashti et al. 2022). Here, we target the processes before and after emergence of triploid saffron crocus. With this, we can look into the past, present and future of this clonal line: (1) **The past: How is chromosomal variability in the progenitor** *C. cartwrightianus***?** We detected large differences in haplotype variability among chromosomes, suggesting that some *C. cartwrightianus* chromosomes have obtained a higher genetic diversity across the Mediterranean than others. This haplotype diversity is fixed in saffron's karyotype, a testimony to the genetic variability of *C. cartwrightianus* 5000 years ago. (2) **The present: Are there signs of somaclonal variability in the saffron clone?** By comparing triploid saffron accessions across the globe, we detect chromosomal variability in three independent instances. We conclude that several saffron lineages evolved somaclonally after emergence of triploid saffron crocus. These saffron lineages have likely spread and are retained by vegetative propagation. (3) **The future: Can the global cultivation of the saffron crocus clone serve as a model for the epigenetics of adaptation?** As the basis for comparative and epigenetic analyses, we are assembling reference genomes of the triploid saffron crocus and the diploid progenitor *C. cartwrightianus*. We show the progress of sequencing, assembly and chromosomal anchoring.

S.24.5 Repetitive DNA elements reveal contrasting evolutionary responses to the polyploid genome shock hypothesis in Brachypodium grasses

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The *Brachypodium* grass species serve as model plants for studying the functional genomics of grass crops, and for elucidating the origins of allopolyploidy and perenniality in monocots. However, significant variations exist in genome sizes among different *Brachypodium* diploid and polyploid lineages. To explore the composition, abundance, and phylogenetic significance of repetitive elements in these lineages, we utilized low-pass genome sequencing data from 44 representatives. Our study aimed to test the potential mechanisms and consequences of the "polyploid genome shock hypothesis" (PGSH) in three distinct evolutionary scenarios, analyzing repeat and genome size variations in *Brachypodium* allopolyploids. Our findings revealed a 3.3-fold difference in the proportion of the genome covered by the repeatome, ranging from 20.77% in *B. stacei*-2x to 67.97% in *B. mexicanum*-4x. Changes in genome sizes were attributed to gains or losses in repeat elements. The most prevalent repeat elements in the *Brachypodium* genomes were LTR-Retand and Tekay retrotransposons.

Repeatome phylogenetic networks exhibited high congruence with plastome, nuclear rDNA, and transcriptome trees, distinguishing ancestral outcore lineages from recently evolved core-perennial lineages. The rDNA 5S graph topologies aligned well with ploidy levels and types of subgenomes of *Brachypodium* polyploids. The core-perennial *B. sylvaticum*-2x displayed a large repeatome, indicative of a post-polyploid diploidized origin. Our study evidenced that expansions and contractions in the repeatome accounted for three contrasting responses to PGSH: the exacerbated genome expansion of the ancestral allotetraploid *B. mexicanum* was a consequence of chromosome-wide proliferation of TEs and not of WGD, the additive repeatome pattern of young allotetraploid *B. hybridum* of stabilized post-WGD genome evolution, and the genome shrinkage of recent core perennials polyploids (*B. pinnatum*, *B. phoenicoides*) of repeat losses through recombination. Our analyses have contributed to disentangling the evolution of the repeatome and the genome size variation of model *Brachypodium* grasses.

S.24.6 A comparative look at genome fractionation in pteridophytes

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Genetic variation created by whole genome duplication (WGD) events can provide beneficial genetic variation for evolution to act upon. However, polyploid genomes comprise many, sometimes unnecessary, duplicated genes. The loss of these duplicates is part of the process of diploidization. One mechanism of diploidization is fractionation, where genes are lost or silenced in one or both homoeologs. Fractionation structurally and functionally alters the genome as only a subset of duplicated genes is retained. This affects the amount of genetic variation present following diploidization, influencing how a lineage will be able to evolve. Despite its evolutionary importance, little is known about how fractionation occurs in different lineages of land plants, particularly in ferns and lycophytes (pteridophytes). In angiosperms, fractionation is thought to proceed quickly, mainly by gene loss. Previous work suggests that genes may be silenced rather than lost in pteridophyte genomes, and chromosomes are retained following WGD. We use newly available published genome sequences for ferns and lycophytes to examine how genome fractionation may be occurring. We find that pteridophyte genomes may fractionate relatively rapidly following WGD, but chromosome order and collinearity are preserved. Including pteridophytes, for the first time, in comparative work on fractionation is a key step to better understanding genome evolution in land plants.

S.25 TOWARDS INTEGRATIVE TAXONOMY. THEORY AND PRACTICE. SESSION 2

S.25.1 Demographic systematics–species circumscription through reciprocal illumination among multiple demographic levels and data sources

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Traditional morphological taxonomy utilises multiple preserved collections that collectively constitute a serendipitous sample of organisms that have been immediately killed and often also dismembered, thereby reducing the number of morphological characters available for subsequent study. The comparative approach typically applied to herbarium specimens prioritises qualitative description above quantitative analysis and cerebral rather than algorithmic assignments of specimens to taxa; it also over-emphasises the holotype – a single point in space and time. The contrasting 'demographic' approach to taxonomy, illustrated here using studies of European orchids, employs a statistically rigorous in situ sampling strategy, and yields large volumes of fully quantified data of two or more kinds obtained from the same spectrum of individual organisms. Each sampled individual is subjected to character-rich morphometric data collection, describing every organ, and to equally detailed population genetic analysis; additional data categories are optional. Each category of data then undergoes multivariate ordination via an algorithm that does not require prior taxonomic assignment of individuals. This approach entails two contrasting forms of reciprocal illumination – the essential element in any truly scientific enterprise. (1) Organisms are aggregated into their source populations, and populations into infraspecific taxa and species, relatively large distances among sets of populations providing the basis of a genuine species circumscription process. (2) Confidence in, and the underlying nature of, the putative species boundaries are then determined through congruence among patterns of similarity in contrasting categories of data, addressed in the context of information gathered on extrinsic properties such as symbiotic relationships, habitat preference and putative geographic distribution. Although the demographic approach consumes considerably more time and resources than traditional taxonomy, it rigorously tests initial species hypotheses and provides far deeper understanding of the resulting species – perhaps even sufficient to predict their behaviour in the face of environmental challenges such as climate change.

S.25.2 Integrating different sources of data to disentangle the taxonomy of Nothoscordum (Allioideae, Amaryllidaceae)

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Nothoscordum (tribe Leucocoryneae) is a New World genus distributed mainly in South America. The huge number of species (ca. 60 new species described in the last three decades out of a total of 89 accepted species at POWO), and the difficulty or impossibility of contrasting the description with types, illustrations, and keys to species has created a taxonomic confusion. This problematic scenario together with the complexity of finding diagnostic characters and the presence of reticulate patterns in the evolution of the genus, has made the identification of the species a real challenge. The aim of our research is to integrate different disciplines to define taxa within *Nothoscordum* as part of the main goal of reconstructing the evolutionary history of the tribe Leucocoryneae. We have gathered 130 specimens and inferred their phylogeny based on the complete chloroplast genome and genome-wide GBS loci, and collected where possible cytogenetic data. Furthermore, we have statistically analyzed morphological data from included specimens in molecular analyses as well as from type specimens (matrix size: 32 characters x 160 specimens). As a result, the gathered information agrees at some taxonomic levels (e.g., sections within *Nothoscordum*) but only partially in other cases (e.g., on the species level). Traditional morphological characters used to distinguish species are in most cases not enough to discern them, and it is important to consider molecular data, phenology, and ecological traits as well. Karyotypes are also helping to discriminate some monophyletic groups. In summary, we dive into the challenges of linking the different datasets, and the new questions that have emerged.

S.25.3 Are all these carnations supported? Insights from integrative taxonomy of the Dianthus virgineus complex (Caryophyllaceae)

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Species are hypotheses about how biological diversity is structured in nature, and robust hypotheses are typically supported by multiple lines of evidence. However, traditionally botanists have been prone to circumscribe species relying just on morphological observations. For instance, the *Dianthus virgineus* complex includes 21 wild putative species/subspecies in the central Mediterranean recognized according to qualitative morphology, but their boundaries await to be explored with other approaches. Thus, we are conducting an integrative taxonomy project to test the current taxonomy of the complex. For this purpose, we collected morphometric, cytogenetic, and genomic (ddRAD-seq) data from over 100 populations belonging to all the 21 taxa. The global structure of the morphometric dataset, built using continuous and categorical variables, suggest the presence of just two main groups. Populations distributed from southern France to peninsular Italy show shorter calyx teeth, epicalyx scales and mucros with respect to populations from Sicily and Corso-Sardinian system (including Tuscan Archipelago). These two groups show sub-clusters, only in some cases mirroring currently accepted taxa. These plants are all diploid with constant chromosome number ($2n = 2x = 30$), albeit relative genome size is slightly higher in populations from Sicily and from Corso-Sardinian system. Genotyping thousands of SNPs revealed a genetic structure that parallels geography rather than taxonomy. Studied populations from the central Mediterranean belong to a unique genetic lineage, structured in two major clines. A first cline extends from southern France to the southern part of the Italian Peninsula, and the other from the Italian Peninsula to the Tuscan Archipelago, Corsica, and Sardinia. Sicilian and Sardinian populations are linked through those originating from Tunisia. All these evidences point to a number of groups lower than currently recognized taxa. In-depth morphometric classification models and multispecies coalescence model-based approaches are currently ongoing to test current and alternative taxonomical settings.

S.25.4 Tackling taxonomy of the mega-diverse genus Begonia

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Large genera are at the forefront of taxonomic endeavour, as they often need a considerable amount of work and represent unique challenges due to the number of species involved, such as how to delimit bite-size groups for revision and how to best work collaboratively. Here we demonstrate an approach to tackling the taxonomy of the mega-diverse genus *Begonia* (2132 accepted species), using a relational database system (PADME) developed at the Royal Botanic Garden Edinburgh to manage nomenclatural and specimen linked data. We built on published hard copy checklists to make an electronic checklist of current nomenclature and taxonomy. We then added images of protologues and specimens, and included specimen-associated information in the database, with currently 60,327 specimens. What emerged was a specimen-driven multi-user dataset, permitting checklist production for any geographic area annotated with current nomenclature plus type and other herbarium specimens, facilitating a new wave of taxonomic work on the genus. Specimen annotations such as phenology and georeferenced localities have supported emergent global scale macroecological studies on the genus. More recently, we have used DNA data to craft a new stable subgeneric classification for *Begonia* in order to facilitate revisionary taxonomy and identification, and also added species descriptions from protologues, revisions and floras in a World Flora Online compliant format. We now have a 50% complete draft WFO account for the world's fastest growing genus. Our approach shows the value of the investment of time in baseline taxonomy, and the facilitatory effects of regional checklists and digitised specimens.

S.25.5 A heuristic approach to species delimitation in the charismatic giant waterlily genus Victoria

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Reliably documenting plant diversity is necessary to protect and sustainably benefit from it. At the heart of this documentation lie species concepts and the practical methods used to delimit taxa. Here, we apply a total-evidence, iterative methodology to delimit and document species in the South American genus *Victoria* (Nymphaeaceae). The systematics of *Victoria* has thus far been poorly characterized due to difficulty in attributing species identities to biological collections. This research gap stems from an absence of type material and biological collections, also the confused diagnosis of *V. cruziana*. With the goal of improving systematic knowledge of the genus, we compiled information from historical records, horticulture and geography and assembled a morphological dataset using citizen science and specimens from herbaria and living collections. Finally, we generated genomic data from a subset of these specimens. Morphological and geographical observations suggest four putative species, three of which are supported by nuclear population genomic and plastid phylogenomic inferences. We propose these three confirmed entities as robust species, where two correspond to the currently recognized *V. amazonica* and *V. cruziana*, the third being new to science, which we describe, diagnose and name here as *V. boliviana* Magdalena and L. T. Sm. Importantly, we identify new morphological and molecular characters which serve to distinguish the species and underpin their delimitations. Our study demonstrates how combining different types of character data into a heuristic, total-evidence approach can enhance the reliability with which biological diversity of morphologically challenging groups can be identified, documented, and further studied.

S.25.6 Reconciling the taxonomy, morphology, and evolutionary history of the coca crops (Erythroxylum spp.)

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Coca represents one of the most culturally significant and oldest crops in the Americas. As the natural source of cocaine, coca is also internationally proscribed under various applications of taxonomy and/or biochemical data. However, recent phylogenetic and phylogeographic studies of the coca crops and closest wild relatives have revealed a complex evolutionary blueprint substantiating taxonomic revisions. The widespread wild species Erythroxylum gracilipes is a paraphyletic taxon containing two or three clades of coca taxa (E. coca and E. novogranatense; each with two varieties) plus the wild species E. cataractarum. Additionally, genetic, and morphological studies indicate intraspecific hybrids are being cultivated for the illicit cocaine market. This presentation provides an overview of the recent genetic and morphological research on the coca clade and discuss various taxonomic proposals that could be more informative of this evolutionary history.

S.26 AFRICAN TAXONOMY: A COLLABORATIVE EFFORT TOWARDS BIODIVERSITY CONSERVATION. SESSION 1

S.26.1 Taxonomic revision of the genus Eulophia R. Br. (Orchidaceae) in Ghana

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Eulophia R. Br. is one of the prominent ground orchids in West Africa and Central Africa, however, there is no complete taxonomic revision of the genus *Eulophia* in Ghana although a revision has been carried out in Nigeria, Cameroon, Equatorial Guinea, Gabon, and the Republic of the Congo. The goal of this study is to determine the range of morphological variations within the genus in order to clarify the delimitation of the taxa in Ghana; evaluate aspects of the ecology and distribution of the genus in Ghana. Field trips to collection sites as cited by the major herbaria in Ghana yielded no live plants although the visits were done following the cited collection dates. Urbanization and land use change is quickly destroying the habitats of the members of this genus. Morphological studies carried out on preserved specimens suggested eight species of *Eulophia* in Ghana, with the most common members found in grasslands. Members of the genus have a cosmopolitan distribution across the country, with the least distribution around the western part. The genus produces flowers and fruits between March to May, with the exception of *E. cristata* (Afzel. ex Sw.) Steud. producing flowers in January also.

S.26.2 A case for the nameless – Accelerating plant taxonomy as a tool for conservation, using Indigofera as a case study

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The saying that we cannot conserve what we do not know presents one of the greatest dilemmas in the face of a probable sixth mass extinction. While many large and charismatic organisms enjoy substantial conservation efforts in terms of funding and public sentiment, thousands of smaller and lesser-known species face the prospect of extinction out of the public eye. We are for fortunate to have one of the best plant red data lists globally that helps to monitor our more than 20 000 plant species in South Africa. Yet, despite a rich history of plant taxonomy in SA dating back to the 1700's, many of our plant species remain undescribed and poorly known. *Indigofera* is an example of a genus that is poorly known and harbors numerous undescribed species. The Greater Cape Floristic Region (GCFR) is home to a diverse assortment of *Indigofera* species, but the last taxonomic account of these species was done in 1862. I aimed, in my PhD study, to taxonomically revise the genus *Indigofera* in the GCFR. Following an intensive regime of field sampling and herbarium analyses, I found 55 undescribed *Indigofera* species in the GCFR, meaning that these 55 species have never received any conservation attention, with some of these species being severely threatened. However, through this study, we now understand and recognize the diversity of *Indigofera* in the GCFR and can inform conservation authorities and landowners of the presence of these previously unknown species. The extensive fieldwork conducted during this study has contributed invaluable information that can be used to help conserve these species by identifying past, present and future threats. This study demonstrates the value of taxonomic studies when combined with extensive field sampling, in firstly helping to understand and quantify species diversity, and through that contribute to the subsequent conservation of biodiversity.

S.26.3 Rediscovery of Nymphaea thermarum Eb. Fisch. in Rwanda

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Nymphaea thermarum is a small waterlily endemic to Rwanda that is being assessed as extinct in the wild since 2010. The species has been rediscovered in July 2023 not far from its *locus classicus*. We report on the rediscovery of *N. thermarum*, identify the current and potential threats for the wild populations, namely mining and overharvesting by collectors, respectively and provide a list of urgent conservation measures and research required to save the species from "re-extinction". The species occupies small muddy ditches fed by hot springs water use to water Avocado plantations and fish pools. The population counts hundreds of individuals including adult reproducing plants and seedlings. In the short term, important conservation actions should include land protection, negotiation to ensure that enough water is reaching the habitat of *N. thermarum* and the reassessment of the species against the IUCN Categories and Criteria to update its status. In a new formal IUCN assessment, the species would quality as Critically Endangered. In the medium-term the creation of a nature reserve, the restoration of the areas already affected by mining and the reintroduction of *N. thermarum* to its original site, would place the species into a better position for its long-term in situ conservation.

S.26.4 Potential impacts of climate change on geographic distribution and conservation of the genus Talbotiella

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Although climate change is a leading cause of species extinction, the effects of climate change on geographic distributions and conservation status of African plants have not seen detailed evaluation. We employed ecological niche modelling approaches to investigate the potential effects of climate change on geographic distributions of the threatened West-Central African genus *Talbotiella*. The results of the study showed habitat suitability was lower in the northern parts of its range in West Africa and at it's southern extremes in West-Central Africa. Potentially suitable areas where new populations or species of the genus could be discovered in West Africa was between Liberia and southwestern Ghana. Model transfers to future conditions showed range shifts and contractions in geographic distributions. Conservation of species of the genus should also include threats by factors such as degradation, agriculture and development of industrial infrastructure. Our study shows how niche modelling approaches could be used to enhance the conservation and discovery of African biodiversity.

S.26.5 Digitization and Enrichment of U.S. Herbarium Data from Tropical Africa to Enable Urgent Quantitative Conservation Assessments

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Herbarium specimens represent a rich source of data on plant diversity. These rich information resources, however, too often remain in analog format only, and have not been digitized and "enabled" in the service of science. This project aims to digitize, enrich, and share openly the rich data resources held in 21 U.S. herbaria that correspond to plants of tropical Africa, which will total more than 1.1 million herbarium specimens. Imaging and data capture is being carried out at each of the herbaria, and data are then aggregated for efficient georeferencing. For most records, georeferencing is being performed automatically, and the remainder will be georeferenced manually by plant scientists in Ghana, Rwanda, Malawi, and Gabon. Finally, project data will be subjected to detailed quality-control assessment and served openly to the scientific community via a dedicated "African Plants" portal on Symbiota (https://serv.biokic.asu.edu/africa/plantae/index.php), as well as integration into biodiversity data portals such as iDigBio and GBIF. The project has thus created a broad, international, intercontinental network of scientists and students interested in and experienced with management and analysis of data about African plant distributions. These rich data resources will be used to understand the conservation status of African plant species in much greater detail than has been possible to date.

S.26.6 Enhancing taxonomy skills in Africa: joining efforts in training and international collaborations

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Plant taxonomy is a diverse and increasingly integrative discipline. With the expansion of digitally available collections, innovative molecular methodologies and geospatial analyses, there is an outstanding opportunity for this field to grow, and for the African continent, in particular, to accelerate the documentation of its plant diversity as never before. However, insufficient specialised human resources, unequal access to resources, and deficient infra-structure could weaken this momentum. Enhancing taxonomy training in Africa is key to filling in the specialists' gap and overcome biases and inequalities in access to these skills. This presentation offers an overview of current challenges and opportunities for plant taxonomy training, particularly in Africa, with suggestions on how to strategically design plant taxonomy training initiatives that efficiently tackle regional needs, fostered by international collaboration.

S.27 A CONTINENTAL SCALE CONSORTIUM APPROACH TO BUILDING GENOMICS CAPACITY AND RESOURCES: GENOMICS FOR AUSTRALIAN PLANTS. SESSION 2

S.27.1 Resolving taxonomy challenges in species complexes using conservation genomics

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Species complexes are often present in floras with high diversity driven by complex evolutionary history and associated high speciation and low extinction rates. Whilst most species are readily identified and described, there are many species complexes where taxa are challenging to resolve though morphological analysis alone. Genomic approaches can assist in this challenge through identification of relationships at the species-population interface providing an evolutionary basis for identifying taxon boundaries, including where ongoing hybridisation confuses morphological relationships. The Genomics for Australian Plants initiative is a national collaborative program that is developing genomic resources to enhance understanding of the evolution and conservation of the diverse Australian flora. One of its three components is application of a conservation genomics approach to taxonomic resolution of challenging species complexes in the Australian flora. This integrated approach brings taxonomists and geneticists together, applying an evolutionary biology lens to identification of taxonomic entities. The focus has been on resolving taxa in complexes where there are likely taxa of conservation concern so they can be defined and considered in conservation listing, facilitating implementation of management actions. The initiative has supported projects covering 11 species complexes and clarified relationships amongst entities, using ddRAD genomic data in combination with morphological assessment. The relative outcomes of ddRAD and the angiosperm 365 bait kit were also tested for four species complexes. These analyses have led to the identification of species of conservation concern, as well as clarification of situations where morphological variation is not reflective of taxonomic separation, or where hybridisation is a complicating factor obscuring morphological relationships. The outcomes demonstrate the benefits of an integrated approach using genomic and morphological methods to facilitate taxonomic resolution of species complexes. This approach may be readily implemented in other highly diverse floras where taxonomic identification of conservation entities is critical to effective conservation action.

S.27.2 Using genomic tools to explore diversity in Southwest Australian plants of conservation concern

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The Southwest Australian Floristic Region contains high angiosperm diversity (>7500 species) often occuring in managed landscapes with varying levels of anthropogenic disturbance, which creates a taxonomic and conservation challenge to understand, classify and protect these organisms. Evolutionary patterns in the flora of this historically stable region are diverse, with widespread, genetically-connected lineages contrasting those with restricted or discontinuous ranges and complex genetic structure. While much of the flora has been described, some groups with morphological complexity or subtlety (and putative evolutionary complexity) have frustrated taxonomists and prompted the use of genomic techniques to help unravel that complexity. As part of the Genomics for Australian Plants initiative, we applied reduced representation genomic approaches (ddRAD, sequence capture) to species complexes suspected to contain cryptic taxa of conservation concern. Our goal was to resolve the taxonomy of these complexes. We present some of our results, along with reflections on the effectiveness and appropriateness of the molecular approaches for our goal. Our findings include unexpected diversity leading to the recognition of more species, as well as the contrasting pattern of unanticipated genetic connectivity leading to fewer species. We also encountered challenges that reflect the complex biology of these systems and highlight the need for fundamental knowledge of e.g. breeding system, ploidy and dispersal patterns when approaching this flora and interpreting genetic data.

S.27.3 A species-level phylogeny of eastern Australian Phebalium Vent. sect. Phebalium Duretto & Heslewood (Rutaceae; Zanthoxyloideae)

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Phebalium Vent. sect. *Phebalium* Duretto & Heslewood is an Australian endemic monophyletic group of species with 14 species distributed in south-western Australia and 21 in eastern Australia. Most species of *Phebalium* have strong horticultural potential, while many are narrowly endemic and of high conservation value. Underpinned by morphological, phytochemical and molecular data, we recognised 15 new species, and we are reinstating four species and raising eight subspecies to the rank of species. From the few previous studies in *Phebalium*, most species-level relationships remained untested or unresolved. Our SNP-based phylogenetic analysis of all eastern Australian *Phebalium* taxa, including the newly delimited species, was carried out using maximum likelihood with IQ-TREE2 and maximum parsimony with PAUP. We also inferred phylogenetic relationships under a coalescent model using SVDquartets. The phylogenetic relationships inferred under all models were concordant. Our analyses recovered three major clades within eastern Australian *Phebalium* corresponding to three species complexes involving *P. squamulosum, P. glandulosum* and *P. nottii.* The monophyly and inter-specific relationships of most of the eastern Australian species of *Phebalium* were resolved and will be discussed.

S.27.4 Phylogenomic analysis of generic limits underpins a systematic study of Chrysocephalum (Gnaphalieae, Asteraceae)

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Chrysocephalum Walp. is a medium-sized genus in the Waitzia clade of the Australian Gnaphalieae (Asteraceae), comprising nine currently recognised species and two phrase-named species. In a recent revision of the *C. apiculatum* and *C. semipapposum* complexes (Wilson 2016), 34 subspecies were added based on morphological characters, with a high level of complexity making distinction difficult among them. Detailed relationships within the clades of the Gnaphalieae remain largely unresolved, and generic concepts have often been based on a small number of morphological characters traditionally considered important. We have inferred a molecular phylogeny of selected Australian native Gnaphalieae (Asteraceae) to test the monophyly of the *Chrysocephalum* using target capture sequences and a bioinformatics pipeline co-developed through the Genome of Australia Plants Consortium. A group of three species form the “core” *Chrysocephalum* clade, *C. apiculatum* (type species), *C. semipapposum* and *C. vitellinum*. Arid zone species form separate clades. We are also resolving species-level relationships with molecular and morphological analyses. This study will resolve long-standing taxonomic issues and, as the study group includes several rare and threatened taxa whose status will be clarified, will also support biodiversity conservation.

S.28 EVOLUTIONARY ECOLOGY OF PLANTS. SESSION 2

S.28.1 Rapid evolution of ecological strategies in Arabidopsis thaliana

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The study of ecological strategies, *i.e.,* sets of co-varying traits that match with environmental conditions in a potential adaptive way, helps to address the role of the phenotype as a whole, rather than individual traits, in adaptation. Because, in the field, covariation between environmental conditions makes it difficult to test for the concrete factors driving ecological strategies, experimental approaches can be valuable. Using experimental evolution, we tested for the evolution of both mean phenotypes and their variance in response to contrasting levels of stress (resource availability) and disturbance (herbivory) in *Arabidopsis thaliana*. By tracking the phenotypic space formed by whole-plant and leaf traits, we found that, after only three generations, *A. thaliana* populations diverged both in terms of phenotypic variation and trait syndromes in response to contrasting resource and herbivory treatments. The most divergent responses were found to evolve under low and high resources without herbivory: a strategy of fast-growth for stress escape and a strategy of slow-growth for competitive ability, respectively. Furthermore, these strategies have been shown to be adaptive and possibly density-dependent. Our results highlight the rapid evolution of plant strategies in response to stress and disturbance and the key importance of population size in ecological analyses.

S.28.2 Plant epigenetics: a contribution to understanding phenotypic variation in changing environments

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Epigenetics investigates phenotypic variation that is not accompanied by changes in DNA sequence, but instead involves the set of chromatin modifications that regulate the ability of a certain genome to produce diverse phenotypes. In plants, DNA cytosine methylation is a key epigenetic mechanism involved in genome stability and developmental change. In the last few decades we have learned that Angiosperms have evolved specific DNA methylation enzymes and pathways (e.g., chromomethylases, RNA-directed methylation) which target cytosines in any sequence context and genomic location, and that genome-wide cytosine methylation level is largely variable across species and has a strong phylogenetic signal and phenotypic correlates within and across plant individuals. Furthermore, changes in DNA methylation induced by environmental stress and transgenerational transmission of some methylation marks have been documented for many plant species. It remains unclear, however, the extent to which inter- and intra-specific variation in the ability of a given genotype to produce phenotypic variants depends on intrinsic genomic features and/or the ecological characteristics of their environments. In our group we have assessed epigenetic variation in wild plant populations at different spatial scales and adopted experimental approaches which combined a controlled alteration of epigenetic features (e.g., by applying demethylating agents) with exposure to selected biotic and abiotic stress factors. I summarize what we have learned from applying these two approaches to a set of non-model plant species. Understanding the relationships between phenotypic traits and changes in DNA methylation in contrasting environments is crucial to uncover the potential impact of epigenetics on fast plant adaptation to changing environments under current scenarios of climate change. Integration of molecular understanding gained from model species and ecological significance assessed in non-model plant species should contribute to better value the contribution of epigenetics in plant adaptation and evolution.

S.28.3 Genetic and phenotypic differentiation in functional traits of Iris pseudacorus L. in native and introduced ranges

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Intraspecific variation in functional traits between native and alien invasive plant species may underlie resilience and invasiveness of aliens facing new physiological limits in response to climate change. Using a common garden experiment, we explored if observed phenotypic variation of *Iris pseudacorus* L. between tidal wetland populations in the native vs. invaded range may be explained by genetic differentiation and/or phenotypic plasticity. Iris seeds were collected from populations under Mediterranean climate along estuarine salinity and inundation gradients within four native and invasive populations in both Guadalquivir Estuary (Andalusia, Spain) and San Francisco Bay-Delta Estuary (California, USA). Germinants were potted (6 plants x 4 populations x 2 ranges; n = 48 experimental plants) and grown for 12 months under uniform environmental conditions. We then evaluated 23 functional traits including growth, biomass allocation, morphological and biochemical responses. Genetic analysis was performed on leaf tissue collected from plants in each seed donor population. Geographic range explained relative intraspecific trait variation segregating native from alien phenotypes. Native plants had lower SLA (-23%) and rhizome TNC concentrations (-63%) than introduced plants, providing evidence of genetic differentiation. Higher genetic diversity in the field and 27% higher phenotypic variation in the CGE for native compared to alien plants indicate longer-term adaptive processes in the native range, while genetic distance of alien field populations increased along with their phenotypic distance in the CGE suggesting rapid genetic differentiation. Phenotypic plasticity also explained some observed inter-range phenotypic differences in response to environmental conditions, since these field differences were not expressed by plants in the

CGE. Management of alien *I. pseudacorus* in the invaded estuary should be established urgently since they represent novel genotypes with key functional traits that can support invasiveness through high competitive ability and physiological stress tolerance responses to sea level rise.

S.28.4 Fitness and barriers to gene flow related to flower colour variation in a snapdragon hybrid zone

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A fundamental question in evolutionary biology is how phenotypes and their underlying genes interact to generate reproductive barriers between populations. The fitness landscape has been an influential framework to model these connections, yet direct measures of how multiple genes interact to create fitness valleys between populations remains challenging to obtain in nature. I present some of the work we've been doing to address this gap by exploiting a natural hybrid zone between subspecies of *Antirrhinum majus* (snapdragons) with a well-defined genotype-phenotype map. This work includes investigations into the molecular genetic basis of flower colour, ecological experiments on the agents of selection, and the development of novel population genomic approaches to detect barriers in the genome. A key focus will be on our multi-generational study, where-by genotyping and phenotyping over 30,000 plants over 14 years, we've obtained a pedigree-based estimate of the fitness landscape separating these recently diverged subspecies. At deeper evolutionary time scales, using whole-genomes along geographic clines we find the absence of a genome-wide barrier to gene flow with only a small proportion of the genome resisting introgression. By linking recent ecological time-scales of fitness variation in nature to patterns of deeper genomic divergence, our goal is to provide a general model for how reproductive barriers arise during the early stages of divergence.

S.28.5 Above- and below-ground trait covariation in perennial herbaceous species

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A fundamental question in plant evolutionary biology is how species that live for multiple years balance resource allocation over time to sexual reproduction (seed production) relative to vegetative growth. One component of this is understanding how reproductive output covaries with vegetative traits (e.g., stem thickness, leaf number, leaf thickness, physiology, root biomass, etc.), how these relationships shift from one year to the next, how they vary under different environmental conditions, and how they change in response to strong selection for increased reproduction output. Although the direction and magnitude of trait correlations can constrain or enhance response to artificial or natural selection, there are few comprehensive studies that describe relationships between traits expressed at early life stages (e.g., seed size and weight, germination timing, germination rate) with traits expressed later in life (e.g., reproductive output, root/shoot biomass ratio in Y1, Y2, Y3, etc.) in perennial herbaceous species. Here, we phenotyped seeds and seedlings of 1,650 plants representing eleven perennial, herbaceous species in the Asteraceae, Fabaceae, and Poaceae families, planted those individuals in a spaced plant nursery in Gray Summit, MO USA, and monitored height, flowering time, and yield over three years. We estimated root traits via soil cores in Y2 and Y3, and then excavated root crowns for further phenotyping. Analyses to date indicate strong correlations within and among life-stages, among reproductive and vegetative traits, and among above- and below-ground traits. These core questions can provide key insights into how perennial, herbaceous species evolve under in nature and under artificial selection and may expedite pre-breeding and domestication of perennial grain crops through early stage selection of traits correlated expressed in seeds and seedling that correlate with desirable traits expressed at later life stages.

S.29 AEROBIOLOGY. ADVANCES IN THE ATMOSPHERIC POLLEN RESEARCH AND CHALLENGES IN THE CONTEXT OF GLOBAL CHANGE. SESSION 1

S.29.1 Metabarcoding and metagenomics techniques in monitoring airborne pollen

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The importance of monitoring the concentration of pollen in the atmosphere has been widely demonstrated from the environmental, ecological and agronomic point of view, as well as from the perspective of human health, since allergenic pollen represents the most important cause of pollinosis globally. Traditionally, pollen concentrations in the air are estimated from analyses based on identification and quantification using optical microscopy. However, the classification of pollen types at the species level using this procedure is limited. This is due to the morphological characteristics of the pollen grains used for their recognition, often shared within genera, families, and even taxonomic orders. An alternative approach is the identification of pollen through molecular sequencing and DNA analysis. Different high-throughput sequencing (HTS) technologies have been used to massively analyse environmental DNA and therefore the airborne pollen. This process requires, before sequencing, the preparation and amplification of the specific library for each sequencing platform. "Ion Torrent" (ThermoFisher), "GenapSys" technology and above all "Ilumina", represent several platforms that sequence with the metabarcoding procedure short DNA fragments (reads) up to a few hundred base pairs in length. Other platforms called "third generation sequencing" such as "PromethION", "GridION" and "MinION" from "Oxford Nanopore Technology" and "PacBio CCS" from "Pacific Biosciences", generate much longer reads (LR) than those obtained in the previous ones, however they are still little used in aerobiology. This study presents a review and the state of the art of airborne pollen studies based on metabarcoding and metagenomics, as well as the limitations of these molecular analyses.

Acknowledgments: This study is conducted in the frame of Cost Action CA18226 (New approaches in detection of pathogens and aeroallergens) and has been carried out by the members of Working Group 2.

S.29.2 Airborne pollen trends in the Iberian Peninsula during the last three decades: flowering timing and intensity

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Airborne pollen significantly impacts air quality, human health, and ecosystems. Effective pollen monitoring is essential for understanding these effects and advancing in air protection strategies. Pollen allergies, affecting a substantial global population, lead to respiratory issues and decreased life quality. Pollen monitoring also informs climate change research, agriculture, and forestry; shifts in pollen seasons indicate the climatic change impacts on vegetation and aiding in fruit production forecasting. Airborne pollen is a good indicator of floral phenology and intensity on anemophilous plants. Historical databases allow to study pollen season timing and intensity. The Mediterranean Climate is wet and mild during winter, and warm and dry in summer. During recent decades, the climate is changing on increasing temperatures and to the lack of water availability, due to a different precipitation pattern with more frequent floods and droughts. These trends are affecting to plant responding to extreme events. Woody plants response more to temperatures, especially those flowering during winter or early spring. Herbaceous plants respond more to water availability. Many recent studies have shown an advance in flowering start, specially on woody plants. However, winter is getting warmer, and the plants are not sufficiently exposed to chilling temperature for break dormancy and budburst; with lack of chilling requirements the forcing process at early spring will not be as effective, that together the lack of water, may cause a delay on flowering. Weeds and grasses respond more to water availability, although in different way, with an advance or delay depending on the species. For this reason, recently there are evidence of longer pollen seasons because more diversity on flowering timing. Regarding flowering intensity, recent studies also support the higher pollen season intensity, probably due to increasing CO2 in the air; however, in the Mediterranean climate it does not always occur due to lack of water.

S.29.3 Effect of long-distance pollen transport on the local and regional airborne pollen evolution

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Long-distance pollen transport, primarily wind-facilitated, profoundly influences local and regional airborne pollen dynamics, impacting genetic diversity, species composition, allergen exposure, seasonal timing, ecological interactions, climate change implications, and biogeographical patterns. The transport introduces genetic material from distant populations, fostering increased genetic diversity within local plant populations for enhanced adaptability to environmental changes. Pollen transport alters the species composition of local and regional plant communities, potentially introducing new species or amplifying the abundance of certain ones, influencing regional biodiversity. The process significantly affects allergen exposure by introducing allergenic species, extending pollen seasons, and altering overall allergen composition, posing implications for public health. Understanding the impact of long-distance pollen transport on seasonal timing is crucial for predicting changes in allergen exposure patterns, with direct implications for public health. Ecological interactions arise, such as competition between introduced and native plant species, leading to cascading effects on local ecosystems and changes in insect and bird populations reliant on specific plant species for food. The complex interplay between long-distance pollen transport and climate change is pivotal for predicting ecological responses, managing biodiversity, and devising strategies to mitigate climate-driven environmental impacts. This interconnectedness contributes to biogeographical patterns, connecting plant populations across geographical regions, vital for maintaining genetic exchange and preventing isolation among plant populations. Monitoring pollen movement aids researchers in assessing the impact of global and regional environmental changes on plant populations. In summary, long-distance pollen transport is a valuable tool for ecological research and environmental monitoring, providing insights into plant dispersal, genetic connectivity, climate influences, and ecological dynamics, contributing to a broader understanding of interconnected processes shaping ecosystems.

S.29.4 Response patterns of calendar and pollen intensity to climate at the southwestern distribution limit of Betula: a 30-year study

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We studied the relationship between the occurrence of *Betula* spp. airborne pollen and climate, during the main pollen season, as well as before and in the preceding year. Our aim was to understand how environmental conditions can influence the main pollen season and the intensity of airborne pollen presence at the meridional boundary of the *Betula* forest distribution in Europe. For this purpose, pollen monitoring was conducted using Lanzoni VPPS 2000 volumetric trap and nearby meteorological data. The study area was located in the northwest of the Iberian Peninsula, specifically in three cities with diverse mesoclimate: Vigo (Atlantic), Ourense (Mediterranean) and Lugo (Cantabrian), which had a distinct oceanic influence. Aerobiological data was conducted based on the Spanish aerobiology network protocol. Weather variables precipitation, maximum, minimum and mean temperature were selected for three-time windows: 1st the main pollen season period, 2nd from 5 to 90 days before the onset of pollen presence, with a cumulative five-day interval, and 3rd the average monthly climate of the previous year. Precipitation delays the onset of the main pollination season and also delays the end of the season, increasing pollen counts in the post-peak interval at all three areas. Temperature during the pollen season affects the duration and pollen integral differently among area. The pollen integral shows an increasing trend over the last decades at all three sites, and the increase in the minimum temperature of the previous summer explains this increase at all three areas from a climatic point of view. In conclusion, the effect of weather before and during the main pollen season has varied effects on the date-related data across the mesoclimate, while the increase in temperature during the summer of the last few decades results in a spring with higher airborne pollen loads for all three locations.

S.29.5 The aerobiology-floral phenology binomial. Phenoclimatic models for pollen forecasts.

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The release of pollen from a plant-source is characterized by a time distribution which is the consequence of the various flowering stages. The beginning of the release of pollen and the quantity of pollen that each plant produces are in relation to a series of biotic factors such as the genotype, the age, the size of the plants, and environmental factors such as the climate, other than edafic and phytosanitary factors. In the aerobiological studies phenological models are used to obtain information useful for forecasting the beginning of pollination of many species, expecially of agricoltural and allergological interst, and to know what will be the severity of the pollination or the quantity of pollen which will be released into the atmosphere day by day. Aerobiological historical data bases on the pollen content in the air, evidence how the climate change is affecting distinct species in different geographical areas. The aerobiology-floral phneology binomial can contribute to the improvement of bio-geographical and ecological information of vegetation, the forest health and vitality being important for the protection of the plant biodiversity. When a predictive model on beginning of pollination is being developed, it is necessary to take into consideration the different responses to environmental factors of the species considered. Temperature-based models are commonly used to predict floral bud-burst as universal models disregarding that they are site- and species-specific. Models working well in some regions might not respond so well in other areas due to genetic characteristics that enable plants to show different tolerance to particular environmental conditions. Modeling to predict the performance of the pollen season with the intention of giving a meaningful result as early as possible has led to the development of many analytical mathematical models, increasingly complex, like time series models, multivariate regression models, Artificial Neural Networks and more.

S.29.6 Real-time airborne pollen monitoring

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Between 20-30% of the European population suffers from pollen allergy, resulting in costs ranging from €50-150 billion per year. For decades, airborne pollen has been monitored using manual methods with counting being done by hand under the microscope and results reported as daily average values from 3-9 days after the measurement. New technologies developed over the past years are revolutionising this field. Combining artificial intelligence with advanced measurement methods, several devices are now available on the market that provide real-time observations of pollen as well as a considerable potential to detect and identify a range of other airborne particles. The EUMETNET AutoPollen Programme has been established in 2018 to take full advantage of the large potential for progress that automatic observations provide. It brings together a consortium from across Europe with the multidisciplinary expertise needed to address the challenges along the entire information chain – from the initial observation through to the final products and services co-designed with end users. As an example, the SwissPollen network, operated by MeteoSwiss, comprises 15 monitoring stations and since the beginning of 2023 provides hourly information in real-time through its website and smartphone app. Furthermore, the real-time observations are integrated into the COSMO-ART model to provide forecasts to end-users.

S.30 MERGING EVOLUTIONARY APPROACHES WITH ETHNOBOTANICAL KNOWLEDGE. SESSION 2

S.30.1 Estimation of Activity Concentrations of naturally occurring radionuclides in selected infant-herbs grown in Igbokoda, Ondo state

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The traditional use of medicinal herbs in treating infant ailments is entrenched in many cultures, including the coastal region of Ondo State, Nigeria. However, there is limited scientific information regarding their morphological characteristics and possible radiological health risks. This study aimed to investigate the morphological features and radiological health effects of six commonly consumed infant herbs. A comprehensive field survey was conducted to identify and collect representative samples of the selected infant herbs: Ananas comosus, Azadirachta indica, Carica papaya, Cymbopogon citratus, Jatropha curcas, Mangifera indica, Ocimum gratissimum, Psidium guajava, Vernonia amygdalina, and Zingiber officinale. Plant identification and classification were conducted morphologically to assess plants' growth habits, stem structure, leaf morphology, and flower characteristics. Radiation levels were measured to evaluate potential risks associated with the consumption of these herbs, using a portable radiation meter. The concentration of radionuclides (specifically, naturally occurring radioactive materials such as uranium, thorium, and potassium) was also determined using gamma spectroscopy techniques. The morphological studies revealed distinct features of each herb, aiding in their accurate identification and classification. Additionally, the radiological health impact assessment indicated relatively low radiation levels in the selected infant herbs, with concentrations of radionuclides falling within acceptable limits set by international regulatory bodies. Thus, the consumption of these herbs was determined to be unlikely to pose significant radiological health risks to infants and young children. This study contributes to the documentation of the morphological characteristics of commonly consumed infant herbs in the coastal region of Ondo State, Nigeria. Furthermore, the radiological health impact assessment provides valuable insights into the safe use of herbs for infant care. The findings can inform healthcare providers, traditional medicine practitioners, and the general public about the potential benefits and risks associated with the consumption of these medicinal herbs, promoting safe and informed choices in infant healthcare practices.

S.30.2 Market integration and changes in traditional practices in West Africa: the case of Shea

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Commercial and development actors influence traditional ecological knowledge (TEK) practices among rural populations in the global south through complex mechanisms. This paper explores this rural transformation dynamic through the case of shea (*Vitellaria paradoxa*). For centuries, women have collected and processed shea nuts into dried kernels, and subsequently butter. Over the last decades, the international demand for kernels has increased as opposed to butter. The results of 1100 household surveys conducted in Ghana and Burkina Faso about women's current and past processing methods and end-use of shea products, reveal that 1) processing methods are being homogenized, and 2) women abandon the butter making process in favor of selling shea kernels. This trend is more visible in Ghana, where especially younger women follow processing methods promoted by big companies and development institutions, in contrast to Burkina Faso, where there remains higher processing diversity, and butter production. Loss of diversity in processing methods may reduce the ability to adapt to external changes, such as market demands and climate change. The decrease in butter production is leading to matrilineal knowledge loss and has implications for the household economy, as women substitute shea butter for industrial, more expensive cooking oils and skincare creams. The study offers a critical analysis of how the dynamic and multidirectional nature of rural transformations and TEK influence resource users and the entire value chain.

S.30.3 Does scent guide Indigenous People's perception of medicinal plants?

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Understanding the interactions between people and plants is of great relevance for both biodiversity and biocultural conservation efforts. The use of plants has been considerably investigated based on morphological traits, but explaining how people recognize a plant's usefulness based on chemistry has been challenging. Here, we explore to what degree the selection and utilization of medicinal plants is influenced by people's smell perception of plants. We assess this through a literature review of works published over 50 years on smell perception and Indigenous People's knowledge of tropical plants. We find that the sense of smell may very well be a nexus between human-plant interactions, but the concept has been relatively complex to establish due to the confines posed by disciplinary perspectives and methodological limitations in most studies. To advance the field, we propose integrating phytochemistry with standard ethnobotanical data collection within study communities to better understand the role of plant scents and smell perception in medicinal plant selection.

S.30.4 Crop domestication is favored by higher competitiveness and resource-capture.

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One of the open questions regarding the relationship between humans and plants is why some taxa are domesticated and become crops while other ecologically and morphologically similar relatives are not. In all likelihood, this is mediated by functional differences between crops and their wild relatives. The identification of this key traits requires accounting for the divergence in ecological and demographic settings between natural populations and crop fields, in which interspecific density is much higher and diversity lower. Traits facilitating growth and survival under these conditions might have thus been relevant for domestication. Using a phylogenetically controlled experiment, we investigated whether domestication might be facilitated by functional traits that increase survival and growth under high density, hyper-competitive conditions. We picked three important annual legume crops, lentil (*Lens* sp.), grasspea (*Lathyrus* sp.) and vetch (*Vicia* sp.) and measured traits that determine competition (lodging; growth rate), resource acquisition (plant height; total aerial and root biomass) and yield (fruit no.). Bayesian models were fitted to these data to quantify the effects of evolutionary divergence between close wild and domestic relatives, as well as between natural and crop (landraces) populations of domesticated taxa. Our results showed important taxonomic differences, likely reflective of different selection pathways. Nevertheless, wild relatives consistently differed from their domesticated congeners in competition and resource acquisition. Never-domesticated taxa consistently produced smaller, slower-growing plants that were more prostrated and allocated less biomass to roots. Conversely, the effect of selection under domestication on vegetative traits was largely negligible, although it appeared to have led to an increase in yield. We conclude that, although domestication processes are always complex and case-dependent, they might indeed favor taxa that are particularly competitive and more effective in resource capture. Subsequent selection under domestication may have targeted reproductive traits (i.e., fruit and seed production).

S.30.5 Molecular authentication, quantification, and in vitro production of metabolites from different Swertia species

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Swertia is ethno-medicinally an important genus belonging to the family Gentianaceae. *Swertia chirayita* is used as an imperative medicinal plant in the Indian system of medicine. However, this species has been frequently adulterated due to its high demand and scarcity. Authentication of this species was needed to protect consumers and conservation measures and to find an alternative source. ITS region proves a robust molecular marker for differing the *S. chirayita* from its related adulterant species. All barcoding regions indicate that *S. chirayita* and *S. minor* both are more closely related than other *Swertia* species. Swertiamarin and mangiferin were estimated from different *Swertia* species and it was revealed that maximum swertiamarin and mangiferin content was found in *S. chirayita*, *S. minor,* and *S. angustifolia* species. Various extraction methods like static extraction (SE), continuous shaking extraction (CSE), and ultrasonic extraction (USE) were evaluated for increasing recovery % of swertiamarin and mangiferin from different *Swertia* species which revealed that SE was more proficient with 24 h extraction gave the maximum recovery in *S. chirayita* of swertiamarin (256.98 mg/g) and mangiferin (155.76 ± 7.78 mg/g). *In vitro* production of swertiamarin from cell suspension cultures of *S. minor* was studied chitosan-treated (25 ppm) cell biomass accumulated higher contents of swertiamarin than salicylic acid and methyl jasmonate. Findings showed that DNA barcoding is an efficient tool for the identification and authentication of *S. chirayita*. *S. minor* is remarkably the best match for *S. chirayita* as per molecular and phytochemical fingerprint is concerned, suggesting an alternative for chirayita. The described protocol can be effectively used for the large-scale propagation, and exploitation of active compounds and will serve as a potential alternative to *S. chirayita* for the fulfillment of over-growing industrial requirements.

S.31 THE ANGIOSPERM REPRODUCTIVE SPECTRUM FROM FLOWERS TO SEEDS. SESSION 2

S.31.1 Variation in fruit and seed dimensions is better explained by dispersal system than by leaf size in a tropical rainforest

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Variation in fruit and seed traits could originate from selection pressures exerted by frugivores or other ecological factors (adaptive hypotheses) and developmental constraints (by-product hypotheses) or chance. We evaluated fruit and leaf traits for nearly 850 plant species from a rainforest in Tinigua Park, Colombia. Through a series of linear regressions controlling for the phylogenetic signal of the traits (minimum N = 542), we tested (1) whether the allometry between seed width and length depends on seed dispersal system (Mazer and Wheelwright's adaptive hypothesis of allometry for species dispersed in the guts of animals = endozoochory) and (2) whether fruit length is associated with leaf length (i.e., Herrera's by-product hypothesis derived from the assumption that both organs develop from homologous structures). First, we discovered a robust negative allometric relationship between seed width and length in endozoochorous species, aligning with our expectations. Surprisingly, this association also held true for anemochorous species. In addition, we found a positive relationship between fruit and leaf length, but this relationship was not evident for zoochorous species. Our findings lead us to the conclusion that the allometric relationship between seed length and width exhibits variability among dispersal systems. This supports the notion that fruit and seed morphology has undergone modifications due to interactions with frugivores and the unique adaptability to rotate, particularly evident in certain wind-dispersed species.

S.31.2 Morpho-anatomy of the flower-to-fruit transition in selected Andean Loranthaceae

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Loranthaceae (Santalales) is a family of hemiparasitic plants that exhibits unique structural modifications, such as: (1) structural reduction of the carpels, compensated by the formation of a massive hypanthium and (2) ategmic ovules, these reduced to the embryo sac; (3) migration of the embryo sac nuclei from the ovary to the style and ectopic fertilization in the style, followed by the repositioning of the proembryo(s) to the ovarian region; and (4) fruits developing from inferior ovaries fused with the hypanthium, with abundant viscine. Other atypical features recorded include the presence of dimorphic embryos (i.e., embryos have foliose or prismatic cotyledons) in the genus *Psittacanthus* and the absence of endosperm described in *Psittacanthus* and *Aetanthus*. Conventional serial sectioning of flowers and fruits at different developmental stages of *Aetanthus colombianus* A.C. Sm., *Gaiadendron punctatum* (Ruiz & Pav.) G. Don., and *Tristerix secundus* (Benth.) Kuijt, allowed us to conclude that the flowers of these species go through: (1) migration of the nuclei of the megagametophyte, which reach the distal third portion of the style; (2) formation of a secretory parenchyma associated with the vascular bundles of petals and stamens; and (3) growth of a sclerenchymatic structure that delimits the megagametophyte in the flower and the proembryo in the fruit. Conversely, the fruit formation follows: (1) development of the pendular embryo, facing the schlerenchymatic tissue, with a conspicuous hypocotyl, and formation and expansion of the viscin in the epicarp; (2) development of two foliose cotyledons surrounded by massive endosperm (ruminate in Gaiadendron), and lack of seed coat; and 3) the fruit proper is delimited by the vascular bundles of the gynoecium, and surrounded by a thick epicarp with extra-carpellary viscin. This work lays the foundation for comparative evo-devo studies on the genetic bases for ovule reduction in hemiparasitic neotropical Santalales.

S.31.3 Anatomy and micromorphology of the two genera with unusual fruit type in Apiaceae (Echinophora and Thecocarpus)

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The genus *Echinophora,* with 10 species is represented in Türkiye by six species, three of which are endemic. *Thecocarpus carvifolius*, is the only representative of the genus. *Echinophora* and *Thecocarpus* are closely related genera with taxonomically controversial history, which are placed in *Echinophoreae*. This tribe is characterized by the remarkable structure of the fruiting umbellules. In this tribe the umbellules have sessile solitary female fruit in the centre, surrounded by the indurated pedicels of the male flower. In this group, different parts of the umbellules take part in fruit formation and in these infructescence structures. The anatomical characters of the fruit are widely used in the taxonomy of Apiaceae. In this study detailed anatomical and micromorphological futures of 7 taxa were done in detail including; *E. tenuifolia*, *E. tournefortii*, *E. chrysantha*, *E. lamondiana*, *E. tricophylla*, *E. orientais*, *T carvifolius*. The relationships of

Echinophora and *Thecocarpus* species grown in Türkiye were discussed based on the micromorphology and anatomy of fruits of 7 species. Plant material was collected from different regions of Türkiye and free hand sections were stained with astra blue and safranin. For scanning electron microscopy, fruits were coated with gold-palladium. We describe the range of variation in the infructescence, to discuss the available taxonomic characters and elucidate micro-morphological and anatomical fruit structure. *Echinophora* mericarps is generally pyriform, glabrous or hairy, located inside thickened structure called the cage or shell. Mericarps contain two carpels or monocarpel by abortion, 6vittae and carpophore. Stomata are absent in some species. *Theococarpus*, fruits called false nuts are hardened, glabrous with two carpels, 4vittae, and carpophore and stomata are present. Fruit structure such as presence and position of stomata, carpophore, vittae size, number and position provided valuable diagnostic characters in the taxonomy of these taxa.

S.31.4 Pleurothallidinae inflorescences: Importance of correct morphology interpretation

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Despite its great relevance, the study of the inflorescence from a typological point of view generally goes unnoticed in taxonomy, which is fundamental for the comparison of structural elements of the same origin. Pleurothallidinae is the most diverse subtribe in Orchidaceae is not the exception, its typology inflorescence remains largely unexplored, causing incorrect interpretations of its structures and misapplication of terms. The morphology of Pleurothallidinae inflorescences is clearly illustrated by photographs and diagrams, and it is analyzed and discussed from a typological point of view, based on the detailed study of structural elements of living material, including more than 82% of genera of the subtribe. The study shows that the subtribe presents a generalized type of inflorescences formed by an abbreviated peduncle and branch system that cannot be seen with the naked eye, which is an uncommon condition in other orchid´s groups. Each branch may produce coflorescences of different lengths with one or multiple flowers, also presenting different patterns of succession that determine the general appearance of the plant. There are two main types of inflorescences in Pleurothallidinae, these with single-flowered coflorescences that are dominant in early divergent clades, ant the multi-flowered coflorescences, which dominate higher clades. A general and practical classification is established for the different types of coflorescences according to the length and number of flowers produced

S.31.5 Evolution of seed dispersal modes in the Orchidaceae: has the Vanilla mystery been solved?

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Orchidaceae seeds are said to have the smallest seeds among flowering plants. They lack an endosperm, and most have only a very small embryo within a thin, spindle-like, transparent seed coat. The seeds are predominantly wind-dispersed, often developed within dry, dehiscent fruits that typically release millions of dust-like seeds into the air. Wind dispersal appears to be a derived state in Orchidaceae and given its predominance, a trait likely associated with enhanced speciation rates. Animal-mediated seed dispersal is a lesser-known phenomenon in the family and predominantly occurs in groups belonging to early-diverging lineages bearing indehiscent, fleshy fruits with hard, rounded, dark seeds. Zoochory primarily occurs in groups derived from early-diverging lineages; occasional reversions suggest a link between dispersal mode and fruit and seed traits. Among the zoochrous groups of orchids, genus *Vanilla* is the most predominant. The more than 120 species of *Vanilla* are native to the Tropical regions of Asia, Africa and America where they grow as climbing vines. Vanillin, the organic compound responsible for the much appreciated vanilla aroma, is synthesized naturally only in the fruits of certain Neotropical species belonging to this genus. This, and related, aromatic compounds play a pivotal role in the multimodal seed dispersal. Ectozoochory occurs in dry, dehiscent fruits, whose seeds are dispersed by (i) male euglossine bees collecting the fruit's vanillin aromatic compounds and (ii) female stingless bees collecting the fruit's mesocarp. Endozoochory occurs in (iii) highly nutritious, indehiscent fruits consumed by terrestrial mammals or (iv) fleshy, dehiscent fruits whose mesocarp is consumed by arboreal mammals. Interestingly, fruits features, such as dehiscence and fleshiness lack phylogenetic signal in *Vanilla* despite their role in determining dispersal modes, suggesting potential environmental adaptability.

S.31.6 Disentangling the Orchid-Euglossini interaction networks in the tropical forest in Costa Rica

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Orchids are one of the most diverse groups of plants, with sophisticated reproductive mechanisms that have allowed the diversification of niches and pollinators, such as Euglossini bees. The study of the reproductive phenology of orchids by means of bee body pollinaria provides a clear understanding of the interaction between plants and pollinators. Also, many bee species have a different phenology in certain ecosystems, which puts pressure on orchids that depend on these pollinators for reproduction. The objective of this work was to characterize the reproductive phenology of orchids and the Euglossini pollinator bee community. The work was carried out at La Selva Biological Station, Costa Rica. During one-year, monthly samplings of three days were carried out, using different chemical attractants to attract Euglossini males, and only those observed with pollinaria or accessory structures on their bodies were captured. The orchid pollinators were identified at the Lankester Botanical Garden and the bees at the School of Biology, University of Costa Rica. *Gongora* and *Euglossa* were the most abundant orchid and bee genera. During the dry season, the abundance of bees was higher than during the rainy season. and the species in flowering vary significantly from season to season, as do the species of bees. This work presents the first bipartite network between orchids and Euglossini bees, considering the two climatic seasons of the year.

S.32 ADVANCES IN SEED CONSERVATION OF WILD SPECIES. SESSION 2

S.32.1 Are seeds of today's endangered plants ready for tomorrow's climate change challenges?

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Seeds operate in a world of physiological limits established by abiotic and biotic factors. These limits represent thresholds that govern not only *in planta* development of high-quality seeds but also seed to seedling transitions via germination. Important plant life history stages such as seed development on mother plants and seedling establishment are crucial to sustaining life on Earth. Yet human induced climate change continues to influence thresholds regulating plant regeneration from seeds. Additionally, many of the predicted impacts of climate change may push seeds beyond limits established during their recent evolutionary history. This predicament may be magnified for seeds of endangered plants and raises a series of important questions. Are the seeds of today's endangered plants ready for the climate challenges of tomorrow? How will seeds have to adapt to climate change? Are we expecting too much from seeds given the potential for increasing levels of stress that may keep seeds at operational limits? This presentation explores those questions by first discussing projected impacts of climate change. It then overlays a current synthesis of seed responses to predicted climate-induced stressors. We conclude with perspectives that may contribute to development of adaptive solutions for endangered species while calling for more attention to seed biology especially in a climate change context.

S.32.2 Elevated spring temperatures promote premature germination in range-wide cork oak populations

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Climate change is facilitating the northward migration of Mediterranean oak species, leading to an expansion of their distribution at their leading edges. Nevertheless, Mediterranean oaks possess desiccation-sensitive acorns that lack the ability to form seed banks, relying instead on post-seed fall climate conditions and the interplay of genetic determinants for germination. In this study, we investigate *Quercus suber* populations' potential adaptation to rising spring temperatures in germination timing and rates. A total of 701 acorns from 9 populations, with 10 mother trees each, were sown at temperatures of 15, 20, and 25 °C, with daily monitoring of germination over a 90-day period. Germination timing was modeled using Cox's proportional-hazards models. Populations' adaptation to the transfer distances associated with spring temperature changes and germination climatic niches under current and the RCP 8.5 scenario for the year 2080 were assessed using fixed-effects models. Variations in germination timing were attributed to both population origin and temperature treatment, while germination rates exhibited sub-optimal tendencies under temperatures exceeding the species' native range. The timing of germination decreased in correlation with rising spring temperatures, with a projected germination occurrence in 2080 anticipated to be 12 days earlier than the present timeframe in central Iberia. Elevated spring temperatures significantly expedite the germination process of recalcitrant Mediterranean species, potentially influencing the developmental environment of seedlings and, consequently, the regeneration and species composition of populations. Consequently, germination timing deserves greater consideration in scientific and stakeholder discourse and should be integrated into forest vulnerability assessments and assisted migration programs designed to foster long-term forest adaptation to climate change.

S.32.3 Functional traits at the service of seed conservation in Brazilian open ecosystems

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Seed-based conservation and restoration are increasingly recognised as cost-effective strategies to protect biodiversity and restore degraded ecosystems. Both strategies depend on seeds' ability to remain viable in medium- to long-term storage, which, in turn, is directly related to seeds' desiccation tolerance —a trait whose assessment is highly time-consuming and challenging to scale to various species. To overcome this shortfall, trait-based models to predict desiccation tolerance using easy-to-measure traits, such as seed mass and moisture content, have been proposed. Here, we used these models to explore the potential of seed conservation in two hyperdiverse yet threatened open ecosystems in Brazil: rock outcrop vegetation and the Cerrado, with the ultimate goal of delivering knowledge about native seed conservation and building capacity for their use in conservation and restoration projects. For rock outcrop vegetation, we built a database of 16 seed traits for 383 species. Unfortunately, data on desiccation tolerance was available for only 34 species, all of them producing orthodox seeds. Still, the available information for seed mass and moisture content for 87 species indicates a high potential for seed conservation, as suggested by the few empirical studies available for these and similar ecosystems worldwide. An ongoing project in the Cerrado is assessing seed desiccation tolerance in 84 species —56 of them with unknown storage behaviour— currently commercialised by local communities in Central Brazil. This species pool includes groups whose seed desiccation tolerance has been little studied, such as perennial grasses, which are a fundamental element of Cerrado plant communities. Ongoing data collection will be compared with the predictions of global trait-based models to assess whether these models produce accurate predictions of seed desiccation tolerance and, thus, used as a tool to facilitate the seed conservation work currently carried out by local communities.

S.32.4 Enhancing Seed Conservation Strategies for Rare and Endangered Plant Species in Bavaria, Germany: Insights from Trait-Based Seed Longevity

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The rapid changes in the environment due to human activities and climate shifts pose a significant threat to the habitats of rare and endangered plant species, pushing them closer to extinction. It remains crucial to preserve these species to uphold the functioning of ecosystems. Our objective is to comprehend the impact of traits like seed morphology and physiology in endangered species on their capacity to endure extended storage periods. By investigating the relationship between these traits and seed longevity, especially in habitats like less fertile soils or transitional zones, our aim is to enhance the prioritization of in situ protection or alternative conservation cultures for certain species, as well as those suitable for long-term ex situ storage in gene banks. Additionally, our analysis of habitat features and seed longevity data using Ellenberg indicator values (EIVs) aims to unveil why particular habitats favor short-lived or long-lived plant species. Our focus within Bavaria, Germany includes understanding how species, including those stored in projects like Bayern Arche establish their abundance in specific habitats based on seed longevity and environmental factors. This research endeavors to establish a direct connection between seed viability and essential traits, providing valuable insights to optimize seed conservation strategies and improve species selection for storage in seed banks.

S.32.5 Green and fatty architecture: how chlorophyll, fatty acids and antioxidants modulate ageing rates in dry seeds

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Orthodox seeds, when dry, solidify their cell's aqueous cytoplasm forming a glass (i.e., an amorphous non-crystalline solid) where most biochemical reactions are inhibited. However, ageing is not completely stopped at this quiescent state and slowly progress mainly via oxidative reactions. Seed ageing kinetics is species dependant, but the causes for these differences are not well known. However, it has been well characterized that the seeds of some particular species age faster than the average. For example, "green seeds" - i.e., those containing chlorophyll at maturity, generally in fully developed chloroplasts - age fast at any storage temperature, like those from Salicaceae species. In addition, diverse "fatty (oily) seeds" age abnormally fast when stored to high subzero temperatures, as those standard in seeds bank (e.g., -20ºC). The causes for the faster ageing rates in these two particular seed types have been related to specific reactions modulated by their "dry architecture" (Ballesteros et al., 2020). In other words, the particular physical-chemical properties of the cell cytoplasm of "green" or "fatty" seeds when dry and stored to low temperatures strongly influences their ageing kinetics. This influence is focused in two aspects: (1) the source of Reactive Oxygen Species (ROS), the target of oxidative reactions, and the antioxidant potential, and (2) the differential physical changes occurring in the glassy aqueous phase of the cytoplasm and the lipid oil droplets distributed therein. In this talk we review the state of art of ageing kinetics in dry seeds with green and fatty architectures. Moreover, we show recent advances on our understanding of this topic using both multicellular seeds but also fern spores as a unicellular model. References: Ballesteros D, Pritchard HW, Walters C. (2020). Dry architecture: towards the understanding of the variation of longevity in desiccation-tolerant germplasm. Seed Science Research 30(2): 142-155.

S.32.6 Call for data sharing and an open invitation to join SeedArc, a global archive of primary seed germination data

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We present SeedArc, a global initiative to mobilize seed germination data that has been produced by decades of studies on seed ecology and conservation. Seed germination is a key stage in a plant's life that is controlled by numerous environmental conditions. Yet, significant amounts of data on germination-environment relationships remain inaccessible and many plant lineages and biomes are underrepresented. Since available information is scattered into a multitude of sources and germination metrics, there is a need for a unified open-science database to archive and share primary seed germination data. To meet this need and to stimulate continental and global eco-evolutionary research, we introduce SeedArc, a global archive of primary seed germination data (www.unioviedo.es/seedarc/; https://doi.org/10.1111/nph.19143). We expect SeedArc to strengthen international collaborative projects in plant science, connecting the seed research community with other data synthesis initiatives. In this session, we demonstrate SeedArc's potential to address major research questions in seed ecology and describe the process for submitting your germination data and participating in collaboration. Most importantly, we extend an open invitation to all holders of seed germination data to submit data and collaborate on SeedArc research projects exploring seed ecology and evolution.

S.33 MECHANISMS AND CONSEQUENCES OF DISPERSAL IN LAND PLANTS: TOWARDS A MORE UNIVERSAL UNDERSTANDING. SESSION 2

S.33.1 Drift in the tropics: Phylogenetics and biogeographical patterns in Combretaceae

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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.

S.33.2 Unraveling the evolutionary history of island floras on the world's most isolated archipelagos.

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The sub-Antarctic archipelagos are some of the most remote and semi-pristine insular habitats in the world. The diverse array of ages of these archipelagos, combined with the large distances between them and to the nearest landmasses, create an exciting area for exploring austral biogeography. This includes phenomena such as extreme long-distance dispersal and colonization, facilitated by marine currents across the Southern Hemisphere. Understanding these dynamics requires reconstructing the patterns and processes explaining biodiversity assembly in the sub-Antarctic archipelagos involved in the sub-Antarctic region. To better understand the biogeography of the sub-Ant-

arctic region we examined four vascular plant species exhibiting different modes of dispersal which are widespread across the region and nearby austral continents, along with three species restricted to a very remote sub-Antarctic province: the Southern Indian Ocean Biogeographic Province (SIOBP). We generated and compiled nuclear and plastid DNA sequence data for each species and estimated phylogenetic relationships, divergence times, inter-island migration rates and island carrying capacities. Our findings reveal that the nearby continental landmasses (South America, Australia or New Zealand) acted as source areas for the dispersal of these widespread vascular plant species to the sub-Antarctic archipelagos. This connection persisted for millions of years, spanning from the Miocene to the present day, and may have been driven by the eastward-moving winds and water currents, supporting long-distance dispersal as a key biogeographic process in this region. In addition, the isolation of the sub-Antarctic archipelagos played a role in the origin of endemics restricted to remote islands. Overall, our study suggests that the sub-Antarctic islands have served as important biodiversity refuges from the Miocene to recent times, emphasizing the need to establish priority conservation plans for these habitats, particularly in light of rapid climate change throughout this region.

S.33.3 Patterns of sex expression and sex ratio with focus on insular bryophytes

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Oceanic islands host remarkable biodiversity richness and represent important hotspots. Laurel forests are the relicts of an evergreen humid forest community, which occurred across the Mediterranean basin about 20 Mya . Since the onset of the Mediterranean climate, laurel forests only persisted in Macaronesia, where the oceanic environment buffered the climatic oscillations of the Pleistocene, and where these forest ecosystems are closely associated with the elevational belt of orographic cloud formation. The Macaronesian laurel forest harbors an exceptionally high diversity of bryophytes, with approximately 33 threatened endemic bryophyte species, the majority of which are dioecious. Dioecious bryophyte species often face challenges in sexual reproduction. Traditionally, asexual reproduction is thought to help maintain well-adapted phenotypes in stable environments, while sexual reproduction enhances genetic variability, increasing the population's chances of survival in new colonizing areas or during periods of environmental change. In contrast to flowering plants, most dioecious bryophytes exhibit a female bias among sex-expressing individuals. However, in a few cases, sex ratios have been found to be evenly balanced or that there is a male bias, as demonstrated in population studies of leafy liverworts. A significantly broader taxonomic range of moss species has been examined, but there is a noticeable lack of data for leafy liverworts. This research will be the first to investigate patterns of sex expression in Macaronesian laurel forest endemic bryophytes. Through the integration of data obtained from fieldwork conducted on the islands of Madeira and Tenerife, along with herbarium material (AZU, C, E, LD, LISU, E, TFC, VAL), we aim to examine the patterns of sex expression and sex ratio in four laurel forest bryophytes (*Exsertotheca intermedia* [endemic], *Frullania polysticta* [endemic], *Frullania teneriffae*, *Porella canariensis*), exploring their implications for effective sexual reproduction across their entire range.

S.33.4 The ultimate dispersers? How dispersal has shaped global patterns of fern biodiversity

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Fern life cycles are characterized in part by their reliance on spores as the primary unit of dispersal. Unlike seeds, which may be a variety of sizes and often rely on animals to assist with dispersal, fern spores are almost uniformly microscopic and wind dispersed, and as a result, these plants have long been recognized as being exceptional long-distance dispersers. We explore the consequences of this dispersal ability for fern distribution and natural history, focusing on recent studies of globally dispersed groups (including genera such as *Asplenium* and *Dryopteris*, and families like Blechnaceae) and how their evolutionary history has been shaped by long distance dispersal. We also discuss the implications for various biogeographical patterns as they apply to ferns, such as island biogeography, classical examples of disjunct distributions, and fern species' ability to colonize of newly available habitats

S.34 FLORAL SPECIALIZATION AND THE GENERALISED NATURE OF POLLINATION INTERACTIONS. SESSION 2

S.34.1 The role of pollinator generalization in co-flowering community assembly

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Pollinators can play a key role in the assembly of plant communities. Due their ability to carry and disperse pollen among flowers they are central in mediating facilitative and competitive plant-plant interactions. These interactions can be direct (via pollen interactions on the stigma) or indirect (by altering pollinator visitation). However, their underlying complexity and their relative role in mediating the assembly of highly diverse plant communities is not fully known. To this end, we collected data on floral traits, phenology and pollinator visitation for over 40 plant species at the serpentine plant communities in California and used network tools to uncover novel patterns of co-flowering and trait structure to help elucidate the role of pollinator generalization in co-flowering assembly. Results show plant species are differentially assembled along multiple trait-axes (flower color and flowering time) depending on the efficiency and specialization level of the main pollinator groups. The assembly of plant species along multiple axes of trait differentiation limits pollinator sharing (competition) and contributes to the maintenance of diverse co-flowering communities. We further collected over 1000 flower visiting insects and plant styles and characterized pollen loads on insect bodies and flower stigmas. We reveal the importance of direct pollen-pollen interactions in community assembly, not only of those that occur on the stigma, but also of those that take place on pollinators bodies during pollen co-transport. Specifically, pollen co-transport networks revealed differences in the number and identity of competitors that pollen species encounter on insect bodies across pollinator taxa. Pollen co-transport networks were modular, indicating some pollen species interact more often on the bodies of pollinators than others. Differences in pollinator generalization can lead to vastly different competitive landscapes during pollen transport and deposition, with important consequences for plant community assembly.

S.34.2 Unraveling urbanization: a tropical perspective on pollinators, plants, and interactions

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Urbanization is a major threat to pollination, due to the transformation of natural landscapes into urban matrices. Previous studies indicate that highly urbanized areas have a higher negative effect on pollinators and their interactions with flowers. However, most of this information comes from non-tropical regions, emphasizing the need for studies in the tropics. Here, we evaluated the impact of urbanization on the richness of pollinators, plants, and interactions in a large tropical metropolis, across twelve sampling points with varying levels of impervious surface. Over a one-year period, we conducted monthly visits to each of these points, sampling over 1 km transects.

During these visits, we observed and recorded all flowering plants, as well as interactions with pollinators. Throughout the study, we recorded 7,603 plants-pollinators interactions, involving 234 plant and 217 pollinator species. Urbanization did not influence pollinator (pseudoR^2= 0.154; p=0.151) and interaction richness; (pseudoR^2= 0.083; p=0.311), but it negatively influenced plant richness (pseudoR^2= 0.357; p = 0.0129). Analyzing seasonal variation, we observed that plant, pollinator, and interaction richness were significantly higher in the rainy season compared to the dry season (t = 3.69, W = 125, W = 127; p<0.001, respectively). The plant species most frequently visited included *Sphagneticola trilobata*, *Tridax procumbens*, *Leucanthemum vulgare*, and *Psychotria carthagenensis*. During the rainy season, *Sphagneticola trilobata* (a native species) emerged as the predominant resource for pollinators, while in the dry season, *Tridax procumbens* (non-native) took precedence. With the exception of *Psychotria carthagenensis* (Rubiaceae), all other frequently visited flowers belong to Asteraceae. These findings offer crucial insights into the impact of urbanization on biodiversity and ecosystem dynamics, with important implications for biodiversity conservation in tropical cities. Additionally, they underscore the substantial potential of Asteraceae plants and non-native species in supporting pollinators in urban areas.

S.34.3 Do pollinator shifts or adaptive wandering explain floral divergence in generalist Dimorphotheca daisies?

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While pollinator-mediated selection undoubtedly contributes to diversification of plants with specialised pollination phenotypes, its importance in generalist plants is less clear. The adaptive wandering model of floral diversification posits that floral divergence in generalists, occurring in response to selection across quantitative pollinator mosaics, does not result in the trade-off in pollinator use (i.e., ecological specialisation) that is the hallmark of the alternate, pollinator-shift model. Here we test the importance of these alternate mechanisms in generating the striking spatially structured floral variation that characterises the annual *Dimorphotheca* daisy complex in South Africa. First we show that the system is underlain by a weak spatial pollinator mosaic because all morphotypes interact strongly with a core group of widespread visitors, with use of these pollinators tracking their relative availability in communities, both within and across morphotype ranges. However, each morphotype is associated with some unique and effective pollinating species that are distributed in a largely qualitative spatial mosaic corresponding to floral morphotype distributions. Field experiments with model inflorescences suggest that, while the core pollinators are not exerting selection, the unique species in the assemblage are selecting on divergent trait phenotypes. Although evidence of trade-offs in pollinator use is limited, divergent floral phenotypes do produce weak but significant pollinator partitioning, and thus ethological isolation, in sympatry. While these results largely align with the adaptive wandering model of floral divergence, the fact that spatially discrete floral variation is underlain by largely qualitative gradients in the availability of a small subset of effective pollinators exerting selection on divergent floral traits is akin to the pollinator-shift model. Against the background of a core widespread generalist pollinator community, our results suggest that relative fitness gains associated with traits improving attraction and effective use of additional range-restricted pollinator species may explain the evolution of floral diversity in *Dimorphotheca*.

S.34.4 A mosaic of local pollinator assemblages underlies floral trait divergence in a pollination-generalized plant.

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Pollinators are a fundamental driver of the diversification of floral traits. Indeed, the astonishing diversity of floral traits represent, in part, an adaptation to the behavioural preferences and functional characteristics of the associated pollinators. The composition of the local pollinator assemblage is expected to differ across the distribution range of a particular plant species, with the potential to generate a geographic mosaic of divergent patterns of phenotypic selection that can represent an avenue of adaptation to the local pollinator assemblage. Thus, studies that relate geographical variation in floral traits to the distinct regimes of phenotypic selection exerted by the local pollinator assemblage are fundamental to understand the interplay between microevolution and macroevolution. This is particularly relevant for generalized plant-pollinator interactions, where a particular plant interacts with a broad range of pollinators. Here, we evaluated whether geographical variation in the composition of the local pollinator assemblage can establish distinct regimes of phenotypic selection and underlie the patterns of divergence in floral traits of *Viscaria vulgaris*. We observed a taxonomically and functionally broad range of diurnal and nocturnal pollinators that primarily included bumblebees, honeybees, solitary bees, syrphid flies, butterflies, and moths. We detected geographical variation in the composition of the local pollinator assemblage and the strength and direction of phenotypic selection on particular floral traits. Despite generalized plant-pollinator interactions, we detected that the observed variation in floral traits was associated with divergence in the composition of the local pollinator assemblage. We argue that generalized plant-pollinator interactions can exert phenotypic selection on floral traits and that distinct local pollinator assemblages can underlie the patterns of divergence in floral traits. Together, these outcomes indicate that specialized plant-pollinator interactions are not required to generate and maintain the diversity of particular floral traits.

S.34.5 Unveiling the paradox: specialized individuals shape generalised networks in seasonal herbaceous communities of Indian Sky-islands

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Floral traits are recognised to play a key role in attracting pollinators, and the competition for limited pollinator resources can negatively impact a plant's reproductive fitness, especially in communities with synchronous flowering. Consequently, plants have evolved strategies to minimize heterospecific pollen transfer (HPT) and ensure efficient pollination. While floral trait diversity has been well-studied for its role in generating specialized interactions, the role of pollinators in maintaining this diversity is often overlooked. We investigated the foraging behavior of native pollinators in highly diverse, annually flowering, herbaceous communities of the Sky-islands of northern Western Ghats. We assessed floral abundance using a transect method across the flowering season to understand: i) the extent of flowering synchrony with respect to floral color and shape, and ii) shifts in plant-pollinator interactions as flowering phenology changed. Additionally, we examined the degree of floral constancy displayed by the most dominant pollinator group—bees—to assess the effect of floral traits and their abundance within a patch in a heterogeneous community. Despite the high species diversity in these seasonal communities, we found that the community as a whole exhibits higher asynchrony in its flowering phenology, potentially reducing competition for shared pollinators. Interestingly, while generalized interactions dominate at the landscape-level, our study revealed that pollinators display high floral constancy towards the most abundant species within a patch. This observation was further supported by the dominance of uni-floral pollen in their loads, highlighting the critical role of individual foragers in preventing HPT and maintaining floral diversity. Our findings unveil the paradox between floral specialization and generalised interactions by showing the presence of low HPT and specialized response of individual pollinators to locally abundant species in a hyper-diverse community with generalised network

S.34.6 Pollination of Dipcadi saxorum Blatt. (Asparagaceae: Scilloideae)

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Dipcadi Medik. (Asparagaceae: Scilloideae), comprises of 44 species distributed in Africa, S. Europe up to Indian Subcontinent. In India, the genus is represented by 13 species and 2 varieties. The genus is characterised by bulbous geophyte plants, bearing long linear flat or channelled leaves, white-green-brick red tubular-campanulate flowers, emitting sweet-foul odour, some odourless. Initially, pollination in Hyacinthaceae (now Scilloideae) was known by bees, birds, butterflies, moths and rodents. Studies of pollination biology on members from Tribe Dipcadieae Speta ex J.C. Manning & Goldblatt, had not been undertaken until Manning *et* al. brought forth the pollination of *Dipcadi brevifolium* (Thunb.) Fourc. by owlet moth *Cornutiplusia circumflexa* (L., 1767) Syn: *Syngrapha circumflexa* (L.) (Noctuidae) from Africa. Scientific study on Pollination of Indian Dipcadi is carried out by the in Mumbai suburban districts, Maharashtra, India during the flowering season from June-August for a period of 2 years from 2020 to 2022. Our work deals with pollination of *Dipcadi saxorum*. The flowers are nocturnal, producing scent and nectar at nightfall which extends up till morning attracting many visitors. The study concludes that the species is self-incompatible, and that the foul-acrid odour it produces is majorly because of aldehydes and esters. Settling moths, *Heliothus peltigera, Chrysodexis acuta* and hovering moths, *Macroglossum stellatarum* and *Cephanodes hylas* are the pollinators of *D. saxorum*.

S.35 METAL HYPERACCUMULATORS: NEW ADVANCES ON A BOTANICAL CURIOSITY. SESSION 2

S.35.1 Tomographic adventures in the selenium-enriched phloem sinks of a hyperaccumulator

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Selenium (Se) is an element beneficial but not essential to plant nutrition, and soils enriched with Se are typically hostile to plant growth and induce toxicity. Uniquely adapted hyperaccumulator plants are capable of growing on these enriched soils and accumulating rather extreme concentrations of Se in their tissues, without exhibiting serious toxicity. In Australia, the legume *Neptunia amplexicaulis* was found growing on seleniferous soils with >4400 µg Se g^{-1} in its tissues, and under controlled conditions this plant is capable of concentrating up to 13,600 µg Se g^{-1} in the youngest leaves. This plant has been shown to retain and circulate its accumulated Se, concentrating Se in phloem sinks such as developing tissues and recycling Se as these phloem sinks become phloem sources. While Se is generally metabolized into a non-toxic organic form (selenocystathioinine), concentrating excessive Se can be a metabolically costly and risky process. Recently we have been able to use cutting edge X-Ray Fluorescence Tomographic Imaging at the German Synchrotron (DESY) to examine the tissue distribution of Se in phloem sinks. These tissues, such as the youngest developing leaves, apical meristem and root tips, would have been difficult to hand section without damaging the tissues or losing any phloem-bound Se. It was found that Se is present in the epidermis of the youngest leaves – unlike maturing leaves, less Se could be found in the vascular tissues of these developing organs. In contrast, the root tips showed ubiquitous Se concentrations in the ground meristem, with a gradual concentration of Se in vascular tissues as they begin to develop. Analysis of this distribution can reveal interesting implications about the mechanisms of Se cycling in this plant, as well as the evolutionary advantages of Se hyperaccumulation.

S.35.2 Screening for metal hyperaccumulators - An analysis of herbarium material from Angola

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For the research on hyperaccumulator plants and their uses in phytomining, phytoremediation of soils and many other applications one crucial part is the identification of species which are able to hyperaccumulate metals. To date there is some research done in the Democratic Republic of the Kongo but only a few on the native plants of its neighboring state, the Republic of Angola. In this context herbaria offer a broad spectrum of native plants that can be scanned for hyperaccumulators. The Herbarium Dresdense contains a big collection of over 3000 specimens from Angola. In cooperation with the Herbarium Hamburgense, for a master's project these were scanned for hyperaccumulating species from different regions of Angola, mainly from the north-western Province of Uíge as well as from the south of the country. The Global Hyperaccumulators Database was used to pre-select genera and families from which Hyperaccumulating species are known. Small samples of each specimen were analyzed for the concentration of several metals using ICP-OES. Over 130 different species, some with several samples from different locations and organs of the plants were tested to examine the influence of these factors on the metal concentrations. We were able to identify several new aluminum hyperaccumulators containing up to 40.000 mg/kg of its leaf dry mass, one new Mangan hyperaccumulator and discover a rather interesting genus for further searches on new hyperaccumulators.

S.35.3 Bioaccumulation of potentially toxic elements in exotic and native woody species growing around a copper mine in Mufulira, Zambia

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There is an international debate on the potential of exotic or native species in phytoextracting potentially toxic elements (PTEs) from contaminated soil to contain the impact of mining activities on forest ecosystems. Exotic and indigenous trees have been evaluated as greenbelts to trap dust and thereby limit the dispersion PTEs. This study compares the potential of native (*Brachystegia longifolia*) and exotic (*Eucalyptus camaldulensis* and *E. grandis*) tree species growing around a copper mine in Zambia to accumulate PTEs and evaluate their ability to biomonitor metal pollution. Tree bark and leaves were collected from trees growing at the same site downwind from a copper-leaching plant. Topsoil was collected one metre from each sampled tree trunk. Portable X-ray fluorescence was used to analyse the elemental composition and concentration of heavy metals in biomass and soil samples. Pollution indices were used to establish the status and degree of soil contamination, while the bioaccumulation factor (BF) determined the ability of studied species to accumulate PTEs. PTEs (Cd, Fe, Cu, Pb, Ni, Mn, and Zn) were detected across biomass and soil samples, with a significant variation between species and plant parts. The pollution indices established that the soil at the study site is highly contaminated with Cu. The concentration of the studied heavy metals varied across species following the order *E. grandis* > *B. longifolia* > *E. camaldulensis* in both tree bark and leaves. The BF indicated that Zn, Mn, and Cd accumulates in all the studied species. Furthermore, a higher concentration of Cu was detected in *B. longifolia* bark, suggesting that this tree species has potential for biomonitoring Cu pollution attributed industrial activities. This study presents new insights in managing polluted environments through biomonitoring and bioaccumulation of PTEs, because these findings can guide policy on species selection when establishing greenbelts.

S.35.4 Mediterranean native plants for the restoration of abandoned mining sites: where we stand and how we move forward

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The Mediterranean Basin experienced a long history of mining exploitation that has left important consequences on environment, human health and biodiversity. In this frame, phytoremediation can help in the restoration of these environments, especially adopting a multidisciplinary approach. A recent review (Boi et al., 2023) has discussed the main issues of metal(loid)s pollution related to mine exploitation in the Mediterranean. A list of native plants suitable for phytoremediation and their related applications were given, categorizing them into four groups basing on their biological forms, vegetation types, and ecology: (1) hydro/hygrophilous vegetation, (2) annual and perennial meadows, (3) garrigues and maquis, (4) high maquis and woods. The study allowed to highlight that mine environments are often rich in *taxa* of phytogeographic and conservation interest which must be taken in account for the remediation of abandoned mines. However, physiological and ecological studies were deserved for a little amount of Mediterranean plants and thus further efforts are necessary to increase knowledge and detect other suitable species. **Acknowledgements:** We acknowledge financial support under the National Recovery and Resilience Plan (NRRP), Mission 4 Component 2 Investment 1.5 - Call for tender No.3277 published on December 30, 2021 by the Italian Ministry of University and Research (MUR) funded by the European Union – NextGenerationEU. Project Code ECS0000038 – Project Title eINS Ecosystem of Innovation for Next Generation Sardinia – CUP F53C22000430001- Grant Assignment Decree No. 1056 adopted on June 23, 2022 by the Italian Ministry of Ministry of University and Research (MUR), and the Municipality of Iglesias in the frame of "Progetto di conservazione e traslocazione di *Limonium merxmuelleri* nella Valle del Rio San Giorgio".

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S.36 CULTIVATED PLANT TAXONOMY: BRIDGING THE DIVIDE

S.36.1 Weeping willow mystery solved: genome-wide DArTseq genotyping reveals origin of Salix babylonica hybrids

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Weeping willow (*Salix babylonica* L.) and twisted willow (*S. matsudana* Koidz.) are prominent ornamental willows in temperate regions of the world. In addition, their importance has been growing in recent years due to their use as a promising crop for biomass production. Despite their distinctive morphologies, the taxonomy of this ornamental group, which also includes cultivars of presumed hybrid origin, has been characterised by uncertainty and confusion. Previous taxonomic concepts lacked exact (genetic) data and relied instead on morphological surveys. The considerable intraspecific phenotypic variation in willows and the lack of knowledge of the genetic relationships of taxa within *S. babylonica*/*S. matsudana* group have prevented experts from reaching a consensus on the number of accepted taxa of weeping and twisted willows. In our study, we used genome-wide genotyping using DArTseq (Diversity Arrays Technology) to analyse all major cultivars of *S. babylonica*/*S. matsudana* and their putative hybrids. By examining thousands of binary SNPs for each chromosome pair, complemented by data on genome size variation (estimated by flow cytometry), we gained new insights into the delimitation of taxa and cultivars within the *S. babylonica*/*S. matsudana* group. The results clearly show their close genetic relationship. We identified three major and four minor hybrid groups, and elucidated the origin of over 20 cultivars, including all the most widely grown cultivars. By providing a solid basis for understanding the genetic relationships between taxa within the *S. babylonica* group, and by providing compelling evidence for the origin of *S. babylonica* hybrids, we propose nomenclatural changes. These proposed changes aim to provide a stable taxonomic concept for this immensely popular, widely cultivated and aesthetically pleasing group of ornamental trees, potentially resolving uncertainties and errors that have persisted for nearly two centuries.

S.36.2 The study of formerly cultivated plants, part of our historical, cultural and biological heritage

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The data obtained by the author during the period 2001-2023 as a result of the study of the Spanish ornamental flora, at present and during the 19th century and the first half ot the 20th, are presented. The results have been used in the publication in scientific journals of numerous articles (more than four hundred) together with several monographs. The author have also participated in the creation, together with other botanist, of Bouteloua, a Spanish journal dedicated to the study of ornamental flora from the scientific perspective, the first volume of wich was published in 2006. The results of this line of work have increased knowledge regarding the number of species and cultivars cultivated and/or commercialised in Spain. Over the course of this study numerous cultivars not mentioned in recent botanical or horticultural literature, and present in the Spanish alien flora, were discovered.

S.36.3 A comprehensive phylogenomic analysis bridges micro and macro-evolutionary scales to explain the evolutionary history of Cannabis

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Cannabis sativa L. has been used by humans for millennia, providing important and versatile services in traditional medicine, for ritual purposes and to produce food and fibre. The process of domestication and subsequent dispersal by humans has resulted in the development of various landraces and cultivars, exhibiting a wide array of morphological features, phytochemical aspects, and an intricate genetic structure marked by numerous hybridisation events. Unravelling the origin of this plant and determining the existence of genuinely wild populations pose considerable challenges due to its complex nature. In this study, we relied on the Angiosperms353 probe set to investigate the genetic origins of over 90 accessions, encompassing a spectrum of wild/feral and landrace representatives. Phylogenomic and population genomics workflows were implemented to analyse the data generated. Both workflows consistently showed East Mongolian accessions as a distinct group, robustly supported as sister to all other sampled accessions. The remaining accessions segregate into two main clades, aligning with the geographical distribution and the classification proposed in earlier studies for the putative subspecies *Cannabis sativa* subsp. *indica* and *Cannabis sativa* subsp. *sativa*. The first clade encompasses accessions from China to Iran and southwards into the Indian subcontinent, with a dispersal to West Africa. These latter Indian and African accessions consist of landraces characterized by high Δ9-tetrahydrocannabinol (THC) content. The second clade is itself divided into two subclades. A Caucasian-Mediterranean clade and a mostly Turanian-Russian clade that also includes some Eastern European accessions. These distribution patterns are consistent with known routes of trade and migrations of human populations, in agreement with previous studies.

S.36.4 Classifying and naming in the network of cultivated plants

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Like done in any plant group, classification and naming are key process to spoke about cultivated plants. The same tools as those used for wild taxa can be used to reconstruct history of cultivated plants, but tools coming from genetics (whether population genetics, genetic diversity or heredity) may also be used to sort out genealogical links. Most of the questions raised by cultivated plants are on the bridge between genetics and phylogeny and have consequences on classificatory and naming process. Using various genera (such as *Rosa*, *Cytisus*...), we show how adding cultivated taxa in taxonomic studies can enlarge some aspects of taxonomic studies. The taxonomic and breeding histories need to be assessed before trying to classify and name some groups in these genera. Various techniques and process can be used to sort out these taxonomic and breeding histories, from purely historical ones to molecular ones. When such histories are reconstructed, in between inter-individual genealogies and inter-specific phylogenies, classification process can be applied in order to delimit pertinent taxa and may question taxa proposed while using wild plants only. In the same way, naming these taxa may need the exact same rules as for wild taxa, but may also rely on rules from the cultivated plant Code, or even other rules. Such situations, intermediate between wild and cultivated, requiring approaches from different disciplines, are common, may be particularly relevant when questioning the naturalness of some individual plants.

S.36.5 Has taxonomy gone to pot? Why the needs and expectations of amateur gardeners and professional botanists lead to opposing desires

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Plant taxonomy is a scientific discipline which output is used directly by a broad range of other parties. Horticultural taxonomy has a particular impact on gardeners and the horticultural trade. This has led to tension between those who dislike any change and those who update names based on new evidence of relationships. The past three decades have seen major changes in plant names and the way plants can be identified due to the development of DNA based data. Through a series of examples, the impacts of nomenclatural changes, reactions to decisions made and the lessons learned from those experiences are examined.

S.36.6 Integrative taxonomy, insights for wild and cultivated tomatoes classification

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Cultivated tomato, *Solanum lycopersicum* L., is a leading vegetable crop worldwide. It is also a model organism for genetics and evolutionary research. Using integrative taxonomy, a predictive classification of tomatoes and closely related groups was proposed, as a framework for further studies (Peralta et al. 2008). Wild tomato species are distributed in Colombia, Ecuador, the Galapagos Islands, Perú, Bolivia and Chile in different ecosystems. The cultivated tomato belongs to a very recently derived group and was domesticated from its wild progenitor, *S. pimpinellifolium*. Domestication process initiated in South America and Mesoamerica, continued in Europe when cultivated tomatoes were introduced in the sixteenth century in Italy, and later its expansion throughout the world as the species was incorporated into consumption. In the 20th century, modern breeding and the emergence of seed companies increased the development of new varieties, and more recently, commercial hybrids mainly with resistance to abiotic factors, pests and diseases, and quality traits. This long process has generated an enormous cultivar diversity due to their vegetative and reproductive growth, and fruit shapes, sizes, colors, and quality characteristics. An attempt has been made to apply a nomenclatural system based on the International Code of Botanical Nomenclature to tomatoes, but it is so complex that it has not been used. Taking into account a comprehensive taxonomy approach, a classification based on the International Code of Nomenclature for Cultivated Plants is proposed, which is simple and easy to apply to describe new tomato cultivars, and potentially useful for harmonizing names and classification of breeding collections among genebanks. Classification criteria must contribute to understand and use the diversity among wild and closely related domesticated species.

References: Peralta I.E., Spooner D.M., S. Knapp. 2008. Taxonomy of Wild Tomatoes and their Relatives (Solanum sect. Lycopersicoides, sect. Juglandifolia, sect. Lycopersicon; Solanaceae) Systematic Botany Monographs Vol. 84

Symposia Session 3

S.37 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 1

S.37.2 Extreme fire severity and fire frequency: evidence for state shift and generation of fire feedback loops of a mesic forest

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Shifts in the fire regime caused by climatic and anthropogenic influences mean that we are currently experiencing more frequent and severe fires at larger scales. Fire is a dominant disturbance in *Eucalyptus* forests in temperate Australia. Wet sclerophyll forests are often bordered by dry sclerophyll and/or rainforests and changes to the fire regime can shift these borders by allowing drier sclerophyll or rainforest species to disperse into current wet sclerophyll forests. The Black summer fires of 2019-20 saw around 50% of the threatened Upland Basalt Eucalypt forests of the Sydney Basin Bioregion ecological community burnt, with some areas experiencing extreme severity fire. Much of this ecological community is often disturbed and fragmented, making it potentially less resilient to disturbance changes, such as extreme fire events. To assess how these wet sclerophyll forests respond to different fire severities, we surveyed areas impacted by the 2019-20 Black Summer fires one-year later. We quantified the mortality rates of dominant tree species including *Acacia melanoxylon, Eucalyptus blaxlandii, Eucalyptus cypellocarpa* and *Eucalyptus radiata,* and compared how the dominance of different functional groups varied across the fire severity gradient. We have uncovered evidence that rainforest trees within wet sclerophyll forests may be highly susceptible to extreme fire events especially and at sites previously subjected to frequent fires. This study highlights the importance of understanding how severity of fire impacts wet sclerophyll forests and can inform management decision on conserving threatened ecological communities.

S.37.3 Improving salinity tolerance in rice: lessons from Oryza coarctata

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Oryza coarctata is the only halophytic relative in the genus *Oryza* that is tolerant to high salinity levels. In this work, we investigated key traits that confer this exceptional salt tolerance in *O. coarctata*, comparing it with responses of cultivated *Oryza sativa* species. We show that *O. coarctata* is utilizing Na^+ for stomata operation and, as result, is capable to maintain unaltered stomatal related traits (size, density, and opening speed). These plants had also enhanced RuBisCO carboxylation and RuBP regeneration in the Calvin cycle. Taken together, these features allowed *O. coarctata* maintain relative steady CO_2 assimilation under salt conditions. Upon exposure to salinity, wild rice also quickly increased xylem Na^+ loading for osmotic adjustment but maintained non-toxic level of stable shoot Na^+ concentration by increased activity of HKT1;5 (essential for xylem Na+ unloading) and a Na^+/H^+ exchanger NHX (for sequestering Na+ and K+ into root vacuoles). In contrast, cultivated rice prevented Na^+ uptake and transport to the shoot at the beginning of salt treatment but failed to maintain it in a long-term. We also show that wild rice limits passive Na^+ entry into root cells while cultivated rice relies heavily on SOS1-mediating Na+ exclusion, with major penalties imposed by the existence of the "futile cycle" at the plasma membrane. Other traits that contributed to superior salinity tolerance in *O. coarctata* included more efficient ROS signalling; desensitization of ROS-inducible cation channels and more superior K^+ retention in the cytosol; more effective control of cytosolic Ca^{2+} homeostasis by Ca^{2+}-ATPase and CAX-mediated Ca^{2+} efflux systems; and ability to prevent salt-induced downregulation of *RBOH* expression that may affect operation of the "ROS-Ca^{2+} hub" and signalling cascades under salinity.

S.37.4 Tracing the resilience of African tree ferns: insights from the African humid period and beyond

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Tropical forests in Africa are rapidly declining due to increasing population, recurrent wildfires, logging, land use changes, agricultural intensification, and other socioeconomic factors. This study utilized maximum entropy modeling, paleoclimatic data, and future climate scenarios to evaluate the historical presence of tree ferns in tropical and Saharan Africa during the African Humid Period (AHP; ca. 14,500-5,000 years ago) and project the impacts of climate change on their future distribution and implications for African forests. Although precipitation increased substantially during the AHP, the distribution was variable and insufficient to support all tropical plant species. We found most African tree fern species persisted in refuge areas that survived the late Pleistocene extinction. These refugia provided a haven for tree ferns, enabling them to survive despite challenging and fluctuating conditions. This highlights the remarkable resilience and adaptability of tree ferns and the critical importance of refugial areas in safeguarding populations during climatic upheaval. Our study further shows tree fern species had differential responses to climate change, with some experiencing minimal range contractions of 5.9% up to over 57% range expansion. Preserving these refugia not only protects tree ferns but also conserves overall forest biodiversity and ecosystem functioning. This knowledge is vital for targeted conservation to promote sustainable forest management and mitigate threats from climate change and human activities in African closed wet forests.

S.37.5 Learning from the adaptive responses of wild emmer wheat to 28 years of global warming

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Global warming has been documented to threaten wild plants with strong selection pressures, but how plant populations respond genetically to the threats remains poorly understood. We characterized the genetic responses of 10 wild emmer wheat (*Triticum dicoccoides* Koern.; WEW) populations in Israel, sampling them in 1980 and again in 2008, through an exome capture analysis. It was found that these WEW populations were under elevated selection, displayed reduced diversity and temporal divergence, and carried increased mutational burdens forward. However, some populations still showed the ability to acquire beneficial alleles via selection or de novo mutation for future adaptation. Grouping populations with mean annual rainfall and temperature revealed significant differences in most of the 14 genetic estimates in either sampling year or over the 28 years. The patterns of genetic response to rainfall and temperature varied and were complex. In general, temperature groups displayed more temporal differences in genetic response than rainfall groups. The highest temperature group had more deleterious single nucleotide polymorphisms (dSNPs), higher nucleotide diversity, fewer selective sweeps, lower differentiation, and lower mutational burden. The least rainfall group had more dSNPs, higher nucleotide diversity, lower differentiation, and higher mutational burden. These characterized genetic responses are significant, allowing not only a better understanding of evolutionary changes in the threatened populations but also for realistic modeling of plant population adaptability and vulnerability to global warming.

S.37.6 Phenological prints of climate change on Mediterranean flora: a retrospective study using herbarium specimens

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Plant phenology is linked to environmental variables. However, in the last century, the global temperature (T) has increased by 1.1 °C, which has caused severe climatic changes that have affected the phenology of Mediterranean plants. In our study, conducted across the western Mediterranean area of the Baetic Range, we used data from herbariums to assess the phenological trends of 98 dominant species from Habitats of Community Interest (Group 4, 5, and 9), along with endemic plants and the overall phenology of the bioclimatic thermotypes present in the area, all over the past 200 years. Significant changes and trends in the day of year (DOY) were detected in the studied phenophases of 71 species, whereas 27 showed no changes. In response to the time variable, seven species displayed significant shifts in the preflowering (FBF), 17 in the flowering (F), one in the fruiting (FS), and 10 in the growth (DVG) phenophase. In response to long-term climatic variables, 16 species showed no changes in FBF, whereas 22 did so in at least one. In F, 23 showed no changes whereas 49 did; in FS, 7 did not, whereas 13 did; and in DVG, 21 did not, whereas 29 did. Regarding overall phenology DOY with time, the thermo-Mediterranean (TM) thermotype showed no changes in the FBF and FS phenophases, whereas advances appeared in F and DVG. In the meso-supra-Mediterranean (MSM) and oro-cryoro-Mediterranean (OCM) thermotypes, all phenophases showed advancing trends. The DOY against climatic variables in the TM thermotypes showed advances in FBF and F, while FS showed no changes, and DVG advanced when P decreased. In the MSM and OCM thermotypes, all phenophases showed trends of advance. Tendencies were stronger in the orophilic than thermophilic group. Those results show the influence of climate change in the phenology of western Mediterranean flora.

S.38 DISSECTING THE EVOLUTION OF SEDGES (CYPERACEAE): PERSPECTIVES FROM MULTIPLE LINEAGES

S.38.1 The evolution and diversity of the genus Bulbostylis (Abildgaardieae, Cyperaceae)

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The genus *Bulbostylis* (hairsedges) includes 227 species worldwide. The taxonomic history of this genus is quite complex, and limited DNA data is available. This lack of data means that species delimitation and evolutionary relationships are unclear, and thus the study of character evolution and biogeographical history of *Bulbostylis* is hampered. Thus, three PhD projects are currently devoted to this genus, working on three centres of diversity of *Bulbostylis*: Africa, Brazil and Madagascar. These different regions respectively include 127, 52 and 25 accepted species of *Bulbostylis*, representing around 90% of the total diversity of the genus. Consequently, the aim of these projects is to gain a better understanding of the diversity, evolution, and conservation of *Bulbostylis* on a large and local scale. To this end, a joint project is underway to reconstruct the evolutionary history of the genus as well as its biogeographical history using a phylogenomic approach. Secondly, integrative taxonomic studies at local scale are ongoing to clarify species delimitation based on phylogenomic data with extensive sampling of species complexes, (micro)morphological and anatomical data; and distribution data. Preliminary results for these regions include: thirteen herbaria visited, ten fieldtrips undertaken, discovery of new species to science (e.g. *Bulbostylis itremoensis* from Madagascar), new herbarium specimens and DNA samples of Africa, Neotropical and Madagascan species, discovery of new anatomical characters for species delimitation; 212 newly extracted DNA samples sequenced with the Angiosperms353 targeted sequencing probes. Our study generates a large, accurate dataset. The future integration of this information may contribute to demonstrate patterns of diversity that allow the identification of important areas for conservation studies and provide new insights on ecological and evolutionary understanding in areas of high biodiversity.

S.38.2 Towards the consolidation of the Southeast Asian sedge knowledge

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Studies on global biodiversity are detecting common gaps in the taxonomic knowledge of tropical areas. While some of these areas are not necessarily considered hotspots, these are still incredibly diverse, and the knowledge gap extends widely to non-woody plants as they tend to be out of focus in regions dominated by tropical forests, which may underestimate diversity levels. For Cyperaceae, the third most biodiverse monocot family and among the top ten in angiosperms, Southeast Asia is the perfect example of such a situation. Despite having diversified worldwide into more than 5000 species with a particular preference for temperate areas in the largest genus *Carex* (40% of the family), there are over 600 taxa native to Southeast Asia. Nevertheless, the lack of historical collections, digitization of herbaria, and lack of support in Cyperaceae expertise for local research groups have turned the region into a darkspot for sedges. To protect current sedge diversity, understand their natural history, and predict their future, we must put forward a set of international collaborations with in-country researchers to improve the available information for this economically and ecologically important family. We hope to start a much-needed new era of collaborations in Southeast Asian sedge-focused projects, aiming to generate taxonomic, geographical, morphological, molecular, genomic, biochemical, and ecological data, accompanied by photographic records of taxa and sets of data that will be publicly available. Objectives such as training resident taxonomists, digitization of local herbaria, or providing international long-term financial support are some of the crucial steps towards the establishment of sedge research lines in Southeast Asia.

S.38.3 Progress on the phylogeny and evolution of Fuireneae s.l. (Cyperaceae)

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Considerable changes to the classification of the large (ca. 5500 spp.), cosmopolitan monocot family Cyperaceae ("sedges") have been made over the past 20 years. This is largely due to the reconstruction of relationships using molecular data. Nonetheless, many groups remain poorly studied, such as tribe Fuireneae *s.l.*, a collection of ca. 153 spp. common to humid and wet habitats worldwide. The group possesses numerous annuals and perennials, and holds ecological and economic importance, often dominating their natural habitats and acting as noxious crop weeds worldwide. Though a recent molecular study found support to divide Fuireneae *s.l.* into four tribes and six genera, only 30% of the tribe's diversity was sampled, sampling was poor where the group is most diverse (Asia), species level-complexes remain unresolved, and tribes could only be divided using impractical microscopic characters. Interestingly, this preliminary data suggested transitions from an annual to a perennial life history strategy, for which few examples are known in angiosperms, especially in monocots. Using a complete taxonomic sample of Fuireneae *s.l.*, and molecular (Hyb-Seq), morphological and embryo characters, we are testing whether current tribal, generic and infrageneric classifications of Fuireneae *s.l.* are natural, and if some perennials in the grade are derived from annuals as suggested by preliminary data.

S.38.4 The relevance of expert curation in taxonomically complex groups: a comprehensive database of occurrences for the genus Carex

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Species occurrences are essential for research requiring spatially-based information. The Global Biodiversity Information Facility (GBIF) is the primary and most popular source of occurrences. However, species identification and georeferencing data in GBIF is often affected by imprecision. Accordingly, a curation process is needed to prevent downstream errors, biases and/or inaccuracies derived from their use. Because of its high species diversity, taxonomic complexity, and wide distribution, occurrence data from *Carex* L. (Cyperaceae) are not exempt from these errors. In this context, we present an expert-curated global compilation of *Carex* occurrences mined from different sources (online databases, herbaria, literature, and fieldwork collections). Beyond basic quality-control procedures, the dataset was reviewed by experts, who curated both geographical inaccuracies and misidentifications. The final expert-curated database contains 397,239 records. During the curation, 16,604 occurrences were flagged as potentially erroneous, and 7,672 taxa names were changed. The resulting dataset has occurrences for 1,679 *Carex* species (c. 80% of all currently accepted species). Finally, we compared the differences between the raw and the expert-curated database. Our work highlights the importance of high-quality taxonomic and geographic data and provides a significantly enhanced *Carex* occurrence database that is made available for future research in the genus.

S.38.5 Niche partitioning or divergence? Sister-lineage comparisons reveal complex patterns of niche evolution in Carex

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With over 2000 species, *Carex* (Cyperaceae) is a nearly cosmopolitan genus with centers of diversity in temperate zones of each hemisphere. *Carex* exhibits tremendous ecological diversity, occupying habitats from coasts to mountaintops, deserts to wetlands, tundra to the tropics, and savannas to forest understories. Divergence across these ecological gradients has long been hypothesized to be a key driver of diversification in *Carex*. This hypothesis has been supported by phylogenetic comparative analyses, which show strong relationships between rates of speciation and niche evolution across the genus. These analyses to date have been based almost exclusively on the estimations of species niches from occurrence records, which are known to contain biased, missing, and incorrect data. Potentially more pernicious problems, however, are that 1) species distributions are dynamic through time; and few species likely 2) occupy the full extent of their fundamental niches or 3) occur in all geographic areas that are ecologically suitable. Consequently, significant findings of niche evolution in *Carex* may be spurious. Here, we use emerging methods that avoid the assumption that present distributions represent the full occupancy of species potential ranges. For nearly 500 sister-species pairs, we perform the Niche Overlap Test, which calculates niche similarity between two species in their total occupied environmental space, and the Niche Divergence Test, which calculates niche similarity in the subset of environmental space that is shared and accessible to both species. These tests are designed to detect whether species occupy distinct niches or simply have access to different environments. We then test whether significant niche evolution between sister species is related to their time since divergence, trait divergence, latitude, and total range size.

S.38.6 Tackling rapid radiations – update on the understanding of the megadiverse genus Cyperus (Cyperinae, Cyperaceae)

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Cyperus or flatsedges represent the second most species-rich genus of Cyperaceae with almost 1000 species distributed mainly in the tropics and subtropics. Historically, many segregate genera were split from *Cyperus* sensu stricto to accommodate the breadth of morphological, functional and ecological variation present in this group. Over the last 15 years, new insights into the evolution, diversity and distribution of this group were gained by integrating molecular phylogenetic data with in-depth morphological and anatomical studies. In the current phylogenomics-based classification, subtribe Cyperinae is monogeneric, placing the 13 segregate genera previously recognised in the morphology-based classification within a broadened circumscription of *Cyperus*. We also have strong evidence that a biodiverse clade of species using the C4 photosynthetic pathway is nested within a grade of C3 species. However, rapid diversification has hampered our understanding of the relationships within the C4 clade. Now, with the advent of phylogenomics, first inroads are made to study trait evolution in *Cyperus*. Yet, to build a complete picture of this megadiverse genus, a concerted effort will be needed to generate a species-level phylogenomic framework to investigate its evolutionary history, generate an infrageneric classification, and resolve species limits. We present the current state of knowledge and explore plans for integrating efforts towards purging the gaps.

S.39 PLANT CONSERVATION GENETICS: FROM IN-SITU AND EX-SITU CONSERVATION TO REINTRODUCTIONS AND RESTORATIONS. SESSION 1

S.39.1 Genomic-guided conservation actions to restore the most endangered conifer in the Mediterranean Basin

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Species with extremely small population sizes are critically endangered due to reduced genetic diversity, increased inbreeding, and the added threat of hybridization. Genomic tools significantly advance conservation by revealing genetic insights into endangered species, notably in monitoring frameworks. Sicilian fir is the most endangered conifer in Europe with only 30 adult trees spread across an 84-hectare area. Using 20,824 SNPs from RAD-seq employing the silver fir genome assembly and a custom 120 SNP-array, we evaluated genetic diversity, mating patterns, and effective population size in adult trees, 118 natural seedlings, and 2,064 nursery seedlings from past conservation actions. We assessed introgression from neighboring non-native fir plantations and established an intra-population assisted gene flow program selecting the most genetically dissimilar individuals and investigating the outcome through simulations. Genomic analysis unveiled significant genetic diversity among adult Sicilian firs, comparable to non-endangered Mediterranean firs with larger populations. However, the genetic diversity of the forthcoming generation declined due to high self-fertilization, leading to marked inbreeding ($F_{IS} = 0.38$) and an alarmingly low effective population size ($N_e = 6$). Nursery seedling monitoring revealed similar selfing rates but significant introgression (~50%) from non-native firs. Although intra-population assisted gene flow could help to mitigate genetic loss, it may not alleviate the species vulnerability to imminent environmental challenges, perpetuating the risk of an extinction vortex. Hence, investigating the impact of Sicilian fir population decline and selfing on inbreeding depression, along with exploring the potential of hybrids for genetic load alleviation and future adaptation, is crucial for effective conservation strategies. This study stands as a compelling model for guiding conservation strategies in similarly imperiled species characterized by extremely small populations.

S.39.2 Plant-animal interactions, population genetics and local community engagement to conserve the Malagasy baobab Adansonia suarezensi

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Adansonia suarezensis, one of the six endemic baobabs in Madagascar, is currently classified as Endangered. Its narrow distribution in the arid areas of N Madagascar is expected to decrease from 1200 km² in 2010 to 17 km2 in 2050 due to climate change, and alarming predictions indicated a likely extinction between 2050 and 2080 without intervention or conservation efforts. Madagascar has lost 37% of its natural forest since 1973, and despite the implementation of conservation programs, deforestation rates have increased in the last decade, mainly because population growth and political instability in the country. Ex situ and in situ conservation actions to recover threatened species require extensive knowledge from diverse disciplines to better understand the reproduction biology, ecology and demography of the target species. *Adansonia suarezensis* belongs to a section named Brevitubae, which include dry-season flowering baobabs with white flowers carrying short-staminal tubes pollinated by fruit bats and lemurs. Recently, a lack of natural regeneration has been observed in natural populations of *A. suarezensis*. In our project, we investigate the life cycle of *A. suarezensis* to reveal factors influencing the natural regeneration of the species, and we designed a restoration plan based on population genomics data by using a whole genome Single Nucleotide Polymorphism (SNP) screening approach (MigSeq). We explore also new plant-animal interactions with fruits, seeds and flowers using camera traps and direct observations. The aim is to elucidate the genetic patterns, investigate the level of gene flow, and explore relationships between population size and genetic variation in the species. The analysis of genetic diversity and population structure allow us to identify priority populations for restoration. Our project demonstrates also the importance of local community engagement in conservation by building nurseries, growing thousands of seedlings of baobabs and other economically plants as part of the conservation plan.

S.39.3 The value of record- and molecular-based conservation management to exceptional species: a case study using Amorphophallus titanum

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If ex situ collections are to effectively conserve species, practitioners should strive to maintain genetically robust ex situ populations by (1) attaining a comprehensive understanding of the current estimates of kinship and other relevant population genetic measures and (2) making informed breeding decisions. The zoological community accomplishes these goals by using a combination of a record-based approach, where extensive documentation of mating between individuals is recorded and used to generate pedigrees, and a molecular-based approach, where individuals are genotyped to reconstruct the pedigree or fill in pedigree gaps. This raises the questions: how well do botanic gardens manage populations of exceptional plant species held across collections, and what lessons on how to manage collections can we learn and implement from the zoological community? We explore these questions and evaluate the utility of the zoo model for conservation using the charismatic arum *Amorphophallus titanum*, an exceptional species native to the Indonesian island of Sumatra that has been cultivated for over 130 years. In this study, we used available accession information to create a pedigree and genomic sequencing to generate a SNP-based molecular dataset. We present our anticipated results that will compare relevant population genetic measures and pairwise kinship estimates and their subsequent recommendations of optimal breeding pairs using the record- and molecular-based datasets. We expect to observe differences between kinship coefficients calculated from each dataset and predict that the molecular-based approach will provide higher precision given notable incompleteness in accession records.

To our knowledge, this is the first study to compare the record- and molecular-based approaches of managing exceptional species in botanic gardens. This work will be an important first step in improving collections management (i.e., standardizing the recording of accession data) and will highlight genomics as an effective tool when managing poorly pedigreed exceptional species.

S.39.4 Conservation genetics of rare and endemic plants: challenges and advances

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Endemic species with limited geographic ranges are more prone to the negative effects of genetic drift and their consequences, especially when their habitat overlaps with economically valuable areas. This is the case of endemic plants associated with the Eastern Amazon cangas, a unique ecosystem limited by high iron concentration in the soils, which faces substantial threats from some of the world's largest iron ore mines. The conservation challenges in this ecosystem arise because just as plants adapted to iron-rich soils exhibit non-random distribution, often clustering in specific microclimatic and edaphic conditions; iron mining activities cannot also be haphazard due to variations in iron ore presence and quality. In response to this conservation dilemma, we have conducted comprehensive studies, integrating ecology and conservation and landscape genomics. By investigating the neutral genomic variation, we have found a scenario of conservation concern for three highly restricted endemic species, with simulations indicating a worsening of such scenario in a few decades if population sizes further decline. Conversely, certain species have demonstrated remarkable resilience, with genetic diversity and gene flow patterns remaining unaffected by mining-induced habitat loss. The use of genotype-phenotype-environment associations has offered further insights into adaptive genomic variation for restoration purposes. For example, our findings indicate that whereas local provenances were found optimal to restore a moderately disturbed site, a mixture of genotypes seems to be the most promising strategy for the recovery of highly degraded mining site. Our studies suggest that vulnerability cannot be easily predicted for co-distributed species, implying the need to obtain species-specific estimates to assess the extinction risks and inform decision-makers for conservation efforts. Based on our studies, we discuss the main challenges in reconciling conservation with mining activities in unique and highly diverse environments.

S.39.5 Intraspecific genome size variation, cryptic speciation and outbreeding depression in Penstemon pachyphyllus

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Outbreeding depression is a main concern when mixing multiple source populations in restoration, as it can reduce seed quantity and quality in seed production fields and restoration sites. The main causes for outbreeding depression are unnoticed taxonomic issues and fixed chromosomal differences, but these aspects are rarely assessed when designing and implementing a restoration project. *Penstemon pachyphyllus* was identified as a restoration priority in the Great Basin, where the Great Basin Restoration Initiative took a regional admixture provenancing approach, combining as many as 18 source populations in pooled seed production fields, to generate large quantities of genetically diverse seeds for wide-scale restoration across this region. However, outbreeding depression was previously reported for this species when mixing populations from two different ecoregions. Because this species extends beyond the Great Basin, we assessed genome size variation across the whole species range to study potential causes of this pattern of outbreeding depression. As we found a geographically structured pattern of genome size variation, with southern populations showing a smaller genome size, we designed a controlled crosses experiment to test if genome size difference is the main driver of outbreeding depression. Moreover, we took a phylogenomic approach to assess species delimitation on our target species including all closely related taxa (i.e., the Coerulei-Gentianoides clade). We found that genome size difference is the main driver of outbreeding depression in this species, with crosses between populations with different genome sizes showing a significantly lower seed production in terms of number and weight, than crosses between populations in different geographic regions but with the same genome size. Species delimitation analyses are consistent with this incipient reproductive barrier.

S.39.6 Using assisted gene flow to save a population from depression

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After the drastic decrease of population sizes of *Arenaria grandiflora*'s population in the Parisian region in the late 20st century, a translocation program was implemented in 1999. A preliminary study revealed that the main cause of the population's extinction was the low genetic diversity and the associated low fitness of the last individuals due to inbreeding depression. To save this species from extinction in this region, non-local and local plants were multiplied by *in vitro* culture and introduced in three sites of their natural area. The three translocated populations were funded with the same mixture of 450 individuals, 2/3 being clones of local plants and 1/3 of clones from non-local ones. To evaluate the outcome of the program, annual monitoring of plant's fitness was carried out over 24 years, coupled with genetic analyses based on 13 microsatellite markers. First results highlighted that the newly-created populations showed an increase in genetic diversity compared to the founders, and displayed lower consanguinity due to higher heterozygosity level. These levels of diversity appear to be fairly stable from year to year, which was encouraging for the program's success. Interestingly, fluctuation in fitness were observed between individuals depending on the proportion of genome inherited from each founder population. To study this model in greater detail and gain a better understanding of the complex genetic processes that condition the success of programs based on assisted gene flow, we are currently resequencing the entire genomes of individuals sampled between 1999 and the present day. By comparing simulations to actual genotypic data obtained from whole genome sequencing, it will be possible to assess whether natural selection phenomena linked to crossbreeding, such as heterosis or hybrid depression, have influenced the patterns of genetic diversity and how introduction of genotypes drove the genetic evolution of the population.

S.40 XYLEM ANATOMY AS A CENTRAL HUB LINKING FLUID TRANSPORT PROCESSES FROM THE INDIVIDUAL PLANT LEVEL TO ECOSYSTEMS

S.40.1 The role of drought on the evolution of woodiness in flowering plants

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Wood formation is a fundamental evolutionary innovation that gave rise to countless woody species (trees and shrubs), offering crucial ecosystem services such as carbon storage and its associated climatic feedback. Most of these species only have woody ancestors, whereas other lineages have independently evolved woodiness from non-woody (herbaceous) ancestors throughout evolutionary history. However, what drives species to become woody and why have so many unrelated herbaceous lineages evolved to new woody species? These key questions have baffled scientists since Darwin, but scientific information has been too fragmented to develop hypotheses that could be rigorously tested. Therefore, we have compiled a unique woodiness database in flowering plants, showing that most woody species with herbaceous ancestors occur in regions with recurrent drought cycles. This has laid the foundation for a novel hypothesis, proposing drought as the major driver of most transitions towards woodiness. We are testing this concept on islands and continents (1) by inferring via modelling whether there is a positive correlation between woodiness and drought, and (2) by assessing via experiments whether woody species with herbaceous ancestors are consistently more drought-tolerant than their herbaceous relatives. By bridging evolutionary biology and ecophysiology, this work shows increasing evidence for a novel strategy that reveals how plants respond to drought stress in a world facing global change.

S.40.2 Assessing drought resistance in a population of cabbage (Brassica oleracea) with contrasting levels of stem woodiness

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As the world's human population continues to grow and droughts become more intense and frequent, monitoring drought-responsive anatomical and ecophysiological traits in crops is crucial to guarantee food security in the future. *Brassica oleracea* is a relevant crop species with cultivars mostly consumed as vegetables. In our research, we crossed a woody accession of *B. oleracea* native to the island of Jersey- commonly known as Jersey cabbage - with an herbaceous, rapid flowering accession TO1000 of the same species. Five F2 genotypes were selected based on their contrasting levels of stem woodiness, along with the two grandparent lines. To evaluate whether stem woodiness is involved in the mechanisms leading to drought tolerance in cabbage, we monitored a broad range of key drought-responsive anatomical and ecophysiological traits under well-watered conditions and during controlled drought. Examples of these traits are stem woodiness, pit membrane thickness, leaf water potential, leaf turgor loss point, embolism resistance in stems and leaves, hydraulic safety margin, and stomatal conductance. We hypothesize that (1) the more woody genotypes are more drought tolerant, (2) the more drought-tolerant genotypes use a coordinated set of anatomical and ecophysiological traits in both stems and leaves to reach a certain level of drought tolerance, and (3) these trait syndromes may differ among the genotypes studied.

S.40.3 The vulnerability to drought-induced embolism-vessel diameter link: what needs explaining, and possible ways forward

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The escalating global tree mortality crisis, with millions of trees succumbing to drought annually, impacts biodiversity conservation. The vulnerability of xylem conduits to drought-induced embolism is a critical factor in determining tree survival during hydric stress. If narrower xylem conduits are less vulnerable to embolism formation, then this vulnerability- diameter link would explain numerous well-established patterns. These include wider xylem conduits in moist environments and narrower conduits in drier environments, the consistent production of conduits that are well below the developmental possible maximum diameter of 700 μm+, widening of the conduits from the tip to the base of the plant, in a way that keeps conductance optimal with height growth, the distribution of wide to narrow conduits in earlywood to latewood, and the differential leaf shedding between plants with wider and narrower conduits. All of these patterns require explanation, and if a vulnerability-diameter link is rejected, alternative explanations are required. As part of a possible explanation for these patterns, we provide data suggesting that the vulnerability-diameter link could involve the association between intervessel pit membrane thickness, vessel wall thickness, and vessel diameter. We show ways in which the vulnerability-pit membrane-wall thickness-vessel diameter associations could account for the link as well as why it is not found in some situations.

S.40.4 Developmental trajectories of the xylem vessel elements from single-cell sequencing data

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Changes in transcriptional profiles are at the heart of development. Understanding transcriptional dynamics at the single-cell level is a central challenge in deciphering developmental processes. Current sequencing technologies allow the estimation of transcription profiles at unprecedented single-cell resolution but the inference of developmental progressions of cells is hampered by sampling sparsity, technological noise, and loss of spatial and temporal information. The xylem cell populations have distinct transcriptional profiles and are ideally suited to reconstruct transitions in transcriptional programs during histogenesis. I use noise-resilient diffusion mapping-based approaches to infer and recapitulate developmental trajectories from large single-cell datasets. Our new methods allow us to reconstruct trajectories that occur on substantially different timescales in development and infer waves of gene expression changes along the developmental progressions. We analyze the development of vessel elements and compare it to the development of other vascular cell types, including sieve elements and companion cells, in different plant organs. We recover known regulators of vascular development that follow expected developmental dynamics based on previous studies and identify putative regulatory factors. We identify waves of gene expression changes of transcription factors and their downstream targets, which provide substantial resolution of transcriptional dynamics in vascular cell development.

S.40.5 Root pressure in tomatoes slightly repairs daily embolism at well-watered conditions, but its role during drought is inconsistent

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Inside plants, water moves from the roots up to the leaves due to a gradient in negative pressure (i.e., tension) generated in the leaf mesophyll cells via transpiration. During intense drought periods, the tension in the xylem sap increases, leading to gas bubbles (embolisms) inside the water-conducting cells (i.e., xylem vessels), thereby obstructing the long-distance water flow. Tomato plants are known to also move water through a positive pressure generated in the roots. We hypothesize that root pressure could help tomato plants remove gas embolism after release from drought after re-watering. Therefore, we used a gantry-based X-ray microCT imaging system, the EMCT scanner at the UGCT (UGent Center for X-ray Tomography, www.ugct.ugent.be), to visualize plant re-hydration and possible embolism repair by scanning the plants before and after drought, and at different times after re-watering. In total, we followed 25 control well-watered plants and 36 drought-stressed plants (covering a wide range of drought intensities). Our results show that all well-watered plants generated root pressure and partially repaired the few embolized vessels overnight. The role of root pressure in plants subjected to drought is more ambiguous: embolism repair after re-watering was also observed, but only in the drought-stressed plants that developed root pressure after re-watering (30%), while no root pressure was detected in 70% of the drought-stressed plants after re-watering. These results show that root pressure development is not an efficient mechanism of tomato plants' recovery from drought but shows the ability of this embolism-vulnerable species to remove the first embolism events generated during the day at well-watered conditions. In conclusion, we show that root pressure in tomatoes can remove the limited daily embolism under well-watered conditions and only occasionally after drought.

S.41 APPLICATIONS OF SPECTRAL REFLECTANCE IN PLANT SYSTEMATICS AND EVOLUTION

S.41.1 The evolution of species specific spectra in a diverse genus of Neotropical trees (Guatteria, Annonaceae) using herbarium specimen

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Leaf reflectance spectra estimated via near-infrared scanning (NIRs) are increasingly used to untangle the intricate complexity of plant diversity and evolution. The variation of these spectra across the tree of life and the impact of the evolution of leaf traits on spectral differentiation between species is still being explored. In this study, we used a framework that combines NIRs of herbarium dried leaves to infer the diversity and evolution of species specific spectra within the most diverse genus of Annonaceae in the Neotropics: *Guatteria*. We scanned herbarium preserved leaves of 148 out of the ca. 180 known *Guatteria* species. Spectra were cleaned, normalized, and analyzed using different multivariate approaches. We tested to see if these data could be used to identify species with similar spectra. We then analyzed this dataset within a comparative phylogenetic framework using a large robust species-level dated phylogeny of *Guatteria*. We tested for the phylogenetic signal of leaf spectra and inferred diversification rates across the evolution of this genus. We tested if changes in spectral diversity when present coincided with shifts in diversification rates within the genus. Our results shed light on the levels of constraint in the different spectral regions, reflecting the evolution of underlying *Guatteria*-specific leaf traits. Finally, our study underlines the importance of herbarium specimens to understand the evolution of diversity and leaf traits using innovative techniques such as NIRs.

S.41.2 Classifying stone oaks (Lithocarpus) in herbaria with reflectance spectra

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Global biodiversity datasets contain key gaps, this is particularly obvious when considering taxa in the Global South. Natural History Collections have the potential to help fill these gaps, however many records are unidentified, precluding them from use. A need to non-destructively sample from these collections further limits their potential. We evaluate the added value gained by taking spectral reflectance measurements of leaf tissue from herbarium specimens. We use a previously undigitised set of 1539 herbarium specimens from the Herbarium at Kew to ask how well we can discriminate between species using spectral data. We also evaluate the feasibility of inferring traits from these herbarium derived spectra. Spectra can accurately be used to identify species, however further work is still needed to extend this application to trait estimates. We highlight that leaf reflectance spectra provide a novel and non-destructive way to add value to natural history collections and can be applied to fill systemic knowledge gaps.

S.41.3 NIRS as a innovative tool for valorizing herbarium specimens: ongoing research at CIRAD

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Near infrared spectroscopy (NIRS) is a promising tool for valorizing herbarium specimens as it allows the gathering information on plants without damaging valuable and historical samples. The CIRAD herbarium is currently testing various approaches. These research can be separated into three areas: Firstly, we are using the NIR spectrum as a trait, studying its covariation with some other more "classic" functional traits such as Specific Leaf Area and leaf thickness. We are working on a dataset of *Combretum* genus from West and Central Africa to assess relationships between functional traits and a rainfall gradient. We are also examining functional traits of a Sahelian species, *Balanites aegyptiaca*, in relation with water availability. Secondly, we are experimenting with NIRS as a tool for systematics discrimination. Assuming that intraspecific variations in the spectrum are smaller than interspecific variations, it may be possible to make identifications in herbarium within some genus, using appropriate calibration. A test was carried out on two *Pistacia* species and their hybrid, with 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. Finally, we are experimenting NIRS for the prediction of leaf chemical composition. As prediction of fodder chemical value is already possible from the use of NIRS on grounded vegetal material, we are building a large calibration set to test the feasibility of applying the same method non-destructively on complete herbarium specimens. We present an overview of the research underway in our laboratory, spanning these three areas with practical case studies and initial results.

S.41.4 Leaf spectral properties and leaf traits of four alpine species of butterworts (Pinguicula L.)

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Understanding the traits that influence the responses of species to climate change is a crucial aspect of predicting future community composition and ecosystem function. Leaf functional traits are informative data to understand adaptation and acclimatization of species to ecological niches. Moreover, different plant species could have unique spectral reflectance signatures that might provide information to recognize and discriminate plant species. We characterized leaf morpho-functional traits of four species of *Pinguicula* with different ecological niches, from dump meadows to rocky walls. Specifically, we studied *P. alpina*, *P. leptoceras*, *P. vulgaris* and *P. poldinii.* Sampling activities took place in the Dolomites, north-eastern side of European Alpine Arc. We measured the following environmental parameters: temperature, relative humidity, light intensity, light spectrum. As leaf functional traits we considered leaf dry matter content and specific leaf area. In order to characterize the photosynthetic adaptation in alpine butterworts, we quantified leaf pigment contents, and we measured photosynthesis *in-situ* and leaf reflectance (400-1000 nm). Also, we observed leaf surface features, trichomes and glands morphology via scanning electron microscopy (SEM). Despite a lower concentration of chlorophylls, *P. poldinii* and *P. alpina* showed a higher photosynthetic efficiency (e.g. yield of open photosystem II reaction centres in light) compared to the other two species. Since the different species showed different leaf reflectance spectra, our findings corroborate the ongoing hypothesis that leaf reflectance can be a useful tool to interpret data related to leaf traits, pigment composition and tissues organization. By providing a comprehensive scenario of leaf morpho-functional characteristics and leaf spectra signature, we show that the studied-species are coherently optimized to their prevailing environmental conditions.

S.41.5 Plants show their true colors: leveraging leaf spectra to understand the diversity and evolution of plant form and function

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Understanding the diversity and evolution of plant function is critical at a time of rapid global change. However, traditional methods for assessing plant function, including measuring their traits and physiological strategies, are too expensive and time-consuming to be done at scale. First, we introduce leaf spectra and how they can be used to rapidly measure plant functional traits and physiological attributes. We cover the basics of leaf optics and techniques used to measure leaves Second, we cover the prospects and challenges of assessing plant function using herbarium specimens instead of fresh leaves. We talk about the challenges imposed by the background mounting paper and glue on the measurements and how to mitigate them. Finally, we describe and exemplify how to model the evolution of leaf spectra and their underlying traits to understand evolutionary rates and convergent evolution.

S.42 CURRENT RESEARCH IN BORAGINALES

S.42.1 An updated phylogeny of Boraginales based on the Angiosperms353 probe set: a roadmap for understanding morphological evolution

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Boraginales are a subcosmopolitan order with ca. 2,700 species recognized in 11 families. We re-analyzed relationships using the Angiosperms353 probe set. In addition to the Angiosperms353 nuclear gene data from 109 Boraginales accessions available in PAFTOL, phylogenomic data from 161 samples were generated, collectively representing all Boraginales families and approximately 84% of genus diversity. The results are consistent with previous phylogenetic studies, with some novelties and overall better resolution. Well-resolved species trees are retrieved with consistently high support for both data sets used (exons and supercontigs) and both analyses implemented (concatenation and multi-locus species tree estimation approach). Among the most important findings, Lennoaceae are found nested in Ehretiaceae and we propose their inclusion in Ehretiaceae. The tribal relationships of the highly diverse Boraginaceae subfam. Cynoglossoideae are fully resolved for the first time. Residual ambiguities remain: Codonaceae are found as basal branch in Boraginales I (sister to [Wellstediaceae and Boraginaceae]) in the exonic data set, in agreement with previous studies, but they are retrieved as basal branch of Boraginales II in reconstructions based on exons and introns. Also, the sister relationship of Namaceae and Hydrophyllaceae is not clear, probably due to limited sampling especially in *Nama*. Similarly, tribe Cynoglosseae was summarily sampled and intergeneric relationships are not at present fully resolved. Overall, the results highlight the effectiveness of the target enrichment probe set for understanding the evolutionary history of Boraginales and pave the way for resolving remaining taxonomic issues and a comprehensive study of the evolution of group-specific morphological traits. Our studies on the internal ovary architecture using scanning electron microscopy and micro-computed tomography reveal that changes in placentation and ovule number are key characters in the macroevolution and divergence of Boraginales families. Combining highly resolved phylogeny with critical morphological analyses promises a deep understanding of evolution trajectories in Boraginales.

S.42.2 Unraveling the evolutionary history of Cynoglossinae (Boraginaceae): insights from molecular dating, biogeography, and diversification patterns

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Cynoglossinae has radiated into a diverse assemblage comprising approximately 200 species, and its evolutionary history has not yet been comprehensively explored. Here, we examine the historical biogeography of Cynoglossinae, employing molecular dating and ancestral area reconstruction to understand how past climate changes and geographical patterns have provoked the diversification of Cynoglossinae. We inferred the evolutionary relationships of Cynoglossinae based on a dataset of 154 taxa, utilizing four plastid markers (*trnL-F*, *rps16*, *rpl16*, and *trnK–matK*) and one nuclear region (ITS) through PacBio sequencing. The monophyly of Cynoglossinae is strongly confirmed under Bayesian and maximum likelihood approaches. However, the nested position of all segregates confirms the broad concept of *Cynoglossum*, encompassing all generic segregates. Our biogeographic analysis results suggest that this subtribe likely originated during the middle Miocene in a large area, including East Asia and the Irano-Turanian region. It underwent rapid initial diversification, subsequently and repeatedly expanding its range both westward to Europe (including the Mediterranean region) and Africa, and southward to Australia during the Middle-Miocene to Pleistocene, with a preferential radiation into northern temperate regions. The timing of the diversification of the species-rich clades corresponds with Miocene tectonic events and global climate changes, resulting in increased aridity across Eurasia. Diversification analyses demonstrated a relatively constant diversification rate for all Cynoglossinae. Our results highlight the complexity of processes shaping diversifications in Cynoglossinae, emphasizing a complex interaction among climatic modifications providing opportunities for diversification.

S.42.3 An update on the phylogeny, classification, and biogeography of the popcorn flowers (subtribe Amsinckiinae, Boraginaceae)

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Subtribe Amsinckiinae, colloquially known as the popcorn flowers, is currently recognized with 17 genera and approximately 302 species. The subtribe exhibits a remarkable diversity of form and is one of the most taxon-rich groups of family Boraginaceae. Several new species in the subtribe have been discovered in the past five years, with more yet to be described. Analyses of new chloroplast DNA and ddRadSeq sequence data resolve some past ambiguities and confirm generally strong support for the monophyly of the 17 genera and of a separate group of *Cryptantha* species termed the *Maritimae* clade. We report the status of resolving "backbone" interrelationships among these major clades, which are often poorly resolved. We summarize major evolutionary shifts in the Amsinckiinae in plant duration, leaf size, fruit morphology, and reproductive biology. Long-distance dispersals within the subtribe occurred a minimum of 18 times, each resulting in an American amphitropic disjunction. Based on sequence data and comparative morphology, we now expand membership of the *Maritimae* clade to include up to 7 North American and 12 South American species, the latter resulting from evolutionary divergence following a single long-distance dispersal event. Finally, we present evidence that the *Maritimae* clade is inclusive of a monotypic genus previously not confirmed as a member of the subtribe, and we evaluate whether the *Maritimae* clade might best be treated as a separate genus of the popcorn flowers.

S.42.4 A systematic analysis of the family Heliotropiaceae Schard. in India based on morphology, anatomy and molecular data

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Systematic concepts of Boraginaceae have been highly problematic and controversial over decades. Traditional classifications subdivided the family Boraginaceae into five subfamilies. Recent molecular data-based results, supports the recognition of eleven families namely the Boraginaceae s.str., Codonaceae Weigend & Hilger, Coldeniaceae J.S.Mill. & Gottschling, Cordiaceae R.Br. ex Dumort., Ehretiaceae Mart., Heliotropiaceae Schard., Hoplestigmataceae Gilg, Hydrophyllaceae R.Br., Lennoaceae Solms, Namaceae Molinari, and Wellstediaceae Novák. under Boraginales. The family Heliotropiaceae Schard. comprises four genera, *Heliotropium* L., *Euploca* Nutt., *Ixorhea* Fenzl and *Myriopus* small. with about 450 species world wide. The members are distributed in the tropics and temperate regions of the world and occur mostly along the plains, coastal areas, dry arid zones. In India, the family is represented by two genera *Heliotropium* L. and *Euploca* Nutt. and with a high percentage of endemism. The members are annual or perennial herbs characterised by scorpioid cymes, epipetalous stamens, bicarpellary gynoecium, tetralocular ovary, terminal style, uniquely modified stigmatic head with annulus base and infertile apex, four seeded fruits. The family is studied in India based on field and herbarium data and the characters were recorded. Entire morphological variation occurring within the family is considered. Diversity and adaptive value of foliar architecture and pollen morphology of species is analysed. Hypodromous, brochidodromous type I, II, III, craspidodromous and reticulodromous venation patterns are noted within the members. Kranz anatomy is restricted to the *Euploca* clade. *Euploca* is characterised by medium-sized pollen grains, except in *E. ovalifolia*. Pollen grains are prolate in *Heliotropium* and prolate spheroidal in *Euploca* with the absence of endocingulum and medial constriction. Phylogenetic analysis using combined sequence data from regions ITS, trnL–trnF, matK and rps16 were conducted. These approaches prove to be highly informative in delimiting members within the family.

S.42.5 Evolutionary trends in gynoecium and fruit evolution in Boraginales

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Boraginales constitute a medium-sized order in the Lamiids with a chequered taxonomic history due to considerable diversity in flower and fruit morphology. In recent decades, molecular phylogenetics established Boraginales as a well-defined order with two major clades. Both comprise families characterised by either capsules or nutlets and capsules, schizocarps and/or drupes. A reduction in ovule number from many to four appears to have preceded the transition from capsular to indehiscent fruits. We address two main questions: Why did indehiscent fruits derived from a bicarpellate, syncarpous gynoecium evolve twice independently? What are the main factors driving fruit evolution in Boraginales? We combine scanning electron microscopy and X-ray micro-computed tomography in the context of recent phylogenies to understand gynoecium and fruit morphological evolution within Boraginales. We focus on three examples from Boraginales II. Our studies of gynoecium and fruit morphology address patterns in ovule and seed number evolution. In Hydrophyllaceae we found multiple transitions from pluri-ovulate to four-seeded fruits, but reversals of this character are rare. We argue that the reduction of ovule number to four fixes an ontogenetic trajectory, ultimately leading to indehiscent, four-seeded fruits. Conversely, in holoparasitic *Pholisma arenarium*, parasitism has likely led to a departure from the "two carpel-four ovule paradigm" in Boraginales, resulting in a multiplication of carpels to increase seed number. Finally, in Heliotropiaceae, we found fruit architecture to be highly conserved and divergent fruit morphology and function is realized by histological changes. Multiple transitions between schizocarps and drupes occurred even within closely related taxa within the family. These morphological and developmental studies underscore the multiple ontogenetic trajectories available for morphological diversification and functional convergence, even where particular character combinations are highly conserved. Traditional Boraginales systematics have emphasised mature fruit morphology – phylogenetic data clearly demonstrate that this often fails to reflect relationships correctly.

S.43 GEOPHYTIC MONOCOTS: TAXONOMY AND THE EVOLUTION OF SUCCULENCE

S.43.1 Delimiting species boundaries in Indian Pancratium (Amaryllidaceae): a cytotaxonomic approach

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Pancratium species grow sporadically throughout the country and individual plants are usually sparsely distributed. The species are ephemeral bulbous perennials. The emergence of scape and flowering mostly depends on the pre-monsoon rain pattern. Following the first pre-monsoon showers, the species flower only once in a year for a short period (10-15 days). Therefore, catching the species in flowering is a difficult task. Consequently, the genus is taxonomically poorly studied. Moreover, the species have been distinguished based on overlapping quantitative characters. Protologues are very brief, and the type specimens are either not available or poorly preserved. Therefore, there is a need to revisit the taxonomy and develop standard taxonomic methods to circumscribe species unambiguously. Accordingly, attempts have been made over the last 20 years to study the Indian species (distributed across ca. 75 accessions from various localities in India) in the field as well as under cultivation. I recognize nine species in India and provide an account of diagnostic characters and standard terminology that can be used to distinguish them. Additionally, chromosomal and crossability data are used to understand species limits. Most of the *Pancratium* species are diploid with $2n = 2x = 22$ chromosomes but a few, viz. *P. triflorum* and *P. zeylanicum* exhibit triploid ($2n = 3x = 33$) cytotypes as well. Karyotypes are represented by m (metacentric), sm (submetacentric), st (subtelocentric) and t (acrocentric) chromosomes. About 60 interspecific crosses involving eight species were made. Interspecific crosses among the Indian species produced fully fertile hybrids indicating that they represent a single biological species. The differences in characters (fixed genetically) among the populations (of species) probably represent ecotypes adapted to local environmental conditions.

S.43.2 Taxonomy of Indian Dipcadi: Does cytogenetics provide all answers?

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Dipcadi Medik. (Asparagaceae) is a bulbous monocot with less than 50 species distributed in Africa, Europe, the Indian subcontinent and Madagascar. India has 13 species with a maximum concentration (11 species) in peninsular India. Cytogenetically the genus is well-known for its bimodal karyotype wherein two sets of chromosomes of contrasting sizes are found. Taxonomy of the genus has always been convoluted on account of the uniformity of morphological features and their short flowering period. Moreover, these species make poor herbarium specimens because of their succulent nature and hence are underrepresented in Herbaria across the globe. Here, we studied the cytogenetics of 23 accessions distributed across 11 species to refine their taxonomy. The variation in diploid chromosome number (2*n*) indicated the presence of three chromosome counts, i.e., 2*n* = 12, 20 and 22 chromosomes. *D. concanense, D. goaense, D. janae-shrirangii, D. reidii, D. saxorum,* accessions collected from Ankai fort, Delhi, Gautala and Mhaismal had 2*n* = 12 chromosomes whereas *D. coimbatorensis, D. krishnadevarayae, D. montanum* var. *madrasicum, D. ursulae, D. ursulae* var. *longiracemosum,* accessions collected from Ajara, Badami, Belgaum, Dapoli, Dolkhamb, Halkarni, Rantale and Yercaud had 2*n* = 20 chromosomes. *D. erythraeum* had 2*n* = 22 chromosomes. The mean chromosome length (MCL) varied from 1.52 – 9.31 µm and the total length of the haploid complement (THL) was 24.76 – 48.91 µm. Both bimodal and trimodal karyotypes were observed. Trimodal karyotypes were confined to species with 2*n* = 20 and 22 chromosomes. Male meiosis was found to be normal. Our findings suggest that cytogenetical information, viz. chromosome number and morphology cannot fully discriminate between species and hence an integrated approach involving molecular cytogenetics or molecular phylogenetics should be applied to resolve the identity of species.

S.43.3 Geophytes in the Anthropocene: an integrated approach to understanding geophyte responses to rapid change

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Geophytes are generally plants with an underground perennation organ (e.g. bulb, corm, tuber, rhizome) that has a storage function and leaves that normally die back annually. This life-form evolved to avoid or cope with adverse environmental conditions and associated stressors both spatially or temporally. A predisposition to stress has arguably resulted in positive and negative consequences, but offers an interesting perspective on responses to rapid global change stressors of the Anthropocene especially climate change. While research focused on geophytism has gained pace recently, more integrated approaches are required. Here we offer recommendations on an integrated approach of understanding geophyte responses to rapid change from evolutionary, ecological, and physiological perspectives for monocots. This approach should begin with a deeper understanding of the evolution of the geophytism (particularly lineages with high levels of geophytism) to determine whether the trait is basal/advanced, when it evolved and under what conditions the trait emerges and persists. Ecological and physiological studies on geophytes focus on distribution, richness, endemism, growth, phenology, reproduction and dormancy. We argue for the implementation of more *in situ* and greenhouse studies (simulated stress scenarios) as these can provide excellent opportunities to understand geophyte responses specifically to climate change at various levels, and potentially provide data for predictive models. Spatial modelling of geophytes under climate change scenarios has been initiated in various parts of the world, but more of such studies are needed. While we have focused on climate change as a primary Anthropocene stressor, we need to acknowledge other interlinked stressors such as land use change, overharvesting, overgrazing, disease, fragmentation, and ecosystem degradation that are increasing the extinction rate of geophytes globally. An integrated approach will allow for a better understanding of the risks posed by climate change and multiple stressors of the Anthropocene, as well as the potential conservation options.

S.43.4 Diversity and phylogeny of the rapidly expanding Asian genus Peliosanthes (Asparagaceae)

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Considered recently to contain only a few species, the genus *Peliosanthes* is currently under active discovery for its taxonomic diversity. Indeed, by the end of the 20th century, it was known to comprise about 15 species, whereas more than 60 formally accepted species are presently known. However, the more taxonomic novelties are published, the less clear the interspecific boundaries become. From a morphological point of view, *Peliosanthes* can hardly be subdivided into species groups. In the virtual absence of molecular phylogenetic data, this makes the ideas of species proximity and their discrimination from each other highly subjective and often ambiguous. We used high-throughput sequencing approaches to obtain sequences of the entire plastid genomes of 20 specimens representing 18 species of *Peliosanthes*. Our results indicate that plastome data allow a well-resolved phylogenetic reconstruction of the genus. In some cases, the reconstruction was in congruence with the morphological similarity between species. For example, *P. triandra* and *P. weberi*, representing the earlier recognized genus *Neolourya*, formed a clade. In other cases, in contrast, the phylogenetic pattern obtained has never been predicted. In particular, our results support the distinctness of *P. graminea*, which was considered to be very close to the widespread and variable *P. teta* but appeared to be distantly related to the latter. We show homoplastic evolution of several structural traits, including the inflorescence type (raceme vs. thyrse), the absence or presence of a pedicel, the shape of the perianth (rotate vs. more or less cup-shaped), and the shape of the androecial corona (entire vs. lobed). We therefore argue that the significance of these characters for the systematics of *Peliosanthes* was overestimated, and we refute a number of earlier proposed interspecific relationships. Supported by the Russian Science Foundation, project 24-44-04001.

S.43.5 New insights on generic circumscription in Hyacinthaceae based on comprehensive morphological, molecular and distributional data

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Generic circumscription and systematics in *Hyacinthaceae* (= *Asparagaceae* subfam. *Scilloideae*), have been controversial in recent decades, with contrasting treatments based on preliminary and partial studies focusing only on morphology and/or limited DNA sequence data. This created considerable instability at both generic level and generic relationships. Recent treatments in subfamilies *Ornithogaloideae* and *Urgineoideae* have recognized a single genus *Ornithogalum* or up to four genera in *Ornithogaloideae* or only two genera in *Urgineoideae*, with a very broadly conceived *Drimia*. These proposals have been accepted for the last years by influential repositories (such as POWO, etc) and represented synonymization of several traditionally accepted genera with very distinct morphology, such as *Galtonia*, *Neopatersonia* and several others into *Ornithogalum s.l.*; several groups traditionally included in *Ornithogalum* into *Albuca s.l.*; or *Schizobasis*, *Thuranthos*, *Litanthus*, etc in *Drimia s.l.* In this way, recognition of such very broad concepts compromise acceptance of most genera in flowering plants and in petaloid monocotyledons and it is our aim to provide an alternative solution based on comprehensive studies combining morphological, molecular and distributional data. Our latest phylogenetic analyses involving plastid and nuclear DNA regions and a selection of 40 morphological characters covers 293 samples of *Urgineoideae* (ca. 80% of its diversity) and yielded 31 well-defined clades or lineages, most corresponding to previously described genera, although some have required description or revised circumscription. Regarding subfamily *Ornithogaloideae*, our studies evidence the existence of 19 lineages that can be accepted at genus rank and are linked to a defined biogeography. As in other monocot families, a considerable degree of homoplasy was observed in morphology, especially in those groups with unspecialized flowers; nonetheless, consistent syndromes of traditional and novel characters are shown to support clade recognition at genus rank.

S.43.6 Integration of genomic phylogeography, morphology and climatic niche to elucidate speciation within Phycella (Amaryllidaceae)

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Phycella (Amaryllidaceae) is a clade of approximately 13 species of lilies endemic to the Mediterranean-type ecosystem of Chile. An unclear taxonomy at the species level and conservation interest makes it a priority to clarify the number and limits of species which hinders addressing questions about speciation mechanisms in this key endemism area. To approach the evolutionary history of *Phycella*, we sampled a total of 137 individuals from 47 populations, including all described taxa throughout the geographic range of the group, and sampled 893 nuclear genes (1135 exons) through hybrid capture. These data largely resolved the phylogeny of *Phycella* with high support and demonstrated substantial phylogenetic resolution at the population level. The combination of high-resolution molecular data with morphological and ecological data further yielded insight into speciation mechanisms, and near-complete plastomes were extracted from raw reads and assembled for all samples to compare with the nuclear framework and examine complex evolutionary processes. Using phylogenetic network and modeling approaches, we identified major cytonuclear discord, attributable to proximity-based gene flow among recently diverged species through the speciation process, largely involving cytoplasmic DNA. Analyses of niche overlap among species and nuclear clades suggest that the diversification of *Phycella* was associated with niche divergence, supporting a predominantly geographic mode of speciation in the group, likely driven by the mountainous landscape characteristic of diversity and endemism center of this clade in central Chile. Finally, we present a major integrative taxonomic proposal that divides *Phycella* into 18 species on the basis of molecular, morphological, and ecological data. Overall, our findings highlight the value of strong sampling of both populations/individuals and genetic loci for speciation studies, which was key to identifying both evolutionary processes and a confident taxonomic framework for contextualizing these processes.

S.44 MECHANISMS UNDERLYING PLANT DIVERSITY PATTERNS IN THE EAST ASIAN–AUSTRALASIAN REGION

S.44.1 What factors contribute to the biased latitudinal species diversity gradient in the East Asia-Southeast Asia-Australasian region?

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The East Asia-Southeast Asia-Australasian region constitutes a continuum of plant diversity hotspots across a broad latitudinal gradient, contributing significantly to global plant diversity. The higher latitudes in the region, including East Asia and Australia, are the richest source of botanical information (i.e., plant species occurrence records) in the world, while the lower latitudes present a global cold spot in such records. This spatial inequality of sample completeness has made it difficult to scrutinize the geographical patterns of plant diversity across the whole latitudinal zone of the region. Recent study reported bias-corrected diversity patterns of global woody plants, and reported a skewed latitudinal gradient in species diversity, peaking in the mid-latitudes of the Northern Hemisphere (southern China). A latitudinal diversity gradient is one of the best-recognized macroecological patterns, and its underlying mechanisms are considered to be due to energy/climatic gradients, and/or tropical niche conservatism, but no consensus has yet been reached. A thorough exploration of the drivers of the skewed latitudinal diversity patterns of woody plants in the region would provide further insight into the geographic, ecological, and evolutionary forces shaping biodiversity. In this presentation, we introduce the results of the examination of the contribution of plant taxonomic components to the biased latitudinal diversity gradient. Then, we aim to identify taxonomic levels, groups, and areas to focus on and in the future and organize hypotheses to be tested in order to elucidate the mechanism of biased latitudinal diversity pattern.

S.44.2 Origin and Australian paleoclimate drives biotic exchange patterns across Wallace's Line

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The convergence of the Sunda continental shelf (Malaysia, parts of Indonesia and the Philippines) and the Sahul continental shelf (Australia and New Guinea) from c. 25 Mya was a significant event in global biogeography that resulted in the exchange of previously isolated floras (the 'Sunda-Sahul Floristic Exchange'; SSFE). Despite the importance of the SSFE in shaping the flora of the region, much remains to be understood about the processes and patterns underlying it. To address this, we used Angiosperms353 target capture data to generate the most densely sampled phylogenetic tree of angiosperm order Sapindales to date, with 448 samples and c. 85% of the genera represented. Our tree resolves the relationships between Meliaceae, Simaroubaceae and Rutaceae and indicates that Nitrariaceae, Biebersteiniaceae and Sapindaceae emerged early in Sapindales, but the order of divergence remains unclear. Bayesian dating with 29 rigorously assessed fossil calibrations indicates that most Sapindalean families arose in the Cretaceous. We then integrated target capture data with legacy Sanger data to produce species-level phylogenetic trees of Sapindales families. Biogeographic analyses of the dated, species-level trees support Sundanian origin for Sapindales families, confirm the eastward bias in exchange from Sunda to Sahul, and highlight the importance of Wallacean emergence in facilitating the exchange. Most interestingly, the results indicate that for some lineages, an origin in Sunda and subsequent colonisation of Wallacea and Sahul explains the observed eastward bias in exchange, while for others, ancestors were present in Sahul, but extinction coincident with Miocene aridification likely contributed to the eastward exchange bias. This study has shed new light on Sapindalean evolution and the SSFE, and emphasises the importance of considering ancient evolutionary history when attempting to understand recent and current biogeographic processes.

S.44.3 Cenozoic dynamics of beta diversity in East Asian angiosperm woody plants: cooling and increased fluctuation of climate drive dist

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We focused on the impact of paleoclimate changes on large-scale taxonomic sorting related to geography; specifically, how cooler and warmer climatic conditions affect the distance-dependency of betadiversity. Using a dataset of Cenozoic fossil assemblages of angiosperm woody plants (7,468 data points; 310 genera in 95 families) in the Japanese portion of the East Asian archipelago (except Ryukyu islands), we modeled the distance-dependency of genus turnover (pairwise compositional dissimilarity) through the Oligocene, Miocene, Pliocene, Pleistocene, Last Glacial Period, Holocene, and present day. The genus turnover of angiosperm woody plants was significantly correlated with geographical and climatic distance only in the Last Glacial Period, Holocene, and present day. During theOligocene to Pliocene, the warmer periods, genus turnover was mostly independent of geographical distance. Spatial/climatic distance-dependent turnover under colder environments involved a climate-induced sorting process to spatially diversify woody-plant assemblages across the archipelago. Moreover, the predominance of distant-independent turnover suggested the effect of dispersal release under warmer, stable climates. Our findings suggest that future tropicalization in temperate habitats could promote geographical homogenization of biodiversity patterns.

S.44.4 Historical biogeography of Maesa (Primulaceae) with an emphasis on the Indo-Australian Archipelago

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The Indo-Australian Archipelago is recognized as one of the world's most geologically and biogeographically complex areas with exceptional floristic diversity. These islands are situated between mainland Southeast Asia and Australia, acting as an area of floristic interchange. However, the pathways of plant dispersal across the region are still unclear. Although west-to-east dispersal into the Pacific is detected in several plant groups, the generality of this pattern remains to be tested. *Maesa* is a genus of shrubs, trees, or woody scramblers in the family Primulaceae distributed in the palaeotropics from Africa to the Pacific comprising approximately 200 species. In this study, we reconstructed dispersal events of *Maesa* focusing on the Indo-Australian Archipelago and the connection to continental Asia and the Pacific islands. We used a comprehensive species-level phylogeny generated from genomic (target sequence capture) data for molecular dating and ancestral range estimation. The phylogeny showed several strongly supported clades, including three geographically structured Asian-Pacific clades. The Asian-Pacific lineage diverged from its African relatives ca. 15 Ma and established in Continental Asia-Papuasia-Philippines ca. 11 Mya. However, the recent diversity of the genus in the Asia-Pacific is a result of rapid radiations that happened ca. 5 Mya possibly related to a warming phase and rapid orogenesis. Papuasia and Continental Asia are inferred as major sources of *Maesa.* We detected two west-to-east dispersal trends: from continental Asia to west Malesia and from Papuasia to Pacific Islands. No connecting path is recovered which might be due to incomplete sampling especially from the Philippines. This study is the first to explore historical biogeography of the genus *Maesa*. Our investigation into the biogeographic history of the genus reveals the events that shape the current distribution of *Maesa* and shed light on the connectivity between the complex Indo-Australian Archipelago and neighbouring islands and continents.

S.44.5 Phylogenomics, pollination biology, floral chemistry, and historical biogeography of Western Australian Darwinia (Myrtaceae)

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We are using a variety of approaches to analyze the relative importance of various drivers of species diversification in the large, relatively young, morphologically diverse genus *Darwinia* (Myrtaceae) from Western Australia. This group is ideal for such a study given the narrow endemism of many species, the sky-island biogeography of several taxa, the apparent lack of long-distance seed dispersal across the group, and the striking diversity of inflorescences and associated pollinators, with the latter including birds, marsupials, and several groups of insects. We are developing a Myrtaceae bait kit for phylogenomic studies of *Darwinia*, and have sequenced and analyzed several hundred single-copy nuclear loci. We are extending these studies now to construct and date nuclear and plastome phylogenies, to reconstruct relationships, character-state evolution, species diversification rates, and historical biogeography in *Darwinia*. We are also investigating the reproductive ecology and pollination syndromes of several representative *Darwinia* species through studies of pollinator behavior, floral morphometrics, and floral volatile and nectar chemistry. Data resulting from these studies will be integrated into analyses of the drivers of taxonomic and morphological diversification in *Darwinia*. This research will shed light on speciation, endemism, adaptive radiation, coevolution, and convergence in a large, threatened clade from the Western Australia biodiversity hotspot based on research by collaborators at the Western Australian Herbarium, Australian Tropical Herbarium, King's Park Botanic Garden, and the University of Wisconsin-Madison.

S.44.6 Phylogeography and conservation of Pedicularis (Orobanchaceae) in the Hengduan Mountains biodiversity hotspot

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Pedicularis (Orobanchaceae) is a genus of herbaceous hemiparasitic plants with highly diverse floral morphologies. It includes ca. 600 species worldwide, more than half of which are native to China and endemic to the Hengduan Mountains, where their greatest diversity is found. Over the past decade, multiple phylogeographic scenarios have emerged to describe the impacts of mountain uplift, Quaternary glacial cycles, and climatic transitions on plant diversification across the Hengduan Mountains. While some studies have documented these large-scale dynamics for species across this region, few have used population genomics to quantify impacts of geographic barriers on population structure. This research highlights the phylogeographic histories of twelve widespread *Pedicularis* species in the Hengduan Mountains, where it is common to find many species of *Pedicularis* flowering in sympatry. With an assembled dataset of ~1,000 specimens, we used a modified ddRAD approach to determine the population structure and divergence time estimates for these twelve species, as well as putative geographic barriers affecting their dispersal ability across the mountain range. Additionally, we compared the genetic diversity between contemporary (post-2018) and historical (pre-2000) *Pedicularis* samples collected throughout the Hengduan Mountains to reveal areas of gene flow, highlighting potential conservation implications of recent infrastructure development in the region.

S.45 TOWARDS A MORE ETHICAL SCIENCE: DECOLONIZING BOTANICAL RESEARCH. SESSION 1

S.45.1 Publishing as ethics: decolonizing as a means towards equitable publishing

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As a means for contributing to the session on decolonizing botany, this paper presents a critical analysis of academic publishing. Because science is a multipronged institution, decolonizing it requires also liberating the colonial hold on the ways information is shared and, moreover, on the information itself. The critical analysis in the presentation is made from my perspective as a publisher and editor with the Society of Ethnobiology and the University of Arizona Press. I also build upon my experiences as a transdisciplinary field researcher, author, and peer reviewer. Additionally, I share key moments from dialogues within the ADIE (Allying for a Diverse and Inclusive Ethnobiology) community related to equitable publishing and data sovereignty about: ethics; iterative project design; research approvals and rapport; co-authoring; regulations, standards and practices; funding and advocacy; procedures for managing vouchers; and ethnobiological methods. By raising questions about what academic publishing would look like in a world where science is decolonized, this presentation provokes considerations related to botanical research. For example, IBC conference attendees might discuss data sovereignty, open access, co-authoring, multilingualism, rank and tenure evaluations, rematriating voucher specimens, collaboration, Indigenizing methods, and epistemological justice. What efforts are being made towards decolonizing publishing? Publishing has made some progress towards decolonizing; particularly with open access, international hip, ethics codes, data sharing, and editorial support for scholars with diverse language backgrounds. What are the barriers in these arenas and what are some additional obstacles to a more equitable publishing? Why are these barriers and obstacles in place, and how could they be overcome? Working within a framework of decolonial theory and born from practical experience, this paper problematizes publishing standards in the colonizers' worlds while it offers pluralizing and otherwising as conceptual mechanisms for decolonizing publishing.

S.45.2 Gender equality and the visualisation of women in ethnobiological research: advances and perspectives

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Achieving gender equality and ensuring a fair representation of women in ethnobiology (and other disciplines) is still challenged by biases deeply rooted in the academic system. These biases lead to practices that reaffirm inequalities towards women. The existence of a gender hierarchy gives rise to a tripartite set of problems that may be manifested in the practice of ethnobiological research. These problems are: 1) maintaining or exacerbating such a hierarchy; 2) failing to examine differences, being insensitivity to differences, and treating people the same when they should be treated differently; and 3) using double standards, treating different groups differently because of their position within a social hierarchy. To explore gender biases in ethnobotanical research, we re-examine our own published works, evidencing gender misconceptions that have become evident in the discursive field and have operated in the conception, methodology, and interpretation of our results. Our conclusions reinforce the idea that it is necessary to open new perspectives that allow considering the feminine dimension when studying place-based knowledge and practice, since it is still veiled in much of the ethnobiological scientific production. The set of problems evidenced in our work and that of other, synthesized in the so-called triangle of bias, can only be corrected with an integral gender approach. Furthermore, we highlight the importance of further research to describe local gender asymmetries in the protagonists' own terms

S.45.3 Co-authorship with Indigenous, Afrodescendant, and local peoples: Opportunities and responsibilities of academia

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Academia has a long history of not acknowledging and/or appropriating the research contributions of traditional knowledge holders in interactions with Indigenous, Afrodescendant, and local communities. Recognizing this history underscores the continued need for more equitable and respectful science, advocating for genuinely collaborative research, and embracing co-hip on scientific publications. This approach presents opportunities for expanded allyship networks, facilitates mutual learning experiences, enriches research methodologies, incorporates diverse perspectives, and fosters ethical and sustainable research outcomes. Co-hip, for example, provides a platform for Indigenous and other local community members to actively participate in the research process, ensuring their voices, perspectives, and knowledge are properly acknowledged and represented. Moreover, collaborative research is impactful when embedded in long term relationships that support agency and self determination with the communities involved. Additionally, papers written collectively are more likely to be expressed in accessible language, enabling more people to build on research and rendering them more meaningful for posterity. This collaborative model foregrounds the significance of cultural sensitivity and respect for local traditions, incorporating the right to veto the publication of culturally-sensitive information. When co-hip is truly collaborative it will promote trust and mutual respect, giving communities a sense of ownership and control over the research process and its outcomes. On the other hand, it is essential to identify and address challenges associated with co-creation of knowledge and co-hip, such as power dynamics, resource imbalances, and the risk of tokenism. Consequently, research methodology should be informed and grounded in empathy as communities may have suffered trauma in the past from exploitative research and colonialism. These challenges should inform future strategies dedicated to nurturing more meaningful and balanced partnerships.

S.45.4 Biocultural heritage of Litekyan in Guam: connecting stories of spirituality and resistance

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The Mariana Islands are characterized by a rich biocultural diversity. The CHamoru people of Guam (the southernmost island) have coexisted sustainably with their islands' biotic communities. When the sacred lands of Tailalo' and Litekyan became threatened by military expansion on Guam, a social movement advocated for the protection of the CHamoru peoples' biocultural heritage and the return of their lands. Maria Hernandez May, an Indigenous CHamoru woman and daughter of a lineage of original Litekyan landowners, continues the legacy of her ancestors in her fight to get their land back. She is at the forefront of the movement, advocating for endangered species, CHamoru culture and ancestral land. The social movement also represents the voices of the traditional healers, fishermen and cultural groups who gather for ceremonies. An ethnographic case study, using methods drawn from Participatory Action and Social Movement Research, analyzed the environmental injustices in a historical and current context. Our research is grounded in learning from those who have mobilized this movement, especially the Indigenous peoples. We documented the spiritual, sacred connections to the land, and how sovereignty rights are tied to CHamoru identity and values. U.S. law disregarded Indigenous perspectives which play a vital role in plant-human spiritual frameworks and the protection of Indigenous biocultural heritage. Despite opposition from the island community and demands for environmental justice, the Department of Defense bulldozed the forest at Tailalo'. More destruction is on the way at Litekyan. This symposium, with a call to action from within the botanical research community, excites us. Maria, traditional knowledge holder and activist, and Else, scientist and activist, share how they support each other to amplify Indigenous voices.

S.45.5 Using photo identification and digital methods to empower local communities to document their own botanical knowledge

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The identification of plants according to the Linnaean system of taxonomy is a cornerstone of ethnobotany, allowing the discipline to be a comparative science. To accomplish plant identification, ethnobotanists have long relied on the collection of voucher specimens and their deposition in herbaria. Nevertheless, the complexity of botanical collecting sometimes hampers the process of local communities self-conducing their own ethnobotanical inventories. Here we bring attention to a new set of methods which could help facilitate this goal: the collection of photographic vouchers and their deposition in digital repositories. The ever-improving quality and ubiquity of smartphone cameras, photographic citizen science applications like Pl@ntnet and iNaturalist, and deep learning techniques of automated photo identification are contributing to a slow revolution in the role of digital data in the field sciences. We propose photographic vouchers as a valid, scientifically rigorous and locally adapted method to inventory local botanical knowledge for and by communities and lay out guidelines for their use.

S.45.6 Ethnobotany in service of food, land, and data sovereignty: examples and barriers

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Ethnobotany, like many fields, was shaped by early Western imperial efforts to colonize people and lands around the world and understand and extract natural resources. Over the last several decades, many ethnobotanists have worked to re-envision the goals of ethnobotany as an anti-colonial science which supports local communities' rights to self-determination. Three case studies will be presented that seek to support food, territory, and data sovereignty of Indigenous Peoples and local communities as well as the challenges faced and lessons learned. First, in many parts of the world, traditional, climate-resilient crops and cropping practices are being replaced with high-input, introduced grains promoted by international and governmental policies. I share work to revitalize traditional grain mixtures in Ethiopia that are being discouraged by agricultural policy. Second, Globally, Indigenous Peoples have shaped landscapes through centuries or millennia of plant stewardship. In the Pacific Northwest of North America, territorial rights can be tied to laws based on misconceptions about traditional land stewardship. I share examples from land-rights cases that incorporate ethnobotany as evidence. Finally, herbarium specimens can contain not only biological data, but also cultural data—notes on local names and uses. In many cases this data was collected without formal approval from communities and/or before Free Prior Informed Consent became standard. I share work by a global consortium of herbaria working to reunite this data with source communities and explore options for community control of their data. Reflections are presented on the social, legal, and ethical complexities involved in these cases as well as faced by contemporary ethnobotanists in general.

S.46 AEROBIOLOGY. ADVANCES IN THE ATMOSPHERIC POLLEN RESEARCH AND CHALLENGES IN THE CONTEXT OF GLOBAL CHANGE. SESSION 2

S.46.1 Vegetation and land-use distribution determine aerobiological risk areas in the Madrid Region

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Pollen is the main source of outdoor aeroallergens, together with fungal spores, and because of allergic respiratory diseases depend on the seasonal occurrence of these aeroallergens, exacerbations of allergic symptoms follow a strongly seasonal pattern. Vegetation distribution and land-use configuration of the territory determine the occurrence and magnitude of pollen exposure, and then the airborne pollen spectrum. The aims of this study were to characterise the airborne pollen dynamics of aerobiological sampling stations of the Madrid Region Palynological Network in relation to the potential pollen sources and to define aerobiological risk areas of the Madrid Region based on homogeneous patterns of occurrence and intensity of the main pollen taxa. Multiple clustering approaches were conducted to group (i) the sampling stations of the aerobiological network and (ii) all pixels of the Madrid Region (central Spain). The clustering dendrogram based on vegetation distribution was compared to those based on airborne pollen characteristics. The results showed a great correspondence between potential pollen sources distribution and airborne pollen dynamics. The Madrid Region was divided into six aerobiological risk areas based on the potential pollen sources. These risk areas were ordered following a clear anthropogenic gradient, with one cluster in the centre covering the most urbanised areas, another one covering agricultural lands in the south and southeast, and four more clusters in the forest-dominated environments of the Madrid Region. Spatial regionalisation in environmental risk assessment favours the application of management plans by the institutions responsible of the management of public health systems and allows resources to be optimised. The mapping of risk areas based on impact of allergenic plant species constitute a step forward in the management of the biological air quality of Madrid Region.

S.46.2 Effects of urbanisation on airborne pollen spectrum in cities

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

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Climate change is affecting plant distribution, but human-driven land use changes are also playing a crucial role in it. Accelerated urbanisation drastically alters the landscape, generating a major impact on herbaceous plant communities in urban environments and, consequently, altering the airborne pollen concentrations in cities. Two of the most relevant impacts are vegetation removal for construction, as well as the introduction of ornamental species. The aim of this study is to analyze trends in the pollination period of herbaceous and ornamental species in the city of Malaga due to urban expansion. To do this, aerobiological data from the period 1992-2023 were used. The data were obtained by means of a Hirst-type volumetric pollen sampler installed on the roof of the Faculty of Sciences of the University of Malaga. The samples were mounted and counted following the methodology proposed by the Spanish Aerobiology Network. The main pollen season (MPS) was defined by fitting a logarithmic function to the accumulated pollen concentrations. Then, trends in the parameters of the MPS were calculated employing linear regressions. The results reveal a significant decrease in the annual pollen integral of herbaceous taxa growing in agroforestry areas such as Amaranthaceae, *Plantago,* and *Rumex,*and a significant increase in pollen from nitrophilous species such as *Urtica membranacea*. *Olea* and *Platanus* pollen types have also increased their presence in the atmosphere due to the expansion of olive tree crops and the growth of ornamental individuals, respectively. The expansion of urban areas causes the loss of habitats as well as the modification of plant communities, which results in a modification of the air pollen content. Therefore, urban expansion can be involved in a significant change in seasonal allergies in the urban population.

S.46.3 Implementation of the PhenoFlex framework for forecasting the start of the main pollen season in the context of climate change

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Climate change is affecting the flowering seasonality of many plant species, disrupting the dynamics of their life cycles and triggering changes in ecosystems. These changes are not uniform across all species and geographic regions, and local monitoring is required to gauge future phenological shifts and to establish mitigation strategies. In this context, aerobiological sampling has proven to be a valuable tool for monitoring the flowering onset in anemophilous species. The start date of the main pollen season for a certain pollen type in a given location is usually linked to the flowering onset of the taxa that produce it. This has encouraged the development of different models in recent years to estimate the start of the main pollen season. However, some of these models rely on rigid assumptions that may not fit the diversity of the environmental conditions in which the plants grow. In 2021, Luedeling et al. developed the PhenoFlex statistical framework to forecast the flowering onset of tree species based on biological processes. This model accommodates for both overlapping and sequential chilling and forcing periods. It also fits all the model parameters for the targeted taxa, avoiding the arbitrary selection of fixed parameters. To date, this framework has not been used in aerobiological contexts. In this study, we delve into the applicability of this framework to aerobiological data and issue some recommendations for model validation and its use in estimating climate change impacts. As an example of application, PhenoFlex models were fitted to aerobiological data for Cupressaceae and *Platanus* from 8 sampling locations within Malaga Province (southern Spain) with 52 sampling years. The models registered mean absolute errors of 7.7 and 4.5 days, respectively, and were used to generate forecasts according to different future temperature scenarios.

S.46.4 Pollen conservation of endangered Hawaiian endemic Hibiscus and Pritchardia species

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Storage of pollen allows for gene exchange between geographically isolated individuals, and for controlled pollination when flowering of staminate and pistillate flowers or individual plants are asynchronous. Desiccation of pollen is essential for the retention of high longevity, yet research into pollen storage behavior is infrequently performed. *Hibiscus clayi* and *Pritchardia minor* are Kaua'i single island endemic plant species assessed as Critically Endangered and Endangered, respectively, by the IUCN Red List of Threatened Species. With respect to these species we asked; 1) How does pollen germination respond to varying sucrose concentrations (5-40%) and substrates (liquid/solid); 2) What is the pollen germination temperature niche breadth; 3) How does pollen viability respond after desiccating to the international genebank standard of 15-25% RH? If desiccation tolerant, 4) how does viability of previously desiccated then hermetically sealed pollen respond to freezing at conventional (-18°C) and -80°C temperatures? Finally, in order to understand relative storage lifespan and the influence of moisture relations, we asked, 5) How does pollen longevity respond to periods of time stored in varying RH environments. To answer these questions, we collected pollen from the National Tropical Botanical Garden's living collections. We desiccated pollen to a range of RHs at ambient temperature (~25°C), hermetically seal, and store at -18 and -80°C, then we tested viability via a germination test at each stage. To assess pollen longevity, survival curves were determined and compared using p_{50} (the time for viability to decrease to 50%). Research into optimal pollen storage methods by species is needed to better understand the effects of desiccation, freezing, and time on pollen viability and longevity. Considering the current rate of plant extinction in Hawai'i, pollen storage is an important conservation tool for conducting controlled crosses that might otherwise not be possible.

S.46.5 Aeropalinology, critical analysis of urban trees in cities with contrasting climates in Chile

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The urbanization in Chile has brought the introduction of arboreal species to the inside of the cities, the same species are used in different type of Climate. For this reason it is desired to show that the trees used as ornamental in cities of our country has no relation to the phytogeographic and climatic zone in which they are inserted, and also in the case of Santiago is expected to demonstrate the effects on the health of people. Four cities of Chile are chosen to research it: Antofagasta, Santiago, Concepción and Valdivia, and from Spain, the city of Barcelona. An analysis of the native arboreal flora is performed and to know the species of the urban trees, the aeropalinological records of the cities involved are used. The results are subjected to the analysis of the Jaccard similarity index. For the case of Santiago, the relationship of the concentration of pollen in the air versus the pollen positive skin tests is given. It is concluded that the trees species of the studied cities are mainly exotic. There is a high degree of homogenization or similarity between the urban tree flora between the cities of Chile and with Barcelona, the species are not related to its bioclimatic area, no native trees are used (if present is a fluke), we do not have original urban landscapes, and tree species in the case of Santiago are directly related to increases in pollen allergies.

S.46.6 Guignardia bidwellii spores ecology in the vineyard, relation to weather factors and phenological development

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Knowledge of the phenology and concentration of phytopathogical fungi in a vineyard is a useful tool to estimate when a phytosanitary treatment is necessary, since today the high use of pesticides leads to subsequent soil contamination that can negatively affect the soil biodiversity and the vine itself. Our aim was to understand how environmental conditions can influence the *Guignardia bidwellii*, causal agent of grape black rot. The study was carried out in two vineyards (Viña Mein and Emilio Rojo) belonging to the DO Ribeiro (Northwest Spain) during 2023 campaign. Phenological study was carried out on 20 selected vines following BBCH scale. To monitor the spores, two Lanzoni VPPS-2010 volumetric samplers are used, one in each study plot. The identification and counting of airborne spores have been carried out following the methodology proposed by the Spanish Aerobiology Network. Meteorological variables have been provided by two meteorological stations, located near the spore trap. The concentration of *G. bidwellii* spores was higher in Viña Mein (2912 spores) than in Emilio Rojo (656 spores). The peak of spore concentration occurred on May 28 with 438 spores/m³ in Viña Mein coinciding with the end of flowering stage (S-6), and 84 spores/m³ on June 23 in Emilio Rojo coinciding with fruit development stage (S-7). When analyzing intraday behavior of *G. bidwellii* spores in both plots, we observed that the highest concentrations occur at dawn (01:00–8:00 a.m.). The meteorological variables that exert the greatest influence on the concentration of *G. bidwellii* were the minimum temperature, dew point, relative humidity and precipitation. Knowledge of the phenological, phytopathological and meteorological variables of a certain region can provide us a valuable tool to know the phytosanitary status of a crop and thus be able to make appropriate decisions regarding the application of different phytosanitary treatments.

S.47 INTEGRATIVE TAXONOMY OF MEDITERRANEAN PLANTS. SESSION 1

S.47.1 Delimiting taxa boundaries in complex plant groups by genomic, morphometric, and ecological data: the case of Helianthemum

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The study of complex plant groups demands a comprehensive approach, encompassing macroevolutionary and microevolutionary scales. By integrating diverse data sources, we aim to offer a thorough perspective that aids in resolving taxonomic and systematic questions. Next Generation Sequencing technologies present a significant opportunity for unraveling the evolutionary processes within these challenging groups. Among these groups, the genus *Helianthe-*

mum stands out as the most extensive genus within the Cistaceae family, boasting over 140 species and subspecies, included in 3 subgenera and 10 sections. Its distribution range extends from Macaronesia to Central Asia, covering North Africa and central Europe. Notably, *Helianthemum* exhibits one of the highest diversification rates in the Mediterranean Basin, attributed to three evolutionary radiations since the Pliocene. These radiations align with the three major sections: *Eriocarpum*, *Helianthemum*, and *Pseudocistus*, resulting in a complex taxonomy and nomenclature with poorly defined taxonomic boundaries. In our research, we employ an integrative approach that combine genomic techniques (GBS, target capture), ecological analyses (soil, climate), and morphological assessments (vegetative, floral, and karyological traits) at both macroevolutionary and microevolutionary levels. Our goal is to unravel the processes contributing to this taxonomic complexity and establish practical boundaries across all taxonomic ranks, from subgenera and sections to species and subspecies. Macroevolutionary findings indicate that higher taxonomic ranks (subgenera and sections) are generally well-defined in terms of phylogenetic, ecological, and morphological criteria. On the microevolutionary front, our investigation of polymorphic species within sect. *Pseudocistus* (*H. marifolium*, *H. cinereum*, and *H. oelandicum*) reveals compelling evidence of some introgression between them and the parallel evolution of characters previously used to define subspecies. This emphasizes the need for a synthetic taxonomic treatment with stable diagnostic characters at the lowest taxonomic levels.

S.47.2 Integrative taxonomy of Centaurea aplolepa Moretti (Asteraceae) and related central Mediterranean species

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Centaurea L., with approximately 600 species, is one of the largest genera of the Mediterranean Region. Due to this species richness and several biological phenomena (hybridization, introgression, polyploidy, etc…), the systematic and taxonomic investigation of this genus is highly challenging. In the central Mediterranean, one of the groups still waiting for a thorough taxonomic revision is that of *C. aplolepa* Moretti. This species is endemic to north-western Italy and, during the last century, a great number of taxa at intraspecific rank was described. Currently, based on qualitative morphological and ecological (e.g., different growing substrate) observations, ten putative subspecies are accepted. Previous phylogenetic studies using ITS and the *rpl* chloroplast region failed to disentangle the relations within *C. aplolepa*. Indeed, its subspecies were all placed in an unresolved clade along with several other central Mediterranean morphologically related species. To understand the systematic relations among the subspecies of *C. aplolepa* and other closely related taxa, we started an integrated taxonomic investigation. During summer 2023, 17 populations of *C. aplolepa* and eight populations belonging to five related and geographically contiguous species were sampled. For each population, 30 individuals were collected for morphometric analyses. A subset of 15 individuals was used to extract DNA for population genetics using AFLP; cypselae were collected for cytotaxonomic studies (chromosome count and genome size estimation). The taxonomic investigation is currently ongoing, but preliminary morphometric results support the distinction of *C. aplolepa* with respect to the related species. Conversely, just three (instead of ten) morphological groups are supported within *C. aplolepa*.

S.47.3 Integrative species delimitation in a Western Mediterranean polyploid complex

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Species delimitation is particularly challenging in polyploid complexes pervaded by reticulate evolution. As allopolyploids are a mosaic of characters of their parental lineages, the simultaneous inference of the evolutionary history (allo- vs. auto-polyploidy) and delimitation of species is impracticable in those groups. For instance, the hybridogenic nature of allopolyploids violates the assumptions of the current DNA-based approaches for species delimitation. *Leucanthemopsis*

(Giroux) Heywood is a genus of the Asteraceae, consisting of six to ten species and several infraspecific taxa, mainly distributed in the western Mediterranean Basin. It is a polyploid complex that includes montane, subalpine, and strictly alpine lineages, which are locally distributed in different mountain ranges of Western Europe and North Africa. We used a mixed approach including Sanger sequencing and high throughput sequencing of amplicons to gather information on single-copy nuclear markers and plastid regions. Nuclear regions were carefully tested for recombinants/PCR artifacts and for paralogy. Coalescent-based methods were used to delimit species among the diploids. For the polyploids, we first sorted homeologs of nuclear genes into parental subgenomes. Therefore, we inferred delimitation among the Iberian tetraploids treating subgenomes separately in the analyses. We corroborated results from the DNA-based approaches with evidence from morphometric analyses of leaf shapes and ecological niche modelling. Based on the results, diploid taxa found growing in the Eastern Iberian Peninsula constitute a single, heterogeneous complex. Concerning polyploids, the analyses inferred Iberian tetraploids as having a clear allopolyploid origins. At least two different polyploidization events gave rise to *L. spathulifolia*, endemic of calcareous outcrops in South-eastern Spain, on the one side, and to all other tetraploid Iberian taxa on the other.

S.47.4 Integrative taxonomy recircumscribes diversity of the Dianthus sylvestris s.l. in the Balkan Peninsula

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Dianthus is one of the most diverse plant genera in the Mediterranean as a result of its rapid radiation in this area. *Dianthus sylvestris* s.l. (Caryophyllaceae) is a species complex distributed across southern and south-eastern Europe and includes a large number of taxa identified based on morphological characters. Previous work has revealed that evolutionary lineages within the complex are not reflected by the current taxonomy, as species boundaries are primarily determined by past demographic events rather than by morphology. Here, we focused on six currently described subspecies distributed in the Balkan Peninsula and applied an integrative approach combining population genomic (RAD-seq), morphometric, genome size and environmental data, to resolve the intraspecific relationships and evolutionary history of the Balkan *D. sylvestris* populations. Population structure revealed a strong divergence of subsp. *tergestinus* from the rest of the Balkan lineage. More detailed genetic variation patterns within the Balkan lineage suggested two major groups of populations which were largely concordant with the two revealed morphological entities. The north-western group included populations well-connected by gene flow, formerly assigned to subsp. *sylvestris* and subsp. *nodosus.* A south-eastern group included more isolated clusters of populations, formerly assigned to subsp. *alboroseus,* subsp. *bertisceus* and subsp. *kozjakensis.* Our combined results (genetic, morphometric, genome size and environmental analyses) suggest survival of the Pleistocene glaciations in two main glacial refugia located along the eastern Adriatic coast, possibly followed by secondary contact in the intermediate area. However, we cannot exclude the existence of multiple smaller microrefugia for the south-eastern group. Finally, our results do not support the current taxonomy. Based on our integrative approach, we propose a species-level treatment for the evolutionary distinct *D. tergestinus*, and the recircumscription of *D. sylvestris* subsp. *sylvestris* and *D. sylvestris* subsp. *bertisceus* to correspond to the north-western and south-eastern genetic clusters, respectively.

S.47.5 Origin and evolutionary dynamics of the octoploid weed Cardamine occulta and its relatives

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The genus *Cardamine* (Brassicaceae), encompassing over 200 species, exhibits a global distribution except of Antarctica. *C. occulta*, an octoploid (2n=64) weed indigenous to Eastern Asia, has become invasive after introductions to various continents, including Europe. In Europe this species first appeared in the Mediterranean region, particularly in Spain and in Italy (here due to rice cultivation near Torino). *C. occulta* shares its Eastern Asian habitat with related species such as the tetraploid (2n=32) *C. kokaiensis* and *C. scutata*, as well as the octoploid (2n=64) *C. dentipetala*. Genomic *in situ* hybridization and large-scale comparative chromosome painting were employed to elucidate the parental genomes and chromosome composition of these *Cardamine* species. All species trace their lineage to a common ancestral *Cardamine* genome (n=8), structurally resembling the Ancestral Crucifer Karyotype (n = 8) but differentiated by a translocation between chromosomes AK6 and AK8. The allotetraploid *C. scutata* resulted from hybridization between the diploids *C. parviflora* and *C. amara*. Conversely, *C. kokaiensis* has an autotetraploid origin related to *C. parviflora*. Notably, the octoploid *C. occulta* likely originated through hybridization between the tetraploids *C. scutata* and *C. kokaiensis*. The octoploid genome of *C. dentipetala* probably originated from *C. scutata* via autopolyploidization. Apart from a five species-specific centromere repositionings and one pericentric inversion post-dating polyploidization events, parental subgenomes remained stable in Asian tetra- and octoploids. Post-polyploid evolution in Asian *Cardamine* polyploids did not involve descending dysploidy or intergenomic rearrangements. The combination of diverse parental (sub)genomes adapted to distinct habitats conferred an evolutionary advantage to newly formed polyploids, allowing them to occupy new ecological niches. The revealed genomic insights into *Cardamine* polyploids not only enhance our understanding of their evolutionary history but also provide valuable knowledge for the targeted management of invasive species.

S.47.6 Using functional traits in integrative taxonomy: the case of the Sonchus asper (L.) Hill (Asteraceae) complex in the Mediterranean

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Functional traits are measurable properties of individuals that determine their basic performance model and role in the communities. The assignment of functional traits allows us to configure the ecological and evolutionary attributes of the individuals conforming a taxon and detect divergences associated to speciation processes. Furthermore, the analysis provides a framework for selecting appropriate operational criteria under the approach of Integrative Taxonomy. *Sonchus asper* (L.) Hill is a relevant case in this sense. It is considered a cosmopolitan self-fertilized annual weed with small, unattractive flower heads. However, the variability within the species' current circumscription revealed the presence of differentiated morphotypes in the Mediterranean, characterized by these functional traits: a) large flower heads, which denotes xenogamous sexual systems; and b) variability in growth habit, from the common annual cycle to creeping rhizomatous life form. A taxonomic revision under a multidisciplinary approach is consistently presented here. Morphologic examination revealed that flowers, leaves, underground parts and fruit traits are important to discriminate between morphotypes. Phylogenetic analysis revealed two separate clades: 1) autogamous with small flower heads; and 2) xenogamous with large flower heads, which includes three monophyletic and one paraphyletic groups. Chromosome number is conserved among morphotypes, with slight differences in chromosome morphology. Post-mating isolation barriers appear to be weak. Therefore, the analysis of ecological and distribution patterns is crucial to understand speciation processes. Our results support these conclusions: 1) The limitation of the name *S. asper* (L.) Hill to autogamous annual forms. 2) The reinstatement of three taxa described in the 19th-century: *S. nymanii*, a rhizomatous creeping Sicilian endemism; *S. glaucescens* subsp. *glaucescens*, a biennial south-eastern French coast endemism; and *S. glaucescens* subsp. *graecus*, an annual widely distributed throughout central and eastern Mediterranean. 3) The existence of a different perennial taxon from mountainous areas of North Africa.

S.48 BIOGEOGRAPHY AND DIVERSIFICATION OF INTERCONTINENTAL TROPICAL PLANT DIVERSITY. SESSION 3

S.48.1 Global patterns of phylogenetic and functional diversity of Scleria (Cyperaceae)

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Scleria P.J.Bergius (1765: 142), commonly known as nut rushes or razor grasses, is the sixth largest genus in the Cyperaceae family with 261 species, and the only genus of tribe Sclerieae Wight & Arn. (subfamily Cyperoideae). Recent studies have disentangled the evolutionary relationships among *Scleria* species and identified major dispersal and niche shifts events. Here, we combined occurrence data, assessments of extinction risk, the latest phylogeny of the genus and trait data collected from herbarium specimens to: (i) explore the spatial distribution of *Scleria* phylogenetic and functional diversity facets, and (ii) identify species and world regions of remarkable interest for *Scleria* conservation. Central America, Western Africa, Madagascar and Northern Australia showed high functional and phylogenetic diversity. We also found that the four *Scleria* subgenera showed contrasting climatic niches, and clear functional segregation in terms of height, blade area and nutlet size. *Scleria* species from Africa and South America include a great diversity of functional types, whereas North America and Oceania are characterised by having shorter species with small leaves. Our results also suggest that around half of the species not yet included in the Red List of the IUCN are potentially threatened with extinction. We found 48 Evolutionary Distinct and Globally Endangered (EDGE) *Scleria*. Evolutionary and ecologically distinct and endangered *Scleria* mostly occur in a few African (Madagascar, Zambia, DR Congo and Tanzania) and South American (Brazil) regions. Protecting these species, we would safeguard 68.47% (41.07 MY) of avertable expected phylogenetic diversity loss in the genus.

S.48.2 Did the drift of Hainan Island occur and affect the evolutionary trajectory of plants?

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Demonstrating whether the plate-tectonic drifts of Hainan Island occurred and affected the evolutionary of plants will disentangle the issue puzzled natural scientists over decades. Here, *Engelhardia roxburghiana* around Hainan Island was selected to identify the genetic structure, diversity, and demographic dynamics using RAD-seq. Three lineages were identified, and the divergence time and genetic structure showed that *E. roxburghiana* dispersed from Chiang-nan to Hainan Island via land bridge during the late Eocene. Hence, drift of Hainan Island did not occur, which was impossible to affect the evolutionary trajectory of plants. Higher genetic diversity in Yunnan-Guizhou Plateau and Chiang-nan Hilly Ranges are the results of mixed populations or refugia, while lower genetic diversity in the Indochina Peninsula due to historical bottleneck. During the late Eocene to Oligocene, the north shift of arid belt driven *E. roxburghiana* expand from Indochina Peninsula to southern China, and main diversification occurred in Miocene within the monsoon system. The climatic oscillations during Quaternary led to the expansion but there was slight contraction after LGM, while southern China was and will be the refugia to climate change. This is the first comprehensive work from large-scale SNP features, providing genomic insights into the geological history of Hainan Island from biogeographic patterns of *E. roxburghiana* it sheds light on geological history of Hainan Island and illuminates the biogeographic patterns of island-mainland in the regions.

S.48.3 Plants on Malagasy inselbergs: exploring the hidden diversity of isolated populations

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Inselbergs are isolated, often monolithic rock outcrops, usually consisting of granite or gneiss. They are ecologically separated from the surrounding landscape and are thus referred to as terrestrial islands. Only relatively few plant species possess adaptive traits that enable them to grow successfully in inselberg habitats, characterised by a lack of soil and nutrients. As a typical floristic element of Malagasy inselbergs, the poikilohydric Velloziaceae can be highlighted. To explore the hidden genetic diversity of isolated populations of Malagasy Velloziaceae, which belong to the genus *Xerophyta,* we used microsatellite markers to assess the importance of geographic and ecological isolation on inselbergs as a trigger for speciation. Usually, species of the *Xerophyta* occur in isolated mats on open rocky slopes. Across all our samples, the analysed loci showed a high genetic diversity. Furthermore, almost all individuals had different multilocus genotypes, excluding clonality. Nevertheless, we were able to identify a few clones in our data. However, the emergence of clones is a relatively rare event. Our previous studies have shown very low gene flow between individual inselbergs regardless of distance, favouring strong genetic and geographic differentiation. The morphological differences between plants from separated localities are probably the result of local adaptations and/or a consequence of phenotypic plasticity. In our analyses, we characterise the genetic diversity of a Malagasy *Xerophyta* species *to* contribute insights into evolutionary processes that may have led to the diversification of lineages of Malagasy inselberg species and to identify more vulnerable regions that require special conservation measures. Currently, Malagasy inselbergs suffer from human impacts (e.g. quarrying, fire), resulting in a dramatic decrease in the genetic diversity of taxa that consist of small isolated populations. It can be concluded that many spectacular taxa (incl. orchids, *Aloe* spp.) are facing similar problems concerning their long-term survival on Malagasy inselbergs.

S.48.4 Multiple losses of structural color in the fruits of Elaeocarpus

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Most plants use pigments to color their flowers, fruits, and leaves, but structural colors are increasingly being described. In contrast to pigments, structural colors are nanostructures that interfere with light to create color. Due to the limited study of structural colors in plants, especially compared to their study in animals, our understanding of how and why structural colors evolve in plants is lacking. Here, we examine the evolution of structural color in *Elaeocarpus*, a tropical lineage with the first described structurally colored fruit. We confirm that *E. angustifolius* has a multilayered structure, but we find that the structure is made of lipids rather than of polysaccharides (as was previously described). The use of lipids to build a multilayer reflector is similar to that of recently described species (*Viburnum tinus* and *Lantana strigocamara*), although the type of lipid is different. Furthermore, anatomically, the structure in *Elaeocarpus* differs in that it occurs in the extracellular space, rather than embedded in the cell wall as in *Viburnum* and *Lantana*. These anatomical and chemical differences indicate that the structure in *Elaeocarpus* has very different evolutionary origins to similar structures described previously. Additionally, we observe that all blue-fruited species in *Elaeocarpus* exhibit the same type of structure, and that the structure was lost multiple times in black-, brown-, yellow-, and red-fruited species. This is the first time that losses of structural color have been documented in plants and suggests that the energetic investment in building large structures out of lipids may not always be advantageous in fruits.

S.48.5 General dynamic model of oceanic island biogeography predicts early diversification dynamics of a highly successful insular plant

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The general dynamic model of oceanic island biogeography (GDM) views oceanic islands predominantly as sinks rather than sources of dispersing lineages. To test this, we conducted a biogeographic analysis of a highly successful insular plant taxon, *Cyrtandra*, and inferred directionality of dispersal and founder events throughout the four biogeographical units of the Indo-Australian Archipelago (IAA), namely Sunda, Wallacea, Philippines, and Sahul. Sunda was recovered as the major source area, followed by Wallacea. The relatively high number of dispersal and founder events originating from Wallacea is attributed to its central location in the IAA and its complex geological history selecting for increased dispersibility in *Cyrtandra*. We also tested if early diversification dynamics in *Cyrtandra* follow predictions of adaptive radiation, which is the dominant process on oceanic islands as per the GDM. Diversification dynamics of dispersing lineages of *Cyrtandra* in the Southeast Asian grade showed early bursts in diversification rates followed by a plateau which is consistent with adaptive radiation. We did not detect signals of diversity-dependent diversification, and this is attributed to Southeast Asian cyrtandras occupying various niche spaces as evident by its wide morphological range, particularly in habit and floral characters. The clade containing mostly Pacific members, which arrived at the early stages of the ontogeny of the Pacific Islands, showed diversification dynamics predicted by the Island Immaturity Speciation Pulse (IISP) model and their morphological range is controlled by the least action effect favoring woodiness and fleshy fruits. Our study provides a first step towards a framework for investigating early diversification dynamics as predicted by GDM in highly successful insular taxa.

S.49 NEW FRONTIERS IN PLANT PHYLOGENOMICS. SESSION 3

S.49.1 Helpful or deceiving? Reference genomes and their influence on phylogenetic tree topologies.

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Recent improvements in genome sequencing, especially long read sequencing techniques like Oxford Nanopore sequencing, provide the means to assemble high quality (draft) genomes for a plethora of species. While these genomes find uses in multiple fields of life sciences, a common application for them is to serve as references in the assembly of high-throughput sequencing reads in phylogenomics. However, it is unclear how quality and phylogenetic position of a reference relative to the investigated dataset influence phylogenomic assemblies and topology of phylogenetic trees. To answer this question, we sequenced and assembled genomes of seven species of *Veronica*, a plant genus known for polyploidization, frequent hybridization and high speciation rates, using Oxford Nanopore sequencing in combination with high coverage Illumina sequencing reads. The assembled references were tested for quality, completeness, contiguity, and possible contaminants. A Genotyping-by-sequencing dataset including 72 samples from *Veronica* subg. *Pseudolysimachium* was assembled denovo, as well as reference-assisted with different parameters, using each draft genome as a reference. We found that not only alignment lengths and number of retrieved loci are changing among the different reference genomes, but also tree topologies and branch lengths, depending on reference taxon and reference quality. These variable results may lead to false conclusions regarding the evolutionary history of the subgenus.

S.49.2 Maximizing the Phylogenetic Yield of Low-Coverage Shotgun Sequencing and Target-Enrichment in Plants Through New Bioinformatic Tools

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Low-coverage shotgun sequencing is a fast and cost-effective method that has been widely used in plants to infer phylogenies mostly from organellar genomes. However, obtaining such data with common organelle assemblers, can be particularly challenging in some plant families with complex genomic structures and rearrangements. In addition, the shallow coverage of the nuclear genome associated with these libraries (<3 x) prevents the use of nuclear sequences, leading recently to an increased use of target-enrichment methods in phylogenomic studies. In this context, we developed ORTHOSKIM a universal and versatile bioinformatic pipeline that allows targeting both organelle and nuclear data in shotgun libraries (enriched or not), with reference sequences and specific modes accounting for paralogous issues as those expected with organelle gene transfers. Nuclear references are however not always available in non-model organisms, and organelle sequences only represent around 10% of the shotgun libraries when not enriched. This results in a tremendous waste of sequencing data. To make use of the 90% remaining data, we also developed REFMAKER that uses a blind approach to create specific sets of nuclear loci, which can be extracted directly from the low coverage libraries (<3 x). These two methods can be jointly used in the same phylogenetic framework to exploit all the produced reads, regardless of their sequencing depth.

S.49.3 Strategies to improve alignment accuracy in large-scale plant phylogenomic analyses

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Despite the large quantities of nucleotide sequences that are analyzed in contemporary plant phylogenomics, the process of multiple sequence alignment (MSA) remains one of its central tenets. Any phylogenomic investigation will only be as reliable as the positional homology established among its underlying sequences, irrespective of their length, genomic origin, or taxonomic representation. Diversifying or further increasing the amount of input sequences is not a substitute for careful and often time-expensive MSA. Instead, the ever-larger data volumes in plant phylogenomics highlight the demand for analysis workflows that accommodate the complexities of nucleotide sequence evolution, especially at the microstructural level. In this presentation, I argue that despite the skyrocketing amounts of sequence data in contemporary plant phylogenomics, the associated MSA process must not be dismissed as a cumbersome side aspect. Specifically, I highlight that while the existing toolkit of MSA software appears sufficiently diverse to tackle the challenges of large-scale plant phylogenomics, their integration into phylogenomic analysis pipelines awaits substantial improvement, especially when accounting for genome-specific idiosyncracies and microstructural mutations. Several empirical examples are presented to support these observations. First, I demonstrate that the correct assessment of positional homology in genome-level sequence data can significantly improve plastid phylogenomic reconstructions in a lineage of South American sunflowers. Second, I illustrate that the manual post-processing of software-generated MSAs significantly improves the reliability of phylogenomic reconstructions among water lilies and that such post-processing can be achieved with reasonable effort even for phylogenomic data. Third, I introduce a software tool that enables the automatic separation of genome sequence data into natural partitions - genes, introns, and intergenic spacers - across thousands of input genomes and automates their individual MSA for different software tools. Based on these results, I highlight the need for an increased effort to develop targeted and customized MSA strategies for plant phylogenomics.

S.49.4 Tracing the phylogenomic roots: revisiting evolution and biogeography in the Tribe Maleae of the Rosaceae Family

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The Rosaceae tribe Maleae, encompassing a wide range of fruit crops, horticultural, and forestry species, displays significant diversity, especially within its subtribe, Malinae. This study undertook a comprehensive Hyb-Seq-based nuclear and plastid phylogenetic analysis of 184 accessions from 159 species across all genera within Maleae. The objective was to place the evolutionary trajectory of Maleae in both a spatial and temporal framework, while also investigating the potential drivers of diversification in Malinae, particularly focusing on the role of whole genome duplication (WGD). The research uncovered two major radiative events within the Malinae subtribe. The first of these events occurred around the Early Eocene in the Madrean Region, and the second during the Middle Miocene in East Asia. These evolutionary radiations were shaped by over 50 million years of changing habitat connectivity, involving the Madrean-Tethyan floristic belt and the Boreotropical forest belt. The patterns of diversity within this plant group were significantly influenced by a series of environmental factors, including habitat disjunction, vicariance, and long-distance dispersal events. A key finding of the study was the impact of WGD at the inception of Maleae evolution. The retention of gene copies post-WGD demonstrated a strong phylogenetic signal, suggesting a pivotal role in the diversification process. Representing the most extensive taxon sampling undertaken to date, the study sheds light on the complex biogeographic history of Maleae. It also reveals evidence of genus-specific diploidization following WGD, highlighting the intricate evolutionary dynamics within this significant plant group.

S.49.5 Phylogenomics and evolution of recently diverged and closely related species: a case study in Rosa sect. Synstylae (Rosaceae)

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Many phylogenetic or evolutionary studies across various plant taxa, particularly those involving recently diverged and closely related species, have historically faced challenges in comprehending species relationships and evolutionary histories within these groups. Recent advancements in genome-wide sequencing technologies and bioinformatics tools have now empowered phylogenomic analyses to unravel robust species phylogenies, offering valuable insights into the intricate evolutionary trajectories of lineages characterized by complex histories. The East Asian wild roses within *Rosa* section *Synstylae* (Rosaceae), recognized as significant genetic contributors to modern ornamental roses, represent a group of species known to have recently diverged and maintained close relationships. Leveraging 1,683 highly conserved single-copy orthologs from the reference genome of *R. chinensis*, a close relative within the *Synstylae* section, we successfully established the first robust phylogenetic relationships among eight species in *Rosa* section *Synstylae*. Moreover, additional phylogenomic analyses unveiled the complex evolutionary history of the *R.* sect. *Synstylae* lineage, likely influenced by a combination of deep coalescence and genetic introgressions. Through comparative ortholog analyses utilizing the draft genome assembly of *R. lucieae*, we discerned patterns of gene family evolution within section *Synstylae*, particularly in response to the adaptation to specific ecological niches. These innovative phylogenomic approaches not only enhance our understanding of the evolution of East Asian wild roses but also offer a framework for comprehending the evolutionary dynamics of other recently diverged and closely related lineages worldwide.

S.50 INTEGRATING CONSERVATION BIOLOGY AND SOCIETY ENGAGEMENT TO ENHANCE PROTECTION OF AT RISK FLORA. SESSION 2

S.50.1 Experiential learning is vital for Plant Conservation

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Being a part of nature adds new dimensions to our perception of it. Experiential learning enhances this perception by providing real-world experiences that help formulate ideal conservation strategies. With the clock of extinction ticking fast, the message on conservation must reach the younger generation swiftly. Admiration arises from experiencing something good; thus, visits to gardens and wilderness areas serve as inspirational platforms for practical education in botany, landscaping, and the conservation of plants and nature. School outreach activities and undergraduate field courses in experiential learning not only bolster conservation efforts but also facilitate the exchange of ideas on genuine conservation practices. Exploring Sri Lankan national parks from Canada through multiple educational field trips enabled students to grasp global concerns and promote awareness, paving the way for making biodiversity conservation in the tropics a reality. My experiential learning field courses have led me to conclude that garden and field visits, hands-on activities in the field, and the commitment of resource personnel are key elements in motivating young generations toward plant and biodiversity conservation.

S.50.2 Plant conservation strategies of the Ministry for Ecological Transition and Demographic Challenge (Spain)

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The Spanish Ministry for Ecological Transition and Demographic Challenge (MTRD) is responsible for planning, formulation of strategies, and establishment of fundamental guidelines for the conservation and sustainable use of natural heritage and biodiversity, in accordance with national and international regulations. Plant species constitute an essential component of biodiversity, and face numerous threats stemming from human activities. Spain, as a country with a high level of endemism, has a significant responsibility for their conservation. In this context, the main working lines of MTRD are: a) Monitoring the conservation status of all protected species, as well as the status, distribution, and trends of invasive alien species; b) Developing strategies for conservation and fight against the main threats to protected plants; c) Launching the Networks of Forestry and Wild Flora Germplasm Bank as tools for ex situ conservation; d) Carrying field tests for the conservation measures applied to protected species; e) Coordinating plant conservation efforts with regional administrations; f) Updating catalogues of protected and invasive species; and g) Coordinating conservation measures addressed to the critically endangered plant Cistus heterophyllus subsp. carthaginensis.

S.50.3 Threatened plant species in agroecosystems: is the coexistence between nature conservation and productivity feasible?

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Agricultural practices are among the most significant threats to plant diversity worldwide. Many threatened species strictly linked to agroecosystems have already disappeared from agricultural areas, particularly in more intensively farmed countries such as in Europe. The recovery of species listed in the Habitat Directive 92/43/CEE, the main legal conservation framework in the EU, is mandatory. However, the reintroduction of threatened species to agroecosystems is constrained by difficulties in recolonizing the original habitat after extirpation. Where populations do avoid destruction, they remain confined to relict habitats which are highly fragmented within an agricultural landscape (*on farm*). There has been a paradigm shift in conservation to restore biodiversity not only in natural habitats but also in semi-natural areas deemed worthy of conservation. Organic and conventional farms with low-input practices have been suggested as having a potentially biodiversity-friendly approach to farming. The increased demand of food from sustainable sources, especially from organic agriculture, has led to improved environmental conditions and consequently assisted in species conservation. However, for nature conservation and agricultural productivity to co-exist, the needs of stakeholders must be considered. These include concerns with detrimental effects on crop yields, a perception of focal species as potential weeds, legal constraints for species protection, and increased costs associated with conservation. However, there are several benefits to farmers of biodiversity conservation in agroecosystems such as *ad hoc* financial incentives (e.g., from the EU Rural Development Plan), improved ecosystem services provisioning, and opportunities for marketing sustainable products. We discuss the implications and limitations of biodiversity conservation in agroecosystems using examples from Europe of the threatened species *Marsilea quadrifolia, Isoëtes malinverniana*, *Lindernia procumbens*, *Bromus interruptus, B. grossus, Agrostemma githago* and *Centaurea cyanus*.

S.50.4 Rapid assessments accurately predict increased extinction risk of megafire impacted flora

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The combined pressures of global climate change and anthropogenic disturbance of the natural world are leading to a rapid rise in the number of species at risk of extinction. For many taxa, these numbers are rising faster than it is currently possible to keep track of leading to an increased need to utilise rapid assessments to accelerate extinction risk assessments and ensure plant species receive timely conservation actions. The 2019-2020 Black Summer fires had extensive impacts on native flora necessitating a prioritisation process to identify the species most in need of rapid and full extinction risk assessments. We used a tiered approach to identify priority species for full extinction risk assessments and compared how well rapid assessments with minimal information predicted extinction risk after full assessment. Some 400 species received rapid assessments and 135 received full assessments. The rapid assessments accurately predicted the final threat status of 59% of species. Higher threat statuses like Critically Endangered and Endangered where more accurately predicted than Vulnerable and Not Threatened. Of the 135 species that recieved full assessments 85%

were found to be at greater risk of extinction following the fires, Our results highlight the value of rapid assessments in response to these landmark disasters with widespread impacts as well as for accelerating comprehensive listings of under assessed flora.

S.50.5 The vision of plant conservation in Europe along the strategies and recommendations

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In last decades it became clear that urgent activities are needed in plant conservation. The area and connectivity of habitats and species will be very important to analyse the direction and intensity of threats of rare species. Although there are new strategies for protecting native species, the scale of the drivers of extinction can be variable and in several cases we don't know the small scale drivers of the life history traits of plant species. Sometimes new ways are needed for checking the feature of species selected for revision and recommendations for example according to the new, accepted strategic plan of Bern Convention between 2023 and 2030. A review and a survey can help member states and experts to analyze the real processes and in characterizing the state of plant species living in Pan-European areas. Different scale has been used and a general, good working conservation methodology have been elaborated together with organizations. The target of making the strategic plan more objective is the multiscale revision of plant species in Annex I. The first step is to determine the main risks in distribution and life history of the species which can be asked through a questionnaire tool. The mutualistic features, seed ecology and the life span also very important factors of protection and restoration success. In connection with the sustainable use of plant species we must take into account the annual or short lived species and their population stability through their interactions in natural habitats.

S.50.6 Conservation of rare arable species through the study of their competitive relationships with crops in the agroecosystem

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After 1950, wild arable plants (hereafter arable species) underwent a dramatic decline due to the rapid intensification of agriculture. In most cases, arable species are considered as weeds and, for this reason, they have been systematically eradicated in conventional farming systems. Arable species extirpated even in sustainable agricultural systems are no longer able to recolonize their former range. Therefore, the reintroduction of arable species within agroecosystems has been proposed to improve their conservation status. Unfortunately, farmers are often reluctant to accept the reintroduction of endangered plants to their lands, as they could reduce crop productivity through competition. Therefore, it is important to understand if farmers' fears of a reduction of crop productivity are grounded in evidence, to engage them to promote coexistence between crops and rare arable species. We studied the mutual competitive effects between two iconic arable species, *Agrostemma githago* L. and *Centaurea cyanus* L., and wheat (*Triticum aestivum* L., variety Palesio) in two densities (5% and 10%) in an open field experiment at the SemeNostrum company (Udine, Italy) in 2022/2023. Analysing the roots/shoots ratio, *A. githago* and *C. cyanus* in competition with the crop significantly reduced the aerial part growth in relation to the root part. The arable species-crop interaction also affected the specific leaf area and chlorophyll content of wild species, which decreased in the presence of wheat. For *T. aestivum*, instead, there was no significant effect on the biomass, specific leaf area or chlorophyll content due to the presence of *A. githago* and *C. cyanus*. Results were consistence in both densities. This first comparative analysis evidences a plausible model of coexistence of arable species and crops. This will provide the baseline for future translocation protocols of threatened species in agricultural contexts.

S.51 FLORAL SPECIALIZATION AND THE GENERALISED NATURE OF POLLINATION INTERACTIONS. SESSION 3

S.51.1 Actinomorphy to Zygomorphy: bilateral symmetry, with correct flower orientation, greatly increases pollen transfer

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While the ancestral symmetry of angiosperm flowers is actinomorphic (radial symmetry), hundreds of lineages have independently evolved zygomorphic flowers (bilateral symmetry). Such shifts are associated with more specialized pollination systems, and lead to significant increases in diversification rates. But what are the actual benefits of zygomorphic flowers for a plant? One little-tested assumption is that zygomorphy maximizes pollen transfer by allowing flowers to place pollen in a more precise and repeatable way on pollinator's bodies. This is supported by the fact that floral orientation tends to be more consistent, and often can be quickly readjusted, for zygomorphic flowers compared to actinomorphic ones. In this study, we performed flight cage experiments with nectar-feeding bats and artificial flowers, testing how floral symmetry and orientation affect pollen removal and transfer. For each flower, four anthers were placed either all of the way around the opening (actinomorphic) or together at one side of the opening (zygomorphic). Nearly twice as much pollen was transferred between zygomorphic flowers, but only when angled at 45º, causing pollen to be consistently placed on the tops of bats' heads. When flowers were positioned flat (i.e., facing upwards), bats approached from many different angles, and zygomorphic flowers performed no better than actinomorphic ones in terms of pollen transfer. Thus, results suggest that shifts to zygomorphy allow more specialized pollination systems which, with the correct floral orientation, maximize pollen transfer success.

S.51.2 The effect of grooming on plant reproduction: a theoretical approach

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The pathway to male reproductive success in plants is affected by events that potentially affect the chance of individual pollen grains reaching the stigma, such as grooming behavior by pollen vectors and the variation in the positioning of reproductive organs. To date, only a few theoretical investigations have attempted to model the effect of grooming on pollen transfer, and empirical studies have been limited to species in which pollen movement can be tracked. Thus, we use a spatially explicit agent-based modeling (ABMs) approach to determine the effect of pollen redistribution and removal in the "pollen landscape" on the vector body, affecting plant reproductive success and mating between floral individuals, associated with variation in reproductive organs. For this, we simulated pollen vector visits and their grooming behavior on a sequence of different flowers in a population. We showed that pollen redistribution and removal restructure the pollen landscape in the body of the bee, in a way that increases the pollen delivery in consecutive visits and the number of pollen donors deposited on the stigmas. We also observed that the mating networks were affected both by the grooming behavior and by the morphological variation of the reproductive organs. So, in the absence of grooming, together with the variation in the positioning of the stigma, makes populations more connected and generalist. The grooming behavior breaks the dominance of some individuals, making the relationships between individuals better distributed. Floral individuals visited by vectors without grooming and that have variation in stigma position are reproductively more generalists. Our model predicts that species pollinated by non-grooming vectors are more variable in stigma position than species pollinated by grooming vector. However, empirical studies will be needed to confirm the predictions we generate with our model, allowing greater knowledge of the factors that may affect pollen transfer.

S.51.3 Does cheating pay off? Influence of floral traits on pollinator behavior and plant fitness in a food-deceptive European orchid

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In food-deceptive pollination systems, plants attract pollinators without offering any reward. The plant lures the insect into pollination by showing traits similar to rewarding flowers. Our research aims to comprehensively understand the pollination ecology within a food-deceptive system (*Orchis militaris*) and to identify key traits influencing pollinator attraction, spatial heterogeneity, pollination success, and consequently, plant fitness. Furthermore, we are investigating the avoidance behavior of pollinators in this deceptive system. We are studying two distinct populations, both located north of the Alps, approximately 650 km apart, covering the broad habitat requirements of *O. militaris*. By identifying effective pollinators of *O. militaris*, along with their co-vegetation, our preliminary results indicate marked differences between the two populations, highlighting a broad pollinator spectrum. The overall pollination success and seed set was high. Main pollinators are Hymenoptera (Apidae), ranging from large (*Apis mellifera*) to small (*Lasioglossum marginatum*). While pollinator abundance appears to be directly linked to plant fitness, current observations indicate that the density of deceptive orchids does not adversely affect pollination success. Notably, we observed that bees seemingly do not exhibit avoidance behavior even in high-density deceptive orchid populations. These preliminary results contradict the hypothesis that pollinators learn deceptive strategies, and therefore show avoidance behavior. As a next step, we aim to understand the mechanisms underlying this observation. To examine the learning process of pollinators, specifically whether they avoid specific floral traits (color) or areas after encountering non-rewarding plants, we are planning to mark bees in the field and to conduct choice experiments with *A. mellifera*. In summary, our study provides insights into pollination ecology and the associated pollinator behavior contributing to the evolution of deceptive systems, which is also of relevance for habitat conservation and management strategies in times of rapid biodiversity declines.

S.51.4 Equal access opportunity: heterospecific pollen tubes grow in the styles of close- and distantly-related species

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In plant communities where generalist pollinators are shared, the likelihood of heterospecific pollen transfer (HPT) increases, potentially affecting female reproductive success. This scenario may drive evolutionary adaptations aimed at either minimizing the occurrence of HPT (pre-pollination) or reducing its impact (post-pollination). While it is commonly assumed that post-pollination mechanisms restrict heterospecific pollen tube growth in the stigma or early in the style, direct measurements of this process are relatively infrequent. When heterospecific pollen tube growth is assessed, studies often focus on intrageneric exchanges, even though plants in diverse communities and may exchange pollen with both close and distant relatives. To explore the impact of HPT in a diverse plant community, we performed experimental crosses involving co-flowering, non-hybridizing plants across a spectrum of genetic distance from an alpine plant community at Rocky Mountain Biological Laboratory (Colorado, USA). Using semi-*in vivo* pollen tube assays, fluorescence microscopy, and ovary size measurements, we examined pollen tube growth and ovary size change following all-by-all reciprocal crosses with 11 species (representatives from Orobanchaceae, Lamiaceae, Phrymaceae, Linaceae, and Fabaceae). Contrary to expectations that pollen tube growth is more likely among closely related species and rare among distant relatives, we observed consistent pollen tube growth among all species pairs, ranging from conspecifics to those in different plant orders. Generalized linear models revealed no significant effects of genetic distance on the probability of pollen tube growth through the stigma and into the style. These results suggest that in plants with close ecological interactions, 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 likely play more significant roles.

S.51.5 Multifaceted strategies ensure prezygotic reproductive isolation of coexisting species of Stenospermation (Araceae)

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Plants reliance on external agents for pollination has led to significant adaptations in floral traits, potentially contributing to the remarkable species diversity observed in this group. Reproductive isolation mechanisms between populations, particularly pre- and post-zygotic isolation in congeneric and sympatric species, play a critical role in minimizing competition for pollinators. Reproductive strategies, including flowering time, visual signals, floral fragrance chemistry, and rewards offered, facilitate coexistence and can act as prezygotic reproductive isolation barriers when gene flow persists, allowing for hybrid formation. We investigated the reproductive systems, isolation mechanisms, and pollination dynamics of coexisting species of *Stenospermation* (Araceae) in two localities of Colombia's central and western Andes. We assessed pollen transfer and the potential for hybrid formation using pollination and hybridization tests. Additionally, we evaluated the effectiveness of phenological and ethological isolation in preventing self-pollination. Floral volatile compounds were analyzed using Dynamic Headspace and GC-MS techniques, and attractiveness assays were performed to determine pollinator preferences. *Stenospermation* exhibits a sexual system with androgynous flowers, and protogyny prevents self-pollination, precluding fruit production through apomixis. Our results demonstrate the possibility of hybridization through controlled experiments. *Stenospermation* communities exhibited low synchronicity or were asynchronous. All species display varying anthesis hours and share their floral volatile chemistry and pollinators at various degrees. We conclude that *Stenospermation* employs a multifactorial approach to prezygotic isolation involving ethological, phenological, and ecological factors, as no single trait thoroughly explains the observed isolation. Pollinator facilitation between syntopic species and complementary life cycles with pollinators contribute to reproductive success. Spathe tissue, the floral chamber and the thermogenesis are crucial floral rewards, particularly for large pollinators like *Cyclocephala*.

S.51.6 Improving flowers to help feed the world: bee responses to field-realistic floral trait variation in strawberry

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A rising global population will need more food, increasing demand for insect pollination services. However, general insect declines conflict with this demand. One way to mitigate this conflict is to grow crop flowers that are easier for insects to find, and more rewarding to those that visit them. Our work quantifies variation in the pollinator-relevant traits of nectar and pollen production, flower size and flower shape in commercial strawberry, finding significant variation between varieties in all traits. Bumblebees could learn to distinguish between the extremes of variation in flower shape, but this learning is very slow, indicating that this variation is at the limit of that which can be detected by bumblebees. Bee preferences for nectar of differing sugar concentrations at field-realistic volumes were consistent with previous observations at larger volumes, suggesting that it is valid to translate lab findings to the field. Our findings build on our knowledge of the range of pollinator reward present in a single cultivated species, and of the impact of field-realistic levels of variation in floral traits on bumblebee preferences.

S.52 AFRICAN TAXONOMY: A COLLABORATIVE EFFORT TOWARDS BIODIVERSITY CONSERVATION. SESSION 2

S.52.1 A taxonomically-vetted checklist shows that species richness of Nigerian plants is underrepresented in major floristic databases

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“Beyond Extrapolations: A Taxonomically-Vetted Checklist of Nigeria’s Vascular Plants” is a new initiative shedding light on the gross underrepresentation of Nigeria’s plant diversity in major global floristic databases. Current estimates of Nigeria’s plant diversity rely heavily on out-of-date extrapolations from the Flora of West Tropical Africa, a publication now six decades old. In response to this critical gap, our consortium is spearheading an ambitious effort to compile a comprehensive, taxonomically-verified, and vouchered checklist of all vascular plants in Nigeria. This presentation unveils the significant findings of our research, emphasizing the disparity between existing global databases and the true botanical richness of Nigeria. We present the second and third outputs in a series of publications stemming from this pioneering effort. Using the historical trend of botanical explorations, we demonstrate that there are still many new plant species to be discovered in Nigeria. To achieve a comprehensive description of these new plant species, a significant number of taxonomists will be needed for an extended period. This demonstrates the significance of capacity building as a milestone in implementing the Global Biodiversity Framework (GBF). It is an urgent priority to find and name these remaining undiscovered species, Red List them, and allocate resources to protect those in need. Recent research has shown that 77% of new plant species at the point of publication today are threatened with extinction. This endeavor serves not only as an update on our progress, but also as a call to action to rectify the prevailing underrepresentation. We offer insights into the challenges faced, methodologies employed, and the significance of our ongoing efforts in advancing

botanical research in Nigeria. Our work establishes a robust foundation for understanding Nigeria's plant diversity, paving the way for enhanced conservation efforts, sustainable development, and a more comprehensive global understanding of the country's botanical wealth.

S.52.2 Synergy of taxonomy and environmental monitoring, an approach to biodiversity conservation: A case study in Ghana.

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The phenomenon of spatio-temporal dynamics occurs as a significant component of environmental monitoring in the 21st century. It deploys sophisticated tools such as satellites and advanced computer applications. Taxonomists believe correctly identifying biological species promotes a universally focused activity such as conservation. Following frequent visits to some portions of the Accra plains of Ghana for plant collection activities, it was observed that some areas and plants are speedily depleted. This concern motivated an investigation at the Shai-Osudoku district occurring on the Accra plains to ascertain the extent of depletion and understand the potential losses and consequences. The Shai-Osudoku district which is enriched with a wide range of medicinal plant species spanning from forest to savannah species was studied to ascertain the rate of land use/landcover change over the past two decades. Using mango plantations as a model, a survey was conducted to verify the spatio-temporal dynamics of mango farming in the Shai-Osudoku district. Images were downloaded from the internet (United States Geological Survey/Global Land Cover Facility) to cross-check survey results. The survey data were analyzed using IBM SPSS 20 and images downloaded were classified using first, ISODATA algorithm with 25 classes and later knowledge-based supervised classification. The results indicated that land use/land cover change has occurred. Also, areas of 'waterbody' and 'mango plantation' increased by 35.62% and 72.14% respectively as 'vegetation' and 'built-up' decreased by 35.20% and 39.55%. Farmers agreed their standard of living improved at the advent of mango production and the market value of mango remained unchanged by Spatio-temporal dynamics but were ignorant about the long-term economic effects of their activities on the increasing depletion population of medicinal plants. Further verification was done using satellite images in comparison with herbarium data to ascertain the erosion of some medicinal plant species from their collection locations.

S.52.3 Conservation of plant diversity in East Africa

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East Africa is home to more than 30,000 species of plants, yet current data reveals significant gaps in floral surveys and studies, with about 16% of the region having zero collections and about 50% being under-surveyed. In the context of China-Africa scientific and technological collaboration under the "One Belt, One Road" initiative, the scientists from China and East African countries have engaged in extensive collaborative researches, focusing on plant taxonomy and conservation biology. For instance, the *Flora of Kenya*, a collaborative project initiated by scientists from China and Kenya. The team carried out studies on numerous pre-surveyed weak areas and discovered more than ten new taxa. These efforts further facilitated the understanding of the diversity of the Kenyan flora as well as its distribution pattern. In Rwanda, the collaborative team discovered more natural populations of dwarf Rwandan water lily (*Nymphaea thermarum*). A comprehensive taxonomic morphology description was undertaken, and active involvement in its conservation efforts ensued. In Madagascar, the conservation genomic studies of baobabs were performed incorporating with in-depth ecological analyses which further raise the concerns on efficient protection of these amazing trees on the island. All these findings and results would provide valuable insights for developing effective and biologically informed conservation strategies for the biodiversity of East Africa in a change world.

S.52.4 Exorcising the demons: subtribal revision of the ironweed tribe (Vernonieae, Compositae) in the Eastern Hemisphere.

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The ironweed tribe, Vernonieae, is one of the most species rich in the daisy family (Compositae) and has a complicated taxonomic history that has led to it being referred to by a number of pejoratives, including the “evil tribe.” A key challenge for taxonomists who work with this tribe was the recognition of a large and poorly defined core genus, Vernonia, which included more than 1,000 species worldwide. In 1999, the genus was re-circumscribed to comprise just 20 species from the Americas and as a result, the necessary reclassification of more than 1,000 species in Vernonia sensu lato was initiated. In the last two decades, significant systematic efforts have resulted in the reclassification of many Vernonieae taxa in the Western Hemisphere. However, comparably little progress has been made toward taxonomic revision of the genus in the Eastern Hemisphere, where ca. 700 species are recognized from West Africa to Southeast Asia and the Pacific islands. Throughout the range of this tribe in the Eastern Hemisphere, there are currently 13 subtribes and 67 genera, but approximately 150 species in this tribe remain in Vernonia and await reclassification. Furthermore, recent studies suggest few of the subtribes currently recognized are monophyletic. We present results of phylogenomic analyses using a combined marker set including Angiosperms353 and Compositae-1061 as well as a greatly expanded sampling of species in this tribe from the Eastern Hemisphere to test the monophyly of subtribes and genera. We also explore morphological character variation in the tribe to understand patterns of evolution and help to support sub-tribal identification of taxa in the field and collections. Lastly, we present a plan to curate and rapidly share taxonomic data using the Global Compositae Database.

S.52.5 Floristic diversity, carbon stocks and degradation factors in two sacred forests in the West Cameroon Region.

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Sacred forests play a valuable role in conserving local biodiversity and provide numerous ecosystem services in Cameroon. The study was carried out in the sacred forests of Bandrefam and Batoufam (western Cameroon). The aim was to estimate the diversity of woody species, carbon stocks and degradation factors in these sacred forests. The floristic inventory was carried out in plots measuring 25 × 25 m for trees with diameters greater than 10 cm, and 5 × 5 m for trees with diameters less than 10 cm. Carbon stocks were estimated using the non-destructive method and the allometric equations of Fayolle et *al.* (2018), Chave et *al.* (2014) and Ntomen (2020). Data on degradation factors were collected using semi-structured surveys in the Bandrefam and Batoufam neighbourhoods. The floristic inventory identified 65 species divided into 57 genera and 30 families in the Bandrefam sacred forest, and 45 species divided into 42 genera and 27 families in the Batoufam sacres forest. The families common to both sacred forests are as follows: Phyllanthaceae, Fabaceae, Moraceae, Lamiaceae, Malvaceae, Rubiaceae, Meliaceae, Anacardiaceae, Sapindaceae. Three genera are present in both sites. These are: *Albizia, Macaranga, Trichillia*. In addition, there are 27 species in common between the two sites. The total carbon stock is 469.26 tC/ha at Batoufam and 291.41 tC/ha at Bandrefam. The economic value varies between 15 823 877.05 fcfa at Batoufam and 9 825 530.528 fcfa at Bandrefam. The study shows that despite the sacred nature of these forests, they are subject to degradation factors such as bush fires (35.42 %), the creation of plantations (23.96 %), illegal timber exploitation (21.88 %), young people’s lack of interest in the notion of conservation (9.38 %), climate change (7.29 %) and growing urbanisation (2.08 %). These factors threaten biodiversity and reduce carbon storage in these forests.

S.52 EVOLUTIONARY ECOLOGY OF PLANTS. SESSION 3

S.53.1 The ecology and biogeography of spiny plants

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Spines are a major ecological innovation supporting plant defence and diversification, present in over 10% of woody plant species. Spine anatomy is diverse, having arisen in multiple plant lineages from many different plant organs and parts of organs, which may be differ in relative advantaged across environmental gradients. We have tried to make sense of this diversity, by address the following core questions. 1. Do spiny plants possess functional trait syndromes that distinguish them from non-spiny plants, and are there differences between spines with different anatomies (spine types)? 2. Where are spines found in environmental space and are there differences between different spine types? 3. What is the evolutionary history of spiny plants? I discuss our ongoing inferences about these topics and future directions we pursue. In brief, our analyses show that different spine types have different functional traits and differ in their distribution across climate and possibly soil gradients. Spines appear to have evolved in response to the evolution of particular mammal lineages on each continent, and that pre-adaptation appears to have been a fundamental part of their diversification in new continents. These combined results emphasise the importance of plant defensive architecture for the spatial distribution of plant diversity, and the substantive role of extinct mammals in structuring modern plant diversity.

S.53.2 Elucidating trait evolution in forest tree species in response to recent climate changes: a review

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One of the main questions in evolutionary biology is whether populations can evolve in response to the ongoing climate change. Understanding past evolutionary trajectories might help us to predict present and future responses. In this review, we aim to identify the main climatic drivers of selection, to detect key traits for adaptation to climate heterogeneity and evaluate the evolutionary potential of forest tree species in response to contemporary climate change. Results from phenotypic selection studies at different temporal and spatial scales report that leaf traits, particularly those related to morphology and physiology are under significant selection. Consistently, a meta-analysis on common garden experiments showed widespread population divergence across species in growth, phenology, leaf economics and allometry. Associations with climate, however, strongly differed across biomes. In general, temperature is the main driver of population divergence in temperate environments whereas precipitation is the main driver in seasonally-dry tropical ecosystems. In Mediterranean environments, both temperature and precipitation have had important roles in population evolution but acting on different traits. Specifically, whereas phenology and growth have evolved in response to minimum temperatures in winter, leaf morphology and leaf economics have evolved in response to precipitation. Studies combining phenotypic and genomic data show that estimated ancestral populations tend to exhibit more conservative resource-use strategies which would provide evidence of adaptation to a colder environment in the past. Synchronic studies also support the existence of evolutionary responses to contemporary climate changes (less than 500 years) in growth, phenology and leaf physiology consistent with population studies and phenotypic selection analyses. Overall, our results suggest high evolutionary potential in forest tree species that has allowed them to respond recent climate fluctuations. However, further studies are needed to elucidate the pace of evolution, particularly through multivariate perspectives that assess trait integration within phenotypes.

S.53.3 Trait evolution reveals fire-prone ecosystems at the origin of the Mediterranean climate: a case study on Juniperus oxycedrus L.

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The Mediterranean climate is known for its summer droughts, resulting in recurrent fires as the primary form of disturbance. With the onset of this climate, newly fire-prone ecosystems emerged, stimulating species diversification and triggering strong selection for traits that enable persistence in response to fire. One such adaptive trait is post-fire resprouting, facilitated by the belowground location of meristematic tissues. *Juniperus oxycedrus*, a gymnosperm species belonging to the cypress family and distributed across the western Mediterranean basin, is reported as the only species within *Juniperus* section *Juniperus* capable of resprouting after a fire. This study evaluated the resprouting capability of *J. oxycedrus* through the examination of 22 burned areas across the Iberian Peninsula. Surprisingly, individuals identified as *J. oxycedrus* subsp. *badia* were not able to resprout. Genotyping-by-Sequencing (GBS), a reduction-representation genome strategy, was employed on 11-12 individuals from each examined population. The objectives were to (1) evaluate the genetic diversity within each lineage and population, (2) examine gene flow levels between lineages and, (3) date the split of the *J. oxycedrus* resprouting lineage.

S.53.4 Amphistomy increases leaf photosynthesis more in coastal than montane plants of Hawaiian ʻilima (Sida fallax)

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The adaptive significance of stomata on both upper and lower leaf surfaces, called amphistomy, is unresolved. A widespread association between amphistomy and open, sunny habitats suggests the adaptive benefit of amphistomy may be greatest in these contexts, but this hypothesis has not been tested experimentally. Understanding why amphistomy evolves can inform its potential as a target for crop improvement and paleoenvironment reconstruction. We developed a new method to quantify “amphistomy advantage”, AA, as the log-ratio of photosynthesis in an amphistomatous leaf to that of the same leaf but with gas exchange blocked through the upper (adaxial) surface, which we term “pseudohypostomy”. We used humidity to modulate stomatal conductance and thus compare photosynthetic rates at the same total stomatal conductance. We estimated AA and related physiological and anatomical traits in 12 populations, six coastal (open, sunny) and six montane (closed, shaded), of the indigenous Hawaiian species ilima (*Sida fallax*). Coastal ilima leaves benefit 4.04 times more from amphistomy compared to their montane counterparts. Our evidence was equivocal with respect to two hypotheses – that coastal leaves benefit more because 1) they are thicker and therefore have lower CO_2 conductance through the internal airspace, and 2) that they benefit more because they have similar conductance on each surface, as opposed to most of the conductance being on the lower (abaxial) surface. This is the first direct experimental evidence that amphistomy *per se* increases photosynthesis, consistent with the hypothesis that parallel pathways through upper and lower mesophyll increase the supply of CO_2 to chloroplasts. The prevalence of amphistomatous leaves in open, sunny habitats can partially be explained the increased benefit of amphistomy in 'sun' leaves, but the mechanistic basis of this observation is an area for future research.

S.53.5 Systematic, evolutionary, and ecological perspectives on the repeated convergent evolution of mimetic seeds in legumes

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Seeds that deceptively mimic nutritious fruits or arillate seeds but provide no nutritive rewards to dispersers have evolved repeatedly in Fabaceae and are one of the most striking examples of phenotypic convergence in the family, yet their evolutionary origins have been little studied. These seeds are associated with a suite of traits, including bright coloration, extreme hardness and impermeability, strong physical dormancy, suppressed abscission, and accumulation of toxic secondary metabolites, that define a parasitic dispersal syndrome targeting naive frugivorous birds. To attract sufficient numbers of dispersers, this strategy requires that seeds remain attached to dehisced pods in the plant canopy for long periods of time, increasing risk of deterioration and exposure to predators. We review the biology of mimetic seeds in the context of the increasingly well resolved phylogeny of legumes and present preliminary data relevant to hypotheses about their origins. We conclude that mimetic seeds have arisen convergently at least 16 times in the family, but only in subfamilies Caesalpinioideae and Faboideae. In most cases the evolutionary transition to parasitism is associated with an abrupt shift to bird dispersal from some other dispersal mode involving one or more non-avian dispersal agents; apparent transitions from mutualistic to parasitic bird dispersal are few. Evolutionary origins of several of the characteristic traits of mimetic seeds—hardness, location in persistent fruits, and toxic secondary metabolites—predate transitions to bird dispersal and mimicry; these traits were likely exapted for their current functions in mimetic seeds. Two other traits—bright coloration and suppressed abscission—are much more closely associated with transitions to mimicry and bird dispersal, and thus likely constitute original adaptations for these purposes. Planned comparative studies on the genetic control of this latter class of traits may be illuminating with respect to the apparent propensity for lineages of Fabaceae to evolve mimetic seeds.

S.53.6 Where mating is overrated: Understanding the evolution and ecology of asexual reproduction in a tropical understory herb

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Flowering plants have a diversity of mechanisms for reproduction. Both asexual and sexual modes represent alternative reproductive mechanisms that plants may adopt in order to counter temporally or spatially variable environments. In plants, it is common to find that a single individual may resort to either mode, resulting in a "mixed reproductive strategy." Our study is focused on the genus *Globba* L., which is a tropical understory herb. It is known for its high diversity in reproductive strategies, with presence of both sexual (andromonecy) and asexual (bulbils) modes of reproduction. The objective of our study is to investigate ecological factors that may have shaped the evolution of bulbils in *Globba*, and to show how this strategy may have helped the genus diversify in the Asian tropical understory. We specifically address the evolutionary significance of asexual reproduction and how it is an efficient reproductive strategy. To study the evolution of bulbils in this genus, we sampled Indian *Globba* spp. from the states of Northeast India and Western Ghats and used sequences from NCBI for the remaining species. A Bayesian phylogenetic analysis using BEAST was carried out on nuclear and chloroplast data set with 89 species. To study the ecological and physiological relevance of asexual reproduction in *Globba*, we also carried out field experiments for 10 species across 15 populations. Our results suggest that the presence of bulbils is an ancestral state and may have evolved multiple times in the genus *Globba*. We also identified obligate asexual taxa differed in their ecological characteristics (such as population size, pollinator visitation rate, natural fruit set, and physiological compatibility). The disproportionate distributional success of obligate asexual species suggested that asexual reproduction by bulbils is clearly an advantageous and an efficient reproductive strategy in some *Globba* species.

S.54 EVOLUTION OF PLANT SEXUAL REPRODUCTION. SESSION 1

S.54.1 Deducing the ancestor of angiosperms from the timeline of molecular evolutionary events associated with flower-specific traits

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The angiosperms, also known as flowering plants, contain numerous traits that are absent from their molecular-phylogenetically identified sister group, the living gymnosperms. Such angiosperm-specific traits include the outer integument of the ovule, the carpel, the perianth, and the bisexual reproductive axis. The extinct gymnosperm orders Caytoniales and Bennettitales have been suggested as strong candidates for ancestors or close stem relatives of angiosperms, but these possess contrasting sets of angiosperm-like features. In Caytoniales, the ovules are enclosed within a cupule, which might (or might not) represent a precursor to either the carpel or the outer integument of angiosperms. In Bennettitales, by contrast, there is no cupule, but a perianth-like structure and a bisexual axis (in some taxa) are present. We are analyzing the evolution of gene lineages that control the development of, or are specifically expressed in, the above-listed angiosperm-specific features. Our aim is to deduce the order of potential neo-functionalization events in these lineages and hence the likely order-of-origin of the traits/organs with which they are associated. In particular, the *epsilon* whole genome duplication, which preceded the radiation of living angiosperms, provides a useful genome-wide time-point to separate earlier and later evolutionary events along the angiosperm stem lineage. The proposition that the outer integument of the angiosperm ovule arose from a Caytoniales-type cupule has been particularly prominent in recent literature, which emphasizes the curved symmetry found in both the cupule and the anatropous angiosperm ovule. A part of our project accordingly focusses on the molecular mechanism of ovule curvature and its degree of conservation between model and early diverging angiosperms.

S.54.2 The role of polyploidy for the evolution of sexual and apomictic reproductive systems in angiosperms

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The predominance of sexual reproduction in eukaryotes despite high costs is still an evolutionary enigma. Major theories propose that sex could provide a twofold DNA restoration tool, i.e. repair of oxidative damage during meiosis, and selective elimination of harmful mutations via recombination. In angiosperms only about 2.3% of genera and <1% of species reproduce via apomixis (i.e., reproduction via asexually formed seeds). Most natural apomicts are polyploids, but the reasons for this association remain still unclear. Previous hypotheses suggested that genome duplication would be the functional trigger for apomixis by altering gene expression and epigenetic control. However, several studies indicate that apomixis already starts in diploid populations at low frequencies and can be inherited by haploid gametes. Transcriptomics on diploid aposporous F2 hybrids suggest that a "lucky combination" of mutations in genes related to reproductive development could be a functional trigger of apomeiosis. However, polyploidy has indirect positive effects to establish apomictic lineages. First, polyploidy can lower abiotic stress, e.g., light stress, which will reduce the trigger of oxidative stress for initiation of meiosis, thereby favouring facultative asexual pathways. Second, polyploidy can buffer short-term effects of recessive deleterious mutations, and only a little bit of facultative recombination (6%) is efficient to for purifying selection even in big polyploid genomes. Third, polyploidy can facilitate niche shifts by adaptations to more extreme environments by epigenetic changes and phenotypic plasiticity, which will be demonstrated by DNA methylation and gene expression analysis. Fourth, polyploidy results in a breakdown of self-compatibility, which allows for self-fertilization and uniparental reproduction in pseudogamous apomicts, which is an advantage for colonization. Experimental and molecular work on *Ranunculus* supports these hypotheses. We conclude that hybridity rather than polyploidy is the primary functional trigger for apomixis, but polyploidy is essential for establishment of apomictic lineages in natural populations.

S.54.3 Anther development and evolution with single-cell RNA-sequencing

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The anther is the developmental housing of pollen of flowering plants. The meiotic cells from which pollen are derived must differentiate *de novo* from somatic anther cells and synchronously develop with the rest of the anther. Understanding the genes that underlie the proper differentiation, developmental landmarks, and functions of each anther cell type is fundamental to plant sciences. Here, we investigated the development of the somatic niche of the maize (*Zea mays*) anther using single-cell RNA-seq (scRNA-seq). We established the developmental trajectories of the somatic cell types from pre-meiosis to post-meiosis, identified putative marker genes for the cell types that previously lacked any known specific functions, and addressed the possibility that tapetal cells sequentially redifferentiate. Finally, we compared these results with anther scRNA-seq data from wheat (*Triticum turgidum*) to assess the evolutionary conservation of anther development. These results are essential for future analyses investigating male-sterile genotypes and the impact of environmental conditions on male fertility in flowering plants.

S.54.4 The role of LEUNIG and SEUSS transcriptional regulators during land plant evolution

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The adaptation of reproductive strategies to the terrestrial environment was one of the crucial steps of the transition from water to land that plants had to overcome. During land plant evolution, various adaptations emerged, from the simple, water-dependent fertilization mechanism of bryophytes to the morphologically highly diverse flowers of angiosperms. This wide range of reproductive strategies makes it especially noteworthy that some of the essential regulators of flower development in angiosperms are present in all major land plant lineages. In *Arabidopsis thaliana*, the transcriptional regulators LEUNIG (LUG) and SEUSS (SEU) play an important role in flower development: LUG and SEU first form a heterodimer, which then can interact with floral organ identity proteins such as APETALA1, and other developmental regulators such as AINTEGUMENTA. The moss *Physcomitrium patens* encodes, like *Arabidopsis,* several homologs of LUG and SEU, raising the questions of (1) how exactly did these regulators co-evolve with each other and other transcriptional regulators to become such important floral regulators, and (2) if their ancestral function was also related to sexual development. We use Yeast-Two Hybrid and Bifluorescence Complementation assays to study protein interactions and the CRISPR-Cas system for multiplex *Physcomitrium* mutagenesis. We present our data on (1) the protein interaction of the *Physcomitrium* and other land plant LUG and SEU homologs and the protein domains important in the co-evolution between LUG and SEU and their interactors, heterodimer formation and for target protein interaction. Further, we show that removing LUG and SEU function from the *Physcomitrium* genomes results in growth retardation and present detailed phenotypic analysis of the LUG and SEU mutants of *Physcomitrium*.

S.54.5 Because sex cells: patterning of gametangia in land plants and specification of gametes in the fern Ceratopteris richardii

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The fundamental sexual reproductive structures of the gametophyte are the archegonium and antheridium (together called gametangia), which produce egg and sperm respectively. The gametangia show remarkable morphological conservation across nonvascular and free-sporing vascular plants but are structurally reduced in seed plants. Many studies have investigated the molecular genetics of gametophyte development in angiosperms, as well as in some Bryophytes, but broad comparative studies are lacking. Furthermore, whether and how the gametes produced by the gametangia are homologous across green algae and land plants is not known. Although analyses of patterning provide strong working hypotheses, contributions from molecular genetics and functional studies will be necessary to determine the complete story of how these structures and the gametes they produce have changed throughout the evolution of land plants. We aim to fill this gap with developmental genetic analyses in the model fern, *Ceratopteris richardii*, using a transcriptomic and candidate gene approach. Using bulk RNA-seq of six developmental stages, we developed a time series transcriptome atlas for the gametophyte of *C. richardii*. This dataset has allowed us to understand broad patterns of gene expression changes throughout gametophyte development, investigate dynamics of shared vs. unique gene expression between life stages, and identify promising targets for further functional analyses. Our candidate approach focuses on TALE homeodomain (TALE-HD) proteins that specify the identity of distinct gametes. Following fertilization, proteins from distinct TALE-HD subclasses form a heterodimer and translocate to the nucleus to initiate the transition from gametophyte to sporophyte in Chlorophyte algae and Bryophytes. However, whether these genes retain this function in ferns is currently unknown. We are combining our transcriptome atlas with in situ hybridization and phylogenetic analysis to understand the evolution of TALE-HD proteins, and leveraging these new data in ferns to create a comparative framework for understanding gametangia evolution.

S.55 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 2

S.55.1 The widespread Quercus ilex L. dieback in Mediterranean forests: investigation of the causes at plant and ecosystem level

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Over the past two decades, the occurrence of extreme climatic events in the Mediterranean region has increased, and this climatic pressure has contributed to the spread of vegetation dieback over several forest communities. Dieback has also affected *Quercus ilex* L., and since this decline has worsened over the last 15 years in many Mediterranean areas, it is crucial to develop effective tools for studying this phenomenon combining different scales of measurement. Our study was conducted over four years (2019-2023) in declining (D) and non-declining (ND) *Q. ilex* stands in southern Tuscany, assessing physiological and biochemical traits such as gas exchange, water relations, carbohydrate analysis in the wood, and xylem sap isotopic signal ($\delta^{18}O$). Dendrochronological and tree-ring $\delta^{13}C$ analyses were combined to investigate the effects of previous droughts on tree growth and water-use efficiency. Lastly, changes in vegetation structure were assessed to monitor the impact of holm oak mortality at the ecosystem level. The results of physiological analyses showed that seasonality had a strong effect on these traits, with the main stress occurring during the summer of 2020, as evidenced by the lowest gas exchange values. According to the results of $\delta^{18}O$ analyses, holm oaks mainly took up water from deep soil sources (bottom soil or ground water) owing to their deep-root systems, resulting in only slightly different ring-width patterns and a low responsiveness to seasonal climatic variations in both stands. By contrast, the $\delta^{13}C$ results combined with SSR genotyping revealed a more conservative water use of the population in the ND stand, underlying the potential of combining these powerful tools for the selection of seed-bearing genotypes putatively tolerant to water deficit. Furthermore, significant changes in the understory plant community highlight that *Q. ilex* dieback strongly affects the vegetation structure of Mediterranean forests.

S.55.2 Tolerance to herbivory is maintained in insular herbivore-extinct ecosystems.

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Plant responses to herbivory play a crucial role in maintaining ecosystem functionality. While a *trade-off* between resistance and tolerance to herbivory has been theorized, recent studies challenged this dichotomy, as they showed that species might possess in-between behaviour. Additionally, the study of enemy release processes suggests that plant responses to herbivory ameliorate after herbivore disappearance. Based on these premises, we set an experiment with the non-palatable insular-endemic shrub *Hypericum balearicum* to assess its capacity to respond to herbivores. We conducted a comprehensive assessment of real herbivore interaction with *H. balearicum* in natural areas and examined plant responses following simulated herbivory. For this, we cultivated *H. balearicum* individuals at the Forestal Centre of the Balearic Islands. From all, we planted 90 in each of two natural areas inhabited by feral goats and sheep. To isolate the impact of herbivores, half of the plants at each site were excluded. Simultaneously, 90 individuals were maintained in a plant nursery for a simulated experiment involving two induced herbivory treatments: moderate and severe. After 45 days, we measured various physiological, biochemical and growth parameters associated with herbivory response. Plants in natural areas showed no signs of herbivore predation, indicating an absence of herbivory on this species. Nevertheless, the response capacity remained evident. Following induced herbivory, we observed maintained net photosynthesis but increased chlorophyll concentration, specific leaf area and Root:Shoot ratio in response to increasing treatment intensity. Severe herbivory simulation induced oxidative stress, and variations in the concentration of 47 leaf secondary compounds were reported across all treatments. Our findings challenge the conventional notion that resistant plants lack mechanisms to respond after herbivory when evolutionary pressures are absent. This study underscores the importance of considering historical factors, such as the presence of extinct herbivores or traits originated by exaptation, in the assessment of plant-herbivore interactions.

S.55.3 Predicting drought tolerance-related biomarkers in maritime pine (Pinus pinaster Ait.) using machine learning

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Knowledge about the molecular and functional mechanisms that control the adaptation of trees to drought is key in the current context of climate change, since recurrent drought is one of the main climatic factors threatening forests, particularly in the Mediterranean region. However, this knowledge is scarce, especially in conifers, due to their huge and complex genomes. *Pinus pinaster* is one of the conifers with the greatest socioeconomic (for wood and resin production) and ecological importance in southwestern Europe, given its adaptive capacity. Recent advances in sequencing technologies enable the generation of large amounts of omics data, introducing a new era of "big data" in biology. Machine learning (ML), a branch of Artificial Intelligence (AI), offers promising approaches to recognize fine-grained patterns and relationships in these large and heterogeneous datasets, helping bridge the gap between our capability to produce and analyze plant molecular data. Here, we explore the potential of machine learning in predicting drought tolerance-related molecular biomarkers in maritime pine (*P. pinaster*). To this end, we used transcriptomic data from grafted rootstocks of genotypes with contrasting response to drought (tolerant and sensitive). Machine learning algorithms were used to analyze the expressed genes on these grafted rootstocks under controlled drought conditions to obtain accurate predictions of their tolerance/sensitiveness to drought. The methodology includes data selection and preprocessing, feature selection, model development, and evaluation. The obtained drought-tolerance molecular biomarkers can be used to guide the design of breeding and management programs, such as marker assisted selection and breeding, which will help improve the conservation, health, and productivity of this conifer in the long term. They can be also used in future drought-response research (e.g. comparative genomic studies, functional transfer across species) which will shed light on trees' molecular adaptive potential to current climate change.

S.55.4 Novel approach to link the physiological response of maize (Zea mays L.) to drought and the occurrence of mycotoxins

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One of the effects of global change is the alteration of hydrological events, which affects many human activities, including agricultural ones. Understanding how maize (*Zea mays* L.), one of the most important staple crops worldwide, responds to these modifications is important to adapt to climate change. Drought stress during maize germination, flowering and pollination can lead to decreased plant growth, nutrient uptake, and grain yields. Prolonged periods of drought can also significantly increase the spread of diseases, which reduces yield quality. In this context we monitored 40 maize fields composed by both irrigated and non-irrigated areas, along a pedoclimatic gradient in NE Italy, throughout the 2022 and 2023 seasons, at four phenological stages (*i.e.*, beginning of stem elongation, flowering, milk maturation, dent maturation). In particular, we considered the plant individual functional response (*i.e.*, plant height, SLA, leaf DMC, leaf chlorophyll, carotenoid and flavonoid content, kernel DW, kernel C:N, kernel δ^{13}C), and the kernel mycotoxins content (aflatoxins and fumonisins), in relation to irrigation conditions and climate data (*i.e.*, total precipitation, mean temperature). We found that the soil structure effect was overruled by the effect of climate and/or irrigation. As we expected, the absence of irrigation and low total precipitation led to a reduction of plant biomass and kernel production, whereas interaction between irrigation and phenological stage had significant effects on leaf pigments (*i.e.*, chlorophyll) and secondary metabolites (*i.e.*, flavonoid). Moreover, irrigation enhanced the kernel C:N ratio and δ^{13}C, whereas reduced the amount of aflatoxins. Our further investigations aim at evaluating the interplay between the climatic variables, the soil structure, and the individual traits on the ultimate content of mycotoxins in the kernel, with two distinct irrigation regimes and at the given different phenological stages, adopting a structural equation modelling approach.

S.55.5 Observing Shifts In Global Tropical Flowering Phenology

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Shifts in flowering phenology can have cascade effects across entire ecosystems and can be indicators of more severe climate change effects. Large scale, multi-taxon studies investigating flowering phenology have been limited to non-tropical latitudes. This study analyzes changes in flowering times at 20 localities across the global tropics. I have found that from 1850 to 2021, flowering times have shifted significantly at all locations, on average 97.6 days across all sites. This ranged from 55.5 days shifted at Las Cruces Research Station in Costa Rica to 109.9 days shifted at Korup National Park, Cameroon. The Neotropics have undergone an average of 80.9 days shifted, the Afrotropics an average of 91.9 days shifted, and Southeast Asia an average of 102.6 days shifted. These shifts could be indicative of greater ecosystem-wide changes. A changing of flowering time can be an indicator for larger impacts of climate change, however it is important to take duration of flowering period into account when analyzing the impact the shift in flowering may cause.

S.55.6 Overexpression of BvNHX1 from sugar beet (Beta vulgaris) confers enhanced salt tolerance in transgenic tobacco

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Salinity is one of the major environmental factors that limit the plant growth and crop productivity worldwide. Tonoplast Na^+/H^+ transporters (NHXs) play crucial roles in regulating the intracellular Na^+/K^+ and pH homoeostasis, which is essential for salt tolerance and development of plants. In the present study, a novel gene *BvNHX1* encoding tonoplast Na^+/H^+ antiporter was isolated in natrophilic crop sugar beet (*Beta vulgaris*) and functionally characterized in tobacco (*Nicotiana tabacum*) plants to assess the behavior of the transgenic organisms in the response to salt stress. The results showed that overexpression of *BvNHX1* significantly enhanced salt tolerance in transgenic tobacco plants compared with wild-type (WT) plants. The seed germination, root length, plant height, and fresh and dry weights in transgenic plants were significantly higher than those in WT plants under salt stresses. The contents of leaf relative water, chlorophyll, proline, soluble sugars, and soluble proteins were significantly higher as compared with WT plants, while malondialdehyde (MDA) contents were significantly lower than those of WT plants under salt stresses. Na^+ and K^+ contents both in shoots and roots of transgenic plants were significantly higher than those of WT plants, and transgenic plants maintained a balanced K^+/Na^+ ratio under saline conditions. Taken together, these results suggested that overexpression of *BvNHX1* reduced damage to cell membrane by reducing osmotic potential of cells, and maintaining relative water and chlorophyll contents of leaves, and finally improved salt tolerance in transgenic tobacco plants.

S.56 PLANT CONSERVATION GENETICS: FROM IN-SITU AND EX-SITU CONSERVATION TO REINTRODUCTIONS AND RESTORATIONS. SESSION 2

S.56.1 Using gene rescue theory to improve the success of conservation translocations

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We present a study that uses genetic rescue (an improved fitness due to the introduction of new genes) theory to help maximise the success of conservation translocations, the deliberate movement of plants for conservation purposes. Species in need of translocations often remain as small, scattered and isolated populations. This makes them vulnerable to genetic problems, such as genetic erosion, inbreeding depression and a lowered evolutionary potential. These genetic problems can decrease plant fitness and consequently make recovery work more difficult. Genetic rescue can help to overcome fitness declines in small populations and mixing genes can be a strong tool for creating more suitable plant material for translocations. Here, we put genetic rescue theory to practice, including all associated steps, such as gathering genetic background information on the study species, cross-pollinations in a nursery, and translocations. We're using the alpine blue-sowthistle (*Cicerbita alpina*) as an example, which is only left in four very small populations in Scotland, UK, where it fails to reproduce. Like so many other species, *C. alpina* is unlikely to recover naturally and could be lost without human interventions. We demonstrate that cross-pollinations improve plant fitness (plant size, survival, flowering) at translocation sites. Mixing genes prior to planting species out can help increase the success of conservation translocations but requires time, space and expertise.

S.56.2 Population genetics for the conservation of three endangered Magnolia species from Chiapas and Guatemala

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Understanding the genetic structure of populations is crucial for conservation purposes of endemic or geographically restricted species, to ensure that ex-situ propagation and conservation efforts include a representative sample of the species' genetic diversity existing in nature. In the case of *Magnolia*, the complex physiographic environment and climatic diversity in southern Mexico and Guatemala results in the existence of species restricted in their distribution to certain mountain ranges, representing examples of either paleo- or neoendemisms. The reduction of habitats due to land use change, deforestation, and climate change consequently places some species in a particularly vulnerable state, requiring urgent implementation of conservation measures to prevent extinction. The species *Magnolia faustinomirandae*, *M. montebelloensis*, *M. quetzal*, are characterized by having highly restricted populations of only a few dozen individuals known in the wild, in addition to those included in propagation programs. Data obtained from the analysis of known wild populations of three species using targeted genomic sequencing revealed rather limited genetic diversity in *M. quetzal*. In the case of morphologically similar species *M. montebelloensis* and *M. faustinomirandae*, the population of the latter from Chiapas highlands demonstrated a genetic identity distinctively separated from the rest of the samples. It was revealed that some individuals morphologically similar to *M. faustinomirandae* in Guatemala are indeed part of *M. montebelloensis* diversity, which has been confirmed by more exhaustive morphological analysis. Therefore, authentic *M. faustinomirandae* is restricted to Chiapas highlands. Regarding *M. montebelloensis*, its populations in Lagunas de Montebello showed genetic similarity with those in Quiché, Guatemala, being the most diverse species in the analysis. The analysis suggested the possibility of a cryptic *Magnolia* species in Guatemala, distinct in its genetic composition, known from a cultivated population in the Monastery site, that is currently under morphological revision.

S.56.3 Genomic signatures of inbreeding depression and mutation load in a threatened African timber tree, Pericopsis elata (Fabaceae)

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Pericopsis elata is a large, gregarious, and light demanding tree distributed in the Western and Central African tropics. Highly exploited for its excellent quality timber, it is listed as endangered on the IUCN Red List and included in the CITES Appendix II. It is a peculiar tropical tree as it has a mixed-mating system, with a high selfing rate, and a lack of regeneration throughout its natural distribution range. Previous results from Democratic Republic of Congo (DRC) showed a high proportion of inbred individuals, with 54% inbreeding in seeds and seedlings, and 20% in adults, indicating inbreeding depression. Recently, two highly differentiated gene pools (F_{ST}=0.53) were identified in DRC (Eastern gene pool), and Republic of Congo and Cameroon (Western gene pool). Along the Western gene pool, we observe a steep westward decay of heterozygosity, and we hypothesize that this is a recent range expansion into Cameroon with founder effects, possibly facilitated by selfing. Our aim is to assess inbreeding depression and mutation load along this westward expansion. Whole genome resequencing data of individuals along this gradient will be used to detect the runs of homozygosity (ROH), which will aid in inferring the demographic history and finding deleterious variants. To detect the mutation load, we test if there is a westward decay of the ratio of synonymous to non-synonymous mutations, and the predicted effect of amino acid substitution on protein function based on sequence homology across closely related species. On the range expansion front, we expect longer ROHs, and an increase in inbreeding coefficient and mutation load towards the west. These analyses, combined with phenotypic data, will help in identifying the effects of inbreeding and informing sustainable management strategies for this threatened timber tree.

S.56.4 Angiosperms353 for population genetics of regionally threatened plant species

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Intra specific genetic diversity is a key component of biodiversity, but it has frequently been overlooked in conservation studies due to the difficulties to study it. Conservation programs often need a genetics assessment of the target populations to guide specific actions, such as source population to use in reinforcement or reintroduction. Here we test the effectiveness of the universal targeted sequence capture approach Angiosperms353 to capture the genetic structure and diversity of small regionally endangered populations within three distinct species for which conservation action plans are developed in Switzerland (*Blackstonia acuminata*, *Eryngium campestre*, and *Lythrum hyssopifolia*). For each of the three species, we could successfully identify a minimum of 900 non-linked Single Nucleotide Polymorphisms (SNPs) in exonic and flanking intronic regions. The analysis of these SNPs revealed contrasting patterns of population structure, genetic diversity, and hybridization levels, even at a very local scale. In *Blackstonia*, our results show the clear differentiation of morphologically similar species (*B. acuminata* and *B. perfoliata*) and reveal in *B. accuminata* a hybridization level indicative of a hybrid taxon likely reproducing through apomixis. *Eryngium campestre* exhibited distinct population lineages associated with the drainage systems in which they were situated. *Lythrum hyssopifolia* revealed both its polyploid nature and significant population differentiation. Although Angiosperms353 was developed to study species relationships due to the high conservation level of the targeted genes, we demonstrate the efficacy of this kit at the population level. Its many advantages such as direct applicability, cost-effectiveness, compatibility with herbarium samples and a better data interoperability could facilitate the use of genetics for rapidly assessing genetic diversity and structure with the aim of informing conservation actions.

S.56.5 Genomics for conservation of Mexican agaves and cactus

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Mexico is one of the few biodiversity hotspots for both wild and domesticated plants in the world. Many species, varieties and landraces can only be found in the region; due to geographical, biological and cultural reasons. Approximately 75%

of species of Agave are endemic and 84% of the cactus found in Mexico are found only here. The most recent assessments from conservationist groups reveal that both Agave and cactus species are the most endangered, threatened of extinction mostly from illegal poaching, change in land use and global warming. Unfortunately, there are still few genomic resources available for both taxonomic groups, and the research community is in high need of tools such as reference genomes, SNP panels and methodological approaches to better understand the biology to these long-lived wild species and inform conservation strategies. During this talk, we explain some of the research initiatives of Desert Botanical Garden in collaboration with several institutions in Mexico and the community to study and preserve both cactus and Agave biodiversity using genomic tools. We leverage on the popularity and economic relevance of two flagship species: *Carnegiea gigantea* (saguaro cactus) and *Agave tequilana*var. Azul ('blue' tequila agave). Although these species are not endangered, through their study we develop tools and raise awareness towards conservation, not only of species but also varieties and landraces. We explain our study of the columnar saguaro cactus and the efforts we are making to involve and actively engage the community to set awareness of climate change and their effects in cactus biodiversity. We also talk about our efforts to document and preserve the almost lost mezcal and tequila traditional Agave landraces, threatened by the enormous demand for only two cultivars that produce the spirits that are highly sought-after in the USA and Europe.

S.57 GENOMIC APPROACHES TO UNDERSTANDING THE ECOLOGY AND EVOLUTION OF SYMBIOTIC AND NON-SYMBIOTIC MICROALGAE. SESSION 1

S.57.1 Genome of the glacier alga Ancylonema and its insights into the evolution of streptophyte life on ice and land

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Contemporary glaciers and ice sheets are home to communities of streptophyte glacier algae that must balance their requirements for photosynthesis and growth with tolerance of extremes in temperature, desiccation and UV radiation. These same environmental challenges have been hypothesized as the driving force behind the evolution of land plants from streptophyte algal ancestors in the Cryogenian (720–635 Mya). Here, we sequence, assemble and analyze the metagenome-assembled genome (MAG) of the glacier alga *Ancylonema nordenskiöldii* to investigate its adaptations to life in ice, and whether this represents a vestige of Cryogenian anydrophyte exaptations. Phylogenetic analysis confirms the placement of glacier algae within the sister lineage to land plants, Zygnematophyceae. The MAG is characterized by an expansion of genes involved in high irradiance and UV light tolerance, whilst lineage-specific diversification led to the novel screening pigmentation of glacier algae. We found no support for the hypothesis of a common genomic basis for adaptations to ice and to land in streptophytes. Comparative genomic analysis revealed that reductive genome evolution in the ancestor of Zygnematophyceae correlates with their reductive morphological evolution. This first genome-scale data for glacier algae supports an Ancylonema-specific adaptation to the cryosphere, as well as shedding light on the genome evolution of land plants and Zygnematophyceae.

S.57.2 From thalli to holobiome genomes: reappraisal of lichens as biomonitors for forest health

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Lichens are one of the most emblematic examples of the mutualistic associations between one fungi and populations of photosynthetic green microalgae and/or cyanobacteria. Aside from these major lichen symbionts, an indeterminate number of other microorganisms, co-occur, intermingled in these associations. Given all of these new "players", the traditional lichen paradigm is evolving into a broader concept of lichen holobiomes. Advances in genomics and bioinformatics have provided a deeper understanding of this diversity. Therefore, lichen thalli are considered microecosystems in which numerous different symbiotic partners can interact. The fine functioning balance established in the thalli is one of the reasons for their recognition as bioindicators. Lichens are sensitive to a variety of anthropogenic disturbances, and are widely used as rapid bioindicators of both small-scale and global change. In the 1990s, a sampling network for the biomonitoring of forests using epiphytic lichen diversity was established in eastern Spain. In 1997, an assessment of the state of lichen communities was carried out and the results were published. In 2022, this previously established biomonitoring network was revaluated. To compare the results obtained in 1997 and 2022, the same methodology was used, and data from air quality stations were included. The results displayed a significant general decrease in the diversity and a generalised increase in damage symptoms in target lichen species, which seem to be the consequence of a multifactorial response (climatic and pollution). Taking advantage of this new sampling, genomic data were obtained from 188 thalli to explore lichen community structure. Our results showed differences in photobiont choice between sexually and asexually reproducing lichens in the epiphytic community. Using metagenomic approaches we explored the differences between the composition of microorganisms amongst healthy and damaged thalli. Our results provide a renewed perspective for biomonitoring.

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S.57.3 Comparative genomics in Chlorophyceae: an exploration to the green OCC clade

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In Chlorophyceae, the OCC clade (Oedegoniales, Chaetopeltidales and Chaetophorales) corresponds to more than a thousand of understudied algae species. They present a variety of interesting features such as the diversity of cellular organization complexity, presence/absence of plasmodesmata, and CO2 concentration mechanisms. However, the lack of genomic resources from the OCC clade limits further investigation into their unique biology. To address this genomic gap, we are currently sequencing four genomes that cover all the three orders in the OCC clade, using a combination of short and long read sequencing, as well as Hi-C scaffolding approach. We expect the resulting chromosome level genome assemblies will not only shed light into the genomic landscape in the OCC clade, but also form the basis for broader comparative analyses across chlorophyte algae.

S.57.4 Comparative genomics sheds light on the ecology and evolution of dryland green microalgae

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In dryland ecosystems, soil microbial communities are intricately linked to ecosystem functioning because they play an important role in carbon and nitrogen cycling, soil fertility and climate regulation. Unicellular green algae are crucial components of these communities with key roles in primary production, food webs, nutrient cycling, soil formation, and modulation of soil texture and structure. Despite its importance and interest in biotechnological exploitation, the phototrophic micro-algal flora represents a vastly understudied component of soil microbial communities. Limited knowledge of the diversity and the adaptive traits important for survival in extreme environments translates into a limited ability to monitor and eventually prevent biodiversity losses. This study aimed to create a genomic library of representative strains of green algae isolated from desert soils worldwide. A collection of 23 soil samples from 14 countries, collected within the framework of the BIODESERT project, was used for this purpose. The newly generated genomes and transcriptomes from several strains representing over 15 genera of the Chlorophyta and Charophyta divisions allow testing the hypothesis of genomic convergence in the adaptation to desert environments in green algae. Our newly genomic library constitutes a novel resource for metagenomics-based monitoring of functional biodiversity in desert soil microbial communities and a better-informed prediction of the ecological implications of climate change on soil biodiversity. Additionally, the results of this initial screening pave the way for the biotechnological exploitation of this vital yet understudied component of desert ecosystems.

S.57.5 How to find the right partner? Omics approaches unveil the mysteries behind the formation of lichen symbiosis

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Symbiotic organisms play a key role in natural communities. However, the mechanisms underlying the selection of symbiotic partners remain largely unknown. Over the past few years, we have aimed to understand the formation of lichen symbiotic associations by examining and comparing the diversity of endosymbiotic and free-living algae in the environment using a combination of eDNA metabarcoding and Sanger sequencing. In many cases, we revealed highly contrasting patterns of diversity, suggesting that the symbiotic inventory of lichen communities does not reflect the diversity of free-living algae. In particular, many symbionts that associate only with asexual lichen species have never been found at a site outside of lichen thalli, although various substrates, including aeroplankton, have been examined for the presence of free-living algae. Such findings strongly violate the paradigm of habitat-adapted symbiosis, as fungal hosts obviously do not select their algal partners from a regional pool of adapted species. Moreover, we hypothesize that some of the symbionts absent from the environment may exhibit a high degree of dependence on the presence of symbiotic fungi or may even represent obligate symbionts that never occur in the free-living state.

S.57.6 The photobiont cookbook: phylogenomics-informed recipes to make lichen-palatable algae

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Lichens are textbook examples of ecologically successful symbioses formed between thousands of fungal species and a handful of green algae. Their biology, ecology and physiology have been studied for centuries, with disproportionate focus on the fungal side of the symbiosis. By contrast, the evolutionary origins and molecular mechanisms of the symbiosis on the side of the green algal partner remain elusive. In this study we explored the evolutionary history and the molecular innovations in green algae at the origin of the ability to establish symbiotic association with fungi to form lichens. For this, we de novo sequenced the genomes or transcriptomes of 12 lichen-forming and closely related non-lichen-forming algae, filling key sampling gaps in the algal tree of life. We then combined this dataset with 129 previously sequenced green algae and performed comparative phylogenomic analyses to find genes discriminating lichen-forming and non-lichen-forming algae. In addition to gene-family expansions, we show that one carbohydrate-active enzyme, the glycosyl hydrolase 8 (GH8), was acquired in lichenizing Trebouxiophyceae by horizontal gene transfer from bacteria. Our results suggest that the ability to degrade the partner's cell wall is a key acquisition for the evolution of symbiotic lifestyle in these algae. Our study unravels an important evolutionary event fundamental to the establishment of symbiotic lifestyle in lichenized algae and paves the way for future functional studies in this understudied yet ecologically important group of organisms.

S.58 STILL STANDING: RIBOSOMAL DNA SIGNIFICANCE IN CURRENT PLANT RESEARCH

S.58.1 Molecular architecture of rDNA loci and evolutionary dynamics of 5S and 35S rDNA repeats in duckweeds (Lemnaceae)

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Duckweeds, represented by 36 species in Lemnaceae family, are small, mostly vegetatively propagated aquatic plants with worldwide distribution and fast growth rate. Sequencing of 35S rDNA repeats in representative species of genus *Spirodela*, *Landoltia*, *Wolffia* and *Lemna* showed positive correlation of the repeats length with genome size, and significant sequence variability of the intergenic spacers. Our genome surveys of two most ancient duckweed species, *S. polyrhiza* (Michael et al., 2017) and *S. intermedia* (Hoang et al., 2020), revealed a very low representation of 35S and 5S rRNA genes, at around 100 copies per genome, and an unorthodox molecular structure of the usually conserved 35S rRNA transcription initiation site (TIS). The low rDNA copy number in *Spirodela* made possible to reveal detailed molecular organization of the species' rDNA loci through a combination of molecular cytology, conventional sequencing and long DNA reads. The relatively GC-rich 35S rDNA and 5S rDNA arrays are imbedded in highly AT-enriched chromosome regions. Further sequence analysis demonstrated that the 5S rDNA repeat clusters, localized on two different chromosomal loci, and composed correspondingly of 40 and 60 repeat units have the non-transcribed spacers (NTS) of different size and different rates of sequence variability, suggesting contrasting evolutional dynamics of the two types of 5S rDNA units. In summary, our findings put duckweeds in the spotlight of rDNA research, promising new insights into basic principles of organization and regulation of rRNA genes.

References: Michael et al. (2017) Plant Journal, 89(3):617-635. Hoang et al. (2020) Scientific Reports, 10(1):19230.

S.58.2 Deconstructing ribosomal DNAs: an overview of ribosomal DNAs evolution and genomic arrangements in the sunflower family

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Here we explore the evolutionary dynamism of ribosomal RNA genes (rDNA), a dynamism that is surprisingly high given their crucial role in the synthesis of ribosomes and thus for life-on-Earth. rDNA units are present in high numbers, from 50 to 13,000 copies per cell that are typically tandemly arranged at one or a few loci. However, despite their importance and abundance, several aspects of the biology remain enigmatic, particularly their mode of molecular evolution and genomic arrangements. We aim to *deconstruct* ribosomal DNA structure to define the model of evolution that best explains its high evolutionary dynamism and the differences in behaviour of 35S and 5S rRNA genes. We have used 74 species in the sunflower family (Asteraceae) as models for this analysis, which together represent a diversity of rDNA arrangements, genome sizes, ploidy levels, and rDNA copy numbers. Indeed, family Asteraceae shows a particularly large diversity of rDNA arrangements amongst its 24,000 species, including in subfamily Asteroideae (tribe Anthemideae and some tribes of the Heliantheae alliance), where there is an exceptional arrangement of 35S and 5S rRNA genes being linked together. Using next-generation sequencing (NGS) and analytical approaches we address central questions allowing us novel, fundamental insights into genomic mechanisms related to concerted evolution, pseudogenisation, the relationship with genome size and rDNAs or their interplay with transposable elements. Our results impact our global understanding of molecular evolution and repetitive DNA organisation in plant genomes.

S.58.3 The plant nucleolus across the seed plants – ubiquitous but mysterious

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The nucleolus is one of the most prominent structures in the eukaryotic cell due to its indispensable role in 35-45S rRNA gene transcription and subsequent ribosomal subunit assembly. In addition to proteins and rRNA, the nucleolus also contains the 35S/45S ribosomal DNA (35S/45S rDNA). These tandemly repeated genes encoding for 18S, 5.8S and 25/28S rRNA are transcribed as a single 45/35S pre-rRNA by DNA-dependent RNA polymerase I (PolI). Despite the presence of nucleolus in almost every eucaryotic cell, many questions about its structure and function remain unanswered. Also, the question of how diverse the nucleoli are among the different seed plant representatives is still pending attention. Hence, in this study, we aimed to shed new light on the seed plant nucleolus structure by integrating insights from the ultrastructure of nucleoli components and through the lens of modern superresolution microscopy. Both the model (such as *Brachypodium distachyon* and *Arabidopsis thaliana*, monocot and eudicot, respectively) and non-model species were analysed. The localisation of the selected nucleolar proteins, *i.e.,* fibrillarin, nucleolin, and subunits of RNA Pol I, were visualized *in vivo* using the GreenGate cloning system. The patterns of selected nucleolar proteins were then compared with the 3-dimensional localisation of the decondensed fraction of 35S rDNA by fluorescent *in situ* hybridisation (FISH). As a result of our study, the functional characterisation of particular nucleolar components has been proposed, shedding new light on the role of the specific nucleolar subcompartments, e.g., the nucleolar vacuoles.

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S.58.4 Conserved sequence elements present in the 5S rDNA intergenic spacer occur in the genomes of distantly related angiosperms

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Tandemly arranged repetitive regions (repeats) that encode 5S rRNA (5S rDNA) are an obligatory component of eukaryotic genomes. Typically, the 5S rDNA repeats within a genome are very similar due to the concerted nature of their evolution. Each 5S rDNA repeat consists of a conserved coding sequence (CDS) and a rapidly evolving intergenic spacer (IGS). The high evolutionary stability of the CDS is the result of purifying selection to maintain the function of the 5S rRNA as a component of the ribosome. In contrast, it is believed that the main part of the IGS probably has no function and therefore evolves at a high rate. To uncover the patterns of IGS evolution in a broad taxonomic context, we applied cloning, sequencing, and bioinformatic analysis to describe the molecular organization of 5S rDNA in 31 genera representing 15 families and 12 orders of angiosperms. It was found that the short-sequence motifs at the 3′ and 5′ ends of the IGS, which are involved in the initiation and termination of 5S rDNA transcription, evolve at a relatively low rate and demonstrate apparent conservation within a genus/family. Surprisingly, our analysis also revealed that in eight genera studied the middle part of IGS harbors conserved sequence elements (CSE), 50 to 200 bp in length, which show clear similarity (70 to 91%) to the genomic sequences of taxonomically distant families. This may be due to presumptive horizontal gene transfer. Alternatively, the CSE may represent ancient sequences that were conserved in some phylogenetic lineages. The function of CSE and the mechanism of its maintenance during long-term evolution remain enigmatic and require further research.

S.262.5 Uniparental silencing of 5S rRNA genes in plant allopolyploids – first evidence from Cardamine (Brassicaceae)

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Introduction: While uniparental silencing of 35S rDNA in interspecific hybrids and allopolyploids is a well-known phenomenon there is no information on whether silencing also affects the 5S RNA component of ribosomes. To address this question, we analyzed the expression of 5S rDNA and 26S rDNA in Cardamine (Brassicaceae) allopolyploids including *C. × insueta* (genome composition ARR, 2n=3x=24), *C. flexuosa* (AAHH) and *C. scutata* (AAPP) (both 2n=4x=32). These combine diploid genomes derived from *C. amara* (A-genome) shared by all three allopolyploids and divergent genomes derived from *C. rivularis* (R-genome), *C. hirsuta* (H-genome) and *C. parviflora* (P-genome) (all 2n=2x=16). Bioinformatic pipelines included high-throughput sequencing of transcriptomes and genomes followed by variant calls and phylogenetic analyses of ribotypes. Genomic organization of rDNA was analyzed by SNPs, clustering and rDNA FISH. Results: In *C. × insueta* allotriploid hybrid we observed uniparental dominant expression of 35S and 5S rDNA loci from the *C. rivularis* genome. In *C. flexuosa* and *C. scutata* allotetraploids 35S rDNA was expressed from the A-genome while 5S rDNA was expressed from the partner H- and P- genomes, respectively. FISH showed relatively intact 5S and 35S loci in *C. × insueta* (twenty populations) while both *C. flexuosa* and *C. scutata* allotetraploids showed copy and locus number changes. Intergenomic translocation of the H-genome 5S rDNA was identified in all populations of *C. flexuosa* which however did not influence its dominant expression. Conclusion: Both 5S and 35S rDNA loci undergo uniparental silencing in Cardamine allopolyploids. In stabilized allopolyploids both rDNA loci are transcribed from different subgenomes. This apparently leads to formation of chimeric ribosomes composed of rRNA molecules originating from different parents. We speculate that epigenetic silencing and rDNA rearrangements generate another layer of variation in multi-molecule ribosomal complexes which may contribute to the evolutionary success of allopolyploids.

S.58.6 Evolving together: Cassandra retrotransposons gradually mirror promoter mutations of the 5S rRNA genes

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The 5S rRNA genes are among the most conserved nucleotide sequences across all species. Similar to the 5S preservation we observe the occurrence of 5S-related non-autonomous retrotransposons, so-called Cassandras. Cassandras harbor highly conserved 5S rDNA-related sequences within their long terminal repeats (LTRs), advantageously providing them with the 5S internal promoter. However, the dynamics of Cassandra retrotransposon evolution in the context of 5S rRNA gene sequence information and structural arrangement are still unclear, especially: 1) do we observe repeated or gradual domestication of the highly conserved 5S promoter by Cassandras and 2) do changes in 5S organization such as in the linked 35S-5S rDNA arrangements impact Cassandra evolution? Here, we show evidence for gradual co-evolution of Cassandra sequences with their corresponding 5S rDNAs. To follow the impact of 5S rDNA variability on Cassandra TEs, we investigate the Asteraceae family where highly variable 5S rDNAs, including 5S promoter shifts and both linked and separated 35S-5S rDNA arrangements have been reported. Cassandras within the Asteraceae mirror 5S rDNA promoter mutations of their host genome, likely as an adaptation to the host's specific 5S transcription factors and hence compensating for evolutionary changes in the 5S rDNA sequence. Changes in the 5S rDNA sequence and in Cassandras seem uncorrelated with linked/separated rDNA arrangements. We place all these observations into the context of angiosperm 5S rDNA-Cassandra evolution, discuss Cassandra's origin hypotheses (single or multiple) and Cassandra's possible impact on rDNA and plant genome organization, giving new insights into the interplay of ribosomal genes and transposable elements.

S.58.7 5S and 45S rDNA monomer organization: lengths, variation, and interruption in tandem arrays from Musaceae species

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Long, single-molecule DNA sequencing shows the organization and structures of rDNA monomers in tandem repeats. Short reads of both 5S and 45S rDNA collapse the arrays during assembly, while older BAC sequences suffer from chaemerism and assembly artefacts. Far from being a continuous array of monomers, we find short deletions, insertions or interruptions in the arrays. Full-length retroelements are found at variable points within some 45S and 5S monomers in the arrays, and there are occasional insertions of uncharacterized sequences. Within monomers, both deletions and short duplications are found. Similar rearrangements have been found in multiple, non-identical, reads, giving evidence for homogenization through unequal crossing-over (and hence duplication of segments of the arrays). The 'starts' of the arrays have been characterized with flanking sequences. Musaceae provides a good model for the comparative study of the rDNA arrays, with long reads available from multiple species, variable chromosome numbers and evolutionary movement of rDNA between chromosomes, independent of other genes. The rDNA is very variable between species, many with one pair sites of 45S rDNA, representing 1% of all the DNA, to Musa beccarii with 3 sites and 5% of the DNA. Monomer lengths are also variable, with the typical length around 400bp found for most 5S monomers but 1056bp in Ensete. The detailed characterization of the arrays shows evolutionary mechanisms and diversity of the ribosomal DNA arrays. Further information and references are given at www.molcyt.com.

S.59 BIOGEOGRAPHIC HISTORY AND ECOLOGICAL PROCESSES OF THE ASIA-AUSTRALASIA FLORISTIC EXCHANGE

S.59.1 Documentation of flora in the Kimberley Gateway to facilitate studies of Sunda – Sahul exchange

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Biodiversity knowledge of north-western Australia's Kimberley region remains low. However, there is a growing body of evidence to suggest that the region has acted as an important gateway for the transfer of biodiversity between Sunda and Sahul due to its proximity to the Indonesian archipelago. We present data based on thirty years of field- and herbarium-based biodiversity discovery demonstrating changes in our understanding of plant diversity in the Kimberley, supporting its regional significance. Covering 100,000 km² in the Australian tropical savanna bioregion, the Kimberley is home to nearly 3,400 angiosperm taxa, of which 40% have only been recognised in the last 30 years. Endemism had been assumed to be low (<10%), but new species records have mostly been localised, and endemism is now >22%. Biogeographic connections are very varied, but include SW, Central, SE and tropical Australia, many parts of SE Asia west to India, and also Madagascar. We present example phylogenies that demonstrate the relevance of the Kimberley region for biogeographic analyses, demonstrating that some groups have followed multiple tracks into and from Australia. We summarise additional groups that would benefit from inclusion in future phylogenetic studies for the purpose of biogeographic reconstructions. Potential mechanisms of dispersal will be discussed.

S.59.2 Exploring the timing and mode of evolution of Asian and Australasian biogeographic exchanges in a framework of global biogeography

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The Asian – Australasian regions harbor rich biodiversity and represent an ideal natural laboratory to explore biogeographic exchanges and pathways, tropical – temperate biome transitions, and plant diversification in response to tectonic movements and climate changes. In this study, we analyze the biogeographic exchanges between Asia and Australasia in a global context in Araliaceae, Calycanthaceae, the Gymnostachydoideae-Orontioideae clade of Araceae, the Leeaceae/Vitaceae clade, *Prunus* of Rosaceae, *Toxicodendron* and its close relatives of Anacardiaceae, and the conifer family Taxaceae. Our analyses reveal extensive biogeographic exchange among major Gondwanan landmasses in the Cretaceous and early Paleogene. Antarctica, Africa, India, and South America played an important role in the biotic exchange of disjunct plants between Asia and Australasia in the early phase, with the existence of the Antarctic land bridge linking Australia, Antarctica and South America, and the Kerguelen Plateau land bridge connecting Antarctica and India. Hence the Asian and Australasian biotic exchanges in the Cretaceous and early Paleogene were mostly via indirect migration and dispersal. Subtropical East Asia and the adjacent tropical southeast Asia developed a rich forest flora that was highly influenced by the East Asian monsoon, the Indian monsoon, and the uplift of the Qinghai-Tibetan plateau. During the Neogene, biogeographic exchange between the Sunda and Sahul regions became highly active after the collision of the Australian continental crust with southeast Asia, with a more dominant Sunda-to-Sahul dispersal pattern. Continental Asia, including tropical Southeast Asia to subtropical East Asia, was a dominant source area for the later Miocene/Pliocene phase of the Asian – Australasian biotic exchanges. Our results also support dispersals from continental Asia to New Guinea, independent dispersals from continental Asia to Sunda and Sahul in a given lineage, and a recent biogeographic corridor linking Taiwan, the Philippines and New Guinea in the late Neogene via long distance dispersal.

S.59.3 Asymmetric migration dynamics of the tropical Asian and Australasian floras

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The tropical Asian and Australasian floras have a close relationship, and is a vital distribution pattern of seed plants worldwide. As estimated, more than 81 families and 225 genera of seed plants distributed between tropical Asia and Australasia. However, the evolutionary dynamics of two floras were still vague. Here, a total of 29 plant lineages, represented the main clades of seed plants and different habits, were selected to investigate the biotic interchange between tropical Asia and Australasia by integrated dated phylogenies, biogeography, and ancestral state reconstructions. Our statistics indicated that 68 migrations have occurred between tropical Asia and Australasia since the middle Eocene except terminal migrations, and the migration events from tropical Asia to Australasia is more than 2 times of the reverse. Only 12 migrations occurred before 15 Ma, whereas the remaining 56 migrations occurred after 15 Mya. The MDE (maximal number of potential dispersal events) analysis also show obviously asymmetry with southward migration as the main feature, and indicated the climax of two direction migrations occurred after 15 Mya. We speculated that the formation of island chains after the Australian–Sundaland collision and climate changes have been beneficial for seed plants migrations since the mid–Miocene. Furthermore, biotical dispersal and stable habitat may be crucial for floristic interchange among tropical Asia and Australasia. Thus, this study provides evidence for the past floristic exchanges between tropical Asia and Australasia.

S.59.4 Biogeographic history and ecological processes of the Asia-Australasia floristic exchange: history, progress and prospect

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The Asia-Australasia floristic exchanges have long attracted the attention from evolutionary biologists with its complex geologic background and remarkable associated biodiversity. The rich floras of Asia and Australasia converge at the unique Wallacea transition zone, which is noted for the well-known Wallace's Line and its outstanding tropical biodiversity. Since the early 19th century, critical insights have been proposed concerning the extent, timing, and routes of the Asia-Australasia floristic exchange, as well as characteristics of the exchanged elements and ecological filters of the exchange processes. We present the early exchanges dated to the supercontinent, the recent affinities during the Quaternary glacial fluctuation, and even the invasive biotic dynamics in the Anthropocene. By integrating distribution data and evolutionary information of plant lineages within the Asia-Australasia convergent region, southwestern Asia showed the highest plant richness, while southern Asia to eastern Australia showed the highest the phylogenetic diversity, indicating that the flora of southern Asia to eastern Australia has together preserved ancient and diverse evolutionary history with frequent interchanges within the region. To better reflect the relationships among floras inside the region, we revisited the regionalization inside the region under a robust phylogenetic framework of the global seed plants and delineated the three phytogeographic areas: the Asia continent and Sunda region, the Wallacea region, and the Sahul region. We found the dispersal exchange among these three areas dominated in a time period after the middle Miocene, consistent to the time when northern and southern shelves in Southeast Asia collided and the migration showed significant asymmetry with the southward dispersal exceeding the northward dispersal. We expect the understanding of the evolutionary history of Asia-Australia flora would shed light on the development history of global biodiversity distribution pattern and provide the theory foundation for biodiversity conservation in addition to new understanding in the biogeography.

S.59.5 Crossing Wallacea: floristic exchange between East Asia and Australasia

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One of the best cases for investigating the history of biotic exchange is the convergence of the Sunda (the southeastern extension of the continental plate of Asia) and Sahul (the tectonic plate of the Australian continent) shelves, where the remarkably diverse Wallacean region is located. Located on either side of the Sunda-Sahul zone, the floras of East Asia and Australasia harbor flourishing, distinctive, and comparable plant diversity and shared a considerable number of taxa, which provide an ideal example to test the effects of geological history and ecological conditions on exchange dynamics, to what extent plants could spread over Wallacea, and the contributions of exchange to floral formation. We investigated the floristic affinities between the Chinese and Australian floras, which represent much of the diversity of the floras of East Asia and Australasia, respectively. Based on a comprehensive genus level phylogeny of the global seed plants and the literature survey of biogeographic studies for the shared genera, we explored the evolutionary relationship between the two floras throughout geological times. Our results suggested that most exchange came up after the Miocene when the emerging islands of Southeast Asia reduced the geographical isolation between the two floras. We also integrated the distribution data to show the spatial pattern of the shared components and correlate the environmental factors which could have impact on migration success. Along with the identification of preference for long life-span and tropical traits, the significant role of habitat filtering during the exchange process between the two floras was indicated.

S.60 BARK STRUCTURE: EVOLUTIONARY, FUNCTIONAL AND ECOLOGICAL IMPLICATIONS

S.60.1 Bark architecture: relationships between appearance and microstructure of covering tissues

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The relations between macro- and microstructure of bark are poorly explored; the most important contribution has been made by T.C. Whitmore (1962). The bark appearance is largely determined: (1) by the ability of the outermost layers of bark to maintain its continuity in the course of dilatation, and (2) by the presence or absence of separation layers, i.e.,the layers of fragile tissues enabling a regular abscission of outer portions of bark. Diverse barks can be classified into four major architectural types (stretched, exfoliating, furrowed and peeling barks) by possible combinations of these conditions. Stretched (e.g., *Adansonia digitata*) and exfoliating barks (e.g. *Celtis africana*) share the ability to conspicuous expansion, usually with lenticels and eye-like markings. The stretched barks have smooth surface, whereas the exfoliating ones bear superficial scars of fallen scales. These barks share a thin periderm underlaid with parenchymatous layer. Supposedly, these architectural types are associated with photosynthetic ability and gas exchange between stem tissues and environments. The furrowed (e.g., *Quercus suber*) and peeling (e.g., *Buddleja saligna*) barks share prominent vertical fissures, without lenticels and eye-like markings. The furrowed barks lack separation layers; they are mostly covered by conspicuous persistent rhytidome or thick single periderm. Such bark architecture can be associated with fire protection as well as with decline of litter accumulation. The peeling barks are distinctive by detachment of relatively thin strips. Their periderms usually serve as separation layers whereas the collapsed phloem perform protective function; occasionally (e.g., *Vitis vinifera*), the functions of periderm and phloem are allocated in the opposite way. The peeling barks are hardly suitable for colonization by epiphytes. Several ontogenetic trends in age transformation of bark types were found. Estimation of bark architectural types along with the bark thickness is a promising approach in ecological research.

S.60.2 Bark anatomy diversity in Mediterranean trees and shrubs

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Scientists often correlate plant stem anatomical features and physical and biotic factors in the nearby environment. These relationships form a basis to hypothesise adaptive strategies as drivers of much of the anatomical diversity that has resulted through evolution. In plant stems, the role of bark encompasses conductive, mechanical, and other physiological functions performed by specifically evolved cell types and their arrangements, thus offering diverse bark anatomies. The extensive plant material collected and anatomically described from the island of Cyprus offered a unique opportunity to analyse the bark anatomy of trees, shrubs, dwarf shrubs, and climbers for ecological trends. This study presents bark anatomical trends I identified by analysing the entire woody flora of a geographically well-defined region. I present how bark features of sieve tube morphology and distribution, sclerenchyma presence and arrangement, rays, phellem, phelloderm, crystals, secretory structures, and appearance under polarised light vary in different lifeforms and environments.

S.60.3 Bark anatomy: what to expect from above- and below-ground in Cerrado species community?

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Covering roots and stems of woody plants, bark is a structurally complex system with functions ranging from conducting photosynthates, and other compounds, to protect the plant. Bark is composed mainly by the secondary phloem, arising from the cambium, and the periderm, arising from the phellogen. Although variation in bark structure across species has been widely examined, little is known about the patterns of bark variation across woody organs. Structural and functional variation would be expected between bark of roots and stems in fire-prone plant communities as a result of the contrasting selective regimes experienced by these above- and below-ground organs. We tested this hypothesis by comparing bark anatomical and functional traits between coarse roots and main stems of species from the Brazilian savanna (Cerrado), the most frequently burnt vegetation globally.

We sampled the barks from coarse roots and main stems of 15 species of trees and shrubs with high phylogenetic diversity and followed standard anatomical techniques. We observed that the secondary phloem is similar between roots and stems, except that rays in roots were taller than stems suggesting adjustments in radial conduction, and storage in roots, likely associated with resprouting after fire and drought tolerance. The periderm showed more protective traits in stems, mainly higher phellem development, indicating protection against fire. This was observed since the formation of the first periderm, and also when rhytidomes were present. These data indicate that, although the cambium is barely influenced by its position in different organs, the phellogen is influenced by the environmental differences to which the organ is exposed.

S.60.4 Shoot-length Scaling of phloem anatomical traits in angiosperm woody species

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Studying the anatomical structure of phloem contributes to our comprehension of how phloem transport plays a role in the ecological success of species. Additionally, integrating both xylem and phloem traits enhances our understanding of how plants strategically adapt their morphological and anatomical features to diverse climates. In recent years, the importance of the scaling relationship between stem length and the size of xylem and phloem conduits has been highlighted for conducting more precise ecological studies. For some species, it has been observed that the intra-specific variance in vessel and sieve element size is more influenced by stem length than by climate. Further, stem length dominates inter-specific variance of vessel traits compared to species habit climate. However, the extent to which climate contributes to the inter-specific variability of phloem anatomical traits is not well investigated. The aim of our study is to examine stem anatomical traits of woody angiosperm species in relation to sample distance from apex and their native climate factors across different biomes. We collected stem cross-section images of species from a wide range of climates. We measured the size and frequency of sieve elements and vessels of outer layer rings. The optimum climate for species was extracted from CHELSA V2.0 based on their occurrence records on GBIF. Our preliminary result shows that when data from all species are aggregated, the radius of sieve elements follows a power law with distance from the apex. After correcting for the scaling factor and phylogenetic correlation, both temperature from the wettest quarter and precipitation in the warmest quarter are related to the radius of the sieve tube element. Our study demonstrates the importance of considering scaling geometry when conducting ecological research on anatomical traits. It also suggests that different phloem traits enable various species to cope with distinct environmental conditions.

S.60.5 Modes of smooth bark formation

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Among the conifer and angiosperm trees, the appearance of bark can vary in a wide range from deeply fissured to smooth one. The bark surface can remain smooth if its outer layers are stretched and/or divided in response to continuous bark increases in circumference as tree grows. We studied different modes of smooth bark formations in several tropical, subtropical (e.g., *Adansonia, Commiphora, Euphorbia, Ekebergia, Heteromorpha, Trichilia, Steganotaenia, Sesamothamnus, Vachellia*, etc.) and temperate (*Betula, Populus, Salix*) taxa. Most of these studied taxa share relatively narrow outer bark (OB) and much wider inner bark. The OB usually consists of a thin periderm with lenticels on the surface and a parenchymatous cortex or pseudocortex whose cells contain chloroplasts. This is why we can see a green underlain layer after scraping of bark. This suite of traits is apparently associated with the stem photosynthesis. The anticlinal divisions and tangential stretching of periderm cells, formation of lenticels, and superficial initiation of arc-like periderms can contribute to the maintenance of continuous OB. The sloughing of smooth bark can be performed by peeling or weathering of outermost phellem layers, or by abscission of thin scales formed by superficial periderms. No prominent rhytidome containing the significant amount of non-conducting secondary phloem found in smooth barks. Their cortex or pseudocortex show meristematic activity, occasionally with formation of dilatation meristems. Shifts from smooth bark to furrowed or tessellated one occur in the older portions of stems in most studied species.

S.60.6 Patterns and causes of carbon allocation to bark across species and ecosystems

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Bark is a conspicuous part of woody stems, but a poorly understood one, especially in comparison with wood. Bark includes the tissues outside the vascular cambium and can be divided, from a functional point of view, into an inner mostly living region (inner bark, IB) and an outer dead region (outer bark, OB). There has been a recent surge of interest in bark functional ecology, but biologists are still far from understanding why some woody plants invest more or less carbon in IB and OB. Bark and wood thickness or cross-sectional areas are good proxies of relative carbon investment, because the density of both tissues covaries strongly. We review the main drivers of IB and OB thickness and area across species and ecosystems at the global level, integrating across-species and ontogenetic approaches. Across mature individuals, across species and environments, woody species allocate more carbon to IB in more seasonal environments in which higher storage of water, non-structural carbohydrates, and nutrients is of selective importance, whereas they allocate more carbon to OB as fire frequency increases. In turn, ontogenetic approaches (along stems or across conspecifics of differing sizes) underscore the role of storage but also of metabolic demands as crucial drivers of allocation in the secondary phloem, a tissue that includes the photosynthate-translocating tissue and a large fraction of axial and radial parenchyma. Regarding OB, ontogenetic approaches show that very frequent fire drives an isometric pattern of carbon allocation to OB along stems. Ontogenetic approaches have not only confirmed across-species patterns, but have also contributed to disentangling the functional roles of poorly-understood bark regions such as the phelloderm and the cortex. Further understanding of the remarkable diversity of bark demands a combination of ontogenetic and across-species approaches to the measurement of structural and functional traits.

S.61 NEOTROPICAL BOTANICAL INVENTORIES: DOCUMENTING WHAT IS LEFT? PERSPECTIVES FROM ACROSS TROPICAL AMERICAS. SESSION 1

S.61.1 Ferns of Colombia: Accelerating lineage discovery to document Neotropical fern diversity

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With more than 1450 known species, Colombia harbors fern diversity that is unparalleled elsewhere in the Americas. However, fern diversity in Colombia remains poorly known: nearly half of the species in the country have been collected only a handful of times, and most species have never been studied in an evolutionary context. The true richness of Colombia's fern flora is surely much higher than what is known today — likely there are hundreds of species that remain either unreported for the country or are still awaiting scientific description. The Ferns of Colombia project, funded by the National Science Foundation of the United States, aims to improve our understanding of Colombian fern diversity through collaborative research involving Colombian and international pteridologists. Our research focuses on four key objectives (1) Addressing major gaps in our knowledge of Colombia fern diversity, (2) Generating unified taxonomic resources for the ferns of Colombia, (3) Producing genomic resources for the ferns of Colombia, and (4) Integrating objectives 1-3 to accelerate lineage discovery and taxonomic research on Colombian ferns. Here we present the progress and some of the most exciting results of this project, which include new species discoveries, new species records for the country, identification of hybrids, and assessments of the extinction risk for selected species using the IUCN Red List Categories and Criteria. These results are the products of three field expeditions, visits to herbaria in the United States and Colombia, and the training of both undergraduate and graduate students. Outreach and networking efforts aimed at establishing a community dedicated to the study and conservation of Colombian ferns have played a crucial role in achieving our goals.

S.61.2 Flora Mesoamericana: a long process with a lasting legacy

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Flora Mesoamericana is an international collaborative project organized by the Missouri Botanical Garden, the Institute of Biology of the Universidad Nacional Autónoma de México and the Natural History Museum in London. Its main objective is to carry out a monographic inventory of the vascular plants existing in the Mesoamerican region, based on a critical analysis of the best available information. Our current estimate is 20,119 species of vascular plants occur in n the region, 41 of which are endemic (8,222 spp.). According to the definition established by the organizers, Mesoamerica extends south of the Isthmus of Tehuantepec to and including Panama, with a total area of 778,238 km^2. In this presentation, a brief account of the history of the project will be given. Likewise, some aspects of its organization, the working method and the results achieved will be described, as well as how the information contributes to larger projects like the World Flora Online. The first volume was published in 1994 and a total of eight volumes have been printed to date, treating 138 families, 1,724 genera, and 11,998 species, representing a 60% of the estimated number of species in the flora. The contents of all volumes, published in Spanish, are also available in a slightly different format on the Internet (http://www.tropicos.org/Project/FM). The progress to date has only been possible thanks to the generous participation of 246 botanists from numerous institutions around the world. Based on the current production rate, we estimate that the remaining five volumes will be released over the course of the next 10 years.

S.61.3 Documenting the multiple dimensions of the Amazonian plant diversity

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Documenting the multiple dimensions (classification, distribution, ecological interactions, and evolutionary history) of the remarkable Amazonian plant biodiversity has been one of the greatest challenges of botanical science, especially in the face of global threats of tropical forest destruction and climate change. While the Amazon is recognized as the home to the world's largest tropical rain forest biome and plays a crucial biogeochemical role in regulating the global climate through essential ecosystem services, little is known about the plant biodiversity itself, the leading player in the evolutionary theater of this majestic forest. For instance: how many different tree species are there throughout the Amazon? When and where did they evolve? What are the primary ecological and biogeographical processes driving their evolution? Addressing such questions requires a synergistic compromise between plant systematists and tropical ecologists. However, recent debates on the number of plant species across the Amazonian rain forests have relied heavily on model estimates, neglecting published taxonomically verified checklists. Ongoing taxonomic and floristic efforts across Latin America, such as the collaborative and dynamic web-based platform of the Flora e Funga do Brasil, are the best way to track progress and updates in near-real time. Detailed taxonomic monographic and phylogenetic works including newly collected specimens and genome-wide sequencing of specimens already held in global herbaria have revealed new species and genera, and how domestication has impacted their evolutionary history. Sustained investment in taxonomy, herbarium collections, virtual herbarium platforms, new collections through field work, and massive DNA sequencing are fundamental in order to document and answer large scientific questions on the origin, evolution, and ecology of the megadiverse Amazon flora in its entirety.

S.61.4 Plants of the ring: Botany of Mexican cenotes

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Sixty-five million years ago, a meteorite struck the Earth near the Yucatán peninsula in south-eastern Mexico, causing global-scale bioclimatic changes that lead to the extinction of all non-avian dinosaurs. Deep and large water-filled sinkholes called cenotes formed along the edge of the crater basin, making a ring around the center of the crater. Cenotes are striking elements of the natural landscape in the Yucatan peninsula and were sacred worship places for the Mayan culture. Urban development is threatening cenotes as they are being polluted or transformed during road and railway constructions. The flora associated with cenotes remain largely undocumented, and it is unknown how many native and endemic plant species thrive around these formations. We have undertaken floristic inventories in several cenotes in the peninsula including localities in the states of Campeche and Yucatan to collect plant data and materials to prepare herbarium specimens. This talk shows our preliminary results on the floristic composition and structure of the plant communities associated with the cenotes. We also highlight the importance of building compelling narratives around floristic research projects to secure funding as well as the involvement of relevant stakeholders including local communities and institutions.

S.61.5 Monitoring tree diversity across the Andes: the Madidi Project and the Red de Bosques Andinos

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Botanical inventories are crucial for understanding, managing, and protecting biodiversity. Tropical regions, despite centuries of study, remain poorly known, and their botanical diversity is undocumented. Collaboration to develop large-scale, long-term research programs is vital in this monumental task. In Bolivia, the Missouri Botanical Garden and the Herbario Nacional de Bolivia have established a program focused on documenting and conserving plant diversity. A cornerstone of this initiative is the Madidi Project on the eastern slopes of the Bolivian Andes. This project merges traditional botanical exploration with a vast network of forest plots, yielding information from nearly 60,000 collections, 200,000 surveyed trees, and 500 forest plots that document more than 3,000 species, including approximately 200 new to science. A significant effort has been made to standardize species names in this large dataset, a common challenge in such endeavors. The data informs various aspects of plant biodiversity, including diversity, ecology, and evolution. It also aids in assessing species' conservation statuses and provides essential biodiversity information to local policymakers. While impactful, the Madidi Project covers a fraction of the Tropical Andes, a global biodiversity hotspot. To address larger-scale biological and conservation challenges, researchers from multiple countries established the Red de Bosques Andinos (RBA). This network includes hundreds of forest plots spanning from Venezuela to Argentina and involves numerous forest biologists. Its formation, primarily by scientists from Andean nations, represents a formidable regional collaboration. The RBA generates vital research on forest ecology and responses to environmental threats. Both the Madidi Project and the RBA exemplify the importance of collaboration and capacity building in long-term forest monitoring and large-scale biodiversity inventories more generally.

S.61.6 How effective have botanists been at sampling Neotropical plant diversity

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For the most part, botanical inventories in the Neotropics have occurred in a haphazard, uncoordinated manner and lacked explicit sampling strategies. We assemble a cleaned version of GBIF biological collections data for the Neotropics to evaluate the gaps and biases in sampling effort to date with respect to predicted diversity, evolutionary distinctness, extinction threat, habitat type and ecosystem services. Whilst not complete, GBIF represents the single most important source of occurrence data for the Neotropics, comprising ca 8 million occurrence records (tracheophyte preserved specimens with coordinates). 'Preserved specimens' the data class corresponding to herbarium collections, comprises occurrence records backed by a physical specimen whose identity can be verified. We downloaded and parsed all occurrence records into unique collection events (Hendrigo Alves de Melo et al, 2023, matched these to a unified taxonomic backbone (World Checklist of Vascular Plant Names, Govaerts et al., 2021) and then projected them onto a map of the Neotropics divided into grid cells of 10 x 10 km. We then overlaid this map with the bserved tracheophyte species richness, IUCN habitat classes . Keith et al. (2020), estimates of predicted species richness, the evolutionary lineage coverage, frequency of threatened species and the estimates of carbon and water value (Jung et al. (2021). This enabled us to identify bias in the sample effort of previous botanical inventories in respect of all the above, and to identify the major gaps in occurrence data for the region.

References: Govaerts et al. (2021) https://doi.org/10.1038/s41597-021-00997-6, Hendrigo Alves de Melo et al. (2023) https://doi.org/10.21203/rs.3.rs-3579370/v1. Jung et al. (2021) https://doi.org/10.1038/s41559-021-01528-7. Keith et al. (2020) https://doi.org/10.2305/IUCN.CH.2020.13.en

S.62 EVOLUTION OF KEY INNOVATIONS IN LAND PLANTS REVEALED THROUGH THE LENS OF EVODEVO. SESSION 1

S.62.1 Transcriptomic landscape of the hornwort sporophyte

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The diploid spore producing sporophyte of land plants is thought to have been interpolated into a primarily haplontic ancestral life cycle as an adaptation to life on dry land. However, between the two monophyletic land plant clades, the bryophytes and vascular plants, sporophyte evolution has followed contrasting trajectories. Bryophyte sporophytes are nutritionally dependent on the gametophyte, uniaxial and monosporangiate, while vascular plant sporophytes have evolved complex branched body plans with a variety of lateral organs to become nutritionally independent. Little is known about how regulatory processes of sporophyte development have evolved and contributed to the diversification of sporophyte functions and morphology. Comparative analyses on sporophyte development and conclusions on developmental homologies have primarily been drawn using the model moss Physcomitrium patens and the liverwort Marchantia polymorpha, in comparison to the well-studied development of flowering plants. However, sporophytes of the three lineages of bryophytes exhibit considerably different growth patterns and insights into shared regulatory mechanisms of sporophyte development can only be achieved by simultaneously investigating all three bryophyte lineages. With the recent establishment of Anthoceros agrestis as a hornwort model, genomic and sporophyte transcriptomic data has become available. Therefore, to gain insight into shared and divergent regulatory mechanisms among liverworts, mosses, and hornworts, we compared sporophyte specific gene expression across the three bryophyte models by creating and analyzing sporophyte and gametophyte enriched transcriptome datasets for M. polymorpha, P. patens and A. agrestis. Furthermore, using laser capture microdissection, we generated tissue-specific transcriptomes for distinct tissues within the A. agrestis sporophyte proliferative zone and analyzed differential gene expression between these sporophyte tissues, to provide the first insight into the genetic control of hornwort sporophyte development. Using fluorescent reporter and overexpression lines we provide our first results concerning the ancestral function of key developmental genes in the sporophyte development of bryophytes and land plants.

S.62.2 The evolution and development of sporangia – the fundamental reproductive organ of land plant sporophytes

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A salient feature of the diploid sporophyte is the development of the sporangium, the fundamental reproductive structure of all land plants. Whether the structure is a cone, strobilus, or flower – all are clusters of sporangia. The sporangium is where meiosis occurs to produce spores, marking the transition between the diploid and haploid phases of the plant life cycle. In all land plants, sporangium development begins when a somatic cell is specified to be reproductive and then undergo a series of stereotypical divisions, and cell fate decisions that gives rise to the sporangium. The developmental anatomy of sporangia has been studied across land plants. From an evolutionary point of view, sporangia are key to land plant success. The evolution of distinct sporangia (heterospory) and retention of the gametophyte evolved three times independently and was a necessary innovation for the subsequent evolution of the seed. The well-known nucellus and pollen sac are the sporangia of flowering plants, and the molecular genetics of their development has been well studied, particularly in *Arabidopsis thaliana*. Despite its fundamental importance, we lack a comprehensive understanding of the evolutionary developmental genetics of sporangia development across land plants. To fill this gap, we are investigating the development and molecular genetics of sporangia in lycophytes and ferns with a focus on the fern model system, *Ceratopteris richardii*. We are studying the development of sporangia in lycophytes and ferns using histochemical staining and microscopy. We are investigating the molecular genetics of *C. richardii* sporangia development using transcriptomics and a candidate gene approach. Despite differences in sporangia cell patterning between *A. thaliana* and *C. richardii*, we found homologous genes pattern sporangia in both species. This suggests that there is a common genetic module that patterns all sporangia and provides a framework for understanding their evolution and development.

S.62.3 Origin and Expression of the silencing peptide RADIALIS in Gymnosperms suggests a role in seed and fruit development.

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An ongoing question in biology is how gene duplication and changes in gene expression may be associated with morphological shifts. One major innovation in plants is the development of ovules and seeds, traits that evolved in the ancestor of all seed plants. Within seed plants, flowers and fruits are synapomorphies arising within angiosperms, while gymnosperms retain the ancestral absence of these structures. Known floral patterning transcription factors RADIALIS and DIVARICATA are closely related MYB proteins whose competitive interaction is associated with the development of carpels/fruits and the establishment of bilateral symmetry in zygomorphic flowers. *RADIALIS* has been described as a silencing peptide that is a truncated paralog of *DIVARICATA*. Through a Bayesian phylogenetic approach, we demonstrate *DIVARICATA* genes underwent two rounds of duplications at the base of vascular plants forming three clades: *DIV-A*, *DIV-B*, and *DIV-C*. We show that *RADIALIS* genes evolved from *DIV-C* genes at the base of seed plants through a premature stop codon that was likely generated by a single-base substitution. This suggests that the RADIALIS-DIVARICATA competitive interaction likely evolved once, at the base of seed plants. We also surveyed the expression pattern of these genes for the first time in a gymnosperm, *Ginkgo biloba*. We find that *Ginkgo biloba RADIALIS* genes are expressed widely but often have higher expression in reproductive organs, especially in megasporangia. This is particularly interesting given that the megasporangium is the evolutionary precursor of carpels/fruits. A key innovation associated with megasporangia of seed plants is that they enclose ovules or seeds. Our work provides suggestive evidence that the evolution of seed habit and the later origin of fruits may be associated with the origin of the silencing peptide RADIALIS

S.62.4 Untangling the developmental genomics of the unique reproductive structures in Gnetales

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The seed is a synapomorphy of all extant seed plants that develops from an ovule, i.e., an integumented megasporangium. As sporangia are conserved throughout vascular plants, the origin of the integument is a defining step in seed evolution. There are some key differences in the number of integuments present in seed plants as well as accessory structures that cover seeds in gymnosperms and some angiosperms. Due to extra structures covering the nucellus, the ovules of Gnetales (*Ephedra*, *Gnetum*, *Welwitschia*) are strikingly different from those of all other extant gymnosperms. In the genera *Ephedra* and *Welwitschia* two envelopes cover the nucellus in contrast to *Gnetum* that has three envelopes. In all three genera of Gnetales, it is generally agreed that the inner envelope is homologous to an integument that elongates and forms the micropyle in other gymnosperms. The homology of the additional envelopes remains equivocal, but it is not debated that these form a unique seed coat in the Gnetales. With an emphasis on the ovulate reproductive structures, here we present the morphoanatomy of the striking differences in the ovulate reproductive structures of representatives of the three gnetalean genera. With a search in our own generated transcriptomic data, we present the differences and similarities with what is already known for angiosperms. Developmental studies on the ovule of *Gnetum gnemon* suggests that canonical genes involved in integument development are not involved in the development of the additional envelopes, suggesting that at least from a molecular perspective there are major differences when compared to angiosperms. A holistic approach involving different perspectives may be required for a better understanding of the complex relationships and evolutionary history of the Gnetales.

S.62.4 Reconstructing the origin of reproductive function for a flower development gene in ferns

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The transition from vegetative growth to flowering in the diploid sporophyte of angiosperms is partly controlled by *LEAFY* (*LFY*), a well-characterized flower meristem identity gene. Less is known about whether *LFY* plays a role in the haploid gametophyte phase and what that role might be. *LFY* orthologs also exist in non-flowering plants, and in mosses, they control the first mitotic division of the zygote. Recent evidence indicates that *LFY* has a vegetative role in fern meristems, but it is unclear where its reproductive function arose. Here, we continue to bridge the gap in investigations into this key floral regulator between mosses and angiosperms to reconstruct the evolution of *LFY*'s reproductive function across land plants. We ask whether *LFY* was co-opted into its specialized flowering function from its previously identified generalized role in regulating meristems by characterizing its two paralogs in the model fern *Ceratopteris richardii*. Transgenic ferns constitutively overexpressing *LFY* orthologs experienced delayed gametophyte fertilization, suggesting a novel role in gametophyte reproduction, and produced overgrown lateral meristems and decreased leaf compounding in sporophytes, providing additional support to the previously characterized vegetative meristem function. Overall, our results suggest that *LFY*'s reproductive role in angiosperm sporophytes may have been ancestrally co-opted from the gametophyte while also supporting previous evidence of their involvement in cell division in both phases of the fern life cycle.

S.62.5 Investigating the origins of phloem development

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Food-conducting cells are present in the major branches of the land plants phylogeny, and specialized phloem tissue is a predicted synapomorphy of the vascular plants. Little is known about the origins of phloem, and when looking at all groups, especially seed-free plants, we can find a great diversity of phloem structure considering the organization of sieve pores and associated parenchyma cells. However, the molecular toolkit necessary for phloem development is mostly described for flowering plants, particularly *Arabidopsis*. To better understand the evolution of genes related to phloem development in other groups, we conducted phylogenetic analyses of some genes related to phloem development. Our gene trees demonstrate that homologs of *OCTOPUS* (related to phloem cell polarization) and *NAC 45/86* (related to cytoplasm and nucleus dissolution) appeared in the ancestor of vascular plants. The main regulator of *Arabidopsis* phloem development, *ALTERED PHLOEM DEVELOPMENT*, a MYB Golden-2-like protein, upregulates several genes in the phloem development pathway (including NAC *45/86*). The ancestral copy of these proteins was present in the common ancestor of land plants. We are now exploring the expression of APL homologs in ferns and lycophytes, and we have identified seven and two APL homologs for the experimental models *Ceratopteris richardii* and *Selaginella moellendorffii*, respectively. Our preliminary data shows the expression of one of the APL homologs in the developing vascular system of *S. moellendorffii*. These findings provide insights into a possibly conserved regulatory network governing phloem development, shedding light on their evolution across diverse plant lineages.

S.63 PLANT DIVERSITY, BIOGEOGRAPHY AND EVOLUTION IN THE TROPICS FOR CONSERVATION, RESTORATION AND SUSTAINABLE USE. SESSION 1

S.63.1 The contribution of indigenous and local people to cataloguing life on Earth

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Indigenous and local peoples' (ILPs) [NV1] contributions to cataloguing life on Earth have been significant but remain under-appreciated. After over 200 years of insights from ILPs to science, the potential contribution of ILPs to current biodiversity research and conservation remains underutilised. The traditional knowledge of ILPs face growing cultural and biological threats. Fostering greater participation of ILPs in research would make science more efficient and conservation more sustainable while also slowing down the erosion of traditional knowledge and skills of ILPs, but formidable obstacles to such participation remain.

S.63.2 Conservation gap analysis of Mesoamerican oaks: establishing priorities for conservation

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Mesoamerica is a global center for oak biodiversity (genus *Quercus*), with an estimated 164 species in Mexico alone. Despite this incredible diversity, for many species, little is known regarding population size, trends, occurrence, or threats. There is an urgent need to coordinate and prioritize conservation action for both *in situ* and *ex situ* populations. We conducted a conservation gap analysis of 59 threatened and Data Deficient species of Mesoamerican oaks to estimate the geographic and ecological representation of species in *ex situ* collections. For species without population-level genetic data, this is a useful proxy to estimate the genetic representation of *ex situ* collections. Between 2017 and 2022 we distributed surveys to *ex situ* institutions with a request for their *Quercus* accessions data. There were 197 institutions that reported living collections of at least one Mesoamerican oak, a majority of which are in the United States (49%) and Europe (32%), with only 5% of the species having at least one collection in Mesoamerica. Twenty-two of our target species are not held in any *ex situ* collections, anywhere in the world. We found that only three of the 59 target species have *ex situ* collections that represent more than 50% of the species' geographic range, and only 19 species have an ecological coverage greater than 50%. Furthermore, approximately one fourth (16/59) of the target species have less than 10% of their native range within protected areas. These results highlight the urgent need for expanding survey and exploration work, increasing representation of oak species in botanic gardens and arboreta, particularly in Mexico and Central America, and identifying priority regions to focus *in situ* conservation efforts, as well as priority activities for the members of the Global Conservation Consortium for Oak (GCCO).

S.63.3 Characterizing and explaining diversification in Haitian Coffee agroforestry systems

Millet Claude Patrick[1,2,3,4], Allinne Clémentine[3,4,5,6], Vi Tram[1,8], Marraccini Pierre[1,7], Verleysen Lauren[9,10], Couderc Marie[1], Ruttink Tom[10,11], Zhang Dapeng[12], Solano-Sanchéz William[13], Tranchant-Dubreuil Christine[1], Jeune Wesly[2,14], Poncet Valérie[1]

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Diversification of cropping systems is a strategy to increase their social and ecological resilience and delivery of ecosystem services. Such practices are prevalent in traditional agroforestry systems, such as those where coffee (*Coffea arabica*) is grown. Indeed, though they face several challenges, Haitian coffee agroforestry systems are important contributors to rural biodiversity and household livelihoods. However, little scientific attention has been paid to these systems. We studied diverse farms in historically important coffee growing regions of northern and southern Haiti and characterized the diversity of several components of their agroforestry systems: coffee plants, shade trees, and associate crops. We tested the relationships between these different levels of diversity and identified key ecosystem services delivered by them, including provision of diversified farm products and carbon storage. In the case of Arabica coffee specifically (Millet et al. 2023), using targeted genotyping, we found significant genetic diversity and complex varietal mixtures. We show that some coffee farms are repositories of historical, widely-abandoned varieties while others are generators of new diversity through genetic mixing despite Arabica's tendency towards autogamy. In the latter, several varieties are often grown together, often in an uncontrolled manner, and are allowed to crossbreed with recruitment from the seed bank common, explaining the frequent admixture detected. Comparing these results with local, vernacular identifications, we found that the diversity in these systems is often under-estimated. These studies are, to our knowledge, the first to genetically characterize Haitian *C. arabica* and one of very few that have looked at Haitian agroforestry system crop and tree diversity.

References: Millet et al. 2023 Haitian Coffee agroforestry systems harbor considerable, dynamic and under-reported variety mixtures and genetic diversity. PlosOne, in revision.

S.63.4 Understanding patterns of biogeography and threat of tree species diversity across the Latin American biomes

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Tropical America has greater biodiversity than any other region of the world, but its biomes are under severe threat from climate and severe land use changes. Over recent years, plot inventory networks have successfully generated syntheses on biodiversity, ecology and ecosystem function. SynTreeSys, a new integrative initiative supported by CESAB (Centre for the Synthesis and Analysis of Biodiversity in France) is gathering knowledge of tree biodiversity across all biomes and gradients of rainfall and climate in Latin America, in order to dissect the patterns of tree diversity, abundance and threats. These inventory plot data offer much to assess species conservation status. Such conservation assessments can be made using herbarium specimen records, but these records have sampling biases and, critically, give no information about species population size and trends. The lack of such basic information prevents us from defining where conservation actions could be strategically implemented to best preserve tree diversity in the region, and to generate future scenarios based on known macroeconomic, climatic and land-use drivers. Here, we present examples from different biomes and regions that examine species' geographic ranges (IUCN criterion

B), and population sizes and potential declines (criteria A, B and D), following the International Union for Conservation of Nature (IUCN) framework. We show how inventory plot data can be used to estimate tree species population size as has been previously done for the Amazon and Mata Atlantica but across other biomes. Population decline can be estimated by crossing such species abundance maps with layes of vegetation cover change. We show how abundance and population estimates can inform more accurately the conservation status of tropical tree species of all the biomes of Latin America.

S.63.5 Insights into the history and evolution of African tropical trees through comparative phylogeography

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Although tropical Africa is home to the second largest tropical rainforest, the origin and evolution of its rich biodiversity remain poorly studied. However, the accumulation of phylogeographic and population genetic studies on tree species makes it possible to look for general patterns. 1. We found that about a quarter of African tree species studied, as delineated by current taxonomy, contain multiple species following the biological species concept, which might double the tree species richness in Tropical Africa and indicate a trend toward taxonomic overlumping. 2. Genome skimming makes it possible to sequence hundreds of plastomes at a reasonable cost, shedding light on the colonization dynamics of species or genera using time-calibrated phylodynamic models. Major distribution range shifts seemed to have occurred c. 200,000 years ago in several unrelated taxa. 3. The comparison of maternally inherited plastomes and nuclear markers provides information on the respective role of seed and pollen dispersal, and highlights situations of extensive plastid capture, suggesting that certain taxa (e.g. several genera of the Berlinia clade, Detarioidea, Fabaceae) could evolve as a syngameon. Finally, phylogeographic data on exploited tree species provide key information to conserve their natural populations or design breeding program for plantation of native species.

S.63.6 Spatial patterns and predictors of seed plants' extinction risks in Asian countries

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Asian countries are experiencing severe biodiversity loss, so it is crucial to develop practical conservation actions and strategies. Threats to species are often dynamic, as their impacts on extinction risk change over time. There is an urgent need to better understand how these factors are interrelated and how they vary spatially with extinction risk. Here, we presented a spatially explicit method to evaluate the dynamic trends and predictors of seed plants' extinction risks across countries, using National Red List data from China, Japan, and Sri Lanka as case studies, by calculating the Red List Index (RLI) and mapping the percentage of seed plants facing increasing risks and pressures. We found overall decrease in extinction risks, however, a substantial number of species, ranging from 328 to 1343 depending on the country, still showed increasing extinction risks. Increasing extinction risks of plants was strongly correlated with changes in threats, such as urban expansion, temperature changes, and tree canopy cover changes, rather than static threat intensity. Specifically, increasing tree canopy cover significantly associated with plant extinction risks in both China and Sri Lanka, where large-scale afforestation and economic forest plantation probably resulted in habitat degradation and species loss. Concerningly, our findings indicated that land-use change was the dominant driver of increased species extinction risk in these two countries, in contrast to climate change in Japan. As governments commit to the Kunming-Montreal Global Biodiversity Framework, we suggest them to make site-specific or taxa-specific policies to ensure the effectively prevention of biodiversity loss.

S.64 RECENT ADVANCES IN THE MEGADIVERSE LEGUME SUBFAMILY PAPILIONOIDEAE. SESSION 1

S.64.1 A new phylogeny of the megadiverse legume subfamily Papilionoideae

Rafaela J. Trad[1], Flávia F. Pezzini[1], R. Toby Pennington[1,2], Gwilym Lewis[3], Bente Klitgård[3], Russell Barrett[4], Anne Bruneau[5], Warren Cardinal-McTeague[6], Domingos Cardoso [7], James Clugston[8,9,10], Manuel de la Estrella[11], Ashley N. Egan[12], Colin Hughes[13], Erik Koenen[13], Todd McLay[14], Daniel Murphy[14], Matt Renner[4], Jens Ringelberg[15], Rowan Schley[2], Mohammad Vatanparast[3], Martin Wojciechowski[16], Darren Crayn[17], Olivier Maurin[3], Raquel Negrão[3], Catherine McGinnie[3], Paul Bailey[3], William J. Baker[3], Félix Forest[3], Gregory J. Kenicer[1]

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Papilionoid legumes occupy every terrestrial biome across a vast array of niches and lifeforms. This charismatic, successful and diverse subfamily (Papilionoideae) is larger than most angiosperm orders and comparable in size to Ericales and Myrtales. The c. 13,800 species constitute around 60% of diversity in the legume family and their value as crops for food, fodder, medicine, soil nitrification, rose wood timber, and an array of other purposes is huge. Due to its size and, until recently, to technical and cost limitations, studies have mostly focused on resolving relationships within specific clades using chloroplast DNA in the subfamily and an extensive nuclear-based phylogeny is still lacking. Additionally, several studies in the most diverse groups of plants have indicated that discordance between nuclear and chloroplast trees is frequent and that phylogenetic estimates for both are necessary to study the evolution of a group. Thus, having a comprehensive nuclear phylogeny for the subfamily is imperative. To this end, we sampled at least one species for over 95% of the 503 papilionoid genera accepted by the Legume Phylogeny Working Group. DNA extraction, library preparation, hybridization with the Angiosperms353 probe set, and sequencing were conducted as part of the Plant and Fungal Trees of Life project at the Royal Botanic Gardens, Kew. We present the first findings of this study, which will contribute to understanding intergeneric relationships and form a basis to enable researchers to investigate many questions across the subfamily on ecology, patterns of diversification, genome duplication. nodulation and character evolution that might help to explain its global success.

S.64.2 Advances in papilionoid systematics: insights from the Dalbergioid clade (from rosewoods to fodder plants and peanuts)

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Dalbergioid legumes form a mostly pantropical clade containing 46 genera and about 1,370 species, of which more than half belong in four big genera: *Adesmia*, *Aeschynomene*, *Dalbergia*, and *Machaerium*. The Dalbergioid legumes encompass three lineages composed of the Adesmia, Pterocarpus and Dalbergia clades. The Amorpheae clade, resolved as sister to the Dalbergioid clade, includes eight genera of shrubs usually with paripinnate leaves, and predominantly North American. The genera form two subclades, the Daleoids and the Amorphoids. The Amorpheae clade is characterised by loss of the papilionaceous flower several times in its evolutionary history, especially in the Amorphoid subclade. This loss also occurs within the Dalbergioid clade, specially within the Pterocarpus clade. Additional to the genus *Acosmium* (moved to the Pterocarpus clade), the newly described *Maraniona*, and the reestablishment of the genera *Steinbachiella* and *Ctenodon*, recent systematic studies on Dalbergioid legumes have elucidated infrageneric relationships in the genera *Aeschynomene* (now excluding *Ctenodon*), *Dalbergia*, *Pterocarpus*, *Adesmia*, *Nissolia* (now encompassing *Chaetocalyx*), *Zornia* and *Stylosanthes*. Studies on floral ontogeny in the Dalbergioid clade have highlighted interesting data. In species of the Adesmia clade genera, variations are observed in the papilionaceous flowers where suppressions, abortions, reduction and/or acquisition of floral parts occur. And other phylogenomic, anatomical and morphological studies are increasing our understanding of many new traits in the Dalbergioid clade. Belonging to Dalbergioid legumes are a wide range of economically important species and their crop wild relatives, the best known being *Arachis hypogea* L. (peanut), *Dalbergia* spp. (rosewoods), and *Stylosanthes* spp. (forage). However, additional genera include tree species with sought after timber. Ensuring that evolutionary relationships and taxonomy are well-understood, provide prerequisites for conservation actions for threatened tree species; and thus, gives plant systematists an even more important role to play.

S.64.3 Revisiting Ebenus L. (Leguminosae): a molecular perspective

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The genus *Ebenus* L. (Leguminosae, Papilionoideae, Tribe Hedysareae) consists of 21 perennial shrubs and subshrubs with high levels of country and regional endemism. It is known from the Arabian Peninsula only in Oman, through the Irano-Turanian region, with a centre of species diversity in Türkiye (14 species) and around the Eastern Mediterranean through North Africa as far as Morocco. As such, its distribution offers a prospective model for understanding aspects of East-West Mediterranean biogeography. The genus was revised by Huber-Morath in 1964 with a focus on groups from Anatolian Türkiye but the taxonomy and biogeography of the genus have never been investigated as a whole. This talk presents the results of the first genomic study of the genus, and indeed the first comprehensive phylogenetic study of the genus. We generated sequence data for between one and five specimens of each of the 21 recognised species, plus four outgroups from other genera in the tribe Hedysareae. These data were assessed using Bayesian and ML analyses to produce a comprehensive phylogeny for the group. The purpose of this presentation is to introduce and discuss the results of these phylogenetic analyses in taxonomic and biogeographical contexts. Particular attention is paid to the relationships between Irano-Turanian and Mediterranean floristic regions, ecoregions and habitat preferences. In addition, morphological patterns such as spinescence, corolla, colour, leaflet pairs, and peduncle are interpreted in the light of the phylogeny.

S.64.4 Towards a comprehensive phylogeny of the largest flowering plant genus: a herbarium-based study of Astragalus (Fabaceae)

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Astragalus (Fabaceae, Papilionoideae), with about 3,000 species, is considered the largest genus of flowering plants and represents a striking example of recent rapid radiation. Our understanding of the evolutionary drivers and adaptive traits responsible for this mega-radiation is fragmentary due to insufficient sampling and poorly resolved phylogenetic trees. It has been suggested that edaphic specialisation and colonisation of extreme microhabitats led to the divergence of lineages in *Astragalus*. To assess the evolutionary radiation and its drivers in *Astragalus*, we are using a target enrichment approach to obtain a robust phylogeny. We designed a large bait set based on 686 orthologous genes (819 exons) specific for the Astragalean clade, which can potentially resolve complex relationships in *Astragalus*. Our sampling is focused on main centres of diversity (Iran, Turkey, and Afghanistan) and relies on the rich *Astragalus* collection at the Botanical State Collection Munich (BSM-SNSB - about 25,000 *Astragalus* specimens from all around the world). We constructed a preliminary phylogeny including representatives of major sections based on 101 species (85 *Astragalus* plus 13 Astragalean clade species and three outgroups). A well-supported phylogeny at the subgenus level was recovered, mainly in agreement with previous phylogenies. Yet, several differences between previous phylogenies and the current sections were recognised, and clear signals of discordance along the backbone were found. We also established a fast and reliable workflow for digitising the *Astragalus* herbarium collection at SNSB. Using manual and automated machine learning techniques allows us to extract morphological traits from specimens and voucher data from labels. Mined data, such as geographic origin and habitat description, can complement genomic data and allow for various studies (e.g., niche modelling, evolution of morphological traits, and much more) to be performed on the extensive herbarium collection, gaining more insights into the drivers of diversification in *Astragalus*.

S.64.5 Progress in systematic studies in the Adesmia clade (Leguminosae: Papilionoideae: Dalbergieae)

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The Adesmia clade encompasses five genera: Adesmia, Amicia, Nissolia, Poiretia and Zornia, and it is sister to the Pterocarpus and Dalbergia clades (Dalbergieae). The clade arose ca. 35 Ma ago, and all genera are monophyletic, but the infrageneric divisions of the two largest genera (Adesmia and Zornia) are paraphyletic. Adesmia is the largest genus of the clade with over 200 species almost exclusively distributed along the western South American Dry Diagonal (wSADD), which stretches from Patagonia to the Peruvian Desert and contains some of the driest environments on Earth. While the ancestor of Adesmia is associated with the wSADD, the ancestor of the clade (i.e., Amicia, Poiretia, and Zornia, ca. 100 species) is associated with the eastern South American Dry Diagonal (eSADD). The eSADD comprises the Chaco, Cerrado, and Caatinga domains, and is marked by a seasonal precipitation regime. Sister to the other genera within the Adesmia clade, Nissolia has a distinct distribution within Seasonal Dry Tropical

Forests. Both vegetative and reproductive characters exclusive to this clade may have impacted the group diversification in the dry diagonals of South America. There are several potential functional traits linked to the occupation, diversification, and maintenance of Adesmia clade species in dry environments. These include a variety of secretory structures, growth forms and life history strategies, underground structures, spinescence, and fruit morphologies, e.g., the evolution of samaroid fruits in Nissolia, shared with other genera in Dalbergieae, suggesting that they may be ancestral to the typical lomentaceous fruit characteristic of the other four genera. Studies of pollen morphology and floral ontogeny bring an important contribution to understand the evolution of the clade and are discussed. Disk-shaped nectary was found in flowers of Adesmia and Nissolia, which have not been previously reported for the clade and may be a morphological character of taxonomic value.

S.64.4 A phylogenetic insight into Astragalus diversification and biogeography

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Astragalus (Fabaceae) represents a remarkable successful radiation of highly similar species in temperate, cold arid regions of Earth. The factors behind its extraordinary diversity have attracted attention from systematists and biogeographers, especially on what sets it apart from less species-rich relatives. Yet its status as the iconic plant megagenus has both highlighted and hindered study of this fascinating diversity. Here, using phylogenomics and an extensive sampling, we ask if *Astragalus* diversification is uniform or characterized by radiation bursts. We additionally test whether the species diversity of *Astragalus* is attributable specifically to its predilection for cold and arid habitats, types of soils, or if it is influenced by chromosome evolution. Finally, we test whether *Astragalus* originated in central Asia as proposed and whether niche evolutionary shifts were subsequently associated with the colonization of other continents. Our results show the importance of heterogeneity in the diversification of *Astragalus*, with upshifts associated with the earliest divergences but not strongly tied to any of the tested abiotic factor or biogeographic regionalization. Chromosome number was the only factor potentially correlated with diversification. In contrast to diversification shifts, biogeographic shifts have a strong association with the abiotic environment and highlight the importance of central Asia as a biogeographic gateway. Our investigation shows the importance of phylogenetic and evolutionary studies of logistically challenging “mega-radiations.” Our findings reject any simple key innovation behind high diversity and underline the often nuanced, multifactorial processes leading to species-rich clades.

S.65 PLANT CONSERVATION IN MEDITERRANEAN AND MACARONESIAN ISLANDS. SESSION 1

S.65.1 Wetland plants in Mediterranean Islands: a checklist of globally or regionally threatened species

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In the Mediterranean Basin, the conservation of plants faces critical challenges due to the historic and ongoing impacts of human land use, placing biodiversity under pressure. This issue is particularly pronounced on islands, where the intrinsic fragmentation of freshwater environments is exacerbated by the limited land area. Consequently, island wetlands, which are generally smaller than their continental counterparts, are more fragile and often overlooked in conservation efforts. Therefore, addressing the need for improved knowledge of wetland plants occurring on islands is a crucial objective that remains largely unresolved. Challenges persist, including cryptic taxonomy within certain genera, and there is still a need for a comprehensive overview of the diversity, distribution, and conservation status of these plants. These knowledge gaps contribute to policy and management shortcomings, hindering effective conservation or recovery efforts. This study seeks to bridge these knowledge gaps by compiling information from local experts on wetland vascular plants occurring on the approximately 10,000 Mediterranean islands and islets. Our work presents and discusses the preliminary results of a checklist of over 200 wetland vascular plants of conservation interest. Remarkably, 20% of these species are globally endangered, 50%

face threats on at least one island, and available information is inadequate to assess the conservation status of 30%. The insights provided in this study can support parallel initiatives, such as the Red List Index of Mediterranean wetland plants. Moreover, they can serve as a reference for planning targeted conservation actions and fostering public awareness about plant diversity in Mediterranean island wetlands.

S.65.2 Importance of small islands of the Mediterranean and Macaronesian regions as refugia of plant biodiversity

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This study aims to show the importance of small islands and islets (ie territories < 1000 ha) of the Mediterranean Basin hotspot, including those of the Mediterranean and Macaronesian biogeographic regions, from the point of view of their plant biodiversity and their role in the conservation of coastal ecosystems.

In the Mediterranean region, there are numerous islands (> 11,000) including a high diversity in term of plant species and of ecosystems' types. These patterns can be explained by complex interactions between a highly heterogeneous historical biogeography and ecological processes. Furthermore, most of the ups and downs of this biodiversity were closely linked with human pressures which have changed many times through the long socio-ecological history of these island landscapes since the Neolithic period. In the Macaronesian region, small islands and islets (named PIMAs, by Médail *et al.,*in prep.) are less numerous (n = 430). Islets with a surface area of less than 1 ha are predominant (88% of the whole PIMAs, i.e.,377 islets), and only 20 islands possess an area comprised between 11 and 1000 ha. These oceanic small islands are characterized by an exceptionally high richness of endemic taxa and constitute outstanding refugia for rare and threatened plant species. These PIMAs are nevertheless impacted by a diversity of human-related threats, notably the presence of invasive alien species, tourist pressure, or overgrazing. The level of knowledge of biodiversity is heterogeneous between the archipelagos and PIMAs are often neglected in conservation policies. If small islands and islets of the Mediterranean and Macaronesian regions have been neglected for a long period,current researches point out their disproportionate role to preserve coastal biodiversity (from genes to landscape). With regards to the biome crisis, they constitute key ecological systems and 'current refugia' to ensure the long-term preservation of this highly threatened biodiversity.

S.65.3 Exploring plant traits that indicate vulnerability among the endemic flora of the Balearic Islands

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The threat categories proposed by IUCN are mostly based on trends in population sizes and geographical range estimates. However, other factors could also be predictors of plant vulnerability, such as those related to the architectural complexity of flowers (e.g. floral shape and symmetry), or plant reproduction (e.g. flowering duration, life form, capability of asexual reproduction). Here, we analysed plant traits that could be potential predictors of vulnerability focusing on the endemic flora of the Balearic Islands, a hotspot of biodiversity and endemicity within the Mediterranean Basin. For this, we compiled the list of entomophilous plant species endemic to the Balearic Islands, categorized their vulnerability according to the regional Red Data Book, and gathered bibliographic data about both intrinsic and extrinsic factors that could affect plant vulnerability. We selected 10 intrinsic factors (floral shape, floral tube length, floral symmetry, corolla segmentation, floral size, floral colour, flowering season, flowering duration, life form and the capability of sexual reproduction) and one extrinsic factor (main habitat). The endemic entomophilous flora of the Balearic Islands comprises 156 taxa, 57 of which (37%) are threatened (EW, CR, EN and VU). We used Generalized Linear Models to test the potential effects of both intrinsic and extrinsic factors on plant vulnerability using a binomial response variable with two categories: "threatened" (EW, CR, EN, VU) and "not threatened" (NT, LC), and obtained optimal models based on the Akaike Information Criterion to select the best predictors for plant vulnerability. Our results showed that flowering duration and habitat were main predictors of vulnerability in the endemic flora of the Balearic Islands. Plants with short flowering duration, and freshwater, littoral and mountain plants were those more threatened. This study emphasizes the importance of studying other useful traits as indicators of species extinction risk in order to enhance plant conservation.

S.65.4 Can we predict the response of Canarian plant commnunities to increasingly dry conditions through leaf physiological traits?

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Precipitation reduction and increasing temperatures are impacting plant communities of the Macaronesian region. Hence, tools for evaluation and classification of plant species according to their vulnerability to increasing air and soil dryness are needed for plant conservation. Ecophysiological studies focused on a single or small group of species provide important information for this goal, but studies on adaptive ecophysiological trait syndromes could quantitative and qualitative improve our capacity to classify species according to their drought resistance. In this study, we measured physiological leaf traits related to drought resistance in more than 70 vascular species distributed across the four National Parks in the Canary Islands. The biomes represented in these NPs comprises a very strong climatic gradient within the generally Mediterranean-type climate, especially in terms of water availability, from the arid climate of Timanfaya to the cloud forests of Garajonay, and from the typical Mediterranean climate of the pine forest in Caldera de Taburiente to the alpine dry environment of Mount Teide and the summits of La Caldera de Taburiente. Leaf traits comprised both drought tolerance (leaf rehydration capacity after dehydration, leaf functionality after dehydration, water potential at full turgor) and avoidance traits (leaf hydraulic conductance, minimal leaf conductance, vein and stomatal density, leaf water absorption capacity and hydrophobicity). In addition, climatic data from the last 20 years recorded by the large weather station network located within the four NPs was compiled to calculate drought indices. Trait average values per species was related to climatic data with multivariate statistical tools aimed to establish groups of species and traits and establish relationships with climatic aridity. The results allowed identifying different trait combinations (syndromes) and their variation along the climatic aridity gradient. We classified the studied species based on those syndromes, thus defining strategies and overall predicted capacity to resist drought.

S.65.5 Plant conservation in the Aegean Archipelago - knowledge building and conservation initiatives

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The Aegean Archipelago is comprised of 123 inhabited islands (Crete, Euboea, Lesbos, Rhodes etc.) and more than 8,000 uninhabited ones. It is divided into 5 floristic regions, with the East Aegean and Crete-Karpathos (KK) ones hosting the richest total floras while KK, Kiklades and West Aegean are richest in endemics. In total, 740 endemic taxa grow in the Aegean of which 62% are regional and 42.4% are Single Island endemics. The first round of conservation status assessments (by HBS in collaboration with IUCN) will conclude by the end of 2023 and a rough estimate of 50% of the endemics seem to be categorised as threatened (CR, EN, VU), most of them facing high extinction risk, uplifting the in situ and ex situ conservation of these plants to an urgent national target. It is noteworthy that ten out of the TOP50 critically endangered Mediterranean plant taxa, and 44% of the plant taxa of Annexes II, IV & V of the Directive 92/43/EEC are found in the Aegean. The Aegean Archipelago also hosts 38% of the Greek NATURA2000 sites, governed by 7 Management Units of Protected Areas; currently, in situ conservation measures for protected or endangered plants are taken mainly within these protected areas. In addition, Plant Micro-Reserves have been established for 7 taxa and one habitat type in Crete while 5 new ones are about to be established in Rhodes, Karpathos and Kastellorizo. Ex situ conservation actions include numerous taxa stored in Seed Banks along with compiling germination protocols and developing plans for in situ population reinforcements. This work, apart from presenting the progress made during the last decades in knowledge building and conservation initiatives, aims to reveal and prioritise the gaps of plant conservation in the Aegean Archipelago.

S.65.6 Ecological forecasting for Aegean endemics: modeling the future of cliff-dwelling plant species

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The Aegean archipelago, the world's second largest, lies at the crossroads of Europe, Africa, and Asia. This unique ecological laboratory comprises approximately 8,000 islands and islets, hosting around 600 endemic species. Among these, certain chasmophytes are confined to calcareous, inaccessible cliffs, a consequence of historical paleogeographical events and ongoing biogeographical processes. These chasmophytes exhibit limited competitive and dispersal capacities, primarily due to the large size of their diaspores and highly specialized niches. Having endured harsh environmental conditions for millennia, these species now confront an unprecedented threat level due to the synergistic impacts of climate change and land-use modifications. This study investigates the potential effects of future climate and land-use changes on the distribution patterns of these endemic cliff-dwelling species. Utilizing a species distribution modeling framework, we assess these impacts across three time periods and propose conservation strategies to mitigate their potential decline.

S.66 NEW FRONTIERS IN PLANT PHYLOGENOMICS. SESSION 4

S.66.1 Genomic incongruence accompanies the evolution of flower symmetry in Eudicots: a case study in the poppy family (Papaveraceae)

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Reconstructing evolutionary trajectories and transitions that have shaped floral diversity relies heavily on the phylogenetic framework on which traits are modelled. In this study, we focus on the angiosperm order Ranunculales, sister to all other eudicots, to unravel higher-level relationships, especially those tied to evolutionary transitions in flower symmetry within the family Papaveraceae. This family presents an astonishing array of floral diversity, with actinomorphic, disymmetric (two perpendicular axes of symmetry), and zygomorphic flowers. We generated nuclear and plastid datasets using the Angiosperms353 universal probe set for target capture sequencing (of 353 single-copy nuclear ortholog genes), together with publicly available transcriptome and plastome data mined from open access online repositories. We relied on the fossil record of the order Ranunculales to date our phylogenies and to establish a timeline of events. Our phylogenomic workflow shows that nuclear-plastid incongruence accompanies topological uncertainties in Ranunculales. A cocktail of incomplete lineage sorting, post-hybridization introgression, and extinction following rapid speciation most likely explain the observed knots in the topology. These knots coincide with major floral symmetry transitions and thus obscure the order of evolutionary events.

S.66.2 Complete chloroplast genome sequence and phylogenetic relationships of some Acanthoideae species (Acanthaceae)

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The plastid genomes of *Acanthoidea were* sequenced and compared with plastome of other sequenced Acanthoideae species to characterize the plastomes, identify the simple sequence repeats (SSRs), detect variations among the cp genomes and to infer their phylogenetic relationships. The plastome was assembled from the whole genome sequences using NOVOPlasty.The cp genomes of the species ranged from 149, 717 bp to 152,217 bp in length with GC and AT contents of 38.3 and 61.7 % respectively and have a quadripartite and circular structure, the genome constitutes of a pair of inverted repeats (IRa and IRb) which are separated by large single copy (LSC) and small single copy (SSC). A total of 131 genes were identified in the genomes, comprising of 80 protein-coding genes, 30 tRNA and 4 rRNA; 113 are unique, 18 were duplicated in IR regions. The analysis of long repeat showed all types of repeats were present in the plastomes and palindromic has the highest frequency. A total number of 98 SSR were also identified in the cp genome of *B. prionitis* and *J. flava* of which majority were mononucleotide A/T. Genome comparative analysis among the plastomes revealed that the IRs regions are more conserved than large single copy and small single copy. In addition, high variation is observed in the noncoding region than the coding. The genes, *ndhF* and *ycf1* are located at the border junction of the small single copy region and IRb region of all the plastome. The sequence divergence analysis indicates that the following genes undergo positive selection (*atpF, petD, psbZ, rpl20, petB, rpl16, rps16, rpoC, rps7, rpl32* and *ycf3*). Phylogenetic analysis indicated sister relationship between Ruellieae and Justcieae. In addition, *Barleria*, *Justicia* and *Ruellia* are paraphyletic, suggesting that Justiceae, Ruellieae, Andrographideae and Barlerieae should be treated as tribes.

S.66.3 Whole genome sequencing deciphering nonbifurcating diversification of Camellia (Theaceae)

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Although increasing evidence suggested that introgression and reticulation might have affected almost all parts of the tree of life, published examples likely represent the tip of the iceberg in terms of the total extent of the ancient hybridization. *Camellia*, the largest genus with significant economic value of Theaceae, has controversial taxonomy and systematics due in part to a complex evolutionary history. Here, we sampled 64 species representing 20 out of 22 sections of *Camellia* according to Chang's system. Integrating a group of data sets such as single copy nuclear genes, single-nucleotide polymorphism (SNP) and plastid coding genes extracted from whole genome resequencing data to investigate the patterns of reticulate evolution of *Camellia*. *Camellia* was divided into eight major clades (C1-C8). Our results yielded much phylogenetic incongruence among topologies reconstructed by three datasets (single copy nuclear genes, SNP, plastid genes) based on different methods (concatenation and coalescent), especially the cyto-nuclear discordance was observed. But all of them support non-monophyletic of sections proposed based on morphological characters. The splits phylogenetic network reconstructed by 508 single copy nuclear genes and ABBA-BABA test conducted by SNP data all support the introgression events in *Camellia*. Four groups based on the minimum CV error value were recovered in Admixture analysis, hybridization events are concentrated on Group II (C2-C6) and Group IV (C8). Although hybridization/introgression have some impacts on the reconstruction of the phylogenetic relationships of *Camellia*, no consistent topologies were detected after removing the putative introgressed loci in SNP. Our study laid a foundation for future researches of *Camellia*, such as plant taxonomy, evolutionary genomics, population genomics, and also provided a theoretical basis for the utilization and protection of important wild plant germplasm resources of the family.

S.66.4 Diversification history of Pedicularis (Orobanchaceae) in the Himalaya-Hengduan Mountains Region

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The *c.* 270 species of *Pedicularis* endemic to the Himalaya-Hengduan Mountains (HHM) region exhibits considerable diversity in geographic distribution, elevational range, and floral morphology. Many of the species, including those with the longest corolla tubes and beaked galeas, fall within a single clade, implying putative *in situ* radiations. We conduct phylogenetic analyses of a clade (informally named

"Clade 3" in our previous work) concentrated in the HHM to infer drivers of diversification and the biogeographic history. Integrating plastome phylogeny, environment data and species distribution data, we revealed the species diversity pattern and identified the key environmental factors of *Pedicualris* Clade 3. Subsequently, we estimated the macroevolutionary rate and reconstructed ancestral distribution and corolla traits. Meanwhile, we evaluated the correlation between distribution overlap and phylogenetic distance. Our results suggest that Northwestern Yunnan–Kangding within the HHM region is the center of species diversity of *Pedicularis* Clade 3 and this pattern is constrained by precipitation and multiple environmental factors; Parallel range expansion from the Sanjiang valley and subsequent allopatric speciation across the HHM are the dominant process in early rapid diversification and may be a major contributor to the high species accumulation of *Pedicularis* spp. Additionally, the evolution of corolla is not associated with the speciation, but as a response of species richness. Our study highlights the importance of integrated evidence for understanding species diversification pattern, and this pattern may be applicable to explain the diversity of other hyper-diverse alpine genera in the HHM region.

S.66.5 Advancing our understanding of oak evolution in the genomic era

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Advances in sequencing and analytical technologies have dramatically changed the field of plant phylogenetics and the ever-increasing availability of high-quality reference genomes now offers a particular opportunity to further reveal the evolutionary history of plant clades. We utilized a new haplotype-resolved reference genome for *Quercus alba* and whole genome resequencing to investigate the history of speciation and introgression in oaks, with a particular focus on North American white oaks. We show that phylogenetic results using a whole genome dataset disagree with previously published relationships among oak species and find widespread phylogenetic conflict across the genome. We further show that a high proportion of polymorphisms are shared across multiple species, which has important implications for time-calibrating the phylogeny of oaks and other species that maintain large population sizes. We investigated introgression among oaks species and identify specific genomic regions showing notable signals of introgression, suggesting that introgression could potentially facilitate adaptive evolution among North American white oak species. As the sequencing and assembly of reference quality genomes becomes ever more routine, whole genome phylogenomic analyses such as these will likely become increasingly relevant and useful to the botanical community.

S.66.6 Cryptic speciation among polyploid mosses demonstrated through phylogenomic analysis

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Whole genome duplication (WGD) is a mechanism critical to evolutionary change and speciation across the plant tree of life. Both conspecific genome doubling (autopolyploidy) and WGD following hybridization (allopolyploidy) may result in morphologically distinct lineages and hence may contribute significantly to species diversity. However, accurate phylogenetic reconstruction of allopolyploids and their component genomes remains a major challenge. The moss *Physcomitrium pyriforme* is a widespread species complex found across North America and Europe that exhibits substantial morphological variation, evident in the recognition of 29 synonyms. We hypothesize that this species complex comprises not only numerous cytotypes and potential species from repeated WGD events, but also population structure among haploid populations that will inform the evolutionary history of allopolyploids and autopolyploids. We sampled over 400 populations of *P. pyriforme* across its North American and use a target capture approach to sequence 648 genes to construct a phylogenetic tree establishing relationships among *P. pyriforme* populations. 60 allopolyploid populations are identified using HybPhaser suggesting that WGD plays a substantial role in the evolution of the *P. pyriforme* complex. Further, structure analysis of haploid populations of *P. pyriforme* offers insights into gene flow and introgression further elucidating the nature of reticulation among haploid, autopolyploid, and allopolyploid populations. These analyses both provide evidence for morphologically cryptic speciation via polyploidy and also provides evidence for the utility of target capture sequencing with an 806 gene bait set for population genomic studies and population demographic inferences.

S.67 TOWARDS A MORE ETHICAL SCIENCE: DECOLONIZING BOTANICAL RESEARCH. SESSION 2

S.67.1 Decolonising biodiversity collections: equity, collaboration, and benefits

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In response to historical inequalities, museums are engaging in the decolonization of biodiversity collections. This entails acknowledging collection histories, enhancing accessibility, and promoting collaborative research. Despite this effort, decolonization remains contentious due to unequal access, biopiracy concerns, and "parachute science" where Global North researchers extract specimens from the Global South without considering local concerns. Internationally the Nagoya Protocol aims to ensure fair benefit sharing, yet scepticism persists. We used a data-driven approach to understand the interplay between research, biological collection, and international collaboration. Focusing on Montserrat and the Cayman Islands, the study analyses collector profiles, their publications, and using data mediated by the Global Biodiversity Information Facility and Wikidata. By using a data driven approach we try to quantify some of the less tangible benefits of biological collection and provide objective information on this issue. Our results reveal specimens from these islands are held predominantly in the USA, Canada, and the UK. Most of the research conducted is related to taxonomy. However, digitization gaps may skew findings. The study emphasises the need for equitable sharing of both monetary and non-monetary benefits. While researchers gain knowledge and prestige, territories should benefit from research outcomes. Open-access publishing, data sharing, and duplicate contributions to local collections are suggested to enhance collaboration. This aims to improve relationships, rectify historical disparities, and inform equitable practices. In conclusion, biodiversity collection decolonization involves recognizing historical imbalances and promoting inclusive collaboration. The study advocates for responsible research practices, acknowledging local expertise, and fostering equitable partnerships. By delving into collection complexities, the study envisions a more equitable future for biodiversity research and conservation.

S.67.2 Pathways to decolonizing botanical research by digitizing biocultural diversity collections at the New York Botanical Garden

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Much can be learned from colonial collections by decolonizing botanical research. Interdisciplinary teams of scholars have recommended a biocultural framework for the continued curation of these collections. Recognizing and protecting biocultural diversity helps to create pathways towards a more ethical botany. Through this objective, botanical collections of colonial projects can find additional purpose. Biocultural diversity accounts for the indissoluble link among language, culture, and humanity's interaction with the biosphere. An NSF funded project on biocultural diversity collections is currently securing, digitizing, and increasing access to voucher specimens that are the product of economic botany, medical botany, ethnobotany, and other botanical studies at the New York Botanical Garden. Digitization of collections through ethical frameworks presents many challenges but offers several potential rewards. Through the curation of these specimens to the currently accepted taxonomy and the inclusion of local and indigenous names, the project seeks to increase access to collections by underserved communities and the general public through its free online collection data portal. Digitization and proper meta-data association aids in the archival return of collections to communities of origin, as well as to diasporic communities of stakeholders interested in botanical disciplines or rediscovering cultural traditions.

S.67.3 Small and in-country herbaria are vital for accurate plant threat assessments: A case study from Peru

Moonlight, Peter[1], Jay Delves[1,2], Joaquina Albán-Castillo[3], Asunción Cano[4], Carmen Fernández Aviles[4], Edeline Gagnon [1,5] Sandra Knapp[6], Blanca [3,7], Jose Luis Marcelo [8], Carlos Reynel [9] , Rocio del Pilar Rojas [10], Eric F. Rodriguez[11], Tiina [1], Rodolfo Martinez[10], Peter W. Moonlight [1,12].

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Herbaria can be considered plant libraries, each holding collections of dried specimens documenting plant diversity in space and time. For many plant species, these are our only evidence of their existence and the only means of assessing their conservation status. Specimens in all herbaria, especially those in small and often under-resourced herbaria in megadiverse countries, are key to achieving accurate estimates of the conservation status of the world plant species. They are also part of a country shared heritage and critical contributions to knowledge of the world diversity. Internationally agreed targets to assess the conservation status of all plant species rely largely on digitised distribution data from specimens held in herbaria. Using taxonomically curated databases of herbarium specimen data for the mega-diverse genera Begonia (Begoniaceae) Solanum (Solanaceae) occurring in Peru, we test the value added from including data from local herbaria and herbaria of different sizes on estimations of threat status using International Union for Conservation of Nature (IUCN) Red List criterio. We find that the Global Biodiversity Information Facility (GBIF) has little data from Peruvian herbaria and adding these data influences the estimated threat status of these species, reducing the numbers of Critically Endangered and Vulnerable species in both genera. Similarly, adding data from small- and medium-sized herbaria, whether in-country or not, also improves the accuracy of threat assessments. [Correction added on 08 September 2023, after first online publication: In the preceding sentence,has been corrected to “little” in this versionA renewed focus on resourcing and recognising the contribution of small and in-country herbaria is required if we are to meet internationally agreed targets for plant conservation. We discuss our case study in the broader context of democratising and increasing participation in global botanical science.

S.68 EVOLUTIONARY ECOLOGY OF PLANTS. SESSION 4

S.68.1 Plant adaptations to city life: lessons learnt from dandelions

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Urbanisation is a globally increasing and highly impactful form of land-use change. Increased temperatures (the urban heat island effect), habitat fragmentation, light pollution, and other human-induced pressures demand rapid biological adaptation from wild species. To discover the necessary adaptations for surviving urbanisation, we looked at a thriving urban plant species: the common dandelion (Taraxacum officinale F.H.Wigg. s.l.). Along urban-rural transects, we found urban plants to be superior in seedling growth at higher temperatures and flowering response at shorter vernalisation exposure. We also found advancements in flowering time for suburban genotypes, both in the field and in controlled environments. These trends were reflected in sequence divergence patterns for genes involved in the regulation of flowering time and heat resistance, where urban plants displayed highly conserved genotypes. Effects were significantly different between urban habitats, where city park plants presented phenotypes intermediate of urban street and rural field populations. Genetic diversity among individuals was lowest for street plants and highest for rural field plants, likely caused by environmental filtering of genotypes in urban environments. In present-day urban environments, the predicted effects of climate change are already normalised, making cities ideal experimental gardens for studying the necessary biological adaptations. Our approach to study relevant traits in urban plant species from both a phenotypic and genomic point of view is therefore a relevant framework to study the effects of climate change on plant evolution.

S.68.2 Running to the hills: changes in plant-pollinator networks structure over time and space, in a mountain region

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Pollinator networks play a crucial role in maintaining biodiversity and ecosystem functioning, especially in mountainous regions. Across an elevation gradient and flowering seasons, 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. In this work, we analyzed the architecture of plant-pollinator networks by recording plant-insect interactions at 10 study sites between 1000 and 1800 m a.s.l., following the two major seasons (from spring to summer flowering seasons) in a Mediterranean mountainous region. Our research aimed to address the following questions: (1) The structure of networks is stable over time-space? (2) How does the topology of networks change over time? (3) Which environmental drivers shape network structure across time and space? We analyzed spatial (elevational) and temporal (weeks) network patterns using generalized linear models (GLMs) and quantified the influence of climate, richness of flowering plant species, and pollinator diversity on network structures using a multimodel inference framework. We recorded 3,343 interactions, 343 pollinators, and 44 plant species of which a majority involved interactions with bees and flies. We found that nestedness and robustness are constant both in space and time. However, we found that the specialization of plant-pollinator networks increased from spring to summer with the rise of the temperature. Further, network modularity decreases across seasons and plant-pollinator interactions were more specialized at higher elevations. We found that flower and pollinator species diversity and abundance, rather than direct effects of climate, better predict modularity and specialization networks. This study highlights changes in network architectures over time and space (elevation) supporting a potential sensitivity of plant-bee interactions to climate change and desertification, putting Mediterranean mountain biodiversity at risk.

S.68.3 A tale of species from two clades: evolutionary processes within Corymbia

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Historical processes driving evolution have left a signature in genetic differentiation and gene flow across the landscape of present-day plant populations. Examining these patterns can enable us to better understand lineage divergence. *Corymbia* is a genus within the eucalypts comprising c. 100 species, most of which are endemic to Australia. Recent phylogenetic analyses suggest that *Corymbia* is paraphyletic (with another eucalypt genus *Angophora* nested within *Corymbia*). In the current study, we sampled leaf material from multiple populations of five co-occurring species from across the two paraphyletic clades of *Corymbia* for genome-wide sequencing. We found two species from one clade (*C. maculata* and a more restricted species, *C. eximia*) to be highly genetically differentiated compared to the other species. In contrast, there was evidence of high levels of introgression among two widespread and morphologically similar species from the other clade, *C. gummifera* and *C. intermedia.* To explore the impacts of climatic factors on species evolution, environmental niche models were generated using Maxent to determine the habitat suitability of each species under the Last Glacial Maximum. Overall, our findings offer unique insights into the processes underlying speciation and influencing species boundaries within complex lineages across diverse landscapes.

S.68.4 Species-soil relationships and their evolution in Amazonian ferns

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Knowledge about plant species niches along environmental gradients is a fundamental prerequisite for addressing many ecological and evolutionary questions. For example, to what degree are plant species distributions and community compositions dictated by species niches in relation to soil properties? And to what degree does evolutionary diversification itself reflect adaptive radiation, where lineages specialize to different edaphic niches? These are especially intriguing questions in the tropical rain forests, where the origin of the high species richness has been a long-standing puzzle, but lack of data has frustrated attempts to find answers. Thanks to long-term extensive field studies across Amazonia, we are now able to model species-soil relationships for many fern species and to place them into an evolutionary context with the help of molecular phylogenies. This makes it possible to analyze niche divergence both as an ecological phenomenon and as the result of an evolutionary process. We are carrying out such analyses using two fern genera, *Adiantum* and *Lindsaea*, as example cases. Both genera are common in the understory of

Amazonian forests, and both have been suggested to be useful as indicators of forest types and soil properties, even though detailed models of their edaphic niches have not previously been available. Our results show that the species' edaphic niches are both relatively narrow and divergent, and that there are clear differences between the two genera. Currently ongoing analyses of niche evolution are expected to shed light on the evolutionary processes within Amazonia.

S.68.5 Exploring ecological strategies in the five bean domesticated species (Phaseolus spp.)

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Despite increasingly robust understanding of the drivers underlying ecological strategies in wild plants, the consequences of plant domestication on the expression of these strategies in crops remains poorly understood. For example, there is debate regarding whether the same patterns of trait covariation observed in wild plants are also found in crops, such as between the leaf (LES) and root economic spectra (RES). To explore patterns of trait covariation in crops, a system with high ecological variation, more than one event of domestication, and a long domestication history is ideal. Beans (*Phaseolus* spp.) represent such a system. The genus includes five domesticated species that represent independent instances of domestication, and hundreds of landraces that grow in a wide range of environmental and management conditions. Although domestication is predicted to produce strong shifts toward acquisitive strategies under the more stable and fertile conditions of agroecosystems, it is less clear whether it would favor uncoupling of the LES and RES. In this study, we cultivated 20 bean landraces (four per domesticated species) in a common garden at a Mexican temperate highland and measured nine functional traits in leaves, stems, and roots before the reproductive phase. Our results indicated that despite strong artificial selection, LES and RES are conserved in beans. However, we found evidence of decoupling between LES and RES, which has also been reported for other crops. There was also wide variation in mean values across landraces along a conservative-acquisitive continuum related to the ecological preferences of the species. This work represents the first effort to understand the consequences of domestication on beans from a functional trait perspective. Understanding patterns and causes of trait correlations in crops is not only important for breeding efforts, but also for predicting plant responses in the context of climate change.

S.68.6 Whitin individual phenotypic and epigenotypic effects of postfire resprouting on a Mediterranean shrub

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Although the ecological and evolutionary effects of wildfires on plants have been widely studied, thus far no attention has been given to the possible effects of wildfires on within-individual plant variability. This kind of variability affects both plant phenotype and epigenotype, and its deeply connected to plant animal interactions and maternal effects. In resprouting species, we hypothesize that wildfires can alter within-plant variability at both levels, since this process might lead to architectural changes and temporal homogenization of plant development. We also hypothesize that the relationship between epigenotype and phenotype might change. To test these ideas, we studied a population of the Mediterranean shrub *Anthyllis cytisoides* (Fabaceae) that was partially affected by a recent wildfire in Valencia. We selected plants that were resprouting after the wildfire as well as plants that were not affected by it to study leaf, flower, fruit and fecundity traits as well as epigenetic traits (i.e.,global cytosine methylation) at a within-individual level. By fitting mixed models to the data, we could see that most traits changed in within individual variance with postfire resprouting, although the sign of change was not always the same: weight related traits tended to be more homogenous within burned plants, while petal size and global cytosine methylation were more variable. In addition, the relationship between methylation level and petal size was not the same in burned and unburned plants. These results highlight the potential role of wildfires in shaping within individual variability of resprouting plants both at the phenotypic and epigenotypic levels and, thus in plant animal interactions and in maternal effects.

S.69 COLLECTIONS, HERBARIOMICS

S.69.1 Museomics and targeted sequencing in Orthosiinae (Apocynaceae) yields undescribed diversity

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Herbaria house an immense collection of plant diversity, primarily in the form of dry-preserved specimens. We present a work protocol in Apocynaceae aiming at advancing Museomic studies in plants using the Andean-centred Orthosiinae in the Neotropical Apocynaceae as model. Exclusively using herbarium specimens (n = 205), some of which are almost 200 years old, we optimised DNA extraction protocols and applied rigorous data processing on target capture sequencing (Hyb-Seq) data using Apocynaceae-specific set with 835 probes. A well-supported species phylogeny is presented comprising approximately 78% of the known species and >50 specimens not yet formally described. Phylogenetic results confirm the generic relationships and the common origin of the species in Orthosiinae. Here, we particularly focus on the relationships inside *Scyphostelma,* a mainly Andean genus with many undescribed species. We measured morphological traits and tested for significant differences among inferred clades, mainly in floral characteristics. We confirm the position of recently described *S. rotorum* and S. *solomonii*, originally suggested for morphological reasons to belong to the *S. harlingii* clade. Our study provides further evidence on the evolutionary relationships of Orthosiinae species. Obtained species trees serve as framework to study the biogeographical history of the group and to quantify how much of the species diversity can be explained by parapatric elevational replacement, which would hint towards ecological speciation (adaptive), and how much by parapatric speciation in isolation (neutral). Our investigation illuminates patterns of evolution of montane biodiversity in the Andes using Orthosiinae as a model group.

S.69.6 Herbarium leaf spectroscopy and estimating functional traits from degraded specimens

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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 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. This 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.

S.69.3 Frozen in time, changing with climate: Alpine endemics speak through herbarium genomics

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The European Alps, undergoing a climate change rate twice as fast as global averages, present a unique opportunity to investigate the genomic responses of alpine flora to environmental shifts. For this project, we chose a few high-elevation, endemic alpine plants (e.g., *Rhizobotrya alpina* (NE), *Saxifraga tombeanensis* (EN)) to assess genomic changes over the past two centuries. For this, we employed a high-throughput genome resequencing approach on historical specimens from diverse herbariums across Europe spanning the last two centuries (1840-2023). By assessing allele frequency changes through time and comparing them with the extant genetic diversity we were able to directly gain insights into climate-driven allele loss and potential adaptations. This study not only sheds light on the evolutionary responses of alpine plants, crucial for their conservation, but also underscores the valuable application of genomics in leveraging natural history collections. The implications of our findings extend beyond the scientific realm, offering critical knowledge for informing conservation strategies and contributing to a deeper understanding of biodiversity in the face of rapid environmental changes.

S.69.4 Filling “big data” needs for biodiversity studies requires a diversity of herbaria and continued collecting

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Massive data resulting from herbarium specimen digitization have started a new era in biodiversity studies, often yielding highly cited publications and stimulating innovations in digitization and biodiversity informatics. A growing recognition of the value of herbarium data for research has, in turn, reinforced funding for digitization of collections. However, digitization grants are temporary and sometimes insufficient for their own goals. In addition, they greatly outweigh and outnumber the (capacity) grants available for collection curation/infrastructure and ongoing botanical collecting, activities also required to maintain the digitized data pipeline. Critically, projects using specimen data often lack any funding support for the herbaria housing those specimens. This situation presents an apparent paradox: herbaria have never been more impactful in terms of contributing specimen data to research, but at the same time, those contributions are increasingly hidden in data download files and burgeoning institutional acronym lists. Such under-acknowledgement exacerbates the long-standing collecting/collections funding crunch. This may be most disadvantageous to smaller or more regionally focused herbaria, where funding needs are most acute. However, we argue that these collections are critical both for geographically equitable access to biodiversity collections and as repositories of specimens representing the spatial and temporal density needed for large-scale analyses. We use data from the Mid-Atlantic Herbarium Consortium (MAHC; https://midatlanticherbaria.org/) of the United States as a case study to examine how plant collecting in this region has contributed to the global data pool. We compare these data to mid-Atlantic specimens available through GBIF to evaluate the uniqueness as well as taxonomic, temporal, and geographic coverage of these specimens. With these analyses, we consider the varying roles of herbaria of different sizes and histories as data sources. We argue for greater support for botanical collecting and the continued support of a diversity of herbarium types to meet our biodiversity research needs.

S.69.5 Unlocking botanical treasures: RBG Kew's digitisation programme, challenges and learnings

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The Royal Botanic Gardens, Kew (RBG Kew), established in 1852, is home to one of the world's largest dried flora and fungi collections, safeguarding around 8.5 million specimens. It encapsulates a remarkable global coverage, containing over 95% of vascular plant genera and representing around 60% of the world's currently known fungi. Significantly, the herbarium serves as an invaluable repository of information for understanding the diversity of the world's living organisms, encompassing their morphological, genetic, physiological and ecological variations. However, most of these botanical treasures remain hidden behind cupboard doors, accessible primarily to academic communities through on-site visits. In turn, this constrains the research potential inherent in the collection. As part of a four-year digitisation program, RBG Kew is recognising this urgency and adapting to the digital era. The objective is to generate high-resolution images and data of the entire herbarium and fungarium collections, ensuring the preservation of the original specimens while unlocking global accessibility. This large-scale digitisation initiative involves overcoming substantial challenges, including the adaptation of workflows to address issues such as mould, pests, and damaged specimens. The Senior Curator Botanists in Digitisation are crucial to the success of the project. They maintain the integrity of the collection by providing intensive training and guidance to all digitisers involved, and by establishing protocols for resolving large-scale issues encountered during digitisation and reporting those issues to the appropriate team or individual. They also link the digitisation project and the core curatorial teams, ensuring constant communication on progress and mediating access to the collections for research while they are being digitised. The endeavour involves not just the conversion of physical specimens into digital formats but also requires the development of strategies to contend with the complexities presented by the collection's varied age and condition.

S.69.6 New perspectives on wood collections: integrated collections at the UNAM Xylarium

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Traditionally, xylaria or wood collections were conceived from a forestry perspective, primarily with the objective of serving as a reference for wood identification for commercial purposes. In the dynamic landscape of botanical collections, the UNAM Xylarium (MEXUw) in Mexico distinguishes itself by transcending traditional boundaries. Our collections encompass a diverse array of samples, organized into four subcollections: traditional wood blocks, entire stem fragments with wood and bark preserved in alcohol for all major orders of gymnosperms and angiosperms, wood anatomical slides, and cores and disks sampled for dendrochronological purposes. A pivotal aspect of our innovation lies in recognizing the unique preservation needs for quantitative wood anatomical studies. In response, the UNAM Xylarium houses an alcohol-preserved collection, a pioneering initiative that retains wood and bark characteristics often lost in conventionally treated wooden blocks subjected to drying, heat and cold. This approach ensures the protection of delicate features essential for comprehensive stem and root analyses. As part of these efforts, collections of wood slides are essential, but the digitalization of these assets remain a neglected frontier. Few institutions have ventured into digitizing their slide collections, and fewer still have made these digital archives publicly accessible, a frontier we are poised to address with the digital resources available at UNAM. Beyond physical and digital preservation, the UNAM Xylarium acknowledges the imperative to modernize organizational frameworks. We've updated all our collections to the APG-IV system, reflecting the most current nomenclature of plant families. The manual effort involved in this process is substantial and time-consuming, emphasizing the need for automation as collections grow and nomenclature evolves. Our presentation aims to highlight not only our advancements in specimen preservation but also our commitment to staying at the forefront of organizational practices as we advocate for increase the donations and trades with other wood collections worldwide.

S.70 INTEGRATIVE TAXONOMY OF MEDITERRANEAN PLANTS. SESSION 2

S.70.1 The Azorean Daucus: a morphological, cytogenomic, phylogenetic and ecological study

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The genus *Daucus* L. contains approximately 45 species, the majority of which are found in the Mediterranean region. The *Daucus carota* complex includes ca. 25 infraspecific taxa, for which there are no or only poorly developed barriers to interbreeding between the wild and domesticated forms. In the Azores archipelago two sub-species occur: the endemic *Daucus carota* subsp. *azoricus* Franco, and the native *Daucus carota* subsp. *maritimus* (Lam.) Batt. Due to the phenotypic diversity observed across the *Daucus carota* complex, the distribution and diagnostic morphological characters of the endemic Azorean species remain unclear. This study aims to clarify the taxonomy of the *Daucus carota* complex in the Azores and determine if the *Daucus carota* subsp. *azoricus* Franco is in fact a distinct taxon. For this purpose, we used molecular, cytogenomic, morphological and ecological data. A total of forty-four specimens of *Daucus carota* subsp. *azoricus* were sampled across the nine islands of the archipelago and the ITS region and the COS region (CA7) sequenced. Estimations of DNA content were performed with flow cytometry to investigate variation between taxa (*i.e., Daucus carota* subsp. *azoricus* and *Daucus carota* subsp. *maritimus*) and populations. Moreover, we measured a total of 31 morphological characters from across the stem, inflorescences, flowers, and fruits. Finally, we performed germination tests in order understand the phenotypical diversity observed and cultivating *Daucus carota* subsp. *azoricus* under different climates and soils. Preliminary results indicate that there are no major morphological differences between the sampled sites. Similarly, with cytogenomic data it was not possible to discriminate between the two subspecies. However, the molecular data revealed variation across the archipelago with different haplotypes obtained from the screened regions.

S.70.2 Disentangling relationships in different lineages of Euphorbia subgen. Esula (Euphorbiaceae)

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Euphorbia subgenus *Esula* is the earliest diverging lineage within *Euphorbia* and with roughly 480 species represents the most significant radiation of the genus in temperate areas of the Old World, with highest diversity in the Mediterranean and Irano-Turanian regions. The overall infrageneric structure has been largely resolved using plastid and nuclear ITS sequences, leading to recognition of 21 sections. In contrast, spatio-temporal diversification within the sections – and partly also the relationships among them – remain poorly understood. I present the outcomes of ongoing studies on the diversification of different species groups within *Euphorbia* sect. *Esula* based on an integrative approach using phylogenetic and phylogenomic data, relative genome size and chromosome number estimations, as well as morphometric and ecological analyses. They are all important for inferring inter-specific boundaries and establishing a stable taxonomy within the subgenus. I address the significance of polyploidisation for diversification within the subgenus and summarise major open questions to stimulate further research on this fascinating group of flowering plants.

S.70.3 Excessive polyploidy and unusual pattern of pollen stainability in Gagea and Ornithogalum species

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Geophyte monocots with their showy flowers are a prominent component of the Mediterranean flora. However, they remain taxonomically challenging due to their low vegetative morphological variability and the presence of polyploidy. We studied genome size as a proxy for ploidy level of selected taxa of Gagea (Liliaceae) and Ornithogalum (Asparagaceae) and we also established their pollen stainability. We asked whether genome size can be used for taxa determination and whether pollen stainability correlates with established ploidy level. We expected a normal pattern of pollen stainability with diploids having the highest proportion of well-developed pollen and even ploidy cytotypes having higher stainability than odd ploidy cytotypes. In both genera, we found an excessive occurrence of polyploidy ranging from diploids to heptaploids. The studied taxa differed in genome size also on the same ploidy level suggesting that genome size can be used for taxa differentiation. Quite surprisingly, pollen stainability varied greatly and it did not follow the expected pattern with higher ploidy and odd ploidy cytotypes usually having a higher proportion of well-developed pollen. A simple mechanistic explanation of this pattern is lacking. Lower stainability in even ploidies suggests past hybridisations and/or meiotic aberrations.

S.70.4 Phylogeny and biogeography unveil taxonomic deflation in the Mediterranean disjunct genus Jasione L. (Campanulaceae)

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Jasione is a taxonomically complex genus with a disjunct east-west Mediterranean distribution pattern. Around 16 species are currently recognized, although more than one hundred taxonomic names have been proposed. The hypothesis that intense morphological stasis is concealing evolutionary relevant variability and hampering correct understanding of the evolutionary relationships in the genus needs to be tested. Internal phylogenetic relationships are investigated after a comprehensive sampling including different populations from most of the proposed names, to prevent a priori exclusion of evolutionary significant lineages. The underlying processes leading to the disjunct east-west Mediterranean distribution pattern are discussed. To address these questions, a five cpDNA loci time-calibrated phylogeny was constructed with 111 terminals. The lineage leading to Jasione originated in the late Oligocene (c. 25 Mya) and the extant lineages of Jasione derive from a much later diversification event, occurring in c. 9 Mya in the Miocene, from an ancestor most probably originated in the western Mediterranean region. Two main clades can be identified, one only present in the western Mediterranean and encompassing species with very different morphologies and another with the extant disjunct distribution pattern. The second clade began to diversify at the beginning of the Pleistocene, probably in the Balkan Peninsula, and at least two east to west dispersal events are identified in this clade, with niche modelling identifying niche conservatism in the eastern group and niche expansion in the western group. The disjunct pattern results from a dynamic biogeographic process in which the two extant areas provided the opportunity both to remain and to disperse, increasing the chances of the lineage to endure. Morphological stasis in *Jasione* led to taxonomic deflation and integrative approaches are addressed. Internal coherence and discontinuities are tested integrating information from key traits, ploidy, ecological niche and adequacy to biogeographical units to support "cryptic" species hypotheses.

S.70.5 Integrative taxonomy and biogeography of Umbilicus (Crassulaceae)

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Umbilicus is a small genus of Crassulaceae with a distribution ranging from the Mediterranean region to Macaronesia, sub-Saharan Africa, and West Asia. The number of species is unclear due to the controversial taxonomy with multiple unresolved taxa and characters traditionally used for species delimitation being rather ambiguous. So far, only genetic analyses at the family level with a very limited number of *Umbilicus* species have been available. Here, we sequenced six plastid genes and spacers (*matK*, *psbA-trnH*, *rps16*, *trnQ*, *trnS* and *trnL*) plus the nuclear ribosomal ITS region of 235 specimens covering most of the distribution range of the genus and most described taxa. We inferred phylogenies with maximum likelihood and Bayesian methods and studied the morphology of herbarium material and photos of observations on iNaturalist. Using Bayesian molecular clock dating with secondary calibration we estimated a stem age of 14 (+/- 6) Million years for the genus. We inferred West Asia as the geographic origin with *Chiastophyllum* as sister lineage. The first diverging clades including *U. albido-opacus* and *U. luteus* as well as species with a paniculate inflorescence are restricted to West Asia, northeast Africa, and southeastern Europe. The remaining species, which all exhibit a racemose inflorescence and mostly greenish tubular flowers, diverged 9 (+/- 6) Ma ago and repeatedly colonized Africa, Europe, and Asia. Within this clade we inferred several cases of long-distance dispersal, most notably the colonization of Cameroon, Angola, and India as well as several independent colonization events of the Macaronesian islands. More data on the pollination biology of the genus, including pollinator shifts and transitions to selfing, will help us understand the discovered phylogenetic patterns.

S.70.6 Unveiling the genetic tapestry: exploring SNPs in the Cyclamen genus

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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.

S.71 BIOLOGICAL DIVERSITY HIDDEN IN EARLY TERRESTRIAL SITES OF EXCEPTIONAL PRESERVATION.

S.71.1 Permineralized plants from the Lydiennes Formation (France): a unique record of early Carboniferous plant diversity and biology

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The earliest Carboniferous (ca 360-330 Mya) is a pivotal time in plant evolution, with the transition between taxa that characterized the first complex plant communities during the middle to late Devonian and more modern groups that later became major elements of the iconic "coal swamps" vegetation of the Late Carboniferous. However, localities with well-preserved fossil plants from that time period are rare worldwide, especially anatomically preserved remains that yield important information on the evolution of plant structure and biology. In Southern France, middle Tournaisian anatomically preserved plants were first reported in the Lydiennes Formation near Cabrières (Hérault) in the late 19th century. Since that time, at least 21 genera have been identified, some of them unknown elsewhere. We present a synthesis of our knowledge of this exceptional fossil flora based on around 450 specimens from the collections of the University of Montpellier, France. The assemblage comprises a mixture of taxa belonging (1) to groups that were abundant and diverse during the Devonian and dwindled during the Carboniferous, such as the cladoxylopsids s.l. and progymnosperms, and (2) to groups that appeared in the Late Devonian and became emblematic members of Late Carboniferous floras such as the Sphenophylllales, Zygopteridalean ferns, and seed plants. In terms of relative abundance, the assemblage is largely dominated by seed plants (>60%). Zygopteridalean ferns, cladoxylopsids, and lycopsids are also relatively abundant (+/- 10%), while the progymnosperms and sphenopsids are rare (1–2%). Anatomically preserved stems and petioles are the most abundant type of remains, while roots and reproductive structures are uncommon. Some of the fossils exhibit an excellent preservation that allows detailed inferences on plant autoecology (e.g., adaptation to aquatic environments), architecture (e.g., the oldest evidence of axillary branching), or development.

S.71.2 The resupinate strobilus spikemoss in the Cretaceous amber might be associated with the rainforest shade aggravation

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Selaginellaceae is a Paleozoic origination with a cosmopolitan distribution. Previous fossil evidence indicates the rainforest floor origin of modern spikemoss and an ecological association between Selaginellaceae and the humid tropics since the Paleozoic. We observed a 99-million-year-old and well-preserved spikemoss branch with the character of resupinate strobilus in mid-Cretaceous Kachin amber, which provides a precious window to glimpse the Selaginellaceae diversification and its specialized habitat. To explore the resupinate strobilus evolution history, we built up the phylogeny including more than 85% resupinate strobilus species, estimated the divergence time, and reconstructed the ancestral state of the sporophylls arrangement and habitat. Resupinate strobilus first appeared in the Early Cretaceous within the Tropical Asia clade and later paralleled in other clade, with the occurrence times strongly related to the rise of angiosperm. In combination with their low-light adaptability and the difference in light response of dimorphic leaves, we further suggested that the current tropical spikemoss diversity originated since the Cretaceous (after angiosperm origin) instead of the evolutionary holdovers from the Paleozoic tropical forest and conjectured the resupinate strobilus was a key innovation of the ground-floor spikemoss adapting to the humidity and shadow rainforests.

S.71.3 Unravelling the diversity of plants and their associated organisms in Devonian and Carboniferous cherts

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Sites of exceptional preservation such as the Devonian Rhynie cherts (Scotland, UK) and the Carboniferous Esnost chert and Grand'Croix cherts (Massif Central, France) preserve remarkable records of early terrestrial ecosystems. The cherts at Rhynie formed as deposits from a hot spring system. Fossilization occurred through episodic inundation of the biota with fluids from a nearby hot-spring system, and the resulting silicification preserved organisms in exquisite detail. Alongside plants, a community of animals, primarily arthropods, and diverse microscopic organisms, including cyanobacteria, algae, amoebozoa, oomycetes and various fungal groups have been described from these sites. At Esnost cherts formed in acidic volcanoclastic sediments associated with peat deposits (now anthracites). At Grand'Croix silicification of the plants was related to silica-charged waters produced during chemical weathering of earlier volcanics. Fossilization preserves both *in situ* plants and transported plant fragments. Preservation is excellent, but the plant remains are fragmentary. In addition to plants, fungi and oomycetes have been documented. The development of Confocal Laser Scanning Microscopy (CSLM) has provided us with a new tool to investigate the biodiversity of these unique sites. Unlike traditional bright-field microscopy, CSLM enhances the image's clarity and detail. Recently we used Fluorescence Lifetime Imaging (FLIM) that delivers information about the spatial and chemical distribution of fluorescent material together with information about its nano-environment. These approaches allow us to document minute three-dimensional structures with unprecedented precision. We present our latest findings on cyanobacteria, testate amoebae, fungi and oomycetes from the Rhynie chert, showing that the components of the bacterial mats among which plants grew were already highly diversified. With the addition of new results on symbiotic and pathogenic fungi and of the newly described oomycetes from the French cherts, we show an increasing knowledge of the diverse interactions that took place in early terrestrial ecosystems.

S.71.4 Uncovering the origins of plant complexity in the Rhynie chert

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Land plants exploded in complexity during the Silurian and Devonian periods during the primary radiation of vascular plants. This radiation saw plants diversify from tiny species, that we predict occupied marginal habitats, and culminated in the origin of the first forests covering large swathes of the terrestrial surface by 385 Mya . The diversification of vascular plants occurred in parallel to, and was likely underpinned by, the origin of the modern vascular plant sporophyte body plan delineated into distinct roots, shoots and leaves and connected by a highly efficient vascular transport system. Despite the evolution of the vascular plant body plan being one of the most important events in plant evolution many key questions still remain about how and when it evolved. The fossil record provides our only direct evidence for the steps involved in the evolution of the complex vascular plant body plan and despite its biased and fragmentary record it remains invaluable for shaping our understanding of plant evolution. Numerous fossil sites from around the world have helped shape our views on the diversification of vascular plants but one of the most important fossil sites has been the Rhynie chert from Aberdeenshire, Scotland. This single fossil site, preserving an entire 407 million year old ecosystem with exceptional preservation, has been transformative for plant evolution. Despite being discovered over 100 years ago new imaging and digital reconstruction techniques are underpinning a resurgence of research on the site. Here I present recent advances in our understanding of the plant species in the Rhynie chert and outline how these fossils are contributing to our understanding of the evolution of plant complexity.

S.71.5 Aglaophyton and Rhynia: ecology, growth and life strategies of the two most common Rhynie chert land plants

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Aglaophyton major and *Rhynia gwynne-vaughanii* are commonly regarded as the less advanced plants from the Early Devonian Rhynie chert. The naked, dichotomizing axes with a simple conducting system were lying on the substrate and lacked root-like structures or rhizomes. Despite their apparent simplicity these plants had rather complex life strategies. The alternation of generations in these two taxa can be reconstructed in great detail, and the excellent and rapid fossilization in the chert even provides snapshots of the release of sperm and the gametophyte-sporophyte junction. Cyanobacterial mats appear to have been crucial for the germination of spores. A symbiosis with vesicular arbuscular mycorrhizal fungi is characteristic of both taxa and was established already in the early gametophyte stage. *Aglaophyton* hosted several other organisms, including cyanobacteria, mites, trigonotarbid spiders and the oldest known bona fide nematodes, the first soft-bodied animals recorded from the Rhynie chert. Apart from sexual reproduction *Rhynia* also propagated vegetatively.

S.72 CITIZEN SCIENCE INITIATIVES FOR THE PROMOTION OF BOTANY

S.72.1 A citizen science initiative to monitor urban plant biodiversity

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"Sauvages de ma rue" (Wild Plants of My Street) is a French citizen science program of Vigie-nature, developed by the National Museum of Natural History and Tela Botanica. Focused on the flora of public spaces in cities, it encourages urban residents to conduct a floristic inventory of their street and submit the data on a website developed by Tela Botanica. Two objectives guided the development of this program: an educational goal to help urban dwellers recognize the plants growing in their daily environment and a scientific goal to understand the ecological role of vegetated micro-spaces (tree bases, walls, pavement cracks, etc.) in the overall functioning of urban biodiversity. This project, initiated in 2011 in the Île-de-France region, was expanded to the entire metropolis in 2012. After about a decade, around 100,000 data points had been collected. This presentation will provide an overview of the list of volunteer participants in the program and the motivations they express. The primary observation is that, in the initial years, individual volunteers submitting data independently have given way to more formalized organizations such as associations, schools, and local authorities, driven by diverse motivations. Additionally, we delve into the scientific outcomes derived from the program.

S.72.2 Photographic field guide to the common grasses of Madagascar

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The grasses and grassy ecosystems of Madagascar have been the focus of Kew's multidisciplinary research, conservation, and development work since 2011, including taxonomic, phylogenetic, ecological and agricultural projects. Madagascar is home to an estimated 38 million hectares of grasslands comprising 146 genera and ca. 590 Poaceae species, of which ca. 220 are endemic to this island. Unfortunately, the lack of specialist expertise and resources has led to a lack of recognition and a failure to utilise this diversity. Madagascar's first colour picture guide to grass genera was printed by Kew in 2018. Field photography of grasses has always been challenging due to their small reproductive organs while living grasses are not easy to recognise from traditional line drawings of spikelets. Using specialist photography training and multiple photographer contributions, we are creating the first photographic guide to species to create a foundational resource for identifying, managing, and using common grasses, making native and endemic forages better known and more valued by the Malagasy people. This bilingual book in English and Malagasy will include 127 genera and 300 species of common and economically significant grass species. Photographs were taken on field trips from 2011 to the present. Ethnobotanical data are gathered from literature as well as smallholder interviews. Morphological traits, distribution, ecology, and economic uses are compiled from GrassBase, project datasets and partner organisations. Field photographs are being edited using Photoshop software, focusing on habits, leaves, spikelets, and caryopses as a rich visual resource for diverse audiences.

S.72.3 Leveraging machine learning and citizen science data to describe flowering phenology across South Africa National Botanical Garden

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Phenological patterns, representing the timing of recurrent biological events, such as flowering, are essential for understanding plant life cycles, ecological interactions, and how species respond to climate change. However, given the diversity of South African flora (ca. 24,000 species), manually recording species phenology presents an immense challenge. In this study, we explore machine learning (ML) application to data sourced from the iNaturalist database and describe the flowering phenology of plants in the South African National Botanical Gardens. We generated a training dataset from 10,000 photographic images, encompassing a diverse range of species from various locations. Next, we applied a Convolutional Neural Network (CNN) to classify images as flowering versus non-flowering. Using metadata associated with each image, including the date the photograph was taken, we were able to derive the timing of peak flower production and length of the flowering season for each species in the database. Our analysis illustrates how ML can leverage the vast wealth of citizen science biodiversity data in South Africa and describe large-scale phenological dynamics across the region. Applying ML and other advanced data tools to big data provides an opportunity for more informed decision-making and sustainable practices in the context of biodiversity conservation and management.

S.72.4 BOTASCOPIA – An open access collaborative collection of descriptions of plants species

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The teaching of Botany in France faces a paradox: waning support in academia contrasts with burgeoning public interest in plant knowledge. The success of French Botanical MOOCs reflects this unprecedented public enthusiasm. In that context, standardized descriptive sheets serve as vital pedagogical tools, offering comparability and accessibility in cataloging vegetation. In 2022, building on a first set of handmade descriptive sheets, researchers from University Paris-Saclay united with pedagogical engineers and informaticians of the French association Tela Botanica to design an open access collaborative botanical knowledgebase, BOTASCOPIA. This platform, curated by experts from different fields (botany, agronomy, ecology), invites continuous contributions from a broad audience. Input fields welcome a variety of data related to plant morphological, ecological and agroecological traits, and have been designed to maximize comparability and extraction of the data, as well as to balance the accuracy of the descriptions with the complexity of the botanical concepts. BOTASCOPIA strives for data traceability and citation of the essential references is a requirement. As output, all the data entered are available online and a subsample can be assembled into nice-looking and illustrated pdf sheets. Initially a pedagogical tool, BOTASCOPIA evolution is now directed towards broader accessibility and should ultimately be part of a larger naturalistic package that will include customizable Bayesian-inference based identification keys. Continual enhancements in structure and interface cater to BOTASCOPIA usability, promising a robust resource for botanical education and research.

S.72.5 TEPIK – A resource for testing and teaching plant identification and botanical knowledge

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Learning plant names is usually considered as a complex and long process, which is even more complex when additional information is added (such as plant size, flowering period, leaf deciduousness, ...). We present the produce of our reflexions in the form of a database associated with a quiz generator, called TEPIK (for Test of Plant Identification and Knowledge). These reflexions have been done with the support of various professional groups and teachers. The produced tool, considered as a complement to teaching with living material, consist in a database fed by certified and free or licensed data. The main feeding sources are eflore from Tela Botanica and Floriscope from Plante&Cité. Selection of the current taxa is based on wild and commercial frequency but any new taxa may be added if needed. For each taxa (more than 4000 are currently included) various characteristics and numerous pictures are present. Each picture is tagged in such way that the part of the plant presented is known by the system. Difficulty parameters are also implemented, whether they rely on the plant (i.e.,some plant parts are more difficult to recognise), on questions (open questions are more difficult that single-choice questionnaire) or on information tested (knowing common name less difficult to learn than soil type). Teachers can generate sets of questions on a precise list of plants, with more or less detailed parameters in order to provide quiz to their students. In addition, thoughts on learning progression are currently developed with Bayesian Knowledge Tracing in order to follow and predict knowledge acquisition.

S.72.6 Breaking the negative trend: Can iNaturalist help boost species knowledge?

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In Sweden, as in many other countries, species knowledge is in decline. There are fewer specialists to teach the next generation and to update floras and keys. We need to use everything we can to help turn this trend around! Engage the general public as well as students at all levels. iNaturalist is a powerful tool in citizen science, such as a bioblitz or inventory competitions. Not only will people get a proposed species name for their observation, they will also be adding valuable data that later can be used in research. When scientists and other experts help identify the observations, a valuable direct link between the scientific community and the public is created. The project function in iNaturalist is a usable asset in for example a floristics course and will make data from inventory projects accessible to the community. We show examples from both a bioblitz for the general public and a floristics course at the University of Gothenburg, Sweden.

Symposia Session 5

S.73 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 3

S.73.1 An overview on the "multi-tasking" enzyme phytochelatin synthase in plants

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My contribution deals, in an evolutionary perspective, with "traditional" and new roles of the phytochelatin synthase enzyme (PCS), the functions of which still appear shrouded in a degree of mystery. I illustrate and discuss the five main key-points that characterize this peculiar "multi-tasking" enzyme in plants: 1) PCS is a "papain-like" Clan CA cysteine peptidase; in particular, the eukaryotic PCS is a gamma-glutamylcysteine-dipeptidyl-(trans)peptidase. 2) PCS is constitutively expressed in plants, algae, lichen chlorophyte photobionts, as well as in other eukaryotes, such as Fungi, some Animalia and Amoebozoa, SAR (especially Bacillariophyceae and Phaeophyta) and, more rarely, Excavata. Moreover, prokaryotic PCSs, which possess significant sequence homologies with those of plants, have been identified in cyanobacteria and in some proteobacteria. 3) Through its transpeptidasic products – i.e., the metal(loid)-binding oligopeptides named phytochelatins (PCn) – PCS detoxifies toxic heavy metals and metalloids (e.g., cadmium, lead, mercury, arsenic, etc.), but can also help regulate the homeostatic needs of metal micronutrients such as iron, zinc, and copper. 4) Being a peptidase (see point 1), PCS can also hydrolyze GSH and GS-conjugated xenobiotics in the cytosolic environment through the cleavage of glycine from GSH. The GS-conjugation capacity of plant PCSs is a feature also detected in prokaryotic PCSs, and the breakdown of GS-conjugates may accordingly be considered a primigenial function of PCS, perhaps older than the biosynthesis of PCn. 5) Lastly, a yet limited number of experimental works is increasingly highlighting the importance of PCS in plant defence against phytopathogens, essentially in terms of microbe-triggered-immunity. Advances in the overall area of knowledge on PCS may well help clarify the evolutionary history and function(s) of this ubiquitous and partly mysterious "multi-tasking" enzyme.

S.73.2 Growth, antioxidative defense, and yield responses of four pearl millet cultivars under elevated UV-B radiation

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Ultraviolet (UV-B) radiation is a well-known potent stress factor on this Earth's surface caused by stratospheric ozone depletion, which alters morphological, physiological, cytological, and biochemical traits in plants. However, its impact on underutilized plant species such as pearl millet is less explored and further, the question of global food security under climate-changing scenarios can be ascertained. This encouraged the present study to investigate the effects of elevated UV-B (eUV-B) radiation (ambient+7.2 kJm^{-2}d^{-1}) on four cultivars of pearl millet (HHB-272, HHB-67, MPMH-21 and MPMH-17) during May to August 2023 under ambient conditions in the Indo-Gangetic plains of India. Maximum increase in plant height (20%), no. of leaves (31.2%), leaf area (35.4%), and panicle length (60%) was recorded in HHB-272 at grain-filling stage (GFS). Superoxide radicals were initially higher in MPMH-21(47.3%), MPMH-17(28.6%) at panicle development stage (PDS), but later decreased by 35.5%, and 15.3% at GFS. To counter oxidative stress, maximum increase in SOD activity was recorded only at PDS in MPMH-21(35.9%), MPMH-17(34.8%), while declined in all the tested cultivars at GFS. Highest phenolic and flavonoid contents was reported at GFS in MPMH-

21(97.2%, 41.7%), and MPMH-17(6.9%,14.9%), respectively. Oxidative damage in terms of malondialdehyde (MDA) content was significantly higher in MPMH-21(46.3%), and MPMH-17(25%), while declined at GFS due to increased phenolic and flavonoid contents, respectively. Yield of tested cultivars was not adversely affected under eUV-B in an ambient tropical condition, but the response varied between them. Grain yield (g m^{-2}) increased significantly in HHB-272(30.2%), HHB-67(55.8%), MPMH-21(83.3%), and MPMH-17(28.6%), respectively. Further investigations are required to assess the impact of elevated UV-B on grain quality characteristics that will be helpful to address the question of food security as well as malnutrition challenges.

S.73.3 Disturbance and nutrient enrichment impacts on plant community dynamics: contributions to a global study

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Herbaceous-dominated ecosystems are found throughout the world in diverse locations that differ in their climate and edaphic factors. This is reflected in a wide range of annual above- and belowground biomass production, plant diversity and canopy density between these ecosystems. Our study aims to understand how nutrient availability and disturbance impact soil trace gas fluxes and how this relates to plant species relative abundance, diversity, and annual aboveground production. Here, we present data on herbaceous-dominated ecosystems found in coastal South Carolina, USA. This study is part of a global network (DRAGNet) of herbaceous-dominated ecosystem study sites distributed globally using identical protocols for treatment application and data collection. We found the relationship between plant species diversity and aboveground biomass production varies. Aboveground biomass and accumulated litter were not correlated, suggesting that the drivers for carbon assimilation and decomposition are different. The combination of disturbance and nutrient enrichment lead to greater CO_2 and CH_4 fluxes, while the relationship between N_2O and the treatments is less clear. This research will serve as the foundation for future research on how nutrients and soil disturbance interact with the amount of carbon assimilation, and if some species show trait variation in response to these treatments in different regions of the world.

S.73.4 Enhancing crop production in acidic soil by mitigating aluminium toxicity

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Wheat is a globally significant staple grain crop due to its high nutritional content and adaptability to a variety of agroclimatic situations. Wheat output must rise on current agricultural acreage to avoid agricultural expansion. Most wheat-growing locations face soil restrictions, including acidity, which hinders crop productivity. Due to excessive usage of ammonium-containing fertilizers and acid rain, 30-40% of global arable soil is acidified. Aluminum (Al) toxicity limits plant development in acidic soil. In Raj 3077, an Al-resistant wheat genotype, an antioxidant defense mechanism against Al-induced oxidative damage and external malate detoxification provides Al-resistance. Raj 4120 (Al-sensitive) inhibited growth more than Raj 3077. Both genotypes' roots were tested for lipid peroxidation and H2O2 concentration. These indicators were greater in Raj 4120 shoots, indicating oxidative stress. Antioxidant enzymes as SOD (EC 1.15.1.9), CAT (EC 1.11.1.6), and APX (EC 1.11.1.11) protected Raj 3077 against Al-induced oxidative damage. Inefficient antioxidant enzyme activity in Raj 4120's roots indicated severe oxidative damage and a greater number of harmful Al ions translocated to the shoot, creating Al stress there. Interestingly, Raj 4120's shoot had more CAT activity than Raj 3077, but it wasn't adequate to counteract Al-induced reactive oxygen species. Raj 3077 had stronger malate efflux and ALMT gene expression than Raj 4120. The root length of Raj 3077 seedlings was especially reduced by niflumic acid, an anion channel inhibitor, suggesting that malate detoxification is needed for root Al-resistance. Al-induced antioxidant defense and external malate detoxifying mechanisms help Raj 3077 cope with Al toxicity.

S.73.5 Diversity in tree hydraulic drought tolerance promotes temporal stability in forests

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Forest biomass productivity is essential for climate functioning and for providing other services to humankind. This productivity, however, is not constant, and it fluctuates between years due to variations in climate and the intrinsic characteristics of tree communities. At the same time, climate change is rising temperatures and climate variability around the World, increasing forest vulnerability to drought, and compromising the stability of forest functioning and services. It is therefore important to understand what factors drive the stability in forest productivity. We explored how tree community characteristics (local climate, vegetation structure and drought-related traits) affected the stability of 40k permanent forest plots across Spain. We used two decades of productivity-related satellite indices (NDVI and EVI) for measuring forest productivity stability, and stand-level data derived from the Spanish National Forest Inventory for measuring tree community structure (maturity and tree density) and mean and diversity of hydraulic drought tolerance traits (P50 and HSM). We found that there are complex interactions determining the patterns of stability, including direct and indirect effects of environmental variables, vegetation structure and tree species drought adaptations. Forests showed higher stability with higher water availability, its stability in time, stand development and density of trees. We also found solid evidence that tree community diversity in hydraulic drought tolerance favoured stability. Results indicated that this diversity influences both, the mean of productivity (positively) and its standard deviation (negatively). Mean drought tolerance at the community level showed a less clear (but mostly negative) effect on stability. These results suggest that drought-related functional diversification would be a good management strategy to secure the stable provision of forest ecosystem services, especially under increasing variability in climate and intensity of droughts.

S.73.6 Adapting to Compound Climate Stresses: lessons from two extremophytes

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Agriculture faces increasing challenges from climate change, introducing complex stressors that reduce crop yields. Rising sea levels and prolonged droughts drive reliance on salt-contaminated water for irrigation. Additionally, extensive use of synthetic fertilizers elevates CO2 emissions and risks depleting non-renewable nutrients like phosphorus. As low-nutrient and high-salt soils become more common, these stresses frequently co-occur, complicating crop responses. When crops face combined stressors, their responses are often integrated rather than additive, presenting a novel challenge. Most stress experiments focus on single variables, leaving the effects of combined stresses largely unexplored. Therefore, developing solutions based on plant biology and genetics to design stress-resilient crops is increasingly important. Extremophytes, wild plants adapted to multiple environmental stresses, can provide insights into enhancing resilient crop growth. Schrenkiella parvula and Eutrema salsugineum are extremophyte models in the Brassicaceae family related to Arabidopsis thaliana. Their reference genomes were recently updated with chromosome-level assemblies. We examined genomic, transcriptomic, metabolic, ionomic, and physiological responses of these two extremophytes to compare their potential adaptive mechanisms in response to high salt and other stresses. S. parvula often adjusted its root architecture in response to single and compound stresses, while E. salsugineum showed minimal change in primary root growth under similar stresses, indicating physiological and genetic diversity within extremophytes in the same family. S. parvula shows stress-ready transcriptomes, while E. salsugineum shows stress-ready metabolomes under salt exposure. Additionally, our results identified several antioxidant and nutrient recycling pathways active under stress conditions in each species. These studies in extremophytes suggest how key genes in stress response pathways may function differently promoting stress-resilient traits, synchronized across developmental stages and tissues, distinguishing extremophytes from stress-sensitive plants. Understanding the genetic mechanisms of these adaptive traits can significantly influence current and future crop development strategies, with extremophytes offering a valuable genetic resource for transformative crop design.

S.74 ADVANCES IN PHYLOGENOMICS AND SYSTEMATICS OF THE BRASSICACEAE. SESSION 1

S.74.1 The Brassicaceae then and now -Advancements in the past two decades

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It is generally agreed that the systematic and phylogenetic relationship within the mustard family (Brassicaceae or Cruciferae) is one of the best known among all of the medium- and large-sized families of vascular plants. One of its species, *Arabidopsis thaliana*, became the model organism of flowering plants about two decades before it entire genome was sequenced in December 2000. The most rewarding developments in systematic botany started when a handful of European and American geneticists, together with their students and others, focused from early to middle 1990's on the study of variation of a single chloroplast gene (e.g., *rbcl*), chloroplast restriction-site variation, or nuclear ITS in several species of a given genus or several genera and assessed the phylogenetic implications of their data on systematic relationships and character evolution. Those pioneering studies led in 2006 to the first phylogenetic tribal classification of the Brassicaceae based on the single chloroplast genes *ndhF*, in which 25 monophyletic tribes were recognized based on a sample of 113 species in 101 genera. That study, together with a global phylogeny of the family based on the internal transcribed spacer (ITS), were the foundation on which based are subsequent studies in the following 17 years that led to the most robust and best available classification of the family using thousands of genes. After 57 years of research on the Brassicaceae, I summarize the major advancement in the phylogenetics and systematic relationships of the family within the past few decades. Brief comparisons of the limits of tribes, genera, and species between what was then and now are presented. Finally, a handful of features that apparently evolved once in the history of the family as we know it now.

S.74.2 Resolving the evolutionary history of Arabideae using phylogenetic placement

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The Arabideae represent the largest Brassicaceae tribe with ~550 species in 18 genera, among them eponymous *Arabis* and the large genus *Draba* with over 400 species. Polyploidy is prevalent in the tribe, with ploidy levels up to hexadecaploid, and hybridization is hypothesized to be common. Previous phylogenetic studies have identified larger clades consistently, but failed to provide resolution at the species level, in part likely due to the presence of paralogs remaining from past whole-genome duplications (WGDs) and hybridizations. We have developed a concept and workflow to infer polyploidization status from target enrichment data and reconstruct the evolutionary history of the taxa of interest using evolutionary placement of paralogs into a diploid reference tree. This method allows us to use information from paralogs despite multiple rounds of WGD and hybridization. Our results provide a solid backbone phylogeny for the Arabideae and pinpoint the ancestral lineages involved in past hybridizations. Within *Draba*, we found strong evidence that one of three main evolutionary lineages originated from hybridization between the other two lineages, with subsequent hybridizations giving rise to further subclades. In total we identified 68% of our samples as ancient polyploids and clustered them in over 40 clades with different patterns of paralog placement, suggesting independent or additional WGDs and hybridization events. Our study highlights the need for novel approaches to phylogenomics in clades with complex evolutionary histories.

S.74.3 Exploring massive parallel evolution towards derived woodiness in the Brassicaceae

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Flowering plants are characterized by a great variation in woody and non-woody (i.e., herbaceous) growth forms. The first flowering plants were woody, but many lineages evolved into herbaceous species. Interestingly, roughly 700 lineages turned back towards a state of phylogenetically derived woodiness. This remarkable case of massive convergent evolution has baffled scientists since Darwin. Recent studies suggest drought as a main driving force, leading to a 'drought hypothesis'. We study the mustard family (Brassicaceae; ~4,000 species), which alone represents one out of seven of all woodiness shifts in flowering plants, making it the perfect model family to understand woodiness evolution. We recently developed a protocol to sequence >1,000 nuclear genes from herbarium specimens, allowing the reconstruction of a robust, time-calibrated Brassicaceae Tree of Life (BrassiToL). This phylogenetic framework will be essential to identify all ~100 woodiness shifts, thereby generating a powerful framework to test for an evolutionary link between woodiness and the environment. Here, we present our initial results, including a robust BrassiToL of over half the family's species, with a focus towards 'woody tribes' like Anastaticeae, Heliophileae, and Lepidieae. Our first analyses of woodiness evolution suggest that drought is correlated with woodiness in at least several of the family's tribes, including Brassiceae and Alysseae. However, we found other factors to also correlate with woodiness, including UV intensity (Arabideae, Brassiceae, Thelypodieae) and aseasonality (Alysseae, Descurainieae, Erysimeae). In the face of global warming and periods of prolonged drought, understanding how plants cope with drought is essential, warranting a thorough assessment of the drought hypothesis.

S.74.4 Eco-physiological features of C3-C4 Moricandia african clade: a range of within-individual phenotypic plasticities

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The majority of plant species on Earth employ C3 photosynthesis. However, more than a quarter of the assimilated CO2 by C3 species can be lost later to photorespiration, which is exacerbated in hot and arid conditions. In response, some plant lineages have evolved carbon concentrating mechanisms to improve net carbon assimilation, either re-assimilating the CO2 released by photorespiration (the uncommon C3–C4 intermediates) or directly inhibiting it (C4 species). There are no

C4 species in the Brassicaceae family, but it contains some C3–C4 species, predominantly in the African clade of the genus *Moricandia*. Most C3–C4 *Moricandia* congeners inhabit the arid and semiarid areas of the Western Mediterranean, where they are able to grow and bloom not only in spring but also during the hot, bright and dry summer, displaying phenotypic plasticity in different functional traits. Phenotypic plasticity, the ability of a genotype to produce alternative phenotypes when exposed to different environments, is pivotal to understand the ecology and evolution of most organism and has important implications for understanding how organisms can rapidly cope with changing environments. Here we show the occurrence of phenotypic plasticity in key traits of the photosynthetic machinery of different *Moricandia* C3-C4 species and compare it to other C3 congeners. C3-C4 congeners exhibit differences in the magnitude of the plastic responses for key leaf traits. Changes across environments in the abundance and size of stomata, vein density, disposition of chloroplasts across leaf cells, and in their CO2 compensation points, all point to different abilities to capture, concentrate and re-assimilate the CO2 released by photorespiration. Compared to C3 species, C3-C4 congeners show improved net carbon assimilation in high photorespiration environments, allowing them to extend their productivity, flowering and production of viable seeds during the harsh season, when most other co-occurring C3 plants are inactive and dormant.

S.74.5 Comparative analysis of ancient genome triplication and diversification of photosynthesis in Brassicaceae and Cleomaceae

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Within both the Brassicaceae and its sister family the Cleomaceae, ancient whole genome triplications (WGT) are thought to have contributed to trait evolution. For example, the role of a WGT to morphological innovation of the Brassica vegetables. We have examined the contribution of independent WGT in Gynandropsis gynandra (Cleomaceae) and to high rates of photosynthetic assemiliation in Hirshfeldia incana (a close relative of Brassica crops). Namely, we have made chromosome-level assemblies of both species and then used a broad comparative genomics framework to analyze patterns of genome fractionation and particular gene retention patterns. By doing so, we establish how these independent WGT events, of approximately the same age, have contributed to the evolution of the photosynthetic capacity of these two semi-desert/Mediterranean climate species.

S.74.6 Multispecies single-cell transcriptome integration in the model clade Brassicaceae

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Brassicaceae are a model plant clade which epitomizes the value of rigorous taxonomic foundation, firm phylogenetic framework, extensive genomic resources, and a cohesive and collaborative research community in creating a rich medium to explore novel biology. As one of the most densely sampled angiosperm groups at the genomic scale, Brassicaceae are the textbook example about how genomes are shaped by evolutionary forces, and complementary efforts aim to uncover how gene expression evolves in this model clade. Recent advances in single-cell transcriptomics, which allows the detection of thousands of expressed genes in thousands of individual cells, has revealed extensive transcriptional heterogeneity reflecting different cell types and cell states. Building upon *Tabula Floris*, our single-cell floral atlas of Arabidopsis thaliana, we have generated comparable developmental floral atlases for eight mustard species, which belong to diverse mustard lineages and span 25 million years of evolution. We have characterized the expression profiles of diverse floral cell populations across these species. Using multispecies embedding based on orthologous genes, we have identified homologous floral cell types and inferred gene co-expression networks underlying their specialized physiology and developmental programs. We have compared these networks to uncover shared nodes and modules, as well as to identify unique network motifs, which may underlie phenotypic divergences. We further focus on the nectary secretory cell to study the contributions of phylogenetic distance and drift to homologous cell types with conserved function among species. These results highlight the enduring utility of model clades in general and of Brassicaceae in particular to address a wide range of comparative questions.

S.75 IAWA SYMPOSIUM - THE CONTRIBUTION OF WOOD IN FOREST: FROM WOOD DYNAMICS TO TRAIT DIVERSITY AND CARBON GAINS

S.75.1 Inter- and intra-growth ring variations of wood carbon fractions in Pinus tabuliformis

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Increasing role of forestry has been recognized in carbon (C) neutrality. Carbon fraction (CF) of trees is essential for quantifying forest C stocks and recognizing the global C dynamics. Considerable attention has been paid to CF variations at various levels, with the exception of inter- and intra-growth rings. This hinders comprehension of C uptake dynamics and impedes innovation and development of C sequestration in forest cultivation. Herein, the inter- and intra-growth ring variation of CF in *Pinus tabuliformis,* one of the most important plantation species in the northern part of China, was investigated in this study. Elemental analysis was performed to obtain CF values of the earlywood and latewood in each growth ring of the xylem. Patterns of CF variation at the growth ring level were then evaluated using mixed effect models. The results showed that latewood CF, 50.6%, was significantly higher than earlywood CF, 49.9% ($p<0.01$). In particular, inter-growth ring variations of CF differed between heartwood and sapwood, as well as between juvenile wood and mature wood. CF values decreased nonlinearly with cambium age toward the heartwood or juvenile wood, with estimated least-squares means of 50.4% and 51.8%, respectively. While CF values were almost unaltered in sapwood, but slightly decreased in mature wood, with estimated least-squares means of 50.0% and 50.2%, respectively. It indicates that patterns of CF variation between juvenile wood and mature wood are important to estimate the C stock of *P. tabuliformis.* Our research provides insights into C gains for forest management and wood utilization. To better understand the impact of forests on global C dynamics, it is necessary to conduct further research on CF values and accurately measure the C stocks they contain. Additionally, it is important to gain a deeper understanding of the patterns, causes, and potential adaptive significance of chemical traits in forests.

S.75.2 Spatial organization and connectivity of wood rays in Pinus massoniana xylem based on high-resolution µCT-assisted network analysis

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Xylem developed from cambium, consisting of diversified wood cells. Spatial organization and connectivity of wood rays are essential for understanding the wood hierarchical architecture, but the spatial information is ambiguous due to small cell size. Herein, 3D visualization of rays in *Pinus massoniana* was performed using high-resolution µCT. We found brick-shaped rays were 6.5% in volume fractions, nearly twice the area fractions estimated by 2D levels. Uniseriate rays became taller and wider during the transition from earlywood to latewood, which was mainly contributed from the height increment of ray tracheids and widened ray parenchyma cells. Furthermore, both volume and surface area of ray parenchyma cells were larger than ray tracheids, so ray parenchyma took a higher proportion in rays. Moreover, three different types of pits for connectivity were segmented and revealed Pits in both axial tracheids and ray tracheids were bordered, but the pit volume and pit aperture of earlywood axial tracheids were almost 10-fold and over 4-fold larger than ray tracheids. Contrarily, cross-field pits between ray parenchyma and axial tracheids were window-like with the principle axis of 31.0 μm, but its pit volume was approximately one third of axial tracheids. Additionally, spatial organization of rays and axial resin canal was analyzed by a curved surface reformation tool, providing the first evidence of rays close to epithelial cells inwards through the resin canal. Epithelial cells had various morphologies and large variations in cell size. Our results give new insights into the organization of radial system of xylem, especially the connectivity of rays with adjacent cells. Furthermore, the diversified structure in the forestry will be better understood and target the goal of carbon neutrality for human society.

S.75.3 Climate change and forest vulnerability: environmental signals in tree-rings of Mediterranean woods

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Ongoing climate change is a major challenge for forest productivity. Indeed, climate change impacts ecosystems directly, through a direct modification of plant growth and physiological behaviour, and indirectly due to the alteration in species composition, thus diversity. Tree vulnerability and forest die-back are rapidly increasing, serious, phenomena, which are attracting more and more attention due to impacts on ecological, social, and economic aspects. The aim of this communication is to highlight how, in the last years, the key role of quantitative wood anatomy in understanding tree acclimation has been more and more recognised, considering that the largest part of global vegetation biomass depends on a thin layer of cells, namely the vascular cambium, whose functioning determines the variability of wood traits. The latter have impact on tree eco-physiological behaviour, given that the limits of metabolic and physiological acclimation are ultimately regulated by the physics of the plant's structure. A focus is dedicated to study cases conducted on tree and shrub species in Mediterranean ecosystems which are particularly vulnerable to climate change. The increase in the frequency of extreme events, such as severe and prolonged drought periods, will likely induce plastic adaptive responses in Mediterranean species, thus affecting plant growth, health, and productivity of forestry systems, with consequences on biogeochemical cycles and ecosystem services. Main findings are discussed regarding xylogenesis and anatomical traits of Mediterranean woods, both under natural and semi-controlled conditions, to unravel signals hidden in tree-rings, as intra-annual-density-fluctuations. Indeed, a correct functional interpretation of such signals must be guided by the study of xylogenesis, which helps relate intra-ring variation of traits with intra-seasonal environmental variations. Understanding how the plants have reacted to past environmental changes can help understanding their plasticity and forecasting their responses to future changes, to evaluate possible consequences on ecosystems.

S.75.4 A theoretical approach to study the relative importance of source and sink controls on annual wood growth and anatomical traits

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Understanding the physiological mechanisms behind plant responses to environmental cues is crucial to assess the effect of global climate changes on forests. In this context, it is important to comprehend the extent to which wood growth is limited by either the availability of carbon sources or by the activity of the sink itself, i.e.,the vascular cambium. Carbohydrates are produced by photosynthesis and allocated to vascular cambium through source-sink dynamics between competing sinks such as primary and secondary meristems in both shoots and roots. The vascular cambium is also directly affected by two main environmental factors, temperature and water availability. Here we present an original process-based modular modelling framework focusing on annual wood growth incorporating the main source and sink dynamics. A first module computes soil water availability and carbohydrates produced by photosynthesis, using temperature and rainfall inputs. A second module estimates the vegetative phenology of primary sinks, both above- and below-ground, and allocates the remaining available carbon resources to secondary growth. Finally, a wood growth module computes the dynamics of cambial cells' divisions and xylem differentiation as a function of three external controlling factors: available carbohydrates, temperature, and water stress. The model outputs are the number of xylem cells produced through the season, the main anatomical traits of these cells (i.e., lumen area and wall thickness), overall wood radial growth and earlywood to latewood ratio. Model simulations are performed under different environmental conditions, representing a wide range of world climates, and the results are analysed and compared with general observed trends of tree ring characteristics. The emergence of Intra-Annual Density Fluctuations (IADFs) is also observed. The model approach seems promising, allowing for a better understanding of the dynamics of wood growth and carbon sequestration in forest ecosystems by an in-depth understanding of the balance between primary and secondary growth.

S.75.5 Is the history of Dipterocarpaceae written in the wood?

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The Dipterocarpaceae family, iconic in Southeast Asian forests, encompasses over 500 tree species. It plays a key role in regional ecosystems and holds substantial economic importance due to timber exploitation. Despite this, the evolutionary history of Dipterocarpaceae remains incompletely understood. While recent refinements have enhanced our understanding of phylogenetic relationships and family nomenclature, uncertainties persist, particularly regarding the placement of certain taxa, such as the largest genera *Shorea* or *Dipterocarpus*. Simultaneously, emerging data supports the hypothesis of an African origin for the family, underscoring the need for insights from the fossil record to address persistent questions. In the case of Dipterocarpaceae, wood constitutes the predominant fossil remains. A question consequently raises: how accurate recognition and identification of Dipterocarpaceae taxa can be? The question is especially relevant as a certain degree of link between wood anatomy and phylogeny was previously acknowledged. However, comprehensive studies about the wood anatomy of Dipterocarpaceae have been scarce, if not absent since the 1960s, posing limitations on contemporary interpretations. We explore the potentials and limitations of the integrated study of wood through examples from both extant and fossil specimens. Emphasizing the necessity of accounting for inter- and intrataxa variability, strengthening the correlation between wood anatomy, phylogeny, and biogeographical history, and reevaluating the fossil record in light of current, more nuanced knowledge, are pivotal considerations.

S.75.6 Vascular cambium and wood characteristics of stem and root from Ulmus pumila and Populus sibirica grown in the semi-arid regions

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The Joint Korea-Mongolia *Green Belt* Project relies on the afforestation of Mongolia's arid and semi-arid areas, as a tool for ecosystem rehabilitation. Since wood formation depends on two main factors, i.e., temperature and water availability, it is reasonable to assume that the extreme climatic conditions in the Mongolian steppe would affect wood formation and the vascular cambium activity of the trees. However, until now, most studies on wood formation have considered the temporal and Mediterranean regions. The present study focuses on vascular cambium and wood characteristics of two species used in the afforestation in the Mongolian steppe, *Ulmus pumila,* and *Populus sibirica.* In detail, we analyzed the vascular cambium characteristics (number of cambial cells and length of cambial cells stack) and wood characteristics (length of last wood increment, earlywood, and latewood xylem area) as a response to 12 combinations of irrigation and fertilization treatments, both in the stem and the root. The vascular cambium characteristics and the length of the last wood increment in *P. sibirica* tend to increase with the increase of the water availability in all three fertilization treatments. However, there is not much difference between the two higher levels of irrigation, which indicates the possibility of reducing irrigation efforts. In *U. pumila* our results indicate that the vascular cambium characteristics and the length of the last wood increment are often not too different between the rainfall conditions and the highest irrigation regime. In both species, the treatments did not impact the early- and latewood xylem area, indicating that they might not be suitable wood characteristics for analyzing the trees' response in semi-arid regions. Thus, using a familiar approach of microcore acquisition and analysis, in both stem and root, could be of value for species and management selection, which are linked with afforestation success in semi-arid areas.

S.76 THE NEW VALUE OF SCIENTIFIC PUBLICATIONS IN THE DIGITAL AGE

S.76.1 Data liberated through the Plazi workflow can enhance the taxonomic backbone and e-Flora of South Africa

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South Africa has had the benefit of an electronic database housing taxonomic and floristic data since the early 1970s. Initially the database only contained the taxonomic backbone with nomenclatural and specimen level data. Leading up to 2003, elementary floristic data (life cycle, growth form, plant height, altitude, distribution) were added. Since 2013, as a result of Target 1 of the Global Strategy for Plant Conservation—to produce an online World Flora by 2020—the floristic data content of the Botanical Database of Southern Africa (BODATSA) was greatly expanded to contribute to the World Flora Online (WFO) through the e-Flora of South Africa project. Since South Africa harbours 5.3% of the global flora with an exceptional species-level endemism (±60%), the country could provide a fair proportion of unique content to the WFO. Information contained in publications were crucial for compiling the e-Flora. However, liberating published treatments were a stumbling block in the initial stages of the project, until a custom plug-in was created to extract information from publications and format it for import into BODATSA, from where it was published to the WFO. The Plazi workflow offers a similar, although more sophisticated, method for extracting taxonomic and floristic data from publications. It has the added benefit that, once a publication has been processed, treatments and related information are available on TreatmentBank for everybody to access and use. Taxonomic and floristic data for South African plants on TreatmentBank can be compiled and extracted via customisable filters. Such freely accessible liberated data can greatly benefit the process of updating and enhancing the taxonomic backbone and e-Flora of South Africa. We present our experiences, tools, and workflows used to integrate data from Plazi databases into our taxonomic backbone and floristic database, as well provide recommendations to taxonomists to facilitate easier data liberation.

S.76.2 Using linked publications as the evidence base for the World Flora Online Plant List

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The World Flora Online (WFO) Plant List is a collaboratively built, consensus classification of the vascular plants and bryophytes of the world. Its primary purpose is as the taxonomic backbone for the WFO portal, but versions of the list are also published twice a year as an API, downloadable files and deposits in GBIF and ChecklistBank. Data for the list is provided by Taxonomic Expert Networks (TENs). There are currently 47 TENs including over 280 active researchers. The TENs submit data in bulk or use an online editing tool called Rhakhis. The WFO Plant List is not a primary data source. Ideally each assertion made in the list should be supported by a scientific publication. The publications provide two types of evidence; nomenclatural and taxonomic. Nomenclatural publications include the original place of publication but also publications associated with other nomenclatural acts such as lectotypification. Taxonomic publications are used to justify the placement of the name within the consensus taxonomy. There are currently approximately 1.6 million names and four hundred thousand accepted taxa in the list. The number of literature citations required are therefore in the millions. Maintaining bibliographic information on all the associated publications would be a major curatorial burden. Furthermore, presenting the user with only bibliographic information would be of little use if the publication referenced was not widely available. This is particularly the case outside major botanical institutions. It would be preferable for the user to simply click a link and be taken to the actual publication. Using persistent identifiers such as DOIs and those from Plazi and the Biodiversity Heritage Library we have now achieved direct links to the literature for over 50% of the names. Our approach and the challenges we face are described.

S.76.3 Beyond the PDF: semantic publishing as gateway to the resources about biodiversity

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The core mission of Natural History Institutions is to contribute to the understanding of the natural world and to disseminate this knowledge. They do so by establishing and maintaining biological collections; conducting scientific research associated with their collections and disseminating scientific knowledge. NHIs have thus been scientific publishers since their creation, publishing journals and floras, in compliance with the regulations of their field, in particular new versions of nomenclatural codes regarding online publications. Over the past decade, the publishing industry has had to face drastic changes and adapt their workflows economically (with a mandate for open access) and technically (with a need to comply with FAIR principles). As scientific and public institutions, NHIs have to ensure research to be easily accessible, interoperable and reusable to facilitate new research. The traditional way of publishing taxonomy and floras is still predominant and does not allow to easily reach the information needed to perform revisions and increase the biodiversity knowledge. Taxonomic papers are not only legal documents that determine the legitimacy of a name of a (new) species; they also cover every creation, description, modification, and use of a taxon. It is crucial to link the information describing a taxon and its history. We present the latest development in publishing, how to semantically structure floras and taxonomic papers to extract (and thus link) all essential parts of the information. Based on a single-source publishing model, the XML file enables to automatically enrich text, and structure domain-specific sections of articles (e.g., Material and methods; Taxon names; Material examined). We demonstrate how the publication can be processed to obtain high quality-controlled biodiversity data extraction and ensure it to be directly usable within WFO as soon as published, and how it enhances the editing of the paper and controls the data before its publication.

S.76.4 Access to the data imprisoned in 500 Million pages of biodiversity publications

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Scientific knowledge about biodiversity is included in billions of statements in an estimated daily growing corpus of 500 million published pages including all the known taxa. All statements are linked by taxonomic names, thus playing a key role in organizing this knowledge, and to access it. Traditionally access has been through the citation of a publication. In the digital age, direct access to the cited statement, such as to taxonomic treatment, material citation, figure, or trait as FAIR (Findable Accessible, Interoperable, Reuseable) data is possible and desirable, especially to leverage the power of machines, and to enable artificial intelligence applications to support research and other usages. A way to make this happen is to annotate the texts with terms that describe the content, such as taxonomic name, collector, material citation, taxonomic treatment for which reference vocabularies exist such as Darwin Core or Taxpub/JATS. In a more advanced step, terms can be linked to references such as the extended catalogue of life, World Flora Online, International Plant Name Index for taxonomic names, or digital copies of cited specimens in the Global Biodiversity Information Facility, DiSSCo or individual collections, or treatments to the Biodiversity Literature Repository, using persistent identifiers. Detailed annotations allow automatic extraction of statements to populate databases such as WFO, GBIF, or ChecklistBank. They can be used as training corpus to teach algorithms to annotate the overwhelming corpus of literature that is currently not accessible digitally. In this presentation an introduction to annotations is provided, and the workflow and access developed by Plazi to annotate and FAIR-izise publications is described, resulting in over 800,000 taxonomic treatments, 450,000 figures in the Biodiversity Literature Repository of which 45,000 datasets are reused by GBIF and ChecklistBank, and over 500,000 treatments in the biodiversity PMC.

S.77 PATTERNS AND PROCESSES DRIVING CLIFF PLANT COMMUNITIES: APPROACHES FOR THE CONSERVATION OF ENDEMIC CLIFF FLORA. SESSION 1

S.77.1 Unravelling evolutionary events that shaped plant life in cliff habitats: the Iberian endemic genus Petrocoptis (Caryophyllaceae)

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Cliffs are fragmented environments that host a great diversity of specialist plant taxa, often with narrow distribution areas. Despite being harsh environments for plant life, they played a key role as refugia during the climatic and topographic changes of the Cenozoic, representing nowadays reservoirs of relict biodiversity. Besides, the challenging conditions that plants have to face in these habitats seem to have promoted radiative diversification of some rock specialist lineages. Here, we focus on the paradigmatic case of Petrocoptis A. Braun ex Endl. (Caryophyllaceae), a genus of chasmophytic plants endemic to the limestone cliffs and overhangs of the northern Iberian Peninsula. In order to try to shed light on the evolutionary processes that may have contributed to shape vascular plant life on vertical rocks, we reconstructed the phylogenetic relationships within the genus following both a target enrichment sequencing and genome skimming approach (i.e., Hyb-Seq). In addition, we measured a set of morphological traits, particularly those referred to seed morphology. The data obtained allowed reconstruction of the whole plastid genome and revealed an evolutionary history that shows strong geographic signal across the genus, which evidences very limited seed dispersal, strong isolation and vicariance, even at population level. The nuclear phylogeny does not generally show such a strong geographic pattern, probably due to higher pollen flow, and supported most of the previously accepted taxa. The integration of morphological data further contributes to support the idea that high phenotypic plasticity may be a key strategy for long term survival of lineages. Finally, we discuss the potential role of this "each valley apart" evolutionary strategy as responsible for the great richness of (narrow) endemics that mid-altitude rocky habitats harbour in the Iberian Peninsula and Mediterranean region, and its implications for plant conservation.

S.77.2 The importance of population size in mating system and genetic differentiation of a narrow endemic chasmophyte

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The mating system plays a crucial role in shaping the genetic structures within and between plant populations. In this study we present *Moehringia tommasinii* (Caryophyllaceae), a chasmophytic plant species with a limited range in the northwestern Adriatic region. Our research focused on examining the population biology of the species by studying all five extant populations. Additionally, we included populations of the co-occurring and much more widely distributed *M. muscosa*, a closely related species with distinct ecological characteristics. To investigate mating patterns, we conducted reciprocal crosses within and between these two taxa. Molecular markers were also utilized to estimate gene flow within populations and between taxa. Our investigation considered various factors, such as the coefficient of inbreeding, population size, seed weight, pollen-to-ovule ratio, flower display size, and the presence of a selfing syndrome. Contrary to our expectations, a high variation in mating systems was observed among populations of M. tommasinii. These populations demonstrated genetic structuring, with population size positively correlated with both seed weight and pollen production. Although a selfing syndrome could not be confirmed due to the majority of selfing resulting from allogamous treatments, the occurrence of selfing was notable. In the presence of *M. muscosa*, particularly in a closely coexisting site, a distinct pattern of fruit production was observed in *M. tommasinii* following various pollination treatments. Molecular and morphometric data provided evidence of hybridization followed by local extinction at this site. Population size emerged as the key factor influencing the mating system in genetically structured populations of M. tommasinii. While populations with higher selfing rates exhibited lighter seeds and reduced pollen production, these traits did not conclusively indicate the presence of a selfing syndrome. The detection of gene flow between *M. tommasinii* and sympatric *M. muscosa* suggested weak reproductive barriers between these taxa, potentially posing conservation challenges

S.77.3 Patterns of evolutionary diversification in cliff-associated plants

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Mediterranean cliffs host unique plant communities composed of taxa with a great adaptive capacity to the severe environmental conditions of these ecosystems. For millions of years, cliffs have been acting as climatic and ecological refugia for an outstanding diversity of species, promoting their specialization. This led to species of high evolutionary interest, which may show high differentiation from their sister generalist relatives. Yet, little is known about these diversification processes promoted by the specialization of plants in cliff ecosystems. In this study, we focus on plants appearing on cliffs of the Iberian Peninsula and Balearic Islands, within the plant diversity hotspot of the Mediterranean region. The aim is to investigate their cliff-affinity and relevant functional traits from a phylogenetic perspective. We extracted a list of 1,398 Iberian taxa of vascular plants potentially inhabiting cliffs from the reference work for the flora of the study area, Flora iberica. To evaluate their degree of cliff-affinity, we contacted 94 experts. A total of 32% of the taxa had cliffs as their preferred habitat and we confirmed that 127 species (9%) grow exclusively on cliffs. As cliff-specialist plants may present a series of efficient strategies and traits to survive in cliffs, we also gathered different ecologically relevant traits for all species, including plant-size, seed-size, flowering period, and altitude range of distribution. After reconstructing a PHYLOMAKER based phylogeny with the majority of the listed taxa, the phylogenetic signal regarding cliff-affinity and selected traits was tested. We also investigated the effect that the degree of affinity has on the different relevant traits under a phylogenetic perspective. Our contribution present and discuss the resulting phylogenetic patterns, helping to improve the understanding of the processes leading to cliff specialization in Iberian flora, and unravelling evolutionary divergences in cliff ecosystems.

S.77.4 Ecology on the rocks: stories from cliff faces in the southeastern USA

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Cliffs harbor unique ecological communities yet face increasing pressure from human disturbance. The Southern Appalachian Mountains (USA) are a biodiversity hotspot for North America, but little is known about regional cliff biota. Many factors shape cliff vegetative communities, including natural variation in slope and surface heterogeneity, and anthropogenic disturbances like rock climbing. However, the interaction between abiotic variability and anthropogenic pressures is largely uneplored. The Southern Appalachian Cliff Coalition (SACC), based in western North Carolina, has been investigating cliff ecosystems of the Blue Ridge since 1997. Much of this work remains unpublished. This talk outlines results from three important SACC cliff studies of cliff vegetation and the impact of rock climbing. We share best-practices for cliff sampling and monitoring, offer recommendations for mitigating the impacts of hiking and rock climbing, and outline future directions for cliff research.

S.77.5 Present and future distribution of insular cliff vegetation in the Balearic Islands

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The study of cliff ecology has long revealed the rich biodiversity of these habitats and their susceptibility to climate change. Similarly, island ecosystems are recognized for their unique biodiversity and high rates of endemism but are also significantly impacted by human activities. This research focuses on the intersection of these two areas: the unique and highly vulnerable insular cliff communities. We conducted an in-depth examination of the spatial distribution of cliff vegetation in the Balearic Islands, identifying key environmental and climatic factors that shape these habitats. Using the WorldClim database, we projected future changes in spatial distribution. Our findings highlight the mountains and coasts as the most suitable habitats, particularly Mallorca's Serra de Tramuntana mountain range. Looking ahead, our models predict that the spatial distribution of cliff vegetation will remain stable in the mountain ranges where habitat suitability is high but will decrease or disappear in other less favourable areas between 2021 and 2040. By 2081-2100, the only areas predicted to be well-suited for cliff vegetation are the high-elevation mountains north of Mallorca. These findings underscore the vulnerability of these habitats to climate change, particularly their susceptibility to aridity and the strict habitat suitability requirements, such as steep slopes. As such, future research should focus on analysing individual species to assess if any cliff specialist species are at risk of extinction due to climate change. This research contributes to our understanding of the spatial distribution and vulnerability of insular cliff vegetation, providing valuable insights for conservation efforts.

S.77.6 Climate change and the future of cliff specialist plants

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Existing plant lineages may have experienced several climate changes during their evolution, and they may have acquired strategies to cope with them. According to many indicators, our planet currently undergoes a very intense warming, which might accelerate extinction rates if plant species cannot adjust fast enough by either migration or adaptation. Cliff environments and their specialist plants are particularly relevant in this context, because they often have limited migration capacity, so their adaptive response might be intense. In this contribution, we present data derived from several experiments conducted with 11 taxa of the chasmophitic Iberian endemic genus *Petrocoptis* (Caryophyllaceae) investigating seed morphology, germination and their interaction with climate. All the species included in the genus showed high viability and *in vitro* germination rate, a couple of traits that might be adaptive in limiting substrates for plant stablishment such as cliffs. In general, warm temperatures decreased *in vitro* germination rate, except for species and populations from warmer climates. We detected a significant mother plant effect on the response of seed germination to temperature, and seeds from mothers behaving contrary to the main population trend were recurrently found. Interestingly, *Petrocoptis* seeds have a hygroscopic strophiole whose size in natural populations is associated with climate. We also conducted common garden and reciprocal *ex situ* cultures of *P. crassifolia* in a 1000-meter altitudinal gradient with contrasting climate. We confirmed the germination dependence on humidity but detected a high tolerance of the species to dry climates once plants were established in the pots. Overall, these results point at population level plasticity as one of the key drivers of cliff plant survival to changes in climatic conditions.

S.78 SYSTEMATICS AND EVOLUTION OF LAMIALES. SESSION 1

S.78.1 Revisiting the classification of Plantaginaceae based on a nuclear phylogenomics

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Plantaginaceae have given rise to discussions about their phylogeny for decades. Established by de Jussieu over 200 years ago, including three genera, the family grew massively to around 107 genera, mainly by including parts of the Scrophulariaceae but also several small families. This circumscription has not changed in the past 20 years, when the first molecular studies targeting those families were published. Nevertheless, despite ongoing research, relationships among genera and tribes are still unresolved, letting the discussion smoulder on until today. Resolving the family-wide phylogeny is the next step to get a more complete picture of the relationships between the included genera and forming tribes as well as helping to place genera within the order of Lamiales. Since the last family-wide analysis was lacking some genera, this study includes some genera for the first time (e.g. *Gadoria,* Antirhineae or *Umbraria*, Gratioleae). To achieve a more complete picture, herbarium samples were used from nearly all genera possibly belonging to the family; large genera were covered by multiple samples. Target sequences were captured via the angiosperms353 toolkit and sequenced by HybSeq. The presentation provides the most complete and reliable analysis up-to-date. The major changes within the family of Plantaginaceae are highlighted together with a discussion about the evolution of the family.

S.78.2 The pangenome of the genus Antirrhinum

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Pangenome analysis can capture structural variants present in genomes from across a group and can be used to understand the evolution of species. Species in the genus *Antirrhinum* (Snapdragons) have been split into three morphological sections, relating to their ecology: *Antirrhinum*, *Streptosepalum* and *Kickxiella*. Section *Antirrhinum* and *Streptosepalum* species are tall, upright grassland plants, whereas section *Kickxiella* are small, prostrate alpines. Phylogenetic analyses indicate there was a basal split of section *Antirrhinum* from sections *Kickxiella* and *Streptosepalum*, but there has been a second independent evolution of *Kickxiella* morphology from within the section *Antirrhinum*. We examined how sharing of genomic structural variants between species provides insights into the evolutionary history of the genus. Long read genome sequencing and assembly was carried out for a species from section *Streptosepalum*, and two species from section *Kickxiella*. Using these genomes, as well as two *Antirrhinum* genomes previously published, a multispecies pangenome was generated and used to identify structural variants. Whole genome short read sequences from samples across the genus were mapped to the pangenome to determine if the identified structural variants are shared by species within an *Antirrhinum* section. This allowed us to gain insights into the evolution of the *Kickxiella* species.

S.78.3 When light is optional: How Orobanchaceae challenges conventional wisdom in plant evolution

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A plant's life is a constant battle for light and water. This autotrophic lifestyle has not only defined Viridiplantae but also profoundly shaped their body plan, physiology, reproduction, and genome. Yet in more than 4000 parasitic species, shifts to heterotrophy have fundamentally altered the selective regime for plants and left major evolutionary footprints. Features that are otherwise rare at the molecular level and beyond have evolved repetitively, including reduced vegetative bodies, shrunk gene repertoire, and an abundance of alien genes. Drawing from my previous work in parasitic plants, I recently proposed a conceptual model to attribute these convergent and predictable evolutionary trajectories to the cascading effects brought about by the loss of photosynthesis. Using Orobanchaceae as a model system, I demonstrate at both molecular and phenotypic levels how repeated losses of photosynthesis in this family have led to convergent evolution in the genome and vegetative architecture. This family contains c.a. 2,300 species spanning the entire spectrum of parasitism from free-living species to non-photosynthetic holoparasites. In particular, I focus on the understudied mitochondrial genome and present the first comparative study of leaf architecture in this family. I also talk about future plans to use this family as a model to study species interaction from analytical chemistry, community ecology, macroevolution, and historical biogeography perspectives.

S.78.4 Phylogenomics sheds new light on the systematics and biogeographic history of the figwort family Scrophulariaceae

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Scrophulariaceae once was the largest family of Lamiales as the order is currently circumscribed, but was based on traits that are ancestral for much of Lamiales. Previous molecular studies identified several unrelated clades within a polyphyletic Scrophulariaceae that are now included in other families, or recognized as separate families, and identified clades previously unassigned to Scrophulariaceae that belong within it. However, uncertainties remain about relationships within Scrophulariaceae, as well as the timing and pattern of diversification of this cosmopolitan clade. To address these questions, we developed a probe set based on five Scrophulariaceae transcriptomes to conduct a target-sequencing approach for phylogenetic analysis of 66 species representing all recognized tribes of Scrophulariaceae plus three genera unassigned to tribe, *Androya*, *Camptoloma*, and *Phygelius*. Ten tribes are recognized based on the resulting phylogeny. Diversification of crown Scrophulariaceae was inferred to have started in the southern hemisphere approximately 60 Mya. A southern African origin is estimated for most tribes with two exceptions, Leucophylleae and Myoporeae. Multiple dispersal events out of Africa gave rise to the contemporary distribution of Scrophulariaceae.

S.78.5 A global phylogeny of the genus Phlomoides (Lamiaceae, Lamioideae)

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As currently circumscribed, *Phlomoides* included seven traditionally defined genera, making the genus is the second largest and perhaps most taxonomically challenging genus within subfamily Lamioideae (Lamiaceae). The genus has undergone major species radiation in Central Asia, the Iranian highland, and China. To date, a robust and broad phylogeny of *Phlomoides* remains absent. Moreover, given the myriad new additions to the genus, the existing infrageneric classification needs to be evaluated and revised. In this study, we attempted to elucidate the phylogenetic relationships within *Phlomoides* using complete plastome sequences and nrDNA regions with a broad taxon sampling of ca. 80% species of the genus. We employed Maximum likelihood (ML) and Bayesian inference (BI) methods to reconstruct the backbone phylogeny of *Phlomoides*. Our results revealed largely congruent topologies of plastid and nuclear DNA data sets, and six major clades were recognized. Several morphological characters (i.e., the root type, appearance of basal leaves, shape of basal and floral leaves, the shape and size of floral bracts, the shape of calyx teeth and spines, the appendages of filaments, the lobes of style, etc.) support the phylogenetic conclusions, indicating the genus can be subdivided into six sections. Hybridization and incomplete lineage sorting may represent potential sources of the incongruence between the plastome and nrDNA data. A purposely integrative design to explore the taxonomy within the genus is required in future.

S.78.6 Toward a synthetic classification of Lamiales

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Nearly ten percent of angiosperm diversity is included in Lamiales, making it one of the largest of all orders. Representatives of this order can be found in nearly all ecosystems around the world and many are well-known for their economic value. This group presents wide morphological and ecological diversity, from aquatic herbs to large trees, and even specialised strategies like parasitism and carnivory. This variation alongside convergent evolution has led to a turbulent taxonomic history, with familial circumscriptions being constantly redrawn even until the present day. Understanding the affinities among lineages of Lamiales has also been challenging, with many inter- and intrafamilial relationships still unknown. In light of these issues, there is a need to undertake deeper research on the phylogenetics of Lamiales not only to understand plant evolution but also to answer questions in related fields such as biogeography and ecology. Understanding of relationships in the order has been impaired by (1) incomplete sampling (at least at generic level); and (2) the abundance of evolutionary processes that affect phylogenetic reconstructions, like rapid radiation, incomplete lineage sorting, reticulation and whole genome duplication. These barriers are now being overcome with the help of modern high-throughput sequencing strategies, large-scale nuclear data and more robust phylogenetic methods. Using the most up to date phylogenomic tree of Lamiales, underpinned by the data produced by the Plant & Fungal Trees of Life (PAFTOL) project at the Royal Botanic Gardens, Kew, we establish a new phylogenomic baseline for Lamiales and reassess the boundaries of families and infra-familial taxa, with the aim of produce a synthetic and stable classification of the order.

S.79 SPATIAL MODELLING OF PLANT NICHES AND DISTRIBUTIONS IN THE ANTHROPOCENE. SESSION 1

S.79.1 Predicting future distribution of an ecoregional invasive species pool with habitat suitability and dispersal modeling techniques

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Biological invasions are causing massive ecological, social, and economic impacts worldwide. Understanding the ecological factors that affect the regeneration of invasive plants is critical to improving action plans that limit the establishment and dispersal of such species. In this study we combine Species Distribution Models (SDMs) with greenhouse experiments to evaluate the regeneration niche of the plant invasive species pool at the regional scale. The central hypothesis is that plant niche, both realized (i.e., current distribution) and potential (i.e., based on dispersal and regeneration), is highly influenced by ecosystem characteristics and plant traits. As the study system, we use the Atlantic region of NW Iberian Peninsula, an ecoregion with high biodiversity value and optimal conditions for the spread of invasive plants in Europe. With a combination of local literature, expert knowledge, and evidence from scientists and managers, we created a complete list of invasive plant species in the ecoregion (~170 species). We used a hierarchical SDM approach to analyze how environmental predictors affected habitat suitability for each species. Using occurrence and environmental data from European and global databases, we found that climatic and soil variables were good predictors of habitat suitability. To evaluate the potential regeneration niche, we combined the habitat suitability estimates for each species with extensions of SDMs implementing dispersal constraints into species projections. Dispersal limitation was approached by estimating geographical barriers, dispersal kernel, and frequency of long-distance dispersal events. We found that dispersal rates across the study ecoregion were species-specific and dependent on species ecological requirements and dispersal potential. Lastly, we conducted greenhouse experiments with the most successful invasive species to evaluate the effect of temperature, water availability, and plant traits on plant regeneration. We found the ecological thresholds for germination and early growth, as well as positive maternal effects on offspring performance.

S.79.2 Unveiling niche-based responses and patterns of local occupancy of dryland species

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Alterations in climate and land use are key drivers of global environmental change in drylands. Understanding the responses of dryland biodiversity to these novel stressors is imperative due to their extensive coverage and their importance in providing key ecosystems services and supporting many human populations. Such importance is further exacerbated due to the high number of endemic species that are unique to these environments. In this study, we explore the Grinnellian niches of the more than 1,500 plant species that inhabit the most important dryland ecosystems worldwide, extracted from BIODESERT dataset. We downloaded and filtered species' occurrence locations from GBIF and BIEN data portals. Then, we used ensembles of Environmental Niche Models (ENMs) to represent the Grinnellian niches of each species, built on an individual species-specific selection of uncorrelated predictors from a set of 74 variables accounting for climate, soil, and topography, at a 10km resolution for the entire world. To ensure a comprehensive representation of the environmental space, we generated pseudo-absences distributed proportionally across 10 strata derived from a Principal Component Analysis (PCA) of the original pool of variables. Finally, for each species, we projected the models onto each of the seven biogeographical realms where the species is currently found, with a presence threshold of at least 1%. This allowed us to validate model projections against the empirical data on dryland communities from the BIODESERT dataset and assess the extent to which potentially suitable locations align with the actual habitats of species adapted to dry environments. This analysis contributes to and may enhance a deeper understanding of the relationship between species' potential distributions and the establishment and sustainability of local populations in drylands, which can ultimately help informing ecosystem-level adaptation strategies to global change in extreme environments.

S.79.3 Species Distribution Modeling Beyond Boundaries: A Comparative Exploration of Hierarchical Strategies

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The heightened vulnerability of Spain's biodiversity, exacerbated by climate change, necessitates innovative ecological restoration initiatives. To guide these actions, we propose a spatially explicit, multidisciplinary tool accessible through an interactive website. The tool utilizes potential species distribution, ecological connectivity, and climate change vulnerability data for various woody and endangered plant species. Ensemble models, combining statistical algorithms, are developed within hierarchical multiscale frameworks covering Spain and Europe under different climate change scenarios. This tool identifies areas for restoration and prioritizes species, optimizing accuracy and applicability. Dynamic connectivity models pinpoint areas crucial for genetic exchange and dispersion towards anticipated distribution areas. By integrating these models with land-use data, priority restoration areas and recommended species are identified at a spatial resolution of 250m. Initial results for 108 species exhibit robust species distribution models (AUC > 0.8). The study anticipates tangible benefits in improved forest management and biodiversity promotion. In addressing challenges associated with species distribution models, our research investigates hierarchical strategies ('covariate' and 'multiply') to overcome spatial truncation issues. We compare their effectiveness against a non-hierarchical model exclusively trained with regional data, considering model performance, predicted range shifts, species richness trends, and extrapolation extent. Findings reveal that hierarchical strategies, particularly the 'covariate' one, outperform non-hierarchical methods in predictive performance and mitigate niche truncation and environmental extrapolation issues. Despite the 'covariate' strategy's superior performance, the study advocates adopting multiple hierarchical approaches to enhance reliability. This research emphasizes the importance of hierarchical strategies in overcoming niche truncation and extrapolation issues, challenging the reliability of non-hierarchical predictions. The results, consistent across diverse species and environmental scenarios, underscore the robustness of hierarchical approaches in improving species distribution modeling for effective conservation and restoration efforts.

S.79.4 GeoPl@ntBERT: modelling plant species assemblages and producing high-resolution maps of habitat types with large language models

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Biodiversity is under severe pressure, as many different disturbance events threaten organisms with extinction and ecosystems with collapse. Therefore, species and habitat distribution modelling are increasingly relevant. They aim to quantify the statistical links between environmental covariates and respectively species or habitat occurrences. Herein, we introduce GeoPl@ntBERT, a novel framework to model species assemblages and produce distribution maps for individual habitats. It leverages a sophisticated deep learning pipeline based on computer vision (convolutional neural networks) and natural language processing (transformers). In particular, it focuses on (i) image classification (plants assemblages are created based on satellite images and rasterized environmental data), (ii) fill-mask (predicted plant species are then translated in context into a modelled ecological process) and (iii) text classification (habitat types are finally assigned to sentences describing species compositions). To train and evaluate the models, millions of heterogeneous presence-only records recently collected by citizens coupled with hundreds of thousands standardized presence-absence surveys from a large database of vegetation plots were used. The resulting dataset covers over ten thousand different European vascular plant species. All steps are validated using a spatial block hold-out procedure (to account for spatial autocorrelation) and reach a high accuracy, as assessed by expert judgement. GeoPl@ntBERT represents a cutting-edge approach, offering a powerful tool for advancing our understanding of biodiversity dynamics and supporting conservation efforts.

S.79.5 Niche-based mechanistic models for spatiotemporal distribution of plant species

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There has been an increasing effort towards developing mechanistic models to understand biodiversity spatiotemporal dynamics and species response to environmental change. This has led to a variety of mechanistic models that vary in their properties, processes implemented and in the ecological level of the agents. This includes models that are niche-based, thus integrating environmental preferences of species, and that simulate agents at lower ecological levels (individuals or populations) across biogegraphical scales. Here, I provide an overview on cross-level mechanistic niche modelling, focusing on recently developed ecological and eco-evolutionary models for plant biodiversity applied to understand and predict species range dynamics across environmental gradients. Featured models are able to depict the distribution of plant species and metacommunities across vertical, depth and elevation gradients, including under natural or human-induced environmental change. These emergent patterns stress how the interplay of ecological traits, spatial processes and local interactions can cascade up to biogeographical levels. This is important, as ecological and evolutionary dynamics at large scales are difficult to experiment in real-world systems, but that can be tackled with dynamic mechanistic models and should be popularized for assessments under non-equilibrium conditions which will dominate the Anthropocene. For this purpose, R and julia packages for niche-based range models are showcased.

S.79.6 Toward hierarchical species distribution models to avoid niche truncation in future projections

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Species distribution models (SDMs) have become a major tool in biogeography, especially in the context of global change assessments. A key application of SDMs is to derive projections in time, e.g. under climate change. SDMs are also based on several assumptions, one being that to make such temporal projection, the full realized environmental niche must be captured. Yet, the niche has a high risk to be truncated if the geographic – and associated environmental – range used to fit the model is smaller than the range occupied by the species, leading to potential mistakes when making temporal projections. A solution to avoid such niche truncation is to build SDMs in a hierarchical nested way, from global to local. Such approaches have already been applied to SDMs, to model invasive species, to downscale large scale models, to support species conservation, or to improve climate change projections. They were recently implemented in the new N-SDM pipeline in R to derive predictions for large numbers of species. However, the importance of using such hierarchically-nested approach has remained rather hidden and confidential so far in the SDM literature. The aim of this talk is to present a review and synthesis of the developments up to now, and to identify solutions and remaining challenges.

S.80 EVOLUTION OF KEY INNOVATIONS IN LAND PLANTS REVEALED THROUGH THE LENS OF EVODEVO. SESSION 2

S.80.1 The investigation of the reproduction in Ginkgo biloba

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Ginkgo biloba is a dioecious gymnosperm belonging to one of the oldest seed plant lineages. A detailed morphological characterization of both ovules and male cones across all their development allowed us to identify the key stages of the reproductive process and the time and space of occurrence of pollination and fertilization. In gymnosperms, pollination and fertilization events are temporally separated (about four months in *Ginkgo biloba*), and during this time pollinated ovules undergo a process of development really intriguing and poorly investigated. *Ginkgo* ovules are windy pollinated: when pollen is ready to be dispersed from the pollen cones, ovules emit a pollination drop from the micropyle in which pollen is captured. The pollen can then enter into the ovule, at the level of the pollen chamber, and can germinate. The pollen tube elongates and penetrates into the available gaps among the nucellar cells, and shortly after, it develops a highly branched haustorial system that anchors the male gametophyte to the nucellar tissue to absorb nutrients and survive during the long time between pollination and fertilization. In the meantime, the ovule goes through a process of growth and development, and the single integument differentiates into the three layers of the seed coat: *sarcotesta*, *sclerotesta* and *endotesta*. Differently from angiosperms, indeed, the seed coat differentiation precedes the fertilization and thanks to our analyses, we pointed out that this process is triggered by pollination, highlighting the critical role of pollen perception and recognition for the further *Ginkgo* ovule development. We therefore believe it is really interesting to understand how the regulation of reproductive development occurs in *Ginkgo*, which are the main gene networks involved and how they interact with hormonal regulation. At this aim, we combine omics-analyses with *in situ* hybridization and immunohistochemical analyses.

S.80.2 Heterochrony and repurposing in the evolution of gymnosperm seed dispersal units

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Seed dispersal units allow the colonization of new environments, the expansion of geographic ranges and gene flow. Two broad categories of seed plant seed dispersal units are dry and fleshy. Knowledge of the anatomy and developmental genetics of fleshy diaspores is much advanced in angiosperms compared to gymnosperms. To improve understanding of the development of the accessory structures of gymnosperm seed dispersal units, we studied the anatomy and histochemistry of seed cone bracts of four species of South American *Ephedra* (Gnetales), three with fleshy bracts and one with dry, papery-winged bracts. We combined ontogenetic comparison of the anatomy and histology of both seed cone bract types to pollen cones and leaves with differential gene expression analysis by RNAseq. On the one hand, our results suggest that seed cone bract fleshiness derives from the accumulation of mucilage within chlorenchyma tissue, also present in juvenile leaves before reaching their mature dry state. Dry bract development, on the other hand, resembles that of leaves, with mucilage chlorenchyma cells turning into tanniferous cells early in development, and hyaline margins growing into “wings”. Differentially expressed candidate genes in the bracts of *E. triandra* during their transformation to the fleshy state included the downregulation of a glucose-hydrolase (polysaccharide degradation), and the upregulation of a pectate-lyase (pectin degradation) and DUF642 domain proteins. We propose an evolutionary model based on the repurposing of leaf structure and heterochronic changes in development, where fleshy and papery-winged seed cone bracts develop from a juvenile stage shared with leaves that diverges towards the pollination developmental stage of ovules. Thus, the ancestral fleshy state of *Ephedra*’s seed cone bracts investigated here represents a novel differentiation program co-opted from juvenile leaf anatomy, while the dry papery-winged derived state would arise from peramorphosis of a pre-existing mature leaf differentiation program.

S.80.3 Genetic changes underlying male gametogenesis evolution in land plants

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Formation of gametes is a prerequisite step for sexual production. Unlike seed plants with highly reduced haploid generation, in which male gametogenesis is confined to few-celled gametophytes (pollens) and sperm cells are delivered by pollen tube, non-seed plants, including bryophytes, lycophytes, and ferns, undergo serial well-defined changes between cell fate determinations and differentiations to produce flagellated sperm cells in elaborate gametophytes. The flagellate sperm cell is regarded as the ancestral trait of land plants and has been lost when seed plants arise with evolution of pollen. Taking advantage of *Marchantia polymorpha*, the model bryophyte species, we drive forward our understanding of genetic networks underlying male gametogenesis, by identifying key transcription factors regulating developmental switches of gametogenic progression. In this talk, we present our recent progress of male gametogenic regulation in *M. polymorpha* and will deliver an insightful understanding of male gametogenesis evolution in land plants, with a particular focus on evolutionary shift of gametophyte-dominant to sporophyte-dominant generation.

S.80.4 Exploring floral reversion in Cleome viscosa: a comprehensive case study on the unique transformation from flower to leafy structures

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Cleome viscosa, the Asian spiderflower, is a fast-growing annual herb with hermaphroditic features, part of the Cleomaceae family. Thriving in warm, humid environments, it prefers full sunlight and is often found in wet soils along roadsides and open areas. In traditional medicine like Ayurveda, it is used for liver ailments, joint pain, and mental disorders. Flowering occurs from August to November, depending on rainfall. An intriguing aspect is the rare floral reversion phenomenon, where floral organs transform into leafy structures. This implies that the flower is a modified shoot, activating shoot meristem into floral meristem, akin to mechanisms in Arabidopsis thaliana using the ABCDE model. Photographic and microscopic documentation reveals this unique transformation, with gynoecium and androecium turning into leaf-like structures. Post-reversion, the plant displays continuous growth, developing single leaves with alternate arrangements. Androecium modification shows leaf/filament or anther development with trichomes, and abnormal pollen grain development. Gynoecium transformation includes improper ovule development. These findings suggest floral reversion results from imbalanced expression of ABCDE genes or plant growth regulators. In conclusion, *C. viscosa's* exceptional floral reversion highlights its adaptability and genetic plasticity. This evidence contributes to our understanding of floral development, with broader implications for plant morphogenesis. Continued molecular investigations promise to advance comprehension not only in *C. viscosa* but in other plant species, fostering progress in plant biology research.

S.80.5 Zinc finger transcription factors in land plants - tracing half a billion years of evolution

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Zinc finger transcription factors are conserved in eukaryotes. The C1-1i ZnF–clade is known to act as transcriptional repressors during different developmental processes. Here we elucidate the evolution of C1-1i ZnFs by phylogenetic, transcriptomic and sequence analysis. Further, we seek to optimize phylogenetic studies on weakly conserved gene-families covering huge evolutionary distances while minimizing the loss of information by using different bio-informatic approaches.

S.80.6 Evolution and expression of the flowering integrator genes AGL24, SVP, and SOC1 in the endoholoparasitic Apodanthaceae

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Floral transition is crucial for successful plant reproduction. This is regulated by multiple genetic pathways activated by environmental and endogenous signals and unified by a limited number of integrators. While floral transitions have been extensively studied in autotrophic plants, less attention has been given to endoholoparasitic angiosperms, which lack stems and leaves; thus they cannot sense environmental signals to initiate the floral transition, yet they still manage to bloom. In this study, we explore how the Apodanthaceae (a family with 12 endoholoparasitic species) achieve this. To this end, we studied three key integrators (*AGL24, SVP*, and *SOC1*) involved in floral transition, in two members of the family, namely, the legume parasite *Pilostyles boyacensis* and the Salicaceae parasite *Apodanthes caseariae*. We identified *AGL24*, *SVP*, and *SOC1* homologs and assessed their copy numbers in the reference transcriptomes of endoholoparasites and their hosts. Subsequently, we determined their phylogenetic affinities. In *A. caseariae* we found one *AGL24A,* one *AGL24B,* and two *SVP* copies. Whereas *AGL24A* likely belongs to the host (Salicaceae), *AGL24B* and *SVP* genes appear to be endogenously transcribed by the parasite. No *SOC1* homologs were identified. In *Pilostyles boyacensis* we found at least one copy of *AGL24A* and *AGL24B*, along with five *SVP* variants, all of them likely belonging to the host (*Dalea cuatrecasasii*). We also found three *SOC1* copies in *P. boyacensis* transcriptomes; however, two belonging to its host, and one likely endogenous. Preliminary data from *in-situ* hybridization in *D. cuatrecasasii* and *P. boyacensis* point to extensive usage of host genes, especially *DacuAGL24A,* by the parasite. Conversely, expression of *D. cuatrecasasii SVP* homologs, the only flowering repressors found in the system, is low in both plants. Our results suggest that endoholoparasites achieve reproductive transition by utilizing specific transcription factors from the host.

S.81 ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS. SESSION 1

S.81.1 Sustainability of medicinal plants gathering in Spain: cultural importance, availability, and conservation status

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Around 7% of the 350,000 vascular plants species of the world are used, mainly as medicines (25,791) (RBG Kew, 2020). The consumption and harvesting of wild medicinal plants are increasing globally, both for self-treatment and for trading. This growing demand is leading to unmonitored commercial gathering and could result in the over-harvest of some species. However, the consequences of harvesting on the conservation status of medicinal wild plants are still barely explored. We have examined the relationship between a species' cultural importance (CI), availability, conservation status, and legal protection, to understand how gathering affects their sustainability. Spain is an ideal case study for this approach because of its rich biological and cultural diversity, which have led to a wealth of traditional knowledge about these plants. We found 1,376 species of medicinal plants with known applications in Spain, which accounts for over a quarter (22%) of the nation's total native vascular flora (16% of which is endemic). There was a positive correlation between species' CI and their abundance (r = 0.466) and area of occupancy (r = 0.495). Only 6% of the traditionally utilized wild medicinal plants in Spain are considered as endangered, and again, just 6% are totally or substantially subject to protection measures. In Spain, the majority of the species used for self-treatment are widespread, easily available, and not threatened. Our results indicate that domestic medicinal plant use does not lead to overexploitation and that traditional knowledge systems of management might safeguard the sustainability of the species. However, this may not be the case for wild species that are gathered for their commercialization.

S.81.2 From traditional mesoamerican use to global medicinal applications (Cempasúchil)

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The traditional use of *Tagetes erecta* L. (Asteraceae), commonly known as Cempasúchil, has been a cornerstone of Mesoamerican ethnobotany, revered in ceremonial and medicinal contexts. This study delves into the historical and ethnobotanical trajectory of T. erecta, tracing its journey from pre-conquest Mesoamerican uses to its current global recognition in pharmacological realms. Originally endemic to Mexico, T. erecta was extensively used in rituals and healing practices associated with Tlaloc, the rain god. The Spanish conquest catalyzed a pivotal shift, recontextualizing this species as an ornamental entity in Europe, known variably as African marigold or African tansy. Linnaeus' classification integrated this species into Western botanical nomenclature, broadening its recognition. The discovery of lutein in T. erecta in the early 19th century marked a significant transition, illustrating the plant's potential in phytotherapy, especially for macular health. Its inclusion in pharmacopeias and designation as Generally Recognized As Safe (GRAS) in the USA signify its dual role in traditional medicine and modern applications, including its economic impact in sectors like poultry feed due to its carotenoid richness. This paper emphasizes the importance of ethnohistorical, pharmacological, and cultural perspectives in understanding the multifaceted roles of T. erecta. It underscores the need for sustainable conservation strategies to preserve traditional uses while fostering modern applications. The global dissemination of T. erecta, intertwined with cultural, historical, and scientific narratives, offers a unique case study in the broader field of ethnopharmacology, highlighting the dynamic interplay between traditional knowledge and modern scientific inquiry.

S.81.3 Current status and future perspectives of ethnobotany in Pakistan

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Ethnobotany is the study of the dynamic relationship between humans and plants that has developed over thousands of years. This particular form of botanical research plays a key role in identifying and preserving traditional knowledge systems, which can lead to the loss of invaluable original knowledge if ignored. Ethnobotanical research focuses primarily on documenting and preserving traditional wisdom, but it also acts as a bridge between traditional knowledge and advanced scientific methodologies. Pakistan is a country with diverse ecosystems and rich bio-cultural diversity. A number of ethnobotanical studies have been conducted on various ethnolinguistic communities throughout the country, mainly in the northern and northern mountainous regions. These studies reported various uses of plants for medicinal, food, cultural, ritual, economic and other purposes. This knowledge has proven invaluable in the identification of potential medicinal compounds, the sustainable management of natural resources and the conservation of local biodiversity. Although ethnobotany is an emerging field in Pakistan, socio-economic changes, climate change and habitat destruction are major challenges that threaten both traditional knowledge and plant biodiversity. Therefore, the future of ethnobotany in Pakistan requires a holistic approach that combines traditional ecological knowledge with modern scientific methods to develop sustainable resource management, biodiversity conservation and economically viable solutions for local communities. Looking ahead, the prospects for Ethnobotany in Pakistan are as follows: a) Active collaboration between ethnobotanists, indigenous peoples and policy makers to develop effective strategies for sustainable conservation and use of bioresources. This strategy aims to achieve a more harmonious balance between human activities and the environment by incorporating local perspectives into conservation strategies and policy frameworks. b) Integrating modern technologies such as GIS mapping and molecular analysis to advance ethnobotanical research. Advanced technologies and data analysis provide opportunities for the systematic documentation and dissemination of ethnobotanical information, which improves its accessibility and usefulness.

S.81.4 The traditional knowledge's dynamism: the first ethnobotanical border study in Valmalenco (Italy) and Valposchiavo (Switzerland)

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Alpine regions are characterized by a rich and complex biodiversity, strictly connected to a distinctive legacy of centuries-old Local Ecological Knowledge (LEK), which led local people to the preservation of autochthonous plant species and their traditional uses. Peripheral Alpine border areas represent a typical hotspot to immortalize the dynamic evolution of LEK, which adapted over time to the threat of climate and socio-economic changes. Within the framework of the European Interreg Italy-Switzerland B-ICE & Heritage and GEMME projects, an ethnobotanical border study was conducted in Valmalenco (Northern Italy, Sondrio) and in Valposchiavo (Switzerland, Canton of Grisons). From 2019 to 2023, semi-structured interviews and participant observation were performed to evaluate the dynamism of LEK circulation across this border. Quali-quantitative analyses of the primary data were performed through pivot tables and ethnobotanical indexes, after database archiving. 470 inhabitants were interviewed, highlighting the use of more than 200 plants (70 families), employed in 10 sectors of use. LEKs differences surfaced among the most cited species: in Valposchiavo, *largù* (resin of *Larix decidua* Mill.) was used to prepare an ointment for thorns and splinters, in Valmalenco its wood represented a natural resource in home-building; since ancient times, in Valmalenco, the decoction of *daneda*'s inflorescences (*Achillea moschata* Wulfen) has been a daily remedy for dyspepsia disorders, and the Swiss remember *malenca* people crossing the frontier during World War II to harvest its flowers as a source of income; elderberry was used in Valmalenco as ink; St. John's worth oleolite for otitis as a peculiarity of Swiss border tradition. Despite the same natural environment, socio-economic and historical contexts may have influenced the bio-cultural popularity of traditional uses in Valmalenco and Valposchiavo. At the same time, homogenization may have occurred between the two LEKs over time, leading to the sharing of plants and popular uses.

S.81.5 Is ethnobotanical knowledge conserved in space and time? A case study in rural Kurdish communities in Iran

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Iran is an important hotspot of biological and cultural diversity with over 8000 species of vascular plants and seven major and many minor ethnic groups. Kurds are a major ethnic group in Iran, that inhabit mainly the country's West. Due to the turbulent second half of the last millennium, many Kurds have been resettled in East and Southeast Iran. Kurds are known for their rich record of traditional ethnobotanical knowledge. It is however unknown if the resettled rural Kurdish communities, especially in remote areas under conditions of cultural assimilation could preserve their original herbalism. We have collected data in 32 Kurdish rural communities in NW Iran and in 22 resettled assimilated rural Kurdish communities in Baluchestan (SE Iran) using ethnobotanical field techniques with a total of 124 informants, collected plant material and compiled databases. The results were used to conduct: a) descriptive analysis to compare qualitative data, b) statistical analysis to compare the numbers of use-reports and species in each group and understand consensus among indigenous people. We have documented in detail the use of 282 medicinal plants for 19 different disease categories. We analyzed potential ethnobotanical links between the two community groups and explored, if 2-3 centuries of resettlement and the drastic change of habitat and surrounding

flora have affected their ethnobotanical knowledge. The complexity of the social structure and the history of the resettlement of the Kurds in Baluchestan, as well as the abrupt change of environment, the linguistic assimilation and the different socio-economic development of both regions has differently affected the ethnobotanical knowledge of both groups. While Kurds in Baluchestan have experienced ethnocultural and ethnobiological assimilation, Kurds in NW Iran have primarily been affected by the continuing loss of ethnobotanical knowledge due to increasing urbanization and the development of the healthcare system.

S.81.6 Early Modern Jesuit Materia Medica, current Philippine remedies: Medicinal plants from Klein's Remedios Faciles (1712)

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Recent literature on Philippine botany has illuminated previously neglected histories of missionary scientific activity during the Spanish colonial period. Between c.1562 and 1815 the archipelago served as the Spanish 'East Indies' from which the Manila-Acapulco galleon trade operated as the critical link between Asia and Nueva España. This paper investigates the medicinal plants prescribed in *Remedios Fáciles* (1712), the most comprehensive surviving representation of missionary medicine during the Spanish period of the Philippines. Written by Bohemian Jesuit Paul Klein (Hispanicised name Pablo Clain), this manual of 'easy remedies' was intended to arm future Jesuit missionaries with the medical knowledge necessary for evangelisation, even without access to the materia medica in the Jesuit apothecary in Manila. Drawing from historical botanical collections, unpublished manuscripts, missionary notes, and archival records, we present case studies from Klein's manual of Philippine medicinal plant uses from the 17th century to the present day and discuss the challenges of linking historically used medicinal plants to modern-day collections and botanical research.

S.82 PLANT DIVERSITY, BIOGEOGRAPHY AND EVOLUTION IN THE TROPICS FOR CONSERVATION, RESTORATION AND SUSTAINABLE USE. SESSION 2

S.82.1 Perspective of change in abundance of floral species utilized by communities and their spatial configuration

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The Polillo Islands in the Philippines is one of the 228 Key Biodiversity Areas in an archipelago of more than 7,107 islands and islets. An island which is an important socio-ecological system (SES), the various provisioning services of the seascape ecosystem is provided by associated diverse floral species, 52 of which are directly or indirectly utilized for various purposes including for their medicinal (i.e.,*Antidesma bunius, Barringtonia asiatica, Bruguiera conjugate, Diospyros multiflora, Hanguana malayana, Hernandia ovigera, Intsia bijuga, Jatropha curcas*), domestic (*Avicennia officinalis, Casearia fuliginosa, Diospyros discolor*) and nutrition (*Caulerpa lentillifera, Ceanothus asiaticus, Diospyros discolor*). The change in abundance through community perspective shows that most (65.38%) are perceived to have been in decline including *Agave americana, Avicennia officinalis, Barringtonia asiatica, Basella alba, Bruguiera conjugate, Calophyllum inophyllum, Calophyllum obliquinervium, Casearia fuliginosa* followed by 23.07% perceived to be stable (*i.e Aegiceras corniculatum, Antidesma bunius, Bruguiera cylindrical, Ceanothus asiaticus, Dentella repens*) and 11.58% were believed to have been increasing (*i.e Alstonia macrophylla, Caulerpa lentillifera, Cymbidium finlaysonianum*). Overlaid with spatial distribution and fragmentation analysis, there is a declining seascape and increasing fragmentation which could have contributed to the change in abundance of the species utilized by communities within the study site. The seascape elements changed with a loss of natural seascape and gain for human habitation and agriculture as well as the reduction of complexity with the changing of beach forest and mangrove areas towards lesser diverse ecosystems as part of the ecosystem response to perturbation where grasses and shrubland replaced beach forest and mangroves. The reduction of natural seascape translates to changing configurations measured by fragmentation indices including Percentage of Landscape (PLAND), Largest Patch Index (LPI), Landscape Shape Index (LSI), Proportion of Like Adjacencies (PLADJ), Patch Cohesion Index (COHESION), Effective Mesh Size (MESH).

S.82.2 Disentangling causes of species dominance in western Amazonian forests from a functional trait perspective

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Many studies have documented dominance by few species in Amazonian forests, but the underlying mechanisms of tree species dominance remain unclear. Given the key role that these dominant species play in crucial ecosystem processes, clarifying the causes of dominance is essential to understand how Amazonian forests will respond to global change drivers. Here, we used an extent plot network encompassing contrasting habitats in Amazonia to study the ecological processes underpinning dominance through the study of their functional traits. We asked whether: 1) dominant species have a different functional profile than non-dominant species and 2) functional traits capture species differences in dominance patterns. We considered six plant functional traits through the compilation of trait information from different projects: specific leaf area (SLA), leaf area (LA), N content per unit leaf mass (LN), maximum diameter at breast height (DBH_{max}), wood density (WD), and seed mass (SM). We found that dominant species can reach greater maximum size than non-dominant species and that trait combinations of dominant species varied between habitat type. Additionally, we found that larger dominant species had higher regional frequency, associated with higher dispersal ability, and lower local abundance, likely due to negative density dependence. Greater SM allowed higher regional frequency of dominant species via greater dispersion and seedling survival. Finally, traits related to resource conservative strategies favored higher local densities, whereas the opposite pattern was linked to higher regional frequency. Our study reveals the potential of trait-based approaches in the study of the ecological mechanisms underlying dominance in tropical forests. Our findings highlight the importance of forest habitat conditions in shaping species dominance. Accounting for both local abundance and regional frequency when studying dominance can improve our understanding and forecasting of species responses to global change drivers and help us to effectively direct new conservation policies in Amazonia.

S.82.3 Scalesia (Asteraceae): ecology and evolution of the most iconic plant genus in the Galapagos Islands

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Darwin's daisies (*Scalesia*, Asteraceae) form an iconic radiation of 15 species endemic to the Galapagos Islands, which are distributed throughout this tropical archipelago. Among them, eight species are endemic to a single island, with small populations distributed across only tens to hundreds of hectares. Our oral presentation will describe an overview of unique findings related to the phylogeny, ecology, distribution and conservation of this emblematic group, summarizing more than 13 years of research. Diversification of extant *Scalesia* species and active phenotypic and genomic evolution appear to have occurred in recent times, specifically in the late Quaternary. However, the present survival and conservation of *Scalesia* species are at high risk, as shown by establishment rates reduced to 5% when competing with invasive plant species. Also, for the first time, we present the most updated distribution maps and ecological niche information for this taxonomic group. We finish by presenting ongoing research and future avenues for the study of this unique plant group. With this presentation, we hope to fill an important gap of information regarding Galapagos plants, particularly for one of the least studied groups of these iconic islands, which serves to create new international collaborations and attract more botanical research on one of the most interesting daisy groups.

S.82.4 Forest typologies in Central Africa based on commercial logging inventory data unveil heavily biased compositional patterns

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In Gabon, that hosts the best-preserved forests in western Central Africa, we lack a consistent and data-driven floristic regionalization needed to design conservation and management strategies. Existing forest typologies rely on logging inventory data which only include a small subset of the canopy tree diversity. Studies demonstrated that the canopy in large parts of Central Africa is dominated by long-living pioneer species that echo widespread historical human disturbance, paleo-climatic disturbances during the Last Glacial Maximum or a combination of both. Additionally, the canopy composition has been altered by industrial logging that selectively extracts large individuals of a few but widespread species. We thus hypothesize that (a) existing typologies draw a heavily biased picture of present-day tree compositional patterns and (b) that the canopy floristic composition is less dependent on environmental factors than the understory. Using a unique dataset comprising 466 vegetation transects inventoried across Gabon including 129,876 trees with a diameter at breast height ≥ 5 cm, we produced two continuous categorical maps, one by excluding and a second by including the understory composition. We identified forest types through hierarchical clustering of the floristic composition of transects and predicted forest types based on environmental and anthropogenic variables obtained through free available raster data through spatially explicit randomforest models. We tested for the importance of each predictor in the model. The V-measure was used to compare both maps and each respective map to those from the literature. The both-strata typology and the canopy typology are incongruent while the latter resembles existing forest typologies more strongly than the former. Human activity variables were of greater importance in predicting canopy-based compared to both-strata-based forest types. Our results emphasize the importance of integrating the understory composition when aiming at unveiling floristic patterns in Central Africa for it is less altered by historical successional dynamics.

S.82.6 Floristic and structural distinctness of monodominant Gilbertiodendron dewevrei forest in the western Congo Basin

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Within the tropical lowland rainforests of central Africa, there is a tree species, *Gilbertiodendron dewevrei,* that forms stands in which up to 90% of the trees belong to just this one species, overturning every stereotype of plant diversity in the tropics. Monodominant *Gilbertiodendron dewevrei* forest covers large areas of the Congo Basin, but it is currently unclear whether it is sufficiently distinct from adjacent mixed *terre firme* forest to warrant separate treatment for conservation planning and carbon calculations. This study aimed to compare the structure and diversity of monodominant and mixed forest, and ask whether there is a unique vascular plant community associated with *G. dewevrei* forest. We utilised a combination of plot data and herbarium specimens collected in the Sangha Trinational (a network of protected areas in Cameroon, Central African Republic, and the Republic of Congo). Plot inventories were used to compare *G. dewevrei* forest and mixed forest for stem density, basal area, above ground biomass, stem size distribution, species diversity, and species composition. In addition, a database of 3,557 herbarium specimens was used to identify species of vascular plants that are associated with *G. dewevrei* forest. We found that *Gilbertiodendron dewevrei* forest is distinct in both structure and species composition from mixed forest. *G. dewevrei* forest has a lower stem number (of trees ≥ 10 cm), but a greater proportion of larger trees (> 70 cm), suggesting higher carbon stocks. The species composition is distinct from mixed forest, with 56 species of vascular plant significantly associated with *G. dewevrei* forest. Monodominant *G. dewevrei* forest in the Sangha Trinational is both compositionally and structurally distinct from mixed forest. We therefore recommend this forest type be considered separately from mixed forest for conservation planning and carbon stock calculations.

S.83 ALPINE PLANT ECOLOGY AND DIVERSITY: FROM SPECIES TO ECOSYSTEMS. SESSION 1

S.83.1 Assembly of regional species pools in the European alpine flora

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Alpine floras contain unique biodiversity above the climatic treeline globally. Understanding such biodiversity needs to consider multiple facets from evolutionary history to the assembly of cold-adapted plant lineages in regional floras and local communities. Here, we summarize recent research on the patterns and drivers of species pools in 23 regional alpine floras of Central and Southern Europe. At the phylogenetic level, we found that climatic changes during the glacial-postglacial periods had an important role in determining current species pools, with closely related lineages in cold and unstable climates. At the taxonomic level, the diversity of European alpine pools is mainly influenced by regional isolation and dispersal limitation. Environmental and topographic heterogeneity complement area effects to explain regional richness, but the area becomes especially critical to maintain species richness in the smallest regions. The taxonomic dissimilarity among regions reflects past glacial connections, but present European alpine floras are strongly isolated, and they are expected to respond differently to regional climatic variation. All these results suggest regional idiosyncrasies in the response of alpine diversity to climate change, concerning spatial, bedrock, and topographic configurations. Since the assembly of European alpine floras may not be in equilibrium with climate, the effects of current warming must be evaluated at meso- and micro-scales within a given species pool, with expected discrepancies among regions. Accounting for multiple regional studies with similar approaches in different regions, especially those supporting relict alpine communities, will be necessary to anticipate future changes in alpine plant diversity.

S.83.2 The diversity and structure of Australian alpine plant-pollinator communities and how global change is impacting these communities

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Alpine ecosystems are highly threatened by climate change. We are observing a fast shrinking of these ecosystems around the world with unprecedented changes of their macroclimate and vegetation. Plant-pollinator interactions play an important role in alpine ecosystems; however, we still know very little about alpine plant-pollinator communities in Australia and how they are affected by global change. Here we analyse the structure and diversity of a plant-pollinator metacommunity networks from the Australian alpine region using two approaches: pollen DNA metabarcoding and flower-visitor observations. Additionally, we analysed historical changes of plant-pollinator communities using insect museum specimens and molecular data. We found that alpine plant-pollinator networks show high spatial turnover of plant species and interaction rewiring as well as showing high phylogenetic diversity driven by micro-climate variability. Our analysis of museum specimens and historical data also revealed that Australian alpine ecosystems have gone through multiple changes of community diversity in the last century as result of grazing, introduced species and climate change. Overall, our findings suggest that the heterogeneity of Australian alpine habitats make these communities partially resilient to climate change, however rapid vegetation changes observed could generate the extinction of some alpine herbaceous plants and key pollinator taxa.

S.83.3 Plant responses to climatic change: insights from tropical alpine plant lineages in the Andes

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Climate change-induced range shifts have been documented extensively in temperate mountains, but the response of tropical alpine species remains understudied. This study aims to address this knowledge gap by focusing on the tropical alpine ecosystem of the Andes while exploring and comparing the responses of four Asteraceae plant lineages to past and future climatic changes. Using curated herbarium-backed occurrence data, we constructed species distribution models (SDMs) based on paleoenvironmental reconstructions and future climate predictions for 113 species from four monophyletic lineages and evaluated their predicted elevation changes, suitable habitat sizes and temperature ranges. We expected that habitat ranges were larger during the Last Glacial Maximum (LGM) and that they would shrink in the future, followed by species elevation shifts. Contrary to expectations, we did not observe a generalized downward shift in elevation during the LGM, and while some lineages had larger ranges in the past, this was not a general trend. Furthermore, we observed differential species' responses to climate change, with species occupying broader temperature ranges having higher habitat stability over time. We speculate that the Andes' complex topography, with high altitude plateaus, might be responsible for the observed patterns, distinguishing it from other tropical alpine ecosystems and highlighting the importance of considering regional and lineage-specific dynamics in understanding the impacts of climate change on habitat suitability.

S.83.5 The seed regeneration niche in Mediterranean high mountains

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The seed regeneration niche encloses 4 main stages (dispersal, persistence, germination and seedling establishment) which are regulated by a complex array of physiological and environmental cues. Understanding the regeneration niche in high-mountain ecosystems is important to track species responses and community dynamics under current and future climate conditions. However, we know very little about the regeneration processes that occur in Mediterranean high mountain vegetation, which faces increasing summer drought periods. Here, we review the topic combining published literature and results from our own research in Iberian mountains. We found inconsistent results in dispersal studies, some of them reporting short-distance dispersal limitation among populations, while others suggesting dispersal-based metacommunities. Our results support that dispersal may not be limiting at the regional level and that community composition is mainly explained by soil properties related to water holding capacity. Seed persistence has rarely been studied, but our data suggest that it is highly species-specific and modulated by microhabitat conditions. Germination is the more studied, showing a general pattern of immediate germination if water is available, even at low temperatures, with complementary effects of cold stratification in some species. Our results support this general trend and provide new insights about drivers such as light, alternating temperatures and soil water potential. Finally, in concordance with existing literature, seedling establishment appears to be the most vulnerable stage, with low chance of survival in the field and in controlled laboratory conditions. Literature suggests that timing of emergence is strongly influenced by temperature cycles, and we found a pattern of increasing radicle length in species linked to warmer microhabitats. In summary, the success of seed regeneration in Mediterranean high mountains seems to be primarily limited by water stress, especially during germination and seedling establishment.

S.83.6 Ecological evolution characteristics of rhizosphere soil microorganism of Oxytropis glacialis on the Qinghai-Tibetan Plateau

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Oxytropis glacialis is an endemic species of alpine grasslands on the Qinghai-Tibet Plateau, and has a strong invasive capacity in degraded grasslands. In this study, a model for the ecological evolution of rhizosphere soil microorganism of *O. glacialis* was constructed using high-throughput sequencing combined with climatic and environmental factor analysis. The results show that the ecological evolution of bacteria is a deterministic process and that of fungi is a stochastic process. The synergy between the fungal and bacterial communities was dominant, and the bacterial communities were more closely interconnected than the fungal communities. The core bacterial groups are Pseudomonas, Gaiellales, Gemmatimonadaceae, etc. and the core fungal groups are Mortierella, Gibberella, Didymella, etc. This study provides data to reveal the role of *O. glacialis* in alpine degraded grasslands.

S.84 NEXT GENERATION ZINGIBERALES: FROM TAXONOMY TO EVOLUTION

S.84.1 Genome size in Zingiberaceae correlates with the life strategies, plant traits and habitat preferences

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Plant species with large genomes tend to be excluded from climatically more extreme environments with a shorter growing season. Species that occupy such environments are assumed to be under natural selection for more rapid growth and smaller genome size (GS). However, evidence for this was so far available only for temperate organisms. We studied the evolution of GS in two subfamilies of the tropical family Zingiberaceae to find out whether species with larger genomes are confined to environments where the vegetative season is longer. We tested our hypothesis on 337 ginger species from regions with contrasting climates by correlating their GS with an array of plant traits and environmental variables. We revealed sixteen-fold variation in GS which was tightly related to shoot seasonality. Negative correlations of GS with latitude, temperature and precipitation emerged in the subfamily Zingiberoidae, demonstrating that species with larger GS are excluded from areas with a shorter growing season. In the subfamily Alpinioideae, GS turned out to be correlated with the type of stem and light requirements and its members cope with seasonality mainly by adaptation to shady and moist habitats. The Ornstein–Uhlenbeck models suggested that evolution in regions with humid climates favoured larger GS than in drier regions. Our results indicate that climate seasonality exerts an upper constraint on GS not only in temperate regions, but also in the tropics, unless species with large genomes find alternative ways to escape from that constraint.

S.84.2 Networked relationships in the family Zingiberaceae – The role of ancient hybridizations in lineage diversification

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Hybridization plays an important role in the evolution of plants and has been observed to occur throughout the evolutionary history. Undoubtedly, determining its role is critical for understanding diversification processes at various taxonomic levels. Recent advances in genomic resources and analytical techniques have allowed for the recognition of ancient hybridization, which has been linked to evolutionary radiations while sometimes preventing further diversification. The causes of ancient hybridizations remain to be explored. The frequency and consequences of ancient hybridization events in Zingiberaceae, a tropical family of over 2000 species that includes economically important crops such as ginger, turmeric, and cardamom, are presented here. We analyzed 1094 nuclear low-copy genes from 250 species, covering most known genera and their geographical distributions. We discovered numerous instances of ancient hybridization using phylogenetic network analysis, which often predated the diversification of entire genera or larger lineages within Zingiberaceae. Such

a commonness of ancient hybridization explains the inability to resolve relationships among and within certain genera, as well as the importance of including historical hybridization analysis when building phylogenies, resolving taxonomic issues, or reconstructing biogeographical history.

S.84.3 Love thy neighbours and create complexes: lessons from the phylogeny of the fragrant ginger lilies, Hedychium J.Koenig

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The genus *Hedychium* (Zingiberaceae), distributed in the Asian tropics, is riddled with species complexes. 'Species complex' refers to a set of taxa that lack morphological distinctness from each other, rendering species boundaries among them to be very hazy. To understand speciation in the genus *Hedychium*, we tackled species complexes as well as phylogenetic reconstructions simultaneously using morphological, ecological, molecular, and genomic approaches. We first noted that the number of species complexes was highest in the Indo-Burmese region, the centre of diversity for *Hedychium*. Using a machine learning approach we analyzed morphological characters of taxa within a complex and we noted that individuals from different species were found to cluster together based on sympatry. This suggested that sympatry may have played a role in maintaining hazy species boundaries. We next looked at intra- and inter-specific reproductive barriers by carrying out directional crossing experiments in the wild, where male and female parents were tracked in each treatment. Although past horticultural studies had indicated the potential for *Hedychiums* to hybridize, our results emphasize the need to look at sympatric associations and directionality in reproductive barriers, especially in taxonomic groups known for the presence of species complexes. Finally, we mapped the flowering phenology and we concluded that the 4-5 months of overlapping flowering phenology of closely related and reproductively compatible taxa may have also facilitated the inter-species crosses in this genus. Our phylogenetic reconstruction of the genus *Hedychium,* therefore shows signatures of hybridization, facilitated by the lack of reproductive-isolation mechanisms. This is further enabled by factors such as sympatric associations and the timing of flowering. What is interesting is that, despite this, the clades were stable and showed biogeographic. Diversifications in *Hedychium* were mostly shaped by geological events such as the uplift of the Himalayas and environmental factors like monsoon intensification.

S.84.4 Extensive introgressions failed to erode species boundaries among multiple sympatric related species

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How species boundaries are maintained among sympatric closely related species experiencing gene flow is a puzzling question in evolutionary biology. Introgression is commonly reported, but the dynamics of, and gene function in introgression have rarely been explored to probe why frequent introgression does not necessarily destroy species boundaries in sympatry. Here we use seventeen morphological traits and whole-genome resequencing data to investigate introgression in five closely related species in *Roscoea* that co-occur in a "sky island" distributional pattern with limited seed and pollen dispersal. Introgression is the cause of phylogenomic discordance between the nuclear and chloroplast genomes. Introgression is largely asymmetrical in intensity and gene function. Introgressive intensity changed over time with a peak at approximately 2-3 Mya Inferred functions of introgressed genes were related to reproductive processes in only one species pair. Our results suggested that closely related species with incomplete assortment of alleles could coexist despite theoretical predictions, reflecting the semipermeable nature of species boundaries as reproductive isolation is accrued, a key conceptual framework for understanding the conflict between introgression and species fate. Our finding offers novel insights into how related sympatric species boundaries can be upheld in the face of frequent gene flow.

S.84.5 The evolution of floral morphology of Kaempferia (Zingiberaceae) in Thailand

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The genus Kaempferia is a member in the ginger family (Zingiberaceae). Its distribution stretches from India to various regions in Southeast Asia. Amongst these, Thailand notably stands out with a rich species diversity of this genus. In accordance with the Flora of Thailand, Thailand hosts approximately 32 accepted species. This perennial herb, renowned for its fascinating medicinal properties, extends beyond its species variety, its significance also permeates into the intricate world of its floral morphology, therefore being the core motivation of this study. Our focus will explore the subgenus Kaempferia, with a specific aim to the evolutionary reconstruction of five intriguing morphological characters: the labellum colour, floral markings of the labellum, the floral plane, the shapes of the anther crest, and the size of the lateral staminodes. Furthermore, our study also aims to reconstruct a phylogenetic tree including 18 Kaempferia species within the subgenus Kaempferia using ITS regions. The DNA was extracted and underwent sequencing from frozen leaf specimens and further underwent Bayesian inference and Maximum Likelihood analysis. Character evolution was then analysed via Mesquite to discover the ancestral states of the genus.

S.84.6 Sequence diversity and chromosome evolution in Musaceae inferred from t2t genome assemblies and molecular cytogenetics

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The family Musaceae, with three genera *Musa*, *Musella* and *Ensete*, belongs to the Zingiberales order, is native to the tropics and subtropics of East-Asia and Africa, and includes important crops and ornamental species. To understand the evolution of Musaceae genomes and species, we combined data from chromosome scale assemblies with fluorescent *in situ* hybridization to describe the chromosomal rearrangements and repetitive DNA composition. Some 50-60% of the genomes are composed of repetitive sequences with LTR-retroelements and DNA transposons predominant and their families distributed among different groups of species. A tandemly repeated 134bp satellite sequence is present at the centromeres of *Ensete glaucum*, *E. ventricosum* and *Musella lasiocarpa*, but no tandem repeat was found at *Musa* centromeres. 45S rDNA and 5S rDNA have variable numbers and chromosomal locations and occupy often otherwise non-syntenic arms. The individual haplotype assemblies of *M. lasiocarpa* showed high degree of alignment at the distal parts of the chromosome arms, but inversions and duplication of repetitive elements near the centromeres, cause haplotype differences in all chromosomes. Within Musaceae, the telomere-to-telomere assemblies, including centromeric positions, enabled us to characterize the syntenic relationships and chromosomal rearrangements. *Musella* and *Ensete*, both x=9, show only few whole arm translocations and large regions of synteny supporting the close relationship but separation of genera, while the x=11 *Musa* species are phylogenetically separate with many more postulated chromosomal rearrangements and genetic differences. This insights into the chromosomal and repetitive sequence evolution of Musaceae genomes along with gene and regulatory sequences in the assemblies, add to a comprehensive and robust pangenome of *Musa* and *Ensete*, valuable to understanding evolutionary mechanisms and genome diversity, adaptation to climate changes and for crop improvement.

S.85 PLANT CONSERVATION IN MEDITERRANEAN AND MACARONESIAN ISLANDS. SESSION 2

S.85.1 Remote sensing identification and mapping of vegetation cover on some listed Algerian islands (Habibas & Rachgoun).

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Despite their proximity to the coast, few studies have focused on identifying and mapping Algerian island vegetation. To fill this gap, we used satellite images and machine learning methods to identify and map the main vegetation groups on two classified islands: the Habibas archipelago and Rachgoun Island, while evaluating the effectiveness of the Random Forest classifier, which is successfully used to study the vegetation of large areas. However, despite the great heterogeneity of their vegetation cover, the use of very high resolution images (Pléaides), through fusion bands and derived bands (NDVI), has enabled us to produce a fairly accurate vegetation map that can be used to establish management and protection plans for these habitats. Our methodological approach produced very satisfactory results, enabling the identification of the plant communities inventoried on the field, while showing high accuracy values, ranging from 0.642 for the halophilic Asteriscus grouping to 1 for the endemic Chasmophyte grouping of the Habibas archipelago. Our methodological approach, and despite the great heterogeneity and very small surface area of our islands and islets, led to very satisfactory results, reflected by good overall accuracy and Kappa index values (overall accuracy > 92% and Kappa index > 0.90).

S.85.2 Diversification and conservation of species and spaces in Macaronesia: an example from the endemic flora of Gran Canaria

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The diversification of the Canarian endemic flora is a dynamic process influenced by multiple biotic and ecological variables, but also greatly related to the geological ontogeny and complex geography of the archipelago. Many current radiations may have evolved from widely distributed ancestors or from ubiquitous endemics (UE, those which occur on all islands), but the selective and stochastic landscapes of the islands trigger fast diversification, so that a widespread occurrence should be an extremely transient distributional feature in most taxa. The SIE are also subject to frequent diversification, and there are numerous examples where molecular tools have discovered sharp genetic discontinuities within this distributional category. We compile data on the existing phylogenetic evidence for the 256 Canarian endemics currently known in one of the most complex and species-diverse islands of the archipelago (Gran Canaria), alongside biotic and abiotic variables associated with their distributions, to gain insight into the factors that influence floristic diversification and conservation status. We show that the closest extant mainland congeners of the UE often occur in distant mainland regions, thereby supporting the hypothesis of extinction of their closest relatives from Western Africa or close Mediterranean regions during the glacial cycles in the late Pleistocene. Our spatial analyses compellingly show that most UE occur in lower regions with less complex relief, tentatively indicating that ecological processes are still an inconspicuous influence on their diversification. By contrast, most of the SIE tend to occur in geographically complex regions, likely reflecting a major role of ecology, relief and stochasticity on their diversification. We analyse multiple data layers related to ecological, geographic, climatic and phylogenetic parameters to suggest restoration strategies to recover areas subjected to high anthropogenic pressure related to renewable energy sources. All calculations were made using the supercomputing platform created by the NEXTGENDEM project (MAC2/4.6d/236).

S.85.3 Biodiversity crisis: two examples of Mediterranean endemic plants struggling with germination issues, climate changes...

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The Mediterranean region is a global hotspot of endemic plant biodiversity. To better understand what destiny awaits some of the most vulnerable plants of Mediterranean flora, we focused on *Petagnaea gussonei* and *Muscari gussonei*, two range-restricted endemic species from Sicily. We specifically investigated the germination capacity of *P. gussonei* and *M. gussonei*, and the temporal trends of climate, desertification and soil-use across the natural range of both species. *P. gussonei* showed high dormancy, whereas *M. gussonei* reported a narrow germination optimum (10–15 °C). The average temperature increased by 0.5–1.5 °C in the period 1931–2020; the land affected by desertification expanded in an alarming way, by reaching values between 50 and 90%. Soil-use changes created also a complex impacting mosaic where 40–85% are agricultural areas. The effective conservation of *P. gussonei* and *M. gussonei* should be multilateral by relying on germplasm banks, improving landscape connectivity and vegetation cover, and promoting climate policies.

S.85.4 Conservation genetics of threatened endemic plants in the Canary Islands: applications and perspectives.

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The study of population genetics has become a fundamental pillar in the management of endangered species. Knowing the distribution and levels of genetic variability within and between populations can help to resolve taxonomic uncertainties, detect bottlenecks and drift in natural populations, identify individuals genetically or detect hybrids, among other things. Nowadays, it is essential to know both the biology and ecology of species and their genetic conservation status in order to support species recovery plans and to optimise resources when carrying out conservation actions, either in situ or ex situ. Due to the biogeographical particularities of island ecosystems, they are an important source of biodiversity, with a high rate of plant endemism. However, due to isolation and small population sizes, island endemics are more vulnerable to anthropogenic disturbances, resulting in an increasing number of threatened species. In this presentation, we highlight some practical cases studied by our research group in the Canary Islands in the last 15 years, showing different scenarios and results, and the diverse practical applications to which they have given rise. To sum up, our population genetic studies have resulted in the description of two new species, assistance in the performance of restoration actions or predictions of distribution changes under climate change. Likewise, the close contact with the managers of the different natural areas is essential for the transferability of the results.

S.85.5 A review of the reproductive biology of endemic Azorean taxa

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The Azorean archipelago is located in the North Atlantic Ocean between 36°55'-39°43'N and 25°00'-31°15'W and is composed of a total of nine volcanic islands divided by three groups. Positioned as the northernmost segment of the Macaronesian biogeographic region, it is considered a hotspot of biodiversity due to the elevated number of endemic species and a significant number of endangered species present. The flora of Azores faces significant threats, primarily stemming from human settlement. The clearing of native vegetation for cereal crops and pasture, along with the introduction of numerous crops, forage, forest, ornamental, and hedgerow plant species, poses a substantial risk. Therefore, it is imperative to prioritize conservation efforts and to implement protective measures to preserve the unique flora of Azores. One approach for *in* and *ex situ* conservation is the combined study of reproductive biology and the genetic characterization of natural populations. There is a considerable lack of information regarding the reproductive biology of the Azorean endemic flora, therefore recent Interreg projects MacFlor (MAC/4.6d/190) and MacFlor 2 (MAC2/4.6d/386) have aimed to improve the knowledge of this particular subject. During the above-mentioned projects, seven endemic Azorean taxa were reviewed: *Hypericum foliosum* Aiton; *Picconia azorica* (Tutin) Knobl.; *Veronica dabneyi* Hochst. ex Seub.; *Frangula azorica* Grubov; *Myosotis azorica* H.C.Watson; *Viburnum treleasei* Gand. and *Laurus azorica* (Seub.) Franco. New data was collected about micro-morphological elements of the flower, phylogenetic relationships, seasonal and floral phenology, palynology, fruit and seed characterization and reproductive success. It was estimated (by ratio Pollen/Ovule) that the target species have xenogamy as their preferable breeding system, which implies that they favour outcrossing as their main reproductive strategy.

S.85.6 Reconstructing the historical biogeography of an (almost) lost ecosystem: Evolutionary genomics of the Canarian cedar, Juniperus cedrus

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The extinction of unique species and the disappearance of various types of vegetation have been recurring phenomena on oceanic islands since human colonization. However, the extent of both prehistoric and colonial anthropic impact, as well as their consequences, remains a subject of debate in many island systems. In this context, the study of historical demography through genetic information preserved by current populations offers a unique opportunity to understand how humans have transformed island ecosystems. Our study leverages recent advances in massive high-throughput DNA sequencing (ddRADseq) and population genomic analyses to address the case of *Juniperus cedrus* Webb & Berthel. in the oceanic archipelago of the Canary Islands. It has been suggested that the Canarian cedar was the primary structuring species of a vegetation type that has now practically vanished due to anthropogenic pressure. Consequently, the Canarian cedar, endemic to the islands of Tenerife, La Palma, La Gomera, and Gran Canaria, is classified as nationally and internationally threatened. Herein, we present the first results of the JUNIPERADAPT project, which aims to: (i) reconstruct the historical biogeography and evolution of the Canarian cedar across its current distribution range through population genomics; and (ii) predict range shifts of the Canary cedar under past and future climate change scenarios through the implementation of species distribution models. By integrating these complementary approaches, we seek to unveil its demographic trajectory, infer the possible impact of societies that colonized the Canary Islands (i.e., both Canarian aborigines and European colonizers), and identify current refuges of genetic diversity.

S.86 RECENT ADVANCES IN THE MEGADIVERSE LEGUME SUBFAMILY PAPILIONOIDEAE - PART II

S.86.1 Combining legacy Sanger with new phylogenomic DNA sequence data to produce a densely sampled papilionoid metachronogram for comparative biology

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Phylogenetic trees are fundamental for understanding the evolution of life on Earth, providing insights into the assembly of biotas, morphological trait shifts, and diversification dynamics. Recent advances in High-throughput sequencing (HTS) technologies are generating an explosion of DNA sequence data and prompting new approaches to enhance phylogenetic resolution. However, sparse sampling of species and intraspecific diversity remains an important limitation for global-scale comparative studies of large clades. Combining numerous species-level phylogenies which benefit from thoroughly curated taxonomy, dense taxon sampling and Sanger sequencing data, with more sparsely sampled higher-level backbone phylogenies presents a useful avenue for generating robust, densely sampled, well curated, time-calibrated phylogenetic metatrees or metachronograms. In this study we present a workflow to integrate large-scale sparsely sampled higher-level backbone trees with fine-scale, clade-specific densely sampled phylogenies. We demonstrate this approach for the species-rich legume subfamily Papilionoideae. We first produced a dated backbone using 20 fossil calibrations and a phylogeny containing 3696 tips representing 20% of known legume species (LPWG 2017). We then searched the literature for well sampled, thoroughly curated phylogenies built for specific Papilionoideae clades using both HTS or Sanger sequencing. When phylogenies were not available, we used the alignments or downloaded the accessions from GenBank to generate phylogenies using MrBayes. We checked ESS values, average standard deviation of split frequencies and whether the topology matched the one in the original study. Those fine-scale phylogenies were then grafted onto the backbone to produce a meta-chronogram. This approach means that diverse data types can be combined to build a single phylogeny, thereby tapping into the full wealth of available DNA sequence data and maximising the number of taxa that can be sampled with molecular data and provides a computationally tractable way to build a large phylogeny with many taxa.

S.86.2 Developments in the phylogenetic and taxonomic studies of Southern African genera of the tribe Phaseoleae

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In southern Africa, the tribe Phaseoleae consists of ca. 185 indigenous, naturalized, and cultivated species distributed among 25 genera, namely, *Alistulus*, *Cajanus*, *Clitoria*, *Decorsea*, *Dipogon*, *Dolichos*, *Dumasia*, *Eriosema*, *Erythrina*, *Flemingia*, *Galactia*, *Lablab*, *Macroptilium*, *Macrotyloma*, *Mucuna*, *Neonotonia*, *Neorautanenia*, *Nesphostylis*, *Ophrestia*, *Otoptera*, *Pueraria*, *Rhynchosia* (including *Bolusafra*), *Sphenostylis*, *Teramnus*, and *Vigna*. A notable challenge in the current understanding of these genera lies in the absence of recent taxonomic revisions for some, resulting in a limited knowledge of their respective species. Furthermore, there is a dearth of information concerning intra- and intergeneric relationships within and between the tribes and genera of the Phaseoleae. This study presents advancements in taxonomic studies of the aforementioned genera and conducting phylogenetic analyses of the subtribes within Phaseoleae over the past decade. While several taxonomic revisionary studies have led to the discovery of new species and many combinations of names, some genera, such as *Galactia*, *Eriosema*, *Teramnus,* still require comprehensive taxonomic revision. Morphological studies revealed a number of characters that can be used to distinguish closely related species within genera, as well as within the subtribes and tribes. These include growth habit, stipule type, leaf indumentum, inflorescence type and length, calyx, and standard petals indumentum. In the realm of phylogenetic studies, our research on southern African *Rhynchosia* has confirmed the polyphyly of the genus within the Cajaninae subtribe. Additionally, the monophyly of Phaseolinae in southern Africa has been substantiated. This study delves into sectional changes within the genera of southern African Phaseoleae, addresses research gaps, and establishes a framework for future investigations into the phylogeny and taxonomy of prominent genera, with a particular emphasis on *Eriosema* in the region.

S.86.3 Phylogenetic resolution of Mirbelieae (Fabaceae) using the Angiosperms353 target-capture probe set.

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An Australian endemic clade, Fabaceae tribe Mirbelieae (bush peas and their relatives), currently consist of 27 genera and c. 756 species, and Core Mirbelieae, the focus of our study, contains 21 genera and c. 540 species, or 32% of Australia's pea flora. Species within the tribe have a wide distribution across Australia, occupying habitats from coastal to alpine zones, and wet forests to arid deserts. However, the phylogeny of Mirbelieae, required to reach consensus on the taxonomic relationships of species and genera within the tribe, has never been adequately resolved using traditional sequencing. To resolve the phylogeny of Mirbelieae, samples were collected from 354 taxa within the core genera, from a combination of wild collected silica dried leaf tissue or herbarium specimens from NSW, BRI, CANB and MEL. Next generation sequencing was then performed using target capture with the Angiosperms353 universal probe set, with the aim of creating a resolved phylogenetic tree for the group to aid future taxonomy. Data assembly resulted in a total of 278 genes being recovered after filtering, with alignments that ranged from 97 bp to 3,575 bp in length. The resulting phylogenetic tree resolved the backbone of the phylogeny and provided statistical support for all major clades within Mirbelieae. We found that 11 genera were monophyletic and six were polyphyletic, including the largest genus *Pultenaea*, which was separated into five distinct clades. Ultimately, we published over 30 new species and recognised four new genera. Our findings shed new light on evolution of Mirbelieae and their phylogenetic relationships, providing a new foundation for the future taxonomic research and classification.

S.86.4 Systematics of genistoid legumes: taxonomy and phylogeny of Argyrolobium (Genisteae, Fabaceae)

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The genus *Argyrolobium* Eckl. & Zeyh. (Genisteae) comprises of ca. 97 species distributed throughout tropical and northern Africa, Madagascar, the Mediterranean, southern Europe and west into the highlands of India. It has its centre of diversity in southern Africa where about 51 species occur. Phylogenetic studies based on a limited sampling of the genus have indicated that the genus may not be monophyletic, and that the generic circumscription needs revision. In addition, the South African species (47) have only been treated synoptically in recent years, based on an unpublished Ph.D. thesis, and the last published comprehensive taxonomic revision of the southern African species dates back to 1862. Several new species remain to be described, and difficult species complexes renders identification of some species problematic. The present study is aimed at producing morphological and molecular data for *Argyrolobium,* based on a globally representative sampling, that will contribute towards resolving the generic circumscription and relationships of the genus. In addition, the taxonomy of the southern African species will be revised. Data from the analysis of nuclear and plastid DNA sequences confirm that the genus is not monophyletic. While a large clade of predominantly southern African species was recovered, the remaining tropical African, Middle Eastern, Asian and Malagasy species form at least two separate clades distributed among other genera of the Genisteae. Options for generic circumscriptions are explored. An overview of the taxonomy of the genus is also presented, along with progress on revisions of several groups within the genus.

S.86.5 Species delimitation and phylogenomics of African Pterocarpus with an implication for species identification tools development

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Reliable delimitation of species is fundamental for establishing sustainable and equitable harvesting guidelines of economically important organisms. *Pterocarpus* (Fabaceae) is a pantropical genus of trees including several highly valuable timber-producing species that face significant threats from intensive logging. However, a lack of taxonomic clarity has hindered the advance of logging regulations and has led to the inclusion of all African *Pterocarpus* populations under CITES (CoP19). In our study, we addressed this issue by reassessing species delimitation of all twelve accepted African *Pterocarpus* species, including neotropical samples of the two pantropical species. Based on DNA sequences obtained by Angiosperms353 probe set, we reconstructed a comprehensive phylogeny combining maximum likelihood and multispecies coalescence approaches. Additionally, we explored the potential of high-copy DNA for identifying African *Pterocarpus* species. This involved reconstructing chloroplast and ribosomal DNA phylogenies, using genome skimming and maximum likelihood approaches. Our results confirmed the monophyly of eleven *Pterocarpus* species and a paraphyletic *P. rotundifolius*, presenting one Angolan subclade with the remaining subclades further subdivided in three geographically coherent groups, suggesting the possibility of cryptic diversity within the complex. A similar situation arose in *P. lucens*, which exhibited two sister clades with disjunct distributions. Species delimitation based on high-copy DNA was congruent with the Angiosperms353 data for most species, indicating the reliability of chloroplast and ribosomal DNA markers for *Pterocarpus* species identification. Our findings give valuable insights into African *Pterocarpus* species delimitation, highlighting the need for further investigation of potential cryptic diversity within *P. rotundifolius* and *P. lucens*. Finally, our study lays the groundwork for developing DNA-based tools aimed at improving logging regulations for African *Pterocarpus* species.

S.86.6 Floral evolution of morphologically unusual papilionoid legumes (Leguminosae, Papilionoideae)

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A key innovation which has evolved in many plant lineages is the elaboration of floral symmetry from actinomorphy (radial symmetry) to zygomorphy (bilateral symmetry), allowing more specialized interactions with pollinators. Genes regulating flower symmetry have been identified in model species including: CYCLOIDEA (CYC), DICHOTOMA (DICH), DIVARICATA (DIV), and RADIALIS (RAD). Changes in these genes underlie symmetry shifts in several lineages. In typical papilionate flowers, CYC and DICH like genes are expressed on the dorsal (upper) side of the flower bud and specific to development of the standard petal via RAD. Several papilionoid lineages have lost the typical floral morphology of 5-petaled, zygomorphic papilionate flower with 10 stamens and have highly morphologically unusual flowers, including those with a single petal, higher number of stamens and even radial symmetry. Here, we explore the key symmetry-regulating genes in the papilionoid legume genera *Andira* (typical zygomorphic papilionate flower), *Cyathostegia* (single petal and multiple stamens), and *Cadia* (radially symmetrical flower). We used draft genome to identify putative ortholog sequences of CYC, DICH, DIV, and RAD, and quantified the expression of these genes in different developmental stages and between the species. Although the three genera bear quite distinct flower architectures, our results show that they vary in expression patterns of genes involved in the establishment of zygomorphic symmetry. Rather than loss or gain of key regulators, differential gene expression may play a major role in the determination of organ identity in florally unusual genera of Papilionoideae. We also provide floral ontogenetic data, allowing insights into the expression of symmetry genes relative to the underlying changes observed in development.

S.87 PLANT CONSERVATION GENETICS: FROM IN-SITU AND EX-SITU CONSERVATION TO REINTRODUCTIONS AND RESTORATIONS. SESSION 3

S.87.1 Improving Seed Germination and Bulb Induction of Allium tuncelianum L. under Aseptic Conditions

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Allium tuncelianum (Kollman) N. Ozhatay, B. Mathew & Siraneci or Tunceli garlic is endemic to Eastern Turkish Provinces of Tunceli, Sivas Erzincan and Munzur mountains. They are edible and bear attractive deep lilac colored flowers with fertile black deep dormant seeds. Tunceli garlic seeds were collected from field grown plants and aimed to break seed dormancy to optimize conditions for induction of bulblets, along with their growth, development and increased bulb diameter. Therefore, these were cultured on MS medium amended with different strengths of $KNO_{3.}$ They were germinated on MS medium with or without 20 g/l sucrose followed by their culture on 1 ×, 2, 4 and 6 ×

1900 mg/l mg/l KNO_3 to increase bulb diameter. Improved seeds germination was noted on MS medium with and without sucrose but with variation compared to previous reports. The bulb formation rate on each of the germinated seeds was not parallel. The results showed 34% and 28.5% bulb induction noted on germinated seeds after 150 and 158 days on MS medium containing 20 g l^{-1} sucrose and no sucrose in the same sequence. The results emphatically noted role of cold stratification on agar solidified MS medium supplemented with sucrose to improve seed germination. The best increase in bulb diameter was noted on MS medium containing 1 × 1900 mg/l KNO_3 after 178 days with bulblet diameter and weight of 0.54 cm and 0.048 g, respectively. Consequently, the bulbs induced on sucrose-containing MS medium could be transferred to pots earlier. Increased (>1 × 1900 mg/l KNO_3) strengths of KNO_3 induced a negative effect on the growth and development of Tunceli garlic bulbs. The strategy of seed germination and bulblet induction reported in this study could be positively used for conservation and protection of this endemic.

S.87.2 Can inbreeding coefficients predict plant progeny fitness? A case study from wild and translocated populations.

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Many threatened species are at risk of extinction or functional extinction due to genetic and reproductive isolation, arising from historic contractions of ranges, and anthropic fragmentation. One method of managing fragmented populations is through genetics rescue, using translocations, particularly supplementations/augmentations and reintroductions. In our study we used a long lived clonal but preferentially outcrossing case study species to assess the impact of inbreeding on fitness of wild and translocated populations. We paired inbreeding coefficients (FIS) with targeted outcrossing to determine if varied fitness of wild plants could be attributed to inbreeding. We also identified if strategic outcrossing resulted in increased growth, seed viability and reproduction of germinants intended for an augmentation translocation and if these strategies could be used to plan more effective and robust plant translocations where genetic rescue is required.

S.87.3 Assessing the restoration potential for the rare sexual populations of Chara canescens, a singular cryptogam, from their oospores

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Chara canescens is a charophyte algae, which plays an important role in the ecosystems that it inhabits. This species is unique within its genus because it presents two different reproductive strategies: parthenogenesis, which is unusual in this genus, and sexual reproduction. Parthenogenetically reproducing populations are known for coastal brackish lagoons worldwide, so they are not considered as rare; however, sexually reproducing populations are restricted to Mediterranean and Pannonian inland brackish water sites, with only a few populations recorded in the last decades. The genetic flow of both populations types through stepping-stone habitats is key to the genetic diversity of the species; and its conservation. The parthenogenetically reproducing populations lack at least some of the genetic recombination mechanisms and consequently are more vulnerable to loss of genetic diversity compared to sexually reproducing species. This fact means that protection measures limited to the coastal stands will not be effective, because the fitness of these stands depends to a high degree on connectivity with inland brackish water sites. With the aim of developing effective transnational conservation strategies, the project "ProPartS" (Biodiversa+) assesses the restoration potential of the species' diaspore bank. The oospores are the charophytes sexual propagules, which can remain viable in the sediment during years and develop new individuals when the conditions are suitable again. Analyzing these oospores (in terms of vitality, germination rate, interfertility assessment...) and assessing the possible differences between the sexually or parthenogenetically produced ones may help to develop effective conservation actions and restoration initiatives for the species. These "hidden biodiversity elements" act as reservoirs and can ensure mid-term resilience of temporary and/or degraded habitats and be potentially useful for the restoration of lost habitats. This is especially important in the context of a changing environment dealing with increased droughts and other threats for the aquatic ecosystems.

S.87.4 Extinct or not? Establishing the status of the urban endemic Hieracium tolstoii (Asteraceae) with taxonomic investigations

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Hieracium is one of the largest plant genera in the Angiosperms and experienced a rapid and recent evolutionary radiation. Due to the massive morphological variation among species, past hybridization events and frequent polyploidization, combined with apomictic reproduction in polyploids, the species concept in *Hieracium* is widely debated and species identification is very challenging. According to recent studies (Davis et al. 2011) most vulnerable species are found within young and fast-evolving plant lineages and several *Hieracium* species are considered extinct or threatened[2]. Taxonomy represents the first fundamental step for every conservation project. Taxonomic investigation can lead to changes in conservation status or to de-extinctions of species[3]. Taxa with doubtful classification are particularly sensitive to this kind of problems. *Hieracium tolstoii* Fen. & Zahn was a narrow endemic species described for the ancient walls of Milan Castle (Italy). Morphologically, this species was considered as intermediate between two other species (*H. pospichalii* and *H. australe*). However, no further investigations were conducted on *H. tolstoii* origin after the first description in early XX century and nowadays the species is considered extinct[3]. To verify the nomenclatural identity of *H. tolstoii*, disentangle its origin and ensure the validity of its current conservation status, we conducted a taxonomic investigation on herbaria specimens of the early XX century. Specimens were studied by morphometric analysis comparing *H. tolstoii* with *H. australe*, *H. pospichalii*, and other closely related species. Finally, we performed phylogenetic investigations using three plastid intergenic spacers (trnH-psbA, trnT-trnL, and trnV-ndhC) and ten nuclear microsatellites to evaluate the genetic relationship between species and assess the possibility of hybrid origin of *H. tolstoii.*

References: Davies et al. (2011), *PLOS Biology*, 9(5):e1000620. 2 Abeli et al. (2021), *Nature Plants*, 7(3):282-286. 3 Orsenigo et al. (2021), *Plant Biosystems,* 155(2):310-335

S.87.5 Using pedigree approach to make management decisions of valuable ex-situ collections

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Historically, ex situ plant conservation has focused on seed banking, however, up to one-third of threatened flowering plant do not produce seeds or produce seeds that cannot be dried and frozen for storage. As a result, these exceptional species must be conserved in living plant collections. This practice of maintaining small, isolated populations often leads to inbreeding, loss of genetic diversity, hybridization between species, and in general, poor conservation outcomes, creating challenges for ensuring their long-term genetic diversity and viability/ An important method used in the zoo community is a pedigree-based management approach, where founding individuals are genotyped and recorded in a "studbook." This allows genetic lineages to be tracked and prevents the breeding of closely related individuals. Optimal breeding pairs are identified and crossed (typically via sperm transfer) to maximize the genetic health of the captive population across institutions. This approach greatly improves conservation outcomes by safeguarding genetic diversity ex situ, creating robust captive populations, and improving reintroduction efforts. By emulating the pedigree approach and creating greater collaboration between institutions, the botanic garden community would be better equipped to safeguard the viability of threatened species in their collections and together manage all ex situ individuals as a "meta collection".

S.87.6 Conserving genetic diversity in the climate change era: strategy used for a rare and threatened conifer in France, Salzmann's pine

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Genetic diversity is essential to evolution and a recognized target of conservation by the Convention on Biological Diversity. Yet, its implementation lags behind other forms of conservation and it is often overlooked in restoration practice. When threats are high and populations are small, in-situ gene conservation needs to be reinforced with an ex-situ approach, where a genetically representative sample of the target taxon is safeguarded in a favorable environment. The fragmented habitat of Pinus nigra subsp. salzmannii (Dunal) Franco 1943 (Salzmann's pine), recognized in Annex 1 of the European Union's Habitats Directive, is threatened by wildfires and land use change. In France, gene flow from massive plantations of other subspecies of black pines since the mid-19th century, also threatens its genetic diversity. Here, using individual tree genotypic data at thirteen microsatellite loci, we identified differentiated lineages for in-situ gene conservation. Discriminating between autochthonous, exotic and hybrid trees, we proposed a method for the creation of an ex-situ core collection. We confirmed that Salzmann's pine is an original genetic lineage within the western European and Mediterranean black pine subspecies. We identified five genetic groups in France that can serve as the basis for in-situ gene conservation as well as for delineating seed zones and guiding forest plantation and restoration practice in a context of increasing interest for this taxon for assisted migration. Maximizing overall genetic diversity while maintaining among population diversity, we identified 80 native and non-hybridized trees that can form the basis of a representative ex-situ core collection. Our cost-effective methods combining in-situ and ex-situ conservation can be easily applied to many forest tree species.

S.88 GENOMIC APPROACHES TO UNDERSTANDING THE ECOLOGY AND EVOLUTION OF SYMBIOTIC AND NON-SYMBIOTIC MICROALGAE. SESSION 2

S.88.1 Genomic divergence and photo-physiological differences within the common lichen photobiont genus, Trebouxia

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The genus *Trebouxia* is a keystone lichen-forming green alga and is known to display a wide range of environmental tolerances. However, knowledge about the genome composition of different strains and what influences the varying levels of tolerance to stress within this genus remains scarce. Here, we report results from two connected studies including (1) a genome-wide comparative study concerning six *Trebouxia* strains, isolated from *Umbilicaria phaea* (*Trebouxia* clade A) and *U. pustulata* (*Trebouxia* clade S) and, (2) an experimental study to examine the photo-physiological performance of the six strains under high light conditions. We have assembled highly complete genomes of the six *Trebouxia* strains, with an average of 96% BUSCO completeness based on the Chlorophyta database. We found extensive genomic variation among, and even within *Trebouxia* clades with genome sizes and numbers of protein-coding genes ranging from 63.08-74.14 Mb and 14,109-18,870, respectively. Interestingly, we found differences in protein-coding genes associated with photosynthesis, suggesting differences in physiological capacities related to photosynthetic performance. To test this hypothesis, we performed an experiment to examine responses of the six *Trebouxia* strains to high light stress, after 1 hour and 3 days of exposure. We measured photo-physiological parameters (photosynthetic efficiency, non-photochemical quenching, chlorophyll *a* concentration) in combination with differential gene expression analysis via RNASeq. Preliminary results show among-strain differences in capacity to withstand high light stress, which likely stem from variation in their genomic composition, particularly regions associated to photosynthesis. Overall, our work demonstrates that unifying physiological and molecular mechanisms can provide important insights into the ecology and evolution of this important and most widespread lichen-forming green algal genus, *Trebouxia*.

S.88.2 Comparative study of asco- and basidiolichen thalli sharing the photobiont Rhizonema

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Relationships between the symbionts within the lichen thallus have been studied extensively, but it is still unclear whether their associations, which are usually specific, are driven by the myco- or photobiont and/or aspects of the thallus structure. Here, we examine the nature of mycobiont-photobiont associations in two lichen fungi clades, one in the Ascomycota (*Coccocarpia*) and one in the Basidiomycota (Dictyonemateae), the latter encompassing the genera *Cyphellostereum*, *Dictyonema*, and *Cora*, which form diverse thalli but are all associating with cyanobacterial photobionts of the same genus, *Rhizonema*. Using microtome sections, light, fluorescence, and scanning electron microscopy, we confirmed the absence of haustorial association in the ascolichen (*Coccocarpia*) and the presence of tubular haustoria in *Cora*, *Dictyonema*, and *Cyphellostereum*. Based on our results, we conclude that formation of penetrative haustoria in *Rhizonema* associations is mycobiont- rather than photobiont-driven and does not correlate with the evolution of a more complex thallus structure in, e.g., *Coccocarpia* or *Cora*. We hypothesize that the absence of haustoria in *Coccocarpia* may be explained by the much older evolutionary age of *Coccocarpia* (Early Cretaceous vs. Oligocene/Miocene in Dictyonemateae), potentially allowing more time to evolve less intrusive non-haustorial photobiont associations in that lineage over time. We also show that the associations within Dictyonemateae lichens appear histologically quite diverse when compared to one another, especially the presence of carbohydrate secretions around the intrahaustorial hyphae but conclude that they likely evolved in their most recent common ancestor and may be a new apomorphy for the clade.

S.88.3 The diversity of lichen phycobiota (microalgae) among thalli and substrates uncovered by an amplicon sequencing approach

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Lichens are considered as microecosystems due to the great diversity of microorganisms that coinhabit their thalli. To encompass the microalgal diversity (including primary and non-primary phycobionts) associated with the lichen symbioses, the term phycobiota is currently used. Here we investigated how the diversity of lichen phycobiota correlates with lichen species and their growth form and ecology. Thalli of five lichen species were collected in a Mediterranean climate zone of the Iberian and Italic peninsulas. The selected species, i.e., *Cladonia foliacea*, *Parmelia sulcata*, *Ramalina farinacea*, *Squamarina cartilaginea* and *Xanthoria parietina* are widely distributed in these regions, have different thallus architectures and grow on different substrates. DNA from five thalli of the same species collected at each locality was extracted, amplified, pooled and DNA metabarcoded for the algal ITS2 marker using an Illumina sequencing approach. This allowed the estimation of the microalgae community present at a certain locality for each lichen species collected there. Furthermore, to corroborate the correct identifications of the lichen mycobionts, barcode identification (of the fungal ITS) by Sanger sequencing was performed. In addition, at each locality three samples of each substrate type present, adjacent to the collected lichens, i.e., soil, bark and rocks were sampled. The substrate samples were used to assess the microalgal background diversity in each locality, i.e., the whole set of algae potentially available for the establishment of lichen symbioses.

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S.88.4 Unraveling the phylogeography and phycobiont diversity of Ramalina farinacea (lichenized fungi, Ascomycota)

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Ramalina farinacea is an epiphytic lichen-forming fungus with a broad geographic distribution, especially in the Northern Hemisphere. To explore the phylogeography of this model lichen and its associated phycobionts (microalgae) diversity, we analyzed over 400 thalli of *R. farinacea* collected in the Atlantic archipelagos of Macaronesia, the Mediterranean Basin, and Temperate/central and Boreal/northern Europe. Data from two nuclear markers (nrITS and uid70) of the mycobiont were obtained to calculate genetic diversity indices, infer phylogenies, haplotype networks, and explore populations structure. Additionally, dating analysis was conducted to provide a valuable hypothesis of the timing of the origin and diversification of *R. farinacea* and its closest allies. Regarding the phycobiont diversity, we studied the climatic niche and bioclimatic distribution of *Trebouxia jamesii* and *T. lynnae*, the predominant symbiotic microalgae in the analyzed populations of *R. farinacea.* Our results highlight that phylogenetic species circumscription in the "*Ramalina farinacea* group" is complex and suggests that incomplete lineage sorting is at the base of conflicting phylogenetic signals. Moreover, *T. jamesii* and *T. lynnae* climatic niches overlapped in a particular zone, but also exhibited restricted zones for each taxon. *T. jamesii* emerged as the most abundant and widespread microalga, which is present in all the bioclimatic belts and biogeographical areas, but *T. lynnae* was identified as the main symbiotic microalga in the thallifrom Western Mediterranean Basin and Canary Islands.

S.88.5 New approaches to understand the effect of anthropic perturbations on lichen communities.

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Lichens, symbiotic organisms consisting of a fungus specialized in obtaining nutrients from a population of unicellular algae or cyanobacteria, have been acknowledged since the 19th century to be highly sensitive to environmental changes, particularly those of anthropogenic origin. This is largely owing to their poikilohydric nature, which lacks active mechanisms for regulating the uptake and loss of gas and water, as well as the symbiosis's fairly delicate equilibrium. Since the mid-20th century, lichens have been utilised as bioindicators for detecting changes that are caused by atmospheric pollution, habitat fragmentation and loss, global warming, etc. However, changes in lichen communities have exclusively been studied from the perspective of fluctuations in mycobiont diversity. There has been little attention to the fate of photobionts and fungal-algal interactions within the community context. Here, we present our recent research results on the impact of anthropogenic disruptions on lichen communities. We utilized metabarcoding tools to characterize species-associated photobiont communities in epiphyte communities along disturbance gradients. Our use of bipartite ecological interaction network analysis tools allowed us to detect much subtler changes than simple analysis of mycobiont diversity and abundance. This enables us to utilise them as an advance indicator of shifts in lichen communities resulting from global change agents.

S.89 NEOTROPICAL BOTANICAL INVENTORIES: DOCUMENTING WHAT IS LEFT? PERSPECTIVES FROM ACROSS TROPICAL AMERICAS. SESSION 2

S.89.1 Flora of the forgotten forests: inventorying the Marañón dry forest in Perú

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Understanding what biodiversity is and where it occurs is crucial if we are to successfully tackle the biodiversity crisis and the climate emergency. Seasonally dry tropical forests contain a high proportion of endemic species yet are particularly vulnerable to conversion to agriculture because they occur on nutrient rich soils. The dry forests of the inter-Andean valleys have been isolated from other dry forests for millions of years and have a level of endemism comparable of that of oceanic islands. We recently surveyed the under-collected Marañón dry forest with the aim of producing the first comprehensive botanical inventory for the area. The process of working with our specimens has highlighted three issues: 1/ The Marañón dry forest contains many species still undescribed by science; 2/ Many tropical families and genera lack taxonomic experts; 3/ Previous floristic analyses of dry forests based on plot data maybe wildly underestimating alpha species diversity in this biome.

S.89.2 Where are we now: state of our knowledge on the evolutionary relationships of Chrysobalanaceae

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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 closely related were found to be distantly related. Analyses using plastomes and more recently nuclear genomes show congruent results as well as incongruences across analyses. We aim to 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. The clade is comprised of four species-poor genera, two Australasian and two neotropical genera.

S.89.3 Risk assessment and categorization proposals for Elaphoglossum species (Dryopteridaceae) in Mexico

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Ferns are indicators of ecological deterioration, as environmental alterations can directly impact their distribution and population density. Studies on the status and conservation priorities of ferns in the Global South are few despite its great diversity in this region. The accelerated loss of biodiversity, particularly in highly diverse countries like those in the American tropics, emphasizes the need to update local fern information and conduct thorough studies to better understand the conservation status of these plants. With 600 species, *Elaphoglossum* is a hyperdiverse fern genus distributed worldwide. In the American tropics, it represents a significant component of the flora with 450 species reported. *Elaphoglossum* is one of the most diverse fern genera in Mexico with 71 species reported, 16 of which are endemic. To contribute to the conservation of the Mexican *Elaphoglossum*, we conducted evaluations for all species based on the categories of the IUCN Red List. We downloaded over 7000 records of *Elaphoglossum* from Mexico through different open-access specimen databases, including GBIF, Pteridoportal, and IBdata. Detailed curation of the datasets involved retaining only accepted names (without synonyms) and removing duplicated records and records from taxa not reported for Mexico or lacking geographic coordinates. The final database included around 4400 unique records. Our preliminary Red List assessment for the 71 reported species in Mexico shows that 90% of them, including all endemics, are threatened –41 critically endangered (CR), 14 endangered (EN), and 16 lacking sufficient data for evaluation–. The main factor contributing to the threat in Mexico is the loss or degradation of habitat due to human activities and overpopulation. Enhanced curatorial efforts of the herbarium collections and updated field collections, will contribute to the accuracy of future assessments.

S.89.4 Understanding the diversity of spikemosses in the American Tropics: An update of the taxonomy of Selaginella in Colombia

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With approximately 700 accepted species, *Selaginella* (spikemosses) is the most species-rich clade of lycophytes and the sole genus in the family Selaginellaceae. Along with the Isoetaceae and Lycopodiaceae, this family holds a critical phylogenetic position as sister to the remainder of the vascular plant lineages and is important for understanding early land plant evolution. The genus *Selaginella* has a cosmopolitan distribution, but the greatest diversity occurs in the American tropics. The taxonomy of *Selaginella* is problematic because of the large number of species, limited morphological differentiation amongst taxa, and a lack of modern taxonomic resources for the group. *Selaginella* diversity in the Americas peaks in Colombia, an understudied global center of plant diversity. This taxonomic impediment limits our ability both to understand global patterns of *Selaginella* diversity and evolution, as well as to advance knowledge of the Colombian flora as a whole. An update to the Flora of Colombia that aims to improve the understanding of the diversity, taxonomy, and distribution of Colombian *Selaginella* is here presented. In total 110 species are recognized, 17 of which are new records for the country, including eight recently described species and four yet-undescribed species. Two species previously included in the Catalog of the Vascular Flora of Colombia are excluded. This update includes a dichotomous key and distribution notes for the 110 recognized species.

S.89.5 Ecuadorian herbaria and their contribution towards botanical documentation in a biodiversity hot-spot

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Ecuador, despite being a small Neotropical country, includes two of the 36 biodiversity hot-spots: Tropical Andes and the Chocó/Darién/Western Ecuador. Per 1000 km^2, Ecuador has more than 6 times the diversity of vascular plants occurring in China, Brazil, Europe, and USA-Canada combined. The literature and direct interviews to personnel from the 18 active Ecuadorian herbaria listed in GRSciColl demonstrate an urgent need for increasing/mobilizing botanical collections as well as the need for support for botanical research in Ecuadorian institutions. Also, it is necessary to highlight the very low number of taxonomists in Ecuador. They, being experts in the area, know how to properly identify and handle these specimens. As such, they are the core of the herbarium operativity. Ecuador registers more than 22,000 vascular plant species names including synonyms, Ecuadorian collections house almost 800,000 specimens, more than 4,900 of which are types. In contrast, only one herbarium from the Global North has more than 600,000 Ecuadorian specimens including +6,000 types. Despite the low average number of Ecuadorian botanists working on herbaria (1-2 FT employees/herbarium), big efforts have been made to digitize almost 400,000 of these specimens. Many of these records are available in GBIF and/or global databases such as Tropicos, and Symbiota as well as in local databases. Potential contributions from Ecuadorian herbaria towards areas such as floristics, molecular phylogenetics, metagenomics, identification with artificial intelligence and accelerated taxonomic efforts are immense. With the climatic crisis we are going through, there is an urgent need for increasing collecting and digitization efforts, describing more plant taxa by local taxonomists, updating/studying the conservation status of the more than 5,000 endemics to Ecuador and repatriating duplicates and/or type images from herbaria from the Global North. Similar situation could be foreseen for other herbaria in biodiversity hot-spots countries from the Global South.

S.89.6 A preliminary palynological study of wild and naturalized vascular plants from the western Andean mountains in the Cotopaxi Provin

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Little is known about palynological information on wild or naturalized species present in the western mountain range in Ecuador. This research compared palynological diversity at three altitudinal levels in the Western Andean Cordillera of Cotopaxi province: evergreen foothill forests (BsPn01) at 300-1400 m, low montane forest (BsBsn04) at 1400-2000 m and montane forest (BsMn03) at 2000-3100 m. Pollen morphology found in this preliminary study of 9 genera in 9 families of vascular plants was mainly perprolate, monoporate and with pollen grain sizes between 26.9 μm and 134 μm. Pollen observed in the range 300-1400 m belongs to: 1) Sambucus sp. (Adoxaceae): 26.9 μm, perprolate and monoporate; 2) Guzmania sp. (Bromeliaceae): 53.7 μm, perprolate and bicolpate; 3) Gasteranthus sp. (Gesneriaceae): 17.9 μm, perprolate and monoporate; and 4) Hibiscus rosa-sinensis (naturalized, Malvaceae): 17.9 μm, perprolate and monoporate.Pollen observed in the range 1400-2000 m belongs to: 1) *Cavendishia* (Ericaceae): 53.7 μm in length, perprolate and monoporate; 2) *Columnea* sp. 1 (Gesneriaceae): 53.7 μm in length, subprolate and tricolporate; 3) *Salvia* sp. 1 (Lamiaceae): 134 μm long, and perprolate; 3) *Oxalis* sp. 1 (Oxalidaceae): 26.9 μm in length and monocolpate; and 4) *Guzmania* sp. 1: see previous description. Pollen observed in the range 2000-3100 m belongs to: 1) *Calceolaria tripartita* (Calceolariaceae): 134 μm, long and bicolporate; 2) *Salvia* sp. 2 (Lamiaceae): 134 μm in length and shape and openings not identifiable; 3) *Oxalis* sp. 1: see previous description and 4) *Guzmania* sp. 1: see previous description. The same species of *Guzmania* (Bromeliaceae) was present in the three altitudinal levels and *Oxalis*, *Cavendishia*, and *Salvia* were found in the two upper altitudinal levels (1400 to 3100 m). These preliminary results need identification of the genera to species and verification and reconfirmation of the pollen grain characteristics.

S.90 CONNECTIONS ALONG THE ATLANTIC FRINGE

S.90.1 Why so few endemic species in oceanic island bryophyte floras? Insights from phylogeographic inference in the Macaronesian region

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Among land plants, bryophytes exhibit the lowest rates of endemism on oceanic islands. This pattern has primarily been interpreted in terms of intense gene flow preventing speciation from the closest continental sources, so that endemism would have to originate from geographically remote sources through chance long-distance dispersal. Here, we test this hypothesis through a meta-analysis of species distribution patterns and phylogeographic analyses in the Macaronesian bryophyte flora. Our results reveal a striking mismatch between the strong similarity of the Macaronesian and Mediterranean floras, and the largely extra-Mediterranean origin of endemism that is, at first sight, compatible with this hypothesis. This hypothesis is, however, at odds with the significant genetic differentiation systematically found among populations disjunct between Macaronesia and the Mediterranean. Our reconstruction of the biogeographic origin of non-endemic species based on ABC analyses in a coalescent framework reveal a complex history of colonization of the archipelago from multiple continental sources, but also of continental colonization from island ancestors. Altogether, our results thus suggest that Macaronesian bryophyte flora originated from different sources depending on the variation of wind connectivity through time, triggering endemic speciation from various sources. While speciation rates may thus not have necessarily been lower than in other land plant lineages, the low rates of endemism among island bryophyte floras result from subsequent dispersal events towards continental areas.

S.90.2 The introduction of heathers to western Ireland indicates an ancient maritime trade route from the Iberian peninsula

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Five species of heather have disjunct 'Lusitanian' type distributions in Europe. They occur as discrete populations along Ireland's west coast, and two also occur on Britain's south-west coast. The nearest, or principal other place they occur is in the Iberian Peninsula. None could have survived the last ice age in Ireland or Britain, and migration northwards, leaving 100s of kilometre gaps *en route,* appears impossible. *Erica mackayana* (Mackay's Heath) does not set seed in Ireland and is restricted to small colonies beside minor routeways inland from the west coast, suggesting it was introduced through smuggling. This was confirmed by a genetic study which found that each Irish population was similar to plants sampled from a different place in north Spain and not to each other. However, while the results are consistent with most of the populations being comparatively recent introductions, the largest, on Roundstone Bog in Connemara, appears to be much older. Other heathers appear to be historical introductions to Ireland, *Erica vagans* (Cornish Heath) brought on smuggled goods and *Erica erigena* (Irish Heath) brought by pilgrims traveling on pilgrimage by sea to Santiago de Compostela, but the single population of *Daboecia cantabrica* (St Dabeoc's Heath), is today that extensive, covering all the available habitat in Connemara and South Mayo, that it must have been brought much longer ago. Eleven other Lusitanian plant species occur in western Ireland including *Arbutus unedo* (Strawberry Tree) shown to be probably introduced 4,300 BP by the first copper miners. Combining the distribution pattens of all those likely to be ancient introductions points at a direct ancient sea crossing from Galicia to western Ireland dating back to the start of the Bronze Age.

S.90.3 Genetic evidence indicates multiple origins of Ireland's tree flora

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Over the past 20 years our understanding of Ireland's tree flora has increased significantly through genetic analysis. While Ireland has among the lowest native forest cover in Europe along with considerable recent planting, the remnants do show a signature of a native flora rather than that of an introduced flora. What emerges from the evidence is a relatively depauperate genetic component, a subset of Europe with reduced genetic diversity. This is to be expected from an island on the western periphery of the distribution of many European trees. We review studies completed to date in Alder, Ash, Birch, Oak and Scots pine. We show that while each species is unique, two overall patterns have emerged. One for species with temperate distributions showing a link with the Iberian Peninsula refugium and another for more cold tolerant and boreal species which shows a mix of Iberian genotypes along with those from a more northerly refugia. This baseline data is essential for situating Ireland's tree flora in a European context. However, many questions remain, such as the sequence and dynamics of invasions through chloroplast capture and the contractions and expansions of populations over time. Further work is ongoing to improve our understanding of the genetic landscape of the native tree flora.

S.90.4 Is Arbutus unedo L. native to Ireland, or was it brought from the Iberian peninsula by Bronze Age copper miners?

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Arbutus unedo, Strawberry Tree, is a small tree occurring widely in central and western Mediterranean regions. It is also found along the Atlantic seaboard, northwards along western France. It is not considered native in Britain, but is in Ireland, where it is virtually confined to the south-west. However, this species could not have survived the last ice age in Ireland and migration northwards leaving such a large gap appears unlikely. Its Mediterranean ecological traits are not adapted to Ireland: it both flowers and fruits in early winter; it is unable to grow on wet soils and is intolerant of shade or grazing, so that it is now confined to cliffs, islands and rocky outcrops. The region around Killarney, Co. Kerry in SW Ireland, supports at least 2,000 individuals of *A. unedo*, or >80% of the total known trees in Ireland. It is here that both a palynological investigation and an archaeological excavation date the first fossil occurrence of the species in Ireland to be around 4,000 – 4,300 BP. The archaeological excavation, on

Ross Island, Lough Leane, was of the first Bronze Age copper mine to be exploited in NW Europe. Using the Botanical Society of Britain & Ireland database, old records and field work, we mapped the distribution of *A. unedo* in Ireland and found a striking association with the occurrence of Bronze Age copper mines. We suggest *A. unedo* was brought by copper miners to Lough Leane from northern Spain, where three copper mines were worked from 4,800 to 4.300 BP, and that it flourished and later spread to other copper mines in SW Ireland, favoured by the extensive forest coppicing associated with the mining and its ability to produce multiple stems from an underground lignotuber. Such an introduction is supported by Irish mythical stories.

S.90.5 Genetic heritage of Arbutus unedo: potential origins of populations from the Atlantic fringe

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The strawberry tree (*Arbutus unedo*) is an iconic plant species that occurs throughout the Mediterranean and the south-western European Atlantic coast. In this talk, we present the initial results of a biogeographic study using wide-genome SNPs (nextRAD sequencing) on over 250 specimens from 38 populations throughout most of its distribution range, with a special sampling effort on Irish populations. At a continental level, we provide evidence of the divergence between Mediterranean and Atlantic populations. In a second analysis at the regional scale, we obtained a consistent linkage among Irish populations, probably due to one or more ancient introductions that have inbred for a long period of time. Here, we describe the main putative patterns of genetic differentiation and will discuss the potential routes and events that may have given rise to these.

Symposia Session 6

S.91 ADVANCES IN FLOWER DEVELOPMENT: THE PIVOTAL TREATISE OF PAYER REVISITED

S.91.1 Merism of Begoniaceae: an issue of numbers

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Floral merism, the number of parts per whorl in the flower, is a relatively conserved and reliable character within major clades, generally with a limited shift between different merisms. Begoniaceae is a family with unisexual flowers which are highly diverse in merism, especially in female flowers. This study aims to understand the original merism and the potential evolutionary trends within male and female flowers. The floral developmental processes of several representative Begoniaceae species were investigated with SEM, and floral characters along the phylogeny of the family were reconstructed to trace back the evolution of different merisms. We also treated early floral buds with 6-BAP to test the effect of size on changes in merism. Our results show that tetramery and dimery shift between each other several times in *Begonia*, and the shifts are the result of space availability or a variation in position in early developmental stages. Trimery is rare and evolved from pentamery. Pentamery is relatively common in the female flower, but is less stable in some species with evidence of shifts from a higher or a lower merism. Shifts towards higher merisms are caused by either the fusing of two tepal primordia or the splitting of one primordium, which also results in the lobed tepal in the section *Eupetalum*. Flowers treated by 6-BAP increase in merism by producing extra organ primordia and this relates to the expansion of floral apex. Female flowers are more diverse in merism than male flowers and possible causes are weaker pressure from bracts on female floral primordia, a higher spatial constraint caused by the development of hypanthium, and the unstability of a high merism. Floral development of Begoniaceae is a good case to understand how different meristic patterns evolved in relation to shifts in space and pressure during early floral development.

S.91.2 The study of flower development and phylogeny, then and now

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Payer was a pioneer in the microscopic study of floral development based on detailed drawings of different developmental flower stages across many angiosperms. He recognized patterns that appeared to be similar in young stages. Some of these were interpreted as indicating systematic relationships. He assumed that in these flowers the development of the androecium was centrifugal. Only in polyandrous Magnoliales and Ranunculales did he find a centripetal pattern. Later improved the observation techniques and the systematic interpretation by phylogenetic analyses. Hirmer worked along similar lines (1918). As a new tool he used microtome sections, which allowed more precise images. Corner emphasized the systematic importance of centrifugal androecia, and unlike other workers, he assumed that this feature was phylogenetically basal, as it occurred in many families of mainly tropical distribution (1949). Corner's view also influenced some later macrosystematists to assume that a number of angiosperm orders together were to be treated as the new angiosperm class Dilleniidae. However, with molecular systematic studies it later was shown that the class Dilleniidae had to be discarded (2018). Further progress was the use of scanning electron microscopy for flower development (Endress 1972) and the use of synchrotron radiation x-ray tomography microscopy for visualizing the inside of fossil flowers (Friis et al. 2014). Progress came also with the focus on still earlier developmental stages, when the developing flowers did not yet have any shape, but were only expressed as an activated meristem, only visible using stained microtome sections. Phylogenetic improvement came with global molecular phylogenetics, at first with the gene *rbcL* (Chase et al. 1993), and then continuously enriched up to the inclusion of all three plant genomes (Soltis et al. 2018). This, in turn, greatly helped to improve the knowledge of structural flower evolution.

S.91.3 The enigma of the grass stigma

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Jean-Baptiste Payer (1857) was among the pioneering researchers of grass flower development. He nicely demonstrated that, taken in isolation, data on gynoecium development in grasses do not contradict its interpretation as a solitary carpel. This conclusion created a need for an explanation of the occurrence of more than one stigma in most grasses. Some scattered angiosperms do have two stigmas per carpel, but a number of grasses possess as many as three (and rarely even more) stigmas. Grass stigmas and their stalks develop as ab initio terete and filiform structures. They differ in this respect from the typical plicate condition of the angiosperm stigma. As first illustrated by Payer (but not documented in full detail with SEM before the present study), at least some PACMAD grasses have stigmas attached to the outer surface of the gynoecium wall, well below the margin of the gynoecium orifice. Consequently, some researchers concluded that the grass stigma is not homologous to the stigma of other angiosperms. Broad comparative analysis in a modern phylogenetic context demonstrates that the grass gynoecium, contrary to the view of Payer, is pseudomonomerous. Each stigma, at least in the hypothetical ancestral grass condition, belongs to its own carpel. A bistigmatic grass gynoecium has two sterile carpels, each producing a stigma, and a fertile carpel that lacks a stigma. Comparison with outgroups is highly important in resolving the morphological interpretation of the grass stigma. Ecdeiocoleaceae are the closest specialised wind-pollinated outgroup of grasses. Our data show that the stigmas of Ecdeiocoleaceae are flat and bifacial, and this condition is apparently plesiomorphic in grasses. The peculiar stigma position found in some PACMAD grasses can be explained in terms of formation of a secondary carpel margin in the region of closure of the gynoecium orifice.

S.91.4 Morphology and development of flowers and inflorescences in Burmannia (Burmanniaceae)

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Burmannia is the largest genus of the pantropical family Burmanniaceae (Dioscoreales). Species of *Burmannia* demonstrate, on the one hand, actinomorphic bisexual flowers with typical monocot trimerous groundplan and, on the other hand, highly elaborated morphology that includes prominent floral tube with large longitudinal wings. We provide comprehensive analysis of inflorescence structure, floral anatomy and floral development for eight species of *Burmannia* with different life strategies (autotrophy, full mycoheterotrophy, partial mycoheterotrophy). In *Burmannia*, the basic inflorescence type is a thyrsoid of two cincinni, which is transformed into a botryoid in the few-flowered species via the reduction of lateral cymes to single flowers. The floral tube in *Burmannia* consists of a hypanthium and a perianth tube. In *B. oblonga*, inner tepals are seemingly absent from mature flowers. However, during early developmental stages of the flower these organs are present; but, their growth is arrested almost immediately after initiation. The gynoecium of *Burmannia* consists of synascidiate, symplicate and asymplicate zones. The symplicate zone is secondarily trilocular. The border between synascidiate and symplicate zones (i.e.,the cross zone) is hard to recognize due to the absence of visible traces of postgenital fusion in the basal part of the symplicate zone. Species of *Burmannia* uniformly possess supralocular septal nectaries, i.e.,located in the upper region of the ovary just below the ovary roof. Finally, species of *Burmannia* reveal a remarkable diversity of stamen-style interactions. The stamens are either tightly appressed to the style remaining free from it, or postgenitally fused with the style by their connectives forming a gynostegium. A gynostegium is otherwise only found in some lineages of Apocynaceae of eudicots that have similar complex synorganised flowers. Acknowledgements: The work was supported by the Russian Science Foundation (project 21-74-10006) and by IITP RAS FFNU-2022-0037.

S.91.5 The legacy of Jean-Baptiste Payer – a need to put floral developmental studies at the forefront of botanical research.

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Morphology has always been the indispensable instrument for the exploration of biodiversity and studies of living organisms. Fundamental questions, such as the origin of flowers and their homology can only be properly answered from the perspective of ontogeny in a phylogenetic framework. Payer was the first to systematically create a comparative study of flowers in great detail, covering as many as 329 species, belonging in 130 families of flowering plants. His masterpiece, *Traité d'organogénie comparée de la fleur*, published in 1857 (1854 for the first edition), was advanced for his time and remains strongly relevant in its extraordinary accuracy and as a valuable counterpart of evo-devo studies. The floral developmental study of Payer has created the perfect conditions for the development of twentieth century schools of dynamic botany set against the more conservative typological approach. Comparative floral developmental studies allow for a better understanding of complex structures and are a key to understanding fundamental trends in floral evolution. As flowers are dynamic structures, often without clearcut boundaries between organs or tissues, an integration of ontogenetic and evolutionary approaches remains the cornerstone in understanding floral evolutionary change. Morphology has always been significant but becomes increasingly so, as the understanding of the floral phenotype is only relevant through integrative studies including pollination systems, gene expression and regulation, and development, demonstrating the importance of spatial constraints. The first part of the talk presents an overview of the significance of Payer as individual. The second part covers his legacy for modern morphological research. The third part explores a case study in the family Anacardiaceae, illustrating the importance of floral developmental evidence for floral studies.

S.91.6 Floral anatomy and vasculature in Peliosanthes (Asparagaceae): refined knowledge of flower structure and implications for systematic

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Peliosanthes is one of Southeast Asian genera of Asparagaceae (Asparagales). Species of *Peliosanthes* (Asparagaceae) are common herbs in tropical and subtropical evergreen forests. We studied inflorescence morphology, flower structure and flower anatomy, with special emphasis on its vascular system, in 13 species of *Peliosanthes*. We revealed raceme and thyrse as two distinct inflorescence types in *Peliosanthes*. Probably, thyrse evolved several times from a raceme in the evolution of the genus, which appeared to be available due to the presence of bracteoles (floral prophylls). A characteristic feature of *Peliosanthes* is the presence of an androecial corona, i.e.,a tube formed by congenitally fused stamens. The corona is absent from the closely related genera of Asparagaceae and therefore can be considered as a synapomorphy of *Peliosanthes*. Our data show that the ovary position (superior, semi-inferior and inferior) is not associated with any differences in the structure of the gynoecium but is a consequence of the different shapes of the ovary roof. According to our results, species differ in the presence of septal nectaries: nectaries are absent from *P. longicoronata* and *P. triandra*, and therefore these species lack an asymplicate gynoecium zone, and their style is formed by a symplicate zone. In the other species, the nectaries are located in the hemisymplicate zone, and the style is formed by the asymplicate zone. The flower vasculature in all the studied species is fundamentally uniform; the interspecific differences are only found in the levels of bundle separation. The structure of the ventral carpel bundles correlates with the presence or absence of the septal nectaries. Our data supplement the phylogenetic findings providing additional evidence for the distinctness of species and lineages within *Peliosanthes*, and also they fulfill the gaps in knowledge on its basic flower structure.

S.92 CAREX: THE EVOLUTION OF A MEGADIVERSE GENUS TACKLED FROM MULTIPLE APPROACHES. SESSION 1

S.92.1 Revisiting the taxonomy of Carex sect. Lupulinae subsect. Lupulinae (Cyperaceae)

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Carex subsect. *Lupulinae* (Cyperaceae) is a well-defined clade of four showy sedge species common in eastern North American swamps that has been the subject of no less than four independent taxonomic revisions in the last 50 years. Although these treatments were all concordant in their species delimitation, extensive fieldwork across the subsection's geographic range in addition to the morphometric analysis of more than 300 herbarium specimens have revealed unexpected morphological extremes and evidence for hybrids that challenge the current circumscription of taxa. Plastid and nuclear sequences were subsequently recovered for more than 100 individuals included in morphometric analyses, and the phylogenies reconstructed from these markers were concordant with the conclusions drawn from morphology and fully support the recognition of an undescribed species endemic to the southern United States Coastal Plain. Moreover, preliminary results suggest that another cryptic species may be hidden in what is currently called *Carex lupuliformis*, a taxon rare throughout most of its range. The discovery of considerable morphological and molecular variation within one of the most extensively studied *Carex* clades in eastern North America not only demonstrates how basic studies in biodiversity continue to be relevant, but also highlights their importance to conservation in even in well-known floras.

S.92.2 Temporal and spatial scales in populations and lineages differentiation in a sedge

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Biologists have debated about how time scale affects evolutionary processes, since the first evolution theories. We present local and regional approaches on the evolution of a common species in the Palearctic *(also in the eastern North America)*: *Carex nigra* (L.) Reichard. In each approach we have assessed which factors are more critical: current ecological conditions or historical processes? In the local approach, microsatellites were used to assess the genetic diversity and structure of 12 populations along an altitudinal gradient in SE Spain. The regional approach involved the application of RAD-seq to explore the phylogeography of *Carex nigra.* Niche modelling analyses were also conducted to evaluate the potential distribution of the *C. nigra* complex. At a local scale, microclimatic and edaphic conditions influenced genetic diversity among populations and shaped the plant's reproductive strategy (clonality vs. sexual reproduction). Notably, lower genetic diversity was observed in colder and nutrient-poor environments where clonality predominated. The genetic structure exhibited a weak pattern, showing no correlation with either climate or geography. Results from the regional approach indicated a strong geographical structure within *Carex nigra* range, distinguishing between three subspecies: *C. nigra* subsp. *intricata,* subsp. *nigra* and subsp. *transcaucasica,* with almost non-overlapping distribution. The significant differences in their climatic niches are, likely, explained by their allopatric distribution pattern. At this scale, historical phylogeography emerge as the main driver of divergence, with these ranges coinciding with different climate refugia during the Pleistocene glaciations. The scale of the evolutionary process plays a crucial role in determining the importance of diversification drivers in *Carex nigra*. Historical phylogeographic factors, such as refugia during Pleistocene glaciations, wielded substantial influence at the regional level. In contrast microclimate and soil conditions did not contribute to population genetic differentiation across altitudinal gradients in a Mediterranean mountain range but determined patterns of genetic diversity.

S.92.3 Genetic and morphological diversity in Carex sect. Siderostictae

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Carex sect. *Siderostictae* is a basal lineage in the whole group of *Carex*. In traditional taxonomy, about thirteen taxa are considered in the group, but the recently proposed phylogeny, 27 taxa are included in the *Siderosticta* group. Unlike other members in *Carex*, the *Siderosticta* group has large and fewer-numbered chromosomes with distinct polyploidization (about 1 µm long and 2*n* = 12 or 24) and miss continuous variation in chromosome number (aneuploidy, agmatoploidy and/or symploidy). The *Siderosticta* group has apparently broad leaves and well-developed rhizomes. Within the section, terminal spikes exhibit diversity with unisexual (staminate) and bisexual (androgynous) flowers. To clarify major lineages within the group and evaluate evolution of major characters, nrDNA (ITS and ETS), cpDNA (*trnC-ycf6*, *aptB-rbcL*, and *trnL-F*), and nuclear low-copy genes (catP and GZF) were utilized. nrDNA and cpDNA do not support monophyly of the traditional section and *C. siderosticta*, which is the most widely distributed in East Asia. However, nuclear low-copy genes support the monophyly of *C. siderosticta*. In addition, *C. siderosticta* + *C. okamotoi* and *C. ciliatomarginata* + *C. splendentissima* + *C. pachygyna* clades were well supported. Multiple polyploidization events were hypothesized in the *C. siderosticta* + *C. okamotoi* clade (2*x*, 3*x*, 4*x* populations). Unisexual terminal spikes are mainly found in diploids such as *C. okamotoi*, *C. ciliatomarginata*, *C. splendentissima*, and *C. tumidula*. Further discussion will be made on cytological and morphological character evolution in major lineages of the *Siderosticta* group.

S.92.4 Jumping for joy: phylogenomic insights on the biogeographic and diversification adventures of Carex sect. Uncinia (Cyperaceae)

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Carex sect. *Uncinia* with c. 70 species is the most diverse lineage of subgenus *Uncinia* and displays a remarkable disjunct distribution in the Southern Hemisphere. It had its ancestral area in South America, where it originated 15 Mya, but it is also present in the Pacific-Southwest Region (Australia-New Zealand), as well as in some Pacific Islands and circum-Antarctic archipelagos. The colonization of these regions was likely facilitated by the presence of an exserted hooked rachilla, which is a syndrome for long-distance dispersal (epizoochory) exclusive of sect. *Uncinia*. A large proportion of the species richness is roughly halved between South America and New Zealand, which have been related to putative evolutionary radiations, especially in the later. Previous phylogenetic reconstructions based on standard DNA barcoding markers failed to disentangle relationships at shallow evolutionary level. We have enhanced phylogenetic resolution within this section by using Hyb-Seq genomic data for an almost complete species sampling. We tried to further studied the evolution within this lineage by obtaining genome size data and by conducting morphometric analyses for shallow species complex with disjunct trans-oceanic distributions (*C. austrocompacta* s.l., *C. brevicaulis* s.l.) biogeographic patterns. Genome size reconstruction analysis reveals that several species of sect. *Uncinia* could be polyploid, as they exceed the average size of the genus. This increase in genome size could be associated to its colonization ability in new ecological niches as previously seen in other Cyperaceae. The dispersal routes of sect. *Uncinia* through the Oceans can be appreciated in some of its species' complex as those of the circum-Antarctic archipelagos: *Carex austrocompacta* s.l. describes a Stepping-Stone pattern from New Zealand in an East-to-West direction. *Carex brevicaulis* s.l., on the other hand, seems to have colonized Pacific, Atlantic and circum-Antarctic islands through several, independent LDD events from South America.

S.92.5 Comparative genomic architecture of chromosomal fissions and fusions in holocentric sedges

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Speciation is a fundamental evolutionary process that has generated and maintained biodiversity. The evolution of reproductive barriers completes speciation, and is therefore key to maintaining species boundaries. In monocentric species, where chromosomes contain a single centromere region, changes in karyotypes often promote reproductive isolation by causing constraints during cell division; however, such chromosomal rearrangements are less likely to be established first. Holocentric species that lack a single centromere but have centromere-like structures across their chromosomes have repeatedly evolved in the tree of life and often show high variation in karyotypes between closely related species. Sedges are a holocentric group with a high diversity of karyotypes between and within species. In sedges, karyotypic changes through chromosomal fusion and fission are associated with changes in transposable elements (TEs). However, the specific underlying genomic architecture is not yet fully understood. Here, we used pairs of sibling species from the genus Carex (Cyperaceae) with different or identical karyotypes to unravel the genomic architecture of chromosomal fission and fusion. For this, we (i) characterized the TEs across rearranged and non-rearranged chromosomes, (ii) measured synteny across species with different karyotypes, (iii) annotated genomes, and (iv) tested whether non-conserved genomic areas differed in gene density compared to conserved regions.

We assembled 10 reference quality genomes from eight Carex species using PacBio Revio and 3D genome-wide chromatin interactions. Through this rare comparative study, we provide detailed insights into genome evolution in holocentric species and its links to speciation by tracing the evolution of changes in genomic architecture and regions associated with reproductive isolation.

S.92.6 The genus Carex (Cyperaceae) in South America: a decade-long study of one of South America's best hidden secrets

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South America harbors an astonishing amount of the world's vascular plant diversity, including more than 120000 species, 6200 genera and five biodiversity hotspots. Systematic and evolutionary studies have been mostly focused on plant lineages greatly diversified in tropical habitats like rainforests, in contrast to the comparatively less studied temperate lineages, which are mostly confined within the continent's colder regions. The genus *Carex* L. (Cyperaceae) is a megadiverse and sub-cosmopolitan group of plants, which, despite being within the ten most speciose plant genera of South America's temperate regions, has been historically overlooked. In this work we present a preliminary systematic synopsis of *Carex* in South America, derived from the results of more than nine years of past and ongoing international collaborative studies involving researchers from all over America and Spain. The main results are the systematic revisions of the two largest lineages within the continent, sections *Junciformes* and *Uncinia*, as well as a series of taxonomical and chorological studies aimed to resolve the systematics of complex groups, describe new taxa, and elucidate biogeographic patterns.

S.93 GLOBAL CONSERVATION CONSORTIA: INTEGRATED PLANT CONSERVATION ON A GLOBAL SCALE

S.93.1 Spatial priorities for the conservation of plant and animal evolutionary history

Sebastian Pipins[1,2,3], Alex Bowmer[2,4], Rikki Gumbs[3,5], Ian Ondo[1,6], Nisha Owen[7], Sam Pironon[1,6], James Rosindell[3], Felix Forest[1]

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The biodiversity crisis is set to prune the Tree of Life in a way that threatens billions of years of evolutionary history. To secure this heritage along with all the benefits it provides to humanity, there is need for conservation prioritisations to be informed by phylogenetics. Furthermore, it is typical for prioritisations to report on vertebrate diversity, biasing our attention away from plants. Here, we contrast global priorities of threatened evolutionary history for seed plants and tetrapod animals, highlighting areas of shared priority and unique concern. We then reveal patterns of Evolutionarily Distinct and Globally Endangered (EDGE) species and consider how areas of shared priority disaggregate at the sub-national scale. With the EDGE index featuring under Target 4 of the Kunming-Montreal Global Biodiversity Framework, it is vital to ensure the world's most unique and imperilled species are safeguarded. This study therefore presents an important examination of the potential synergies to be found in conserving across the Tree of Life.

S.93.2 Ex situ gap analyses: informing prioritization for conservation action

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Botanic Gardens Conservation International (BGCI) is leading a global initiative to create a cost-effective, botanic garden-driven system for conserving and managing plant diversity. This initiative involves forming consortia of experts knowledgeable in genera that pose conservation and management challenges. These consortia operate under a unified framework to meet the conservation needs of these endangered plant groups. A key strategy for the most threatened species includes establishing ex situ metacollections, networks of living collections across various locations, and managed as unified populations. These metacollections aim to conserve a broader range of genetic diversity, mitigate risk by distributing collections across multiple institutions, and lower maintenance costs. The Global Conservation Consortium (GCC) is at the forefront of promoting best practices for these metacollections through cross-sector collaborations. They have also developed new methodologies for conservation gap analysis to evaluate existing plant group collections, identify species at the highest risk, and prioritize conservation actions. The presentation will showcase case studies from the GCC on managing metacollections for Cycads, Magnolias, and Oaks. These studies will illustrate the value of data sharing amongst botanic gardens in the application of Conservation Gap Analysis, establishment of collaborative conservation orchards, and best practices for managing collections with a genetic focus. This talk will introduce the GCC's gap analysis tools, underscoring the potential for collaborative opportunities and inviting new partners to participate in the GCC's global conservation efforts.

S.93.3 Improving oak micropropagation and cryopreservation through GCC collaborations

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Oaks are flagship species that act as keystones in many communities. However, oaks worldwide are increasingly threatened by novel pests and diseases, habitat loss, and climate change. Protection of global oak biodiversity must include ex situ banking, but as oaks are considered exceptional species overall, they cannot be banked using conventional seed banking methods and instead are best banked long-term using cryopreservation. The first step in developing many cryopreservation protocols is initiation into tissue culture. However, tissue culture propagation in oaks is difficult, with protocol response often specific to species and even genotype. Developing universal tissue culture protocols would make it vastly easier for practitioners worldwide to quickly and effectively bank the biodiversity necessary to ensure these charismatic species survive into the uncertain future. As a beginning step towards this goal we selected eight focal oak species, including six threatened species, from across the United States to study the factors affecting tissue culture initiation in *Quercus* in preparation for cryopreservation. Eighteen institutions across North America, organized through the Global Conservation Consortium (GCC) for Oak, collaborated to send cuttings from their collections. Using 91 genotypes taken from across the species' range, we initiated shoot and somatic embryo cultures using a standard experimental protocol to test the effects of species, genotype, climate conditions, anti-microbials, silver thiosulfate, sterilization methods, and other factors in the initiation of *Quercus* to tissue culture. First year results showed survival at three months across species ranging from 41.3% (*Q. rubra*) to 1% (*Q. boyntonii*), with an average survival of 15.7%. Comparison of four new sterilization methods reduced the contamination rate from 73.9% to 18.2%. This project is an example of how the GCC can be used to facilitate large-scale studies on the improvement of ex situ conservation methods. (Research supported by IMLS).

S.93.4 Establishing ex situ conservation collections through collaborative partnerships

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Effective conservation of tree genetic diversity requires the integration of *ex situ* and *in situ* conservation approaches. A network of coordinated living collections at multiple sites managed as a single population —a metacollection— is the most effective and efficient way to conserve genetic diversity of threatened exceptional plants (plants that cannot be conserved in conventional seed banks), *ex situ*. Metacollections can be used for research, education, restoration, and act as an insurance policy against extinction. Botanic gardens and arboreta have the expertise to identify, collect and propagate exceptional plant species, but they often lack sufficient space to establish coordinated collections at the scale needed to capture sufficient genetic diversity. The public garden community has long known that we are more impactful working together than on our own, but how does that translate to living collections? To address this challenge, the Global Conservation Consortia (GCC) have created a solution that brings partners from different sectors to solve the challenges of *ex situ* conservation of exceptional plants. More specifically, the GCC's have led cross-sector partnerships that advance and maximize the different strengths and skills of GCC partners to successfully establish genetically diverse metacollection sites. Partners such as traditional botanic gardens and arboreta, those that have the staff capacity and infrastructure to collect and propagate seedlings, cuttings, and grafts of rare and threatened species are partnering with other sectors such as government agencies or land trusts, those who have more space or capacity to manage and monitor large-scale plantings long-term. Throughout this presentation, the GCC for Oak, Magnolia and Cycad will provide case-studies of successful, collaborative metacollection site establishment. This talk will present opportunities to engage with the GCC's to establish more partnerships to protect the depth and breadth of genetic diversity found in wild populations of the priority at-risk plant species, globally.

S.93.5 Understanding the dynamics of ex-situ living collections: a longitudinal, contextual, and global meta-data approach

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The ex-situ living collections of Botanic Gardens are distinct from other horticultural landscapes in being "documented", in other words they are defined by the data that describe the collections. Consequently, ex-situ living collections individually and globally amass vast quantities of data, as they seek to track and document the transient flow of biodiversity within and through networked ex-situ collections. But these data are rarely if ever comprehensively analysed to understand the performance, strengths and limitations of ex-situ collections. At the Cambridge University Botanic Garden, we have developed a bioinformatic pipeline called BGSmarR which will thouroughly analyse the data of a living collection in order to reveal the quality (or otherwise) of collection management - itself crucial for the sustainable maintenance and conservation of ex-situ diversity. Furthermore, by combining these analyses across the multiple globally distributed living collections, we can reveal the global dynamics that enable and limit the functioning of ex-situ conservation. Here we report on the findings of these global meta-analyses, describing the rise and fall of ex-situ living collections over time, and the surprising and counterintuitive patterns that emerge from longitudinal and contextual approaches. On the basis of these analyses we identify global and cultural forces in play that are limiting our collective ability to manage high performance living collections, and preventing us from realising the our full portential to deliver ex-situ conservtaion in perpetuity.

S.93.6 Beyond Botanic Gardens – establishing and maintaining an ex situ conservation metacollection with non-botanic garden partners

Hannah Wilson

Ex situ conservation is crucial for preventing species extinction, yet many conifer species are exceptional and cannot be preserved through traditional seed banks. These species must be conserved as living collections, a challenge compounded by the substantial space required for cultivating large, slow-growing trees. The International Conifer Conservation Programme (ICCP) at the Royal Botanic Garden Edinburgh has pioneered a solution over the past 35 years, establishing a vast conifer conservation metacollection across the British Isles. This network spans over 270 diverse sites, from botanic gardens and private estates to zoos, hospitals, and hotels, encompassing over 23,500 individual plants and nearly half of all conifer taxa.

This talk will explore the ICCP's journey, emphasizing the unique benefits and complexities of collaborating with non-botanic garden partners. By expanding beyond traditional botanic gardens, the ICCP has enhanced its conservation capacity and created new opportunities for public engagement, education, and outreach. Special attention will be given to the educational and outreach efforts that have transformed participants from conservation novices to enthusiastic advocates. This talk will highlight the significant added value of non-traditional partnerships in achieving botanic garden conservation goals and fostering a widespread commitment to preserving threatened species

S.94 LARGE-SCALE GENERATION AND UTILISATION OF REFERENCE-QUALITY GENOMES FROM PLANTS

S94.1 10KP sequencing of genomes from phylodiverse species: new discoveries and new technologies

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Seven years ago at the IBC in Shenzhen, we announced a plan to sequence the genomes of 10,000 phylodiverse plants. Much has changed since those days. The technology of sequencing, especially long reads, has raised the standards for assembly. But the COVID-19 pandemic and growing geopolitical conflicts have made international collaborations increasingly difficult. We have adjusted to these realities and continued to produce data, albeit at a lower rate. Much of the data produced by 10KP have been for algae provided by Michael Melkonian. The most notable discovery, echoed by other publications not affiliated with us, is the ubiquity of horizontal gene transfer. We have identified two mechanisms for the gene transfer, involving phages and DNA viruses, depending on the nature of the donor organism. The mechanisms are not unique to plants and may be shared across eukaryotic evolution, included metazoan evolution. As for land plants, and in particular the angiosperms, long reads will be essential to create the high-quality assemblies that plant scientists rightly demand. To this end, BGI has developed an in-house long reads nanopore sequencing platform. We are adopting this new technology as an alternative to the otherwise more expensive options currently available.

S94.2 Pangenome and multiple origin dynamics of the Brachypodium distachyon - B. stacei - B. hybridum grass allopolyploid model system

Miguel Campos Cáceres[1,2], Rubén Sancho[1,2,3], Bruno Contreras-Moreira[2,3], Ernesto Pérez-Collazos[1,2], Li Lei[4], John Vogel[4], Pilar Catalán[1,2]

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Pangenome analyses help to unveil the genome landscape and the evolutionary traits and trajectories of complex plant groups. We generated a large pangenome for 282 native Mediterranean representatives of the diploid-allopolyploid *Brachypodium* grass model system (118 *B. distachyon*-2x, 35 *B. stacei*-2x, 129 *B. hybridum*-4x) accounting for a total of 411 assembled genomes and subgenomes. Filtered syntenic SNPs from whole (sub)genomes were used to reconstruct the evolutionary trajectory of the 'Brachy' lineages and to perform population genomics. *B. hybridum* showed a general additive pattern of TEs in its two progenitor genomes, our analysis detected a slight proliferation of transposons in the allotetraploid compared to the diploids, probably as consequence of the allopolyploidization process. Maximum Likelihood (ML) and coalescent-based trees uncovered several genomic clusters in the diploids *B. distachyon* and *B. stacei*, which were shaped by evolutionary history and geography, and revealed three independent and recurrent origins for their derived allotetraploid *B. hybridum* from local parents. Population genomic structure also revealed three clusters for, respectively, the ancestral western Mediterranean and the two recent western and eastern Mediterranean hybridization events, and overall large homogeneities in both subgenomes. A thorough genomic analysis of intraspecific individuals exhibiting genetic admixture showed a homogeneous distribution of admixture markers across all chromosomes suggesting a genome-wide level occurrence of admixture.

S94.3 Genomic fruits from the Darwin Tree of Life project

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The field of evolutionary genomics is at a turning point, where many unresolved questions can now be addressed using high quality reference genomes for non-model species. The Darwin Tree of Life (DToL) project aims to sequence all eukaryotic genomes in Britain and Ireland and has recently hit the milestone of generating 1,000 reference genomes including over 50 plants. I show how these plant genomes can be integrated with the wealth of knowledge on the diversity of the British flora to investigate evolutionary processes. Comparative genomic analyses reveal the wide range of plant genomic diversity, shaped by various attributes such as mating system and extent of natural hybridisation. A 'deep dive' into the genome of the European mistletoe (*Viscum album*), the largest genome ever sequenced (90Gb), reveal its giant genome size has been achieved via extensive repeat proliferation and degradation rather than recurrent polyploidy. Future large-scale floristic analyses promise to combine the benefits of broad-scale analyses of diverse species, with the precision to infer evolutionary process from whole genome sequence data.

S94.4 From plastomes to genomes – pitfalls and prospects

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Nuclear reference genomes can have many uses, e.g. serving as a basis for genetic marker development in conservation, for tracing the origin of genes conferring special phenotypic properties, or for studying genome evolution, especially at the structural level or at small genetic distances (such as in partially clonal / apomictic populations). However, several technical obstacles still hamper progress towards high-quality nuclear reference genomes "for all". By fostering exchange and collaboration between experts throughout Europe and beyond, as well as the development of protocols, tools and standards, the European Reference Genome Atlas initiative (ERGA) seeks to ease the way for future genome sequencing projects and maximize the benefits which can be obtained from such data. While nuclear reference genomes are often still work in progress, their "smaller siblings", i.e.,plastid genomes, rapidly become broadly available and might serve as a test case for large-scale genome sequencing. Though they have some peculiarities, such as a smaller size and a more uniform structure, the overall workflow for their generation parallels that for nuclear genomes. We tested several bioinformatic tools for the assembly of plastid genomes and found considerable differences in reproducibility and sensitivity to sequencing coverage, which have the potential to cause misinterpretations of the biological data. Based on our findings, we developed PlastidPipeline, an open bioinformatic pipeline producing highly reproducible, fully annotated and structurally standardized plastid genome assemblies from short read sequence data. Finally, we ask how far we can extrapolate from plastome to nuclear genome sequencing projects – what will we gain, and which pitfalls can we potentially avoid?

S94.5 The benefits and value of large-scale reference genome generation in plants

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The genomes of green plants vary tremendously in size, transposable element content, and structural complexity, making sequencing, assembly, and annotation challenging. Although many published plant genomes are complete or nearly so at the gene sequence level, their assemblies remain fragmentary, precluding certain types of comparative analyses. However, recent advances in sequencing technology and analytical software are enabling chromosome-level assemblies even for large and complex genomes. Thus, high-quality reference genomes are being generated for many clades, providing key insight into specific genotype-to-phenotype relationships and facilitating comparative genomic analyses on an unprecedented scale. Large-scale community sequencing projects have been particularly effective at generating genomic anchors for diverse clades, and notable insights are emerging. Key among them is the consistent evidence for widespread whole-genome duplication, with even very small genomes bearing signatures of multiple duplication events. In other cases, expansions of gene families and the identification of gene clusters are being linked to production of key metabolites, defense compounds, and disease resistance. One of the most surprising discoveries is the frequency of ancient reticulation, based on extensive gene-tree conflict. How general are these results to date? Ongoing large-scale sequencing projects will continue to generate new genomes, but the number of plant species is immense, and many more such efforts are needed, particularly as the concept of the reference genome evolves from a high-quality assembly for a single individual to a pangenome that represents a species. Fortunately, the tools for sequencing, assembling, and annotating genomes are improving rapidly, and we can look forward to novel discoveries and the possibility of any plant species becoming a genomic model.

S94.6 Single-cell spatial transcriptomic drives a new era in plant research

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Dissecting the delicate and complex plant tissues and cell types in single-cell resolution facilitates us to discover plant developmental mechanisms and how plants respond to various environmental stimuli. Based on the developed Stereo-seq technology and plant cell wall staining, we developed the sc-Stereo-seq (Single-cell SpaTial Enhanced REsolution Omics-sequencing) technique that enabled us to show the *in situ* spatial transcriptome profiles in various plant tissues at the real single-cell resolution. By analyzing *Arabidopsis* leaves, we successfully distinguished cell sub-types that show subtle but significant transcriptomic differences, including the upper epidermis and lower epidermis, spongy mesophyll and palisade mesophyll. We also discovered cell-type-specific gene expression gradients from the main vein to the leaf edge for the first time. Furthermore, we managed to apply scStereo-seq in various plants and tissues. For example, the spatiotemporal developmental atlas of nodules enabled us to reveal the new function of stress-related genes in regulating nitrogen fixation, and the most refined spatiotemporal atlas of *Arabidopsis* seed facilitated us to define the subtype of endosperm cells generated by differentiation during germination. Altogether, these findings show the crucial role of scStereo-seq in discovering new cell types and exploring their spatiotemporal cell-fate transition characteristics, and scStereo-seq will significantly advance our understanding of plant morphogenesis, plant-microbe interactions, and stress tolerance mechanisms in the future.

S.95 ECOLOGICAL AND EVOLUTIONARY DYNAMICS AT THE REAR EDGE UNDER CLIMATE CHANGE

S.95.1 Evolutionary history affects adaptation at the rear edge

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How past evolutionary dynamics have shaped range limits remains a central and timely question in ecology and evolutionary research, especially when predicting how species ranges will respond to future climates. The rear edge – remnant populations persisting in former glacial refugia – is particularly exposed to climate change as these populations often occur at the warmer range limits. However, this range limit is largely overlooked in evolutionary research so we lack a clear picture of how past evolutionary dynamics may affect adaptation in these populations. Rear-edge populations may have served as distinct genetic diversity reservoirs during successive glaciation periods. High genetic diversity and differentiation may have provided beneficial variation to adapt to continuously warming post-glacial climates and will be crucial for the ability of these populations to persist and adapt to future climates. At the same time, rear-edge populations may be at particular risk for extinction, as strong genetic drift resulting from a history of demographic decline and isolation in marginal habitats may reduce their genetic diversity and constrain adaptation. This interplay of opposing evolutionary forces may result in a mosaic of adaptive capacities at species' rear edges. Here we assessed how past evolutionary dynamics shape climate adaptation at the rear edge of the North American herb *Campanula americana*. We studied populations from the core and the rear edge and found greater phenotypic differentiation among populations and greater adaptation to the marginal climates in rear-edge populations. These results will be discussed in a climatic, population genetic and phylogenetic context.

S.95.2 Climate change and traits interact to explain abundance shifts in the aridity edges of Iberian trees

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Climate change is expected to exert an amplified influence on the climate edges of species distribution owing to their proximity to ecological tolerances. However, a notable ambiguity persists regarding the interplay between climate change, plant functional traits, and their collective role in driving shifts in plant abundance at climate edges. Furthermore, the influence of historical land-use legacies in moderating this interaction remains unclear. Leveraging data from approximately 300,000 monitored trees spanning 66 widely distributed species in Spain, we quantified shifts in tree species abundance at aridity edges (i.e., cold and wet vs. warm and dry conditions) over 25 years. We also examined the relative significance of the interplay between climate change and tree traits in driving these abundance shifts. To evaluate the shifts in tree species abundance at aridity edges, we used a null model to test the hypothesis that such shifts occur randomly concerning gains and losses of trees across the entire aridity gradient. Our investigation revealed an overall increase in tree species abundance over time across the studied region. Notably, a non-random increase in tree species abundance was observed at the cold and wet edge, while the increase at the warm and dry edge appeared to follow a random pattern. Furthermore, shifts in tree species abundance across the entire aridity gradient, including its edges, correlated with forest densification within the surveyed plots. The influence of climate change on shifts in tree species abundance was notably mediated by the traits of these species at the aridity edges. Consequently, our study offers species-specific insights into the dynamics of tree abundance at climatic edges, presenting valuable information pertinent to informed decision-making in formulating conservation, management, and restoration strategies within the context of anthropogenically-induced global environmental changes.

S.95.3 Evolutionary rescue of wild monkeyflower populations during extreme drought

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Populations declining due to extreme climate change may require adaptive evolutionary change in order to persist. While evolutionary rescue is well-established by theory and demonstrated in microbial experiments, its relevance to the persistence of natural populations facing climate change remains largely unknown. Here we document range-wide patterns of rapid evolution and evolutionary rescue in scarlet monkeyflower after an exceptional natural drought event in the western United States. We combine 10 years of field demographic monitoring with whole-genome sequencing across 55 populations prior to the exceptional drought ("baseline" genomics), and whole-genome resequencing of 12 populations throughout the drought ("time series" genomics). Range-wide population decline during the drought was most closely associated with precipitation anomalies. Genome-environment associations in baseline samples identify approximately 600 snigle-nucleotide polymorphisms associated with spatial variation in historical climate. In the time series samples, the heat- or drought-associated allele at these 600 climate-associated loci increased more than expected by chance throughout the drought, consistent with rapid evolution by natural selection. Finally, rates of demographic recovery were predicted by genetic variation, not climate anomalies. Specifically, populations that recovered most quickly had higher nucleotide diversity at climate-associated loci in the baseline samples and greater rates of temporal change in climate-associated loci in the time series samples. Genetic variation, rapid evolution, and demography showed weak latitudinal clines across the species range, with rear edge populations facing some of the steepest demographic declines, the lowest segregating genetic variation, and the weakest response to selection. These findings demonstrate evolutionary rescue in the wild, showing that some populations can evolve to recover from climate-change induced population decline and that genomics tools can have an important role in predicting recovery capacity via evolutionary rescue.

S.95.4 Forest ecosystem dynamics at rear edges in a changing world

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Forests are home to a large part of terrestrial biodiversity and underpin critical ecosystem processes, including climate regulation, and carbon and nutrient cycling. Unfortunately, ongoing anthropogenic climate change is reshuffling the geographic distributions of tree species with far-reaching implications for the beneficial contributions of forests to human populations. It is typically assumed that climate change-related risks to forests are higher at species rear edges, i.e., the low latitude and altitude edges of species distributions, because rear edge populations tend occur at the limit of the species' climatic tolerances. Yet evidence on uneven patterns of rear edge population loss and retention is accumulating. This variability in population responses may result from the large ecological heterogeneity at species rear edges, including site-level abiotic conditions decoupled from the regional climate, functional trait variability across populations or species interactions. Importantly, climatic stressors and other global change drivers such as anthropogenic land-use changes interact and strongly impact biological communities and may influence species redistributions. Here we present recent and ongoing research on these major regulating factors of forest dynamics at species rear edges. Refining our predictive understanding of species rear edges is essential to advance our ability to monitor and plan for the impacts of climate change on forest biodiversity and functioning.

S.95.5 Genetic structure and mating system shift at a trailing edge of Sphagnum fuscum

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Rear edge populations match in many cases with the extreme of species´ niche. During the Holocene, one strategy for cold-adapted species has been migrating to refugia while conserving their ecological niche, in what is known as trailing edges. In such populations, long-distance dispersal is thus a crucial trait that may be under selective pressure. In the genus *Sphagnum* L. (peat mosses) such function relies on spores. Its production may be compromised by the species mating system, with sporophytes being less frequent in dioicous species rather than monoicous. Here, we studied the genetic structure and demographic traits of *Sphagnum fuscum* (Schimp.) Klinggr., a putative dioicous species, on its rear edge in the Pyrenees. We entirely genotyped seven populations through 16 microsatellite loci, and we assessed the production of sporophytes in each population. Genetic diversity within populations is extremely poor, harbouring only one to three private genotypes per population. Each genotype constitutes a separate group according to a Bayesian cluster analysis. Surprisingly, we found sporophytes in some monoclonal populations. We suggest that *S. fuscum* is a glacial relict in the Pyrenees. Its current genetic structure can be explained by a demographical contraction and altitudinal migration upwards after the Local Last Glacial Maximum. The remarkable uniqueness of every genotype may result from independent founder events and strong isolation. Our findings indicate that *S. fuscum* may have shifted to monoicy in the Pyrenees. This trait would enhance the fitness of small populations with limited and fragmented suitable habitat. Consequently, we think that *S. fuscum* would be a good model to study the molecular mechanisms underlying sex determination in the genus. Furthermore, it could provide valuable insights to understand mating system transitions in *Sphagnum* under an evolutionary ecology perspective.

S.96 GRAPEVINES (VITIS SPP.): A MODEL FOR MULTIDISCIPLINARY APPROACHES TO CONSERVING AND USING CROP WILD RELATIVES

S.96.1 Optimized design of a genetic reserve network for the in situ conservation of wild grape Vitis vinifera subsp. sylvestris

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Wild grape is important for Spain because it is a) the third largest wine producer in the world, b) one of the most climate-affected European countries, and c) a rich source of wild grape diversity. As part of the implementation of the National Strategy for the Conservation and Utilization of Crop Wild Relatives and Wild Food Plants of Spain, we aimed at inventorying the occurrences of wild grape populations in Spain and developing an optimized design of a network for the establishment of wild grape genetic reserves. 796 wild grape populations were identified from various sources. An ecogeographic land characterization (ELC) map was created for Spain to estimate genetic differentiation between wild grape populations. 309 populations that occur in protected areas were found in 9 of the 10 ecogeographical categories in which the species occurs in Spain. Using a complementarity analysis, seven protected areas including nine populations were finally selected for the establishment of the genetic reserves. An eighth site in a non-protected area was also selected to cover the ecogeographic category that was not represented in the protected area populations. The proposed network is distributed across a latitudinal gradient including sites located in Navarra, Aragón, Madrid and Andalucía. The establishment of these genetic reserves would provide protection and enable access to the genetic resources for the breeding of new cultivars adapted to the forthcoming environmental conditions.

S.96.2 Conservation and sustainable use of crop wild relatives for food security

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A valuable resource for agrobiodiversity, sustainable agriculture, and overall food security are crop wild relatives, or CWRs. Genes for advantageous characteristics like high nutritional value, disease and pest resistance, resource efficiency, and climate adaptation may be present in CRWs. Their innate genetic diversity and the microbiota that coexists with it provide an abundance of resources for creating resilient, nutrient-dense, and productive crop varieties as well as for diversifying agricultural systems. Despite their value, a wide range of CWRs are threatened and face pressures, e. g. from the consequences of climate change, urbanization, pollution, and intensive agriculture. However, there is still a dearth of information regarding their deployment in breeding and conservation. As a result, there is a lack of understanding regarding the diversity that is present and the specific ways in which it can be applied to farming and crop improvement. Wild relatives of crops are an essential source of adaptive traits and genes, which can be used in plant breeding to improve sustainable food security in the face of obstacles like population growth and climate change. These traits and genes include resistance to diseases, pests, and stresses like drought and extreme temperatures. Crop wild relatives are valued at more than 120 billion US dollars annually (PwC, 2013). Their significance for maintaining agriculture in the future has been acknowledged internationally in the Convention on Biological Diversity (Aichi target 13), International Treaty on PGRFA, FAO Global Plan of Action, and The Sustainable Development Goals (SDG 2- Zero Hunger). The conservation of crop wild relatives is still an underfunded field of study, despite their economic significance to agriculture and the centuries-long influence they have had on the development of our food crops.

S.96.3 Using phylogenetic relationships and species delimitations of North American Vitis to inform crop breeding and conservation action

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The North American *Vitis* species are of considerable economic importance and have played a significant role in saving the viticulture industry since the 1870's. With the recent advances in genomics and collections-based informatics, the taxonomy of *Vitis* is experiencing a new era of revolution. We conduct extensive phylogenomic analyses to unravel the complex evolutionary history of North American *Vitis* by densely sampling all New World species with representatives from Eurasia and by using a newly developed bait set target-capturing 1013 nuclear genes. We also target the sampling of several species complexes including the taxonomically challenging *Vitis aestivalis*, *V. arizonica* and *V. cinerea* complexes. Our analyses reveal extensive introgressive hybridizations of North American *Vitis* at the deep and shallow levels. Introgressive hybridization is a major mode of speciation in North American *Vitis*, driving the evolution of several species including *V. californica*, *V. novae-angliae*, and *V. shuttleworthii*. Geographic isolation plays an important role in generating morphological variations in the *V. aestivalis*, *V. arizonica* and *V. cinerea* complexes. *Vitis* is herein classified into three subgenera: subgenus *Mesoamericana* J. Wen (subg. nov.), subgenus *Muscadinia* (Planch.) Rehder and subgenus *Vitis*, and the North American *Vitis* subgenus *Vitis* is placed into eight taxonomic series. The taxonomic framework, evolutionary relationships, phenotypic variations, geographic distribution, and ecological characters provide fundamental insights into crop breeding and conservation actions. We call the attention to further assess the distribution and conservation status of *V. novae-angliae*, a species that is supported to be of hybrid origin between *V. labrusca* and the common ancestor of *V. riparia* and its close relatives. Furthermore, *V. shuttleworthii* of peninsular Florida should be more closely monitored as the coastal narrow endemic can be threatened by rising ocean levels associated with climate warming.

S.96.4 A multidisciplinary and collaborative model for conserving North American grapes (Vitis spp.)

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Crop wild relatives are wild plants closely related to domesticated crop species. The genetic diversity found in crop wild relatives is utilized to improve crops in many ways, including increased resistance to pests and pathogens, and tolerance of heat, cold, and drought. Grapes are one of the most economically valuable crops globally, but production of grapevines is hindered by pests, pathogens, and climatic changes. North American wild grape germplasm was critical in providing resistance to the pest, phylloxera, that plagued many European vineyards in the late 1800s. North America is a major center of grape diversity, with about 25 taxa native to the United States. Several native North American *Vitis* taxa are used as rootstock for the cultivated grapevine (*V. vinifera*) or for scion breeding. North American wild grapes have been cultivated for their fruit for centuries, particularly muscadine grapes (*Vitis rotundifolia*). Due to changing climatic conditions, North American native grapes are increasingly important to improving the cultivated grapevine. As with other native plants, crop wild relatives are becoming more threatened, and further efforts are needed for conservation. However, information on the complementary conservation (*in situ* and *ex situ*) of North American native grapes is lacking and scattered among different stakeholder groups. To more comprehensively conserve North American *Vitis*, we convened a collaborative workshop in November 2022, which brought together 20 scientists from the agricultural and conservation communities to identify conservation gaps in North American native grapes. We discuss the conservation status of native grapes, the importance of hybrid wine grapes for sustainability, and a roadmap for the complementary conservation of North American grapes. We also address the positive outcomes from collaborating with multiple stakeholder groups to conserve crop wild relatives.

S.96.5 Natural variation in North American Vitis species used as rootstocks influences shoot system phenotypes in grafted grapevines

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North American grapevines (*Vitis* spp.) represent a morphologically, genetically, and ecologically diverse group of taxa that are important contributors of regional and global viticulture. Although few North American species are grown directly for grape production, these species have been used for more than one hundred years in the generation of disease-resistant hybrid vines derived from crosses between North American species and the European grapevine (*V. vinifera*). Beyond their use in hybrid vines, North American *Vitis* species have also been used as rootstocks: roots of domesticated *V. vinifera* are susceptible to damage caused by the North American aphid phylloxera, but North American *Vitis* species can withstand infestation. As a result, North American Vitis *species* and their hybrid derivatives are widely used as rootstocks for *V. vinifera* vines on multiple continents. In perennial woody systems like grapevines, a fundamental question is how variation within and among species in below-ground features influences traits expressed in structures above ground, including leaves, flowers, and fruits. In this study, we used a rootstock experimental vineyard in which the clonally propagated grapevine cultivar 'Chambourcin', a European-American hybrid, was growing ungrafted and grafted to three hybrid rootstocks derived from crosses between *V. cinerea ssp. berlandieri, V. riparia*, and *V. rupestris*. Data collected over three years demonstrate seasonal and annual variation in rootstock effects on 'Chambourcin' phenotypes including leaf ion concentrations, gene expression patterns and epigenomic signatures, among others. These data indicate that natural variation grapevine root systems have a detectable influence on a multitude of traits observed in a grafted clonal scion. Additional work is required to document natural variation in wild grapevine species and it's genetic and environmental influences, in order to fully leverage these taxa in ongoing efforts to adapt global viticulture for consumer preferences and changing climates.

S.96.6 Importance of wild Vitis germplasm in historical and modern grape breeding

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Grapes, and its diversity offer a unique opportunity to tell the importance of germplasm for modern plant breeding while simultaneously highlighting the need for its conservation for future generations. Because of their abundance in our food system (as raisins, wine, juice, jelly, and for fresh eating), as well as their role in sacrament, grapes hold cultural significance in many ways. The history of grape breeding in both Europe and North America is rooted in controlling fungal diseases (powdery and downy mildew) and insects (phylloxera) which persist as the main breeding targets today along with high quality. Due to the narrow genetic base of *Vitis vinifera*, the predominantly grown grape in production worldwide, other *Vitis* species from Asia and North America have been critical for introgressing pest resistance and solving vineyard problems. This review will cover the importance of wild *Vitis* germplasm through several examples/historic events that continue to impact the viticulture community. Grapes can be a model to exemplify the importance of wild species in impacting human life, culturally and economically, and the need for conservation in protecting important genetic resources. Modern plant breeding, although empowered through new genetic and genomic tools, at its core relies on access to the diversity for genetic improvement for sustainability and human benefits.

S.97 SOLANACEAE: BIOLOGY, SYSTEMATICS AND EVOLUTION. SESSION 1

S.97.1 The anatomical and genetic bases of fruit diversity in Solanaceae

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The diversity of fruit patterning and seed dispersal strategies in Solanaceae is outstanding. The family exhibits berries, capsules, drupes, pyrenes and intermediate forms of thin fleshy fruits that dehisce or thick fleshy fruits that dry out. The optimization of fruit type onto a phylogenetic framework results in a unidirectional shift, from dry fruits to fleshy fruits, in the specious Solanoideae. However, independent acquisitions of fleshy fruits have occurred at least in *Cestrum* and *Duboisia*, and reversals to dry fruits take place in members of Daturae. We have undertaken comparative anatomical studies coupled with genetic studies to understand the evolution and development of different fruit types across Solanaceae. We have been documenting the carpel-to-fruit transformation in distantly related species across the family including *Brunfelsia*, *Brugmansia*, *Capsicum*, *Cestrum*, *Petunia*, *Nicotiana*, *Nierembergia*, *Nicandra*, *Nolana*, *Salpiglossis*, *Saracha*, *Schizanthus*, and *Solanum*, which have allowed us to assess key anatomical homologous and convergent features. We have reconstructed the evolution of specific anatomical features during the diversification of the family. We have also evaluated genes that are critical for fruit patterning, taking as reference the genetic network for fruit development established in *Arabidopsis*, where major transcription factors control valve identity (i.e., *FRUITFULL*), replum development (i.e., *REPLUMLESS*) and the differentiation of the dehiscence zones (i.e., *SHATTERPROOF*, *INDEHISCENT* and *ALCATRAZ*). Our data indicates that the fruit developmental genetic network in the Brassicaceae cannot be extrapolated to the Solanaceae, due to independent duplication events and changes in expression patterns for key genetic hubs. We present data on their expression and function in species with different fruit type with Solanaceae emphasizing those convergent fruit types in *Cestrum* and *Brugmansia* and we discuss the implications of our findings in fruit evolution studies across the family

S.97.2 Transposable Element Activity as Genome Evolution Driver: The Nicotiana Suaveolentes section Case

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Nicotiana is an herbaceous plant genus of the Solanaceae family with 90 naturally occurring species divided into 13 sections. Five sections contain allopolyploids formed by interspecific hybridization between diploids. The largest section is Suaveolentes which includes 38 species, such as the well-studied *Nicotiana benthamiana*. The origin of this paleopolyploid clade is dated 6 MYA. Our previous work showed that Suaveolentes derives from the hybridization of the Alatae/Sylvestres and Noctiflorae/Petunioides ancestors. The polyploid genomes evolve to a diploid state in which repetitive elements are purged and some duplicated genes lose their function becoming pseudogenes or get removed by non-homologous recombination between the subgenomes. The transposable element analysis has revealed an explosion of LTR/Copia elements at the time of the diversification of the clade, shaping the gene space of the most recent Suaveolentes species.

S.97.3 Evolution of sacred plants

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Plant species that produce tropane alkaloids (TAs) have been used by humans for millennia as medicines, stimulants, and for mystical-divinatory purposes. We ignore how the longstanding interaction with humans has shaped the genomes and metabolism of these sacred plants. We studied the evolution of TAs in members of the Solanaceae family, which includes multiple TA-producing species that are sacred to cultures around the world. We conducted a search for regulatory networks associated with TA evolution by integrating transcriptomic and metabolomic variation in hundreds of Solanaceae species. Our findings show that TAs are produced by independent phylogenetic clades, indicating the independent acquisition or loss of the TA pathway. Notably, TA genes are components of the same co-expression networks as genes involved in the production of other alkaloids, steroidal glycoalkaloids (SGAs), implying a regulatory tradeoff linking the two pathways. We identified candidate alkaloid genes whose expression shows a correlation with SGA and TA levels across samples. These genes could play a role in metabolic switching between TAs and SGAs during the evolution of the Solanaceae. A genomic analysis of the distribution of TA genes across the Solanaceae phylogeny highlights the significance of genomic clustering, gene duplication, and gene loss in the evolution of alkaloid pathways. Finally, we found that viruses and endophytes have shaped the use of TA-producing species by humans. Our study provides a unique view of the evolution of medicinal plants with potential applications for metabolic engineering of TAs.

S.97.4 Evolution of steroidal glycoalkaloid (SGA) metabolism in medicinal and wild plant species of Solanaceae

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The Solanaceae family constitutes a promissory group for genomic and metabolomics studies. This condition is attributable to the morphological diversity, agronomic importance, and few polyploidy events for most taxonomic groups. Within Solanaceae, wild species in the Neotropic are a valuable source of diversity to study the phylogenomic evolution of different plant clades through specialized metabolism. Steroidal glycoalkaloids (SGAs) are among the most interesting compounds of plant origin due to their medicinal, antibiotic, and defensive properties against pests. These compounds have been mainly studied in the domesticated species of the *Solanum* genus. Genomic synteny and gene expression studies in species such as potatoes, tomatoes, and eggplants have allowed the identification of genes that determine the production of SGAs. These analyses have shown that the genes associated with the metabolism of SGAs are grouped in genomic regions, forming what is known as biosynthetic clusters (BCs). The expression and gene composition of these BCs define the evolution of SGAs in cultivated species. However, the genes that have generated the diversity of SGAs in wild species have not yet been studied. Understanding the genetic causes of the diversification of SGA metabolism in non-highlighted species is fundamental to understanding the evolution of metabolism in Solanaceae and characterizing these compounds for biotechnological purposes. Our project proposes to fill this gap by studying the evolution, metabolism, expression, and genomic organization of genes associated with the production of SGAs in wild and medicinal species of the Solana-

ceae family. Specifically, we identify candidate genes using co-expression and correlation analysis using the transcriptomes and metabolomes of dozens of species. In addition, we performed synteny analysis to characterize the BCs variation between cultivated and wild *Solanum* plants. Moreover, we validate some candidate genes using overexpression techniques to find new and promising compounds for medicinal purposes.

.S.97.5 . Repetitive DNA in the Cyphomandra clade (Solanum, Solanaceae)

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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.

S.98 KIN DISCRIMINATION AND KIN SELECTION IN PLANTS

S.98.1 Kin recognition and kin selection from an experimentalist's view

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Some plants are able to discriminate and alter their competitive phenotype towards a conspecific neighbor, depending on its genetic relatedness. This has spurred a large interest in studying kin selection in plants during the last two decades. The ability to show positive kin discrimination may create positive frequency dependent interactions in plant communities with implications on species co-existence and assembly as well as consequences for agronomy where selection of crops with more "co-operative" behaviors may prove fruitful. Whether plants actively avoid competing with their kin and the fitness consequences of such "behavior" is, however, tricky to study experimentally as alternative hypotheses may predict similar outcomes. Questions of importance are, what type of experiments could we conduct, which plant traits should we study and what are the results to expect in order to decide if we find evidence of kin recognition and kin selections or not? I present examples from different experiments and discuss how we may or may not interpret these as evidence for kin recognition and kin selection.

S.98.2 How to use kin selection models in plants: a theoretical perspective

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Inclusive fitness theory of kin selection has been very successful in evolutionary biology, which provides both conceptual and theoretical explanations for the evolution of numerous traits ranging from social behaviors, microbial interactions, and disease evolution. There are also cases where inclusive fitness theory has been applied to plant ecology, for example, the evolution of sex allocation, seed dispersal, pollen dispersal, and dormancy. However, the conceptual gap between inclusive fitness theory and plant ecology is still large, rendering the powerfulness of the theory at most in its intuitiveness. In this talk, I tell you a bit about why inclusive fitness theory should be (re-)advocated in plant ecology. Specifically, I show some classical, elementary predictions derived from inclusive fitness theory, including (i) the effect of local competition on the evolution of interaction among relatives, (ii) kin recognition as unnecessary conditions for inclusive fitness theory, and (iii) the effects of plant reproductive traits (selfing, pollen dispersal, and seed dispersal) on inclusive fitness theory. Finally, I draw an example from the evolutionary dynamics of plant reproductive traits to highlight plant reproductive traits as model systems of inclusive fitness theory theory.

S.98.3 Plant growth of Chenopodium quinoa (Willd.) is better when growing with kin than with non-kin regardless of soil nutrient condition

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Plants have the ability to recognize their kin neighbours, which may be a beneficial trait that increase inclusive fitness, by suppressing individual growth to support the combined growth of the group. However, the advantages of kin cooperation (known as kin selection theory), may differ across environmental gradients, with competition between related individuals potentially being detrimental under resource limitation (following niche partitioning theory). The study aimed to understand how quinoa (*Chenopodium quinoa* Willd.) plants grow with kin or with non-kin under different nutrient supply rates. Plants were grown in treatments post-germination for 70 days. Biomass accumulation, allocation to organs, and organ traits related to resource acquisition were measured at the end of the experiment. Total mass and shoot mass were greater for plants grown with kin than with non-kin across nutrient treatments. Plants grown with kin had greater root allocation than with non-kin under low and high nutrients. Allocation to leaves, specific leaf area, and average leaf mass were greater for plants grown with non-kin than kin under high nutrient supply but did not differ under low nutrient supply. Allocation to stem was greater for plants grown with kin than non-kin under high nutrient supply but did not differ under low nutrient supply. Specific taproot length and specific stem length were respectively positively and negatively related to increased fertility, but unrelated to kinship. Our results suggest that both niche partitioning and kin selection processes may be at play in quinoa, depending on whether soil nutrient competition is more important. Under both situations, quinoa plants always grew better with kin than non-kin regardless of soil nutrient conditions.

S.98.5 Specificity and context-dependency of plant-plant communication in response to herbivore and pathogen attacks

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Over three decades of work on airborne plant communication have demonstrated that plants send, receive, and respond to volatile organic compounds (VOCs) emitted by neighboring plants. Much of this research has focused on the consequences of plant-plant communication on resistance against herbivory, with studies showing that VOCs emitted by herbivore-damaged plants increase resistance of neighboring undamaged plants. This phenomenon of plant communication is thought to be widespread and an increasing number of studies have proposed the use of plant VOC-mediated signaling as an alternative for sustainable crop protection against pests and diseases. However, a key aspect that has received relatively less attention concerns the ecological specificity and context-dependency of this phenomenon. Knowledge on this is crucial for assessing the ecological mechanisms that govern plant communication, determining its biological significance under natural conditions, as well as designing effective strategies for its use in crop plant resistance. Here, we talk about the ecological specificity of plant communication, as well as the chemical mechanisms underlying this phenomenon, based on three main aspects: plant-based specificity, enemy-based specificity, and the importance of the abiotic context.

S.98.6 The fitness consequences of sharing pollinators with relatives

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Recently, it has been shown that the genetic composition of the intraspecific neighborhood can influence a plant's investment in attracting pollinators. Specifically, plants surrounded by kin exhibit significantly larger floral displays compared to those grown with non-kin. This increased floral display in kin groups could enhance plant inclusive fitness by attracting shared pollinators to other nearby kin. To investigate this hypothesis, we conducted an experiment using the model plant species Moricandia moricandioides. We established an experimental population of 560 plants, divided into 80 groups of seven plants each. Half of these groups consisted solely of half siblings, while the other half contained a random sample of genotypes. We then measured pollinator visitation rates and female reproductive success. Our findings provide the first experimental insights of the potential effect of kin selection on floral display evolution.

S.99 USING GENOMIC DATA TO UNDERSTAND THE BIOLOGY AND EVOLUTION OF LICHENS

S.99.1 Exploring Biosynthetic Gene Clusters in Lichens: Insights into Secondary Metabolites Evolution

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Lichens, symbiotic organisms comprising fungi and photosynthetic partners, are known for their diverse array of secondary metabolites with pharmaceutical, ecological, and adaptive significance. The biosynthetic pathways responsible for these compounds are encoded within biosynthetic gene clusters (BGCs). In this study, we investigate the evolutionary processes shaping BGCs in lichens, focusing on the genetic mechanisms driving secondary metabolite diversification, particularly in cortical secondary metabolites such as usnic acid and atranorin, and a medullary substance as fumarprotocetraric acid. Advances in genomics and bioinformatics have provided a deeper understanding of the diversity and organization of BGCs across lichen-forming fungi. Comparative analyses reveal that BGCs have undergone dynamic evolutionary processes, including gene gain, loss and rearrangements. Furthermore, environmental and ecological pressures may have influenced the evolution of BGCs, shaping the secondary metabolite profiles, including those in the cortex of lichens. Insights into BGC evolution enhance our knowledge of lichen secondary metabolism and its adaptation to various habitats, paving the way for potential applications in biotechnology and environmental sciences.

S.99.2 Speciation continuum in non-model organisms: revisiting the species-pair concept in lichens

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Evolutionary biologists have long pursued understanding the continuum in which populations flow, interact, and evolve to eventually diverge into different species. Traditionally, these discussions have centered around model organisms and reproductive isolation. Lichens, redefined as complex ecosystems, show impressive evolutionary mechanisms that are far to be accounted for by mainstream speciation definitions. Unlike in other organisms, the so-called species-pair concept of closely related taxa that only differ in their reproductive mode is frequently documented in lichens. We investigated this species-pair concept in the iconic beard-like lichen *Usnea* using a comparative approach through reference-based RAD-seq combining multivariate and model-based methods. Species pairs in *Usnea* showed contrasting scenarios of lineage divergence along the speciation continuum. The reproductive mode emerged as a major factor shaping lineage differentiation, promoting upgrading the species-pair concept into a continuum landscape of speciation. Ultimately, this study contributes to expanding the speciation continuum framework towards non-model organisms and advancing our understanding of the consistency of speciation patterns across the tree of life.

S.99.3 The genomic landscape of recombination in a fungal syngameon (Pyrenodesmia, Teloschistaceae)

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The role played by reproductive isolation in fungal speciation remains poorly understood. Several studies, especially based in in vitro experiments, show that some fungi maintain open reproductive boundaries with more or less distantly related species, in a strategy that can be best described as “first mate and then figure things out”. In nature, however, sexual isolation is shaped by multiple factors that act simultaneously as barriers to the flow of genetic information at different scales and levels of organization. Geographic and ecological boundaries limit gene-flow between populations, while molecular factors implied in recognition, development or simply completeness of gene content, impose limits to the viability of hybrid genotypes. The lichen genus *Pyrenodesmia* s.s. provides a good example of the limitations of phylogenetic methods of species delimitation, and of the importance of interspecific hybridization in natural populations. The phylogenetic study of Western European specimens of the genus identified widespread interspecific mating, i.e., low pre- zygotic isolation as well as discrepancy in phylogenetic signal linked to hybridization. All species are interconnected in a supraspecific syngameon in which species remain partly distinguishable but also produce hybrids and phenotypically intermediate morphs. Comparative genomics data on selected specimens, provides evidence that genome concertation plays an important role in fungal hybrids. The mechanisms implicated in genome simplification and in the concertation of gene content are still a matter under scrutiny. IN our survey we discuss the role played by heterochromatin related genome defense mechanisms, such as RIP, and the proliferation and silencing of transposable elements in the regionalization of the genome into areas of reduced and increased recombination. We hypothesize that this regionalization is largely responsible for the evolutionary success of this mating strategy, as it allows maintaining a stable core genome while allowing for the incorporation of xenologous genes of adaptive value in subtelomeric regions.

S.99.4 Insights into the evolution of lichens using large-scale phylogenomic analyses

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The growing availability of genomic data from lichens enables us to test hypotheses about their evolution based on the information from entire genomes. Robust phylogenetic trees derived from the analysis of many genes not only resolve taxonomic relationships but also lay the groundwork for various downstream analyses. This has recently led to several novel findings about the evolution and inner workings of lichen symbioses. While the potential of genome based phylogenetics in lichen research remains huge, challenges in analyzing large genome-scale datasets reliably, reproducibly, and fast also persist. To mitigate common problems encountered in phylogenomics, we developed phylociraptor (http://github.com/reslp/phylociraptor), a tool facilitating streamlined phylogenomic analyses based on the information of hundreds to thousands of genomes. Starting from genome and transcriptome assemblies or sets of proteins, phylociraptor identifies genes, infers orthologs, performs and filters multiple sequence alignments and calculates phylogenomic trees using various methods. Finally, we showcase recent advancements in our understanding of lichen evolution by presenting large-scale phylogenomic analyses of lichens performed with phylociraptor. We concisely introduce the software and show how it helps to overcome several typical methodological challenges, while employing innovative strategies to enhance the robustness of phylogenomic analyses. The exploration of lichens using large-scale phylogenomic analyses promises to deepen our understanding of these fascinating symbioses, with implications extending to nearly all facets of lichen research.

S.99.5 Intraspecific genomic differentiation in lichen-forming Umbilicaria species along climatic gradients

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Many species of lichen-forming fungi have wide geographic ranges, and can occur in more than one biome. These species have evolved broad ecological tolerances to cope with different climatic conditions. Here we ask, how climate affects genome architecture and variation in populations of lichenized fungi. We study populations of different species of the rock-inhabiting genus *Umbilicaria*, collected along elevation gradients. The gradients are located in Europe and North America, and span different climate zones, e.g. the Mediterranean and cold temperate zone. In my talk I summarize research in my group over the past few years, which overall has shown that there is substantial and abrupt genome-wide divergence between high elevation and low elevation population groups, largely corresponding to biome borders. I report on fungal genes and genomic features affected by climate, and differences in genomic differentiation of sexually and asexually reproducing species. Furthermore, I discuss the symbiotic green algae associating with *Umbilicaria* (*Trebouxia* spp.), which show community turnovers along elevation, and preferred altitudinal distributions, suggesting that environmental filtering is one driver of symbiont distribution. All in all, our findings contribute to piecing together the complex picture of environmental adaptation in the lichen symbiosis.

S.99.6 Using genomic data to assess species of conservation concern in western North America

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The northern North American Cordillera is a globally significant center of endemism. In western North America, imperiled arid steppe habitats support a number of unique species, including several endemic and threatened lichens. However, processes driving diversification and endemism in this region remains unclear, and genomic data can play critical roles in informing conservation decisions. Here, we investigate diversity and phylogeography of the threatened wanderlust lichens (mycobiont=*Rhizoplaca* species) which occur free on calcareous soils in steppe habitats in western North America. Wanderlust lichens comprise three species of lichen-forming fungi (LFF) – *Rhizoplaca arbuscula*, *R. haydenii*, and *R. idahoensis* (endangered, IUCN Red List) – which occur in fragmented populations in Idaho and Wyoming, with limited populations in southeastern Montana and northern Utah. Using a genome-skimming approach, we generated a 19.1Mb alignment, spanning ca. half of the complete LFF genome, from specimens collected throughout the entire range of wanderlust lichens. Phylogeographic analyses suggest that both dispersal and vicariance played a significant role throughout the evolutionary history of the vagrant *Rhizoplaca* clade, with most of the dispersal events originating from the Salmon Basin in eastern Idaho – the center of diversity for this group. This has resulted in an unexpected number of morphologically distinct, and geographically restricted lineages. Furthermore, niche modelling suggests that vagabond lichens don't fully occupy the areas of highest distribution probability. In fact, documented records often occur in areas predicted to be only marginally suitable. These data suggest a potential mismatch between contemporary habitats outside of the center of diversity in eastern Idaho with the most suitable habitat, adding to the vulnerability of this imperiled complex of endemic lichens. We discuss how the implications of these findings can help guide conservation strategies for imperiled regional endemic lichens.

S.100 ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS. SESSION 2

S.100.1 Identifying Hmong postpartum medicinal herbs via DNA Barcoding

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The Hmong people are an ethnic group that primarily live in China and Laos. However, post-Vietnam War, many Hmong were forced to leave Laos as refugees, with a large portion settling in the U.S. Today, one of the largest communities of Hmong in America is in the Twin Cities of Minnesota. In traditional Hmong culture, to recover from giving birth a new mother will follow a strict diet of chicken soup with medicinal herbs for 30 days postpartum. In the Hmong diaspora, some Hmong women brought these herbs with them and began growing them in their new homes, including Mayyia Thao Lee. Now an organic farmer outside St. Paul, MN, she and her daughters, Mhonpaj and Zongxee, sell postpartum herbs to regional hospitals for culturally relevant care. While they have extensive knowledge of the plant's Hmong names and uses, the scientific names are either unknown or tentative. Noticing that many younger generations of Hmong are either skeptical or lacking knowledge about the herbs, Mayyia and Zongxee requested help assigning Latin names to their soup herbs, so they could continue selling to hospitals and preserve their knowledge. Complicating species identification, many of them do not flower outside of tropical/montane Asia, and keys for this area are limited. Given these challenges, DNA barcoding is the best option for assigning scientific names. To identify these medicinal herbs, we sequenced the ITS and rbcL loci of these herbs, BLASTed them against NCBI GenBank, and inferred the phylogeny of our sequences and their close matches from GenBank. Taxonomic issues and limited publicly available sequences in some taxonomic groups complicated species identification for several of the plants. However, we were able to barcode 45 Hmong medicinal herbs, with 29 identified to species, 14 to genus, and 2 to family.

S.100.2 Consequences of climate change on potential geographic distribution of some threatened African medicinal plants

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Climate change is anticipated to have significant impacts on medicinal plant distribution and populations. However, the effects of climate change on many African medicinal plants have not been evaluated. As such, we evaluated the anticipated climate change effects on the geographic distributions of three threatened but commonly used African medicinal plants (*Garcinia afzelii*, *Khaya ivorensis,* and *K. senegalensis*). We used primary biodiversity data records from GBIF and climatic data for the present and future, the latter characterized by two IPCC representative concentration pathway (4.5, 8.5) future emissions scenarios and 27 general circulation models for a 2050-time horizon. The modelled present-day distribution of the medicinal plants generally showed more suitable habitats in the south-eastern parts of its known distribution for *G. afzelli* and *K. ivorensis* whereas that of *K. senegalensis* was similar to it's known distribution. Our results showed drastic range reductions and shifts, and only modest gains for the three medicinal plants under future climate change. Thus, climate change may reduce local availability of these medicinal plants which are considered to be threatened.

S.100.3 Maya Q'eqchi' phytotherapy in Guatemala: transdisciplinary research to advance the evidence base for medicinal plants

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Maya Q'eqchi' phytotherapy plays a vital role in Guatemala's socio-natural capital, being one of the key elements in traditional healthcare provision services, which co-exist alongside the national public health system. The historical marginalization of indigenous communities, alongside biodiversity loss, habitat degradation, urbanization, monocultures, and invasive species compromises plant resources. This jeopardizes access to medicinal plants, hindering their availability, research, utilization, and benefits for traditional knowledge in meeting basic needs, like medicine. To understand the role of herbal therapies within traditional Maya systems and the potential for commercial scaling, the Green Health Project aimed to propose an implementation framework for the sustainable use, access, and distribution of benefits of biological species within the Convention on Biodiversity (CBD) protocols. Under a transdisciplinary format 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, an ethnographic and ethnobotanical research on Maya Q'eqchi' phytotherapy was conducted, proposing a protocol of access and benefit-sharing framed within the CBD. From 2019 to 2021, 15 Ajilonel (traditional healers and herbalists) from Guatemala participated in documenting 764 patient treatments in Epidemiological Booklets deriving a list of medicinal plants employed, to later collect specimens for identification. The UVG research team effected thirty-two transect walks in Guatemala, where indigenous community researchers helped gather 42% of the ethnobotanical data and plant samples. Of the 251 specimens collected, 132 morphospecies were identified across 51 taxonomic families and 92 genera. The healers addressed 130 physical and 36 energetic-spiritual conditions. Based on the Cultural Importance index, 11 species, including *Drymonia serrulata*, *Petiveria alliacea*, and *Anthurium pentaphyllum*, stood out for treating multiple conditions. Understanding plant-use relationships is crucial to comprehend sociocultural dynamics in traditional medicine, enabling the implementation of conservation efforts, benefits, and healthcare policies in the country.

S.100.4 The medicinal plant Buddleja asiatica and its relation to the welfare of local people in the Pan-Himalayan region: past, present

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Buddleja asiatica Lour. (Scrophulariaceae) is widely distributed across the Pan-Himalayan region. It has traditional medicinal applications and cultural value, as well as ecological significance. We conducted an ethnobotanical study combining field surveys from Nepal and Xizang, China with a literature review to assess the ethnobotanical, phytochemical, and pharmacological aspects of this species. We also employed *in silico* computational techniques to confirm the pharmacological findings. Our study highlights the cultural significance of *B. asiatica* within indigenous communities, and in particular the use of the leaves to make a starter culture for the preparation of wine. The origin of plant use as a starter culture is likely to be vertical transmission, as inferred from the phylogenetic comparative method. However, an evident intergenerational gap in knowledge transfer exists. The phytochemical investigation revealed the presence of various chemical classes (carbohydrates, terpenoids, flavonoids, saponins, esters, steroids, glycosides, fatty acids). The potential medicinal properties of these chemicals include anti-inflammatory, antioxidant, cytotoxic, antihepatotoxic, antimicrobial, and anti-cholinesterase activities and our *in silico* molecular docking and molecular dynamics simulation support the efficacy of iridoid glycosides as potent anti-inflammatory agents. We combine these lines of evidence to show the prospects for the livelihoods of local people across this region and propose future research directions.

S.101 ALPINE PLANT ECOLOGY AND DIVERSITY: FROM SPECIES TO ECOSYSTEMS. SESSION 2

S.101.1 Re-distributions of alpine plant species in the Anthropocene

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Mountain ecosystems remain comparatively natural and harbor disproportionately high levels of biodiversity. Yet, they are warming about twice as fast as the global average and are additionally affected by nitrogen depositions from the lowlands. Recent warming caused individuals of plant species already previously present to grow taller, and the overall plant community height increased. This increase of community height is, however, not only driven by intraspecific trait variation. The composition of plant species communities changed as well. A few plant species increased substantially in abundance at the expense of the majority of species which decreased in abundance. In addition, species shift their ranges to higher elevations to track the climatic conditions they are adapted to. Taller-growing nutriphilous and thermophilic species from lower elevations seem to profit by shifting their distributions faster than the less competitive, more specialized, and unique flora of higher elevations. These trends led together to a significant greening of the European Alps above the tree line. Yet, the vast majority of species is lagging behind recent trends, implying that even if climate change was halted now, its effects were likely to continue. Climate warming is, however, not slowing down but is rather accelerating. Potentially increasing lags might therefore become too large to overcome in the future, resulting in species extirpations. These local to regional extirpations might be reinforced by more competitive and faster shifting neophytes that start to arrive and spread in mountain ecosystems. Predicting these future responses of alpine plant species to global change is crucial to conserve global biodiversity. For accurately predicting the future it is, however, inevitable to first understand the past and its legacy effects.

S.101.2 The importance of facilitative interactions for the plant diversity of alpine plant communities

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Facilitation among plants occurs when the fitness of one species increases in the presence of neighboring plants. It has been suggested that the importance of facilitative interactions among plants increase with the environmental harshness. In high-elevation (alpine) habitats the abiotic harshness increases with elevation, and several studies have addressed how the intensity of facilitation among plants change along elevational gradients. However very few have addressed the frequency and importance of these interactions for the diversity of alpine environments. Using a dataset spanning 78 sites and 5 continents, we assessed the relative importance of facilitative interactions in determining plant diversity in alpine ecosystems. We focused on alpine plant communities dominated by cushion plants, a particular growth form that act as nurse plant for other species. Samples from cushions and open areas were combined in a single matrix accounting for the difference in cover between both microhabitats, and through rarefaction curves we assessed how many more species are added to the community due to the presence of cushions. In general, the presence of cushions consistently increased species richness at the entire community level. The magnitude of these increases in species richness varied with habitat severity where cushion species enhanced species richness more in systems with harsher environments and hence inherently impoverished in local diversity. Facilitative interactions with the nurse species appear to act as a "safety net" sustaining diversity under harsh conditions, demonstrating the importance of positive interactions among species in determining the diversity of alpine habitats in general.

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S.101.3 Endemic species in the aerobiome? Evidence from floristic and aerobiological studies in the Italian Alps

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Pollen as a proxy for plant diversity helps to interpret vegetation and/or to model vegetation shifts under climate change scenarios. Within the BIOALPEC project "Biodiversity in Alpine Ecosystems," we investigate the qualitative-quantitative input of pollen and spores on the bioaerosol of high altitudes exploring implications for ecosystem functioning and biodiversity. Here we present how the local flora and surrounding vegetation are sources of the bioaerosol at alpine receptor sites in Trentino, Italy. The methodology applied involves floristic studies and bioaerosol sampling with passive gravitational traps. We surveyed the flora at different local scales starting from the aerobiological sampler: i) within a circle of 10 m radius; ii) in 5 randomized 2 x 2 m plots within a circle of 100 m radius; iii) along a transect of 1000 m x 2 m. The bioaerosol was analyzed by microscopy and eDNA metabarcoding. Microscopic analysis permits the identification and quantification of pollen, while molecular analysis goes beyond morphological identification allowing for deeper taxonomic resolution and, thus, biodiversity assessment. Results of floristic studies indicate the presence of Italian endemic species, including *Anthyllis vulneraria subsp. alpestris*, *Galium baldense*, *Knautia baldensis*; and alpine endemits such as *Primula daonensis*; *Eritrichium nanum*, *Arabis caerulea*, *Alchemilla pentaphyllea*, *Achillea erba-rotta subsp moschata*, *Adenostyles leucophylla*, and *Bupleurum stellatum*. The bioaerosol analysis will verify the presence of pollen from endemic species in alpine ecosystems. Complementing floristic data with the results from optical microscopy and eDNA will be a step forward in exploring the potential of air to monitor terrestrial plant biodiversity.

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S.101.4 Upscaling the functional response of plant communities to summer drought in alpine tundra

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Climate change is causing remarkable impacts on plant species distribution and communities in cold biomes, with particular concern to arctic and alpine tundra. One prominent effect is the progressive increase of vegetation cover that is leading arctic and alpine greening, with far reaching consequences for the species persistence and the overall plant diversity. Nonetheless, the greening magnitude is expected to be significantly shaped by the increasing frequency of summer heat waves and drought, in the alpine domain as well. Climate change induces plants to acclimate by both morphological and physiological traits due to their phenotypic plasticity. A functional trait approach is hence crucial to foresee the responses of dominant species, whose changes could also affect the entire community and ecosystem functioning. To get new insight into the ecological mechanisms involved in these changes, it is important to promote innovative upscaling approaches, for linking field monitoring evidence to remote sensing data. We here present the results of a rain exclusion experiment conducted in alpine tundra (i.e., grasslands and dwarf shrub communities) in two localities of the eastern Alps. We measured individual growth and physiological traits, as well as community and ecosystem response to experimental treatments. Concurrently we carried out close-range and UAV (Unnamed Aerial Vehicle) multispectral surveys, obtaining remote sensing-derived vegetation indices for the upscaling of plant responses. We found that precipitation induced a trait-mediated plant community response affecting the ecosystem functional response. We also found remote sensing-derived indices to be related to the analyzed plant traits, showing promising perspectives for the upscaling of plant responses to drought. Our findings shed new light on the potential use of remote sensing tools for understanding of the response of alpine vegetation to the future climate scenarios, proving to be a promising method for long-term monitoring of such plant communities.

S.101.5 Species responses to harsh environments in Alpine communities with contrasting regional pools

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Unravelling assembly processes that explain the composition and abundance of coexisting species is a backbone of community ecology. Local communities emerge from the filtering of species present in the regional pool in response to assembly processes such as the suitability of environmental conditions. Understanding how plant communities with distinct levels of turnover respond to their environment is crucial for comprehending these species-environment relationships. The regional pool limits the amount of functional variation among species, and hence, their ability to cope with contrasting environments. However, we often lack information about niche requirements of all species present in the community, especially for rare ones. To shed some light on this regard, we analysed the distribution of plant species across two mountain ranges with contrasting levels of regional richness (63 and 159 species, Mediterranean and Temperate respectively). We applied Hierarchical Modelling of Species Communities (HMSC) to quantify species-specific environmental responses (to elevation, soil fertility and radiation) and how they are affected by 3 functional traits (vegetative height, LDMC, leaf thickness). Despite differences in species turnover between communities, we detected common signals of filtering with plant height and leaf harness (LDMC, thickness) modulating the effects of environmental stress (elevation and radiation). Contrary to our expectations, functional responses of species were more diverse in the species-poor Mediterranean region. We found positive and negative responses to elevation, whereas in the Temperate area negative responses prevailed. In addition, in the Mediterranean area, species also responded to soil fertility according to their growth strategies (height and leaf thickness). Taken together these findings highlight the importance of functional traits related to growth strategies and leaf economic spectrum in shaping species environmental responses in high mountain contexts. Also, they suggest that contrasting environmental stress (drought in summer and cold in winter) may trigger diverse functional responses in species poor mountains.

S.101.6 Are differences in soil fungi communities between the High Andean Forests and Paramos preventing the upslope migration of trees?

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Despite rising temperatures, treeline is stable (i.e., not shifting upslope) in many montane areas. Indeed, recent studies have shown that treeline has remained unchanged in Peru and other parts of the tropical Andes for at least the last 40-50 years even as many trees are shifting their distributions upslope within the forested areas below treeline. Treeline stability suggests that factors other than temperature must play essential roles in determining the upper elevational limit of tree growth and the dynamics of the forest-grassland ecotone in these systems. One factor that could influence treelines is the composition and abundance of symbiotic soil fungi, which are known to play important roles in determining tree species performance in different habitats and shaping forest ecosystems. To explore the possible role of soil fungi in determining treeline location and stability, we are studying the composition, diversity, and abundance of soil arbuscular and ectomycorrhizal fungi in the Eastern Andes Cordillera of Colombia from 3,000 to 3,500 masl. At each of our sites, we collected soil samples in each habitat: the High Andean Forest (~3,000 - 3,200 masl), treeline ecotone (~3,200 - 3,400 masl), and Páramo (>3,400 masl). At each sampling site, we also measured the soil's pH, mineral nitrogen, total nitrogen, available phosphorous, cationic exchange capacity, exchangeable acidity, potassium, calcium, magnesium, and oxidizable organic carbon. Microbial DNA was extracted to determine soil fungi composition, diversity, and abundance, and the ITS and SSU regions were sequenced for ectomycorrhizal and arbuscular mycorrhizal fungi, respectively. By April 2024, we used HMSC models to assess what are the environmental drivers of arbuscular and ectomycorrhizal fungi communities from the High Andean Forest to the Paramo. These data provide valuable insight into the role of microbes in determining tropical montane tree species distributions and the dynamics of the Andean treeline.

S.102 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 4

S.102.1 Savannas retain water better than grasslands in central Brazil: findings from a novel Sentinel-1 derived vegetation water content

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Assessing vegetation water content (VWC) dynamics is essential for understanding plant growth, water and carbon cycles, and ecosystems' drought response and stability in the face of climate change. However, acquiring field-based VWC estimates, consistently through space and time, is challenging due to time and resource constraints. Therefore, in this study we explored the potential of Sentinel-1 Synthetic Aperture Radar (SAR) data for estimating VWC in natural ecosystems in central Brazil, ultimately using the generated VWC dataset to answer how the studied vegetation types (i.e., savannas, dry grasslands, and waterlogged grasslands) respond to seasonal dry periods in terms of water content. Field data from 82 plots, spanning various seasons and vegetation types, served to calibrate and validate the VWC estimation model. The calibrated model, with an R^2 of 0.519 and RMSE of 0.412 kg/m², was then applied to Sentinel-1 SAR backscatter data to generate monthly VWC maps for grassland and savanna ecosystems at 30 m spatial resolution between April 2015 and March 2023. These maps, combined with rainfall and potential evapotranspiration data, provided insights into how these ecosystems respond to water scarcity during dry seasons. More specifically, savannas showed to be able to retain higher water content levels during dry periods, likely attributed to their woody component's enhanced water-holding capacity and deep-root systems, enabling access to deeper groundwater. This research underscores the potential of Sentinel-1 SAR data for monitoring VWC in natural ecosystems, opening avenues for assessing ecosystem responses to drought events and alterations in their functioning, ultimately guiding informed land management decisions in the face of climate change.

S.102.2 Mangrove forests: natural laboratories for studying epigenetic and climate changes

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The tolerance adaptations of mangrove trees to osmotic stress, high temperatures, and low nutrients make them a promising model system for studying trees' molecular responses to stress, which must occur relatively quickly to outpace climate change. Little is known about the transcriptomic and epigenomic contributions to stress responses and rapid local adaptation in mangroves. In Okinawa Japan, which near the global northern range limit of mangroves, we investigated the genomic, transcriptomic, and epigenetic contributions to stress adaptation over a local salinity gradient. Here, our data focuses on the mangrove *Bruguiera gymnorhiza* (Rhizophoraceae), which grows over a wide salinity but experiences stunted growth at the ocean. We focused on two patches of *B. gymnorhiza* growing within the same population but in two different saline environments – one brackish (15 psu) and one oceanside (34 psu). Individuals within each patch display remarkable morphological and physiological differences which may be associated with the observed differential expression of stress responsive genes from transcriptomic analysis. In addition, trees in saline environments had genome-wide DNA hypermethylation, especially of transposable elements (TEs) indicating marked epigenetic structuring in the absence of population genetic differences. DNA hypermethylation was concurrent with the transcriptional regulation of chromatin modifier genes, suggesting robust epigenomic regulation of TEs in the mangrove genome under osmotic stress. We then performed a reciprocal transplant of mangrove propagules between sites to investigate if and for how long the trees “remember” their parental environmental conditions at the transcriptomic and epigenomic level. Following whole genome methylation and transcriptome analysis, our results provide evidence for the transient persistence of DNA methylation and gene expression pattern for several weeks after transplantation. These results provide a first glimpse into the mechanisms underlying wild trees’ adaptive capacities under novel stress conditions, which may be critical for understanding their responses to climate change more generally.

S.102.3 Responses of southern European forest understorey species to macro and microclimatic variations

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Forests can mitigate climate change effects on understorey plants by maintaining microclimatic conditions which create local refugia for many species under ongoing climate warming. However, these microrefugia are today reduced and threatened by increasing forest fragmentation, land use change and anthropogenic or natural modification of the canopy cover, reducing the temperature buffering capacity of forests and exacerbating the negative effects of climate change on plants. Especially for species with a narrow ecological niche, such as forest specialist plants, their ability to respond to climate change through habitat tracking remains questionable, particularly in highly fragmented forest landscapes. Here, we assessed the functional trait responses of eight understorey plant species from southern Europe through a multi-factorial experiment performed in two deciduous forest types (thermophilous and mesophilous forests in Italy and Belgium, respectively) and along macro and microclimatic gradients (in open vs dense forests and at the forest edge vs forest interior). A total of 576 individuals were transplanted within their range (Italy) and beyond their northern range limit (Belgium): 288 individuals derived from lowland forests and 288 from highland forests. Individuals of all species were sourced from Italian forest sites as seedlings, bulbs or rhizomes collected from local native populations and grown in nurseries for one year. Specifically, during two growing seasons, we investigated the individual responses in terms of survival, number of flowers, ground cover percentage, number of leaves, plant height, SLA and LMA. This allowed us to estimate infraspecific trait plasticity for all species along the experimental gradients. Preliminary results showed strong effects of forest structure and edge vs interior position on plant growth and performance with significant interactions between the two regions for most species, i.e., in contrasting ways depending on macroclimate.

S.102.4 Regeneration response of Vepris dainellii, an endemic species of Ethiopia to disturbance in moist forest ecosystem

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Examining the regeneration response of species is one of the key ecological analyses vital to understanding and predicting the spatial structure of plant populations and designing specifc management plans in the face of anthropogenic and climate change factors. Despite the ecological and traditional importance of *Vepris dainellii* species, little is known about the efects of anthropogenic disturbances on its natural regeneration patterns and recruitment structure. This study investigates the regeneration and recruitment response of *V. dainellii* and its correlation to disturbance particularly clear-cut in Sirso moist evergreen Afromontane forest, Ethiopia. By employing transect sampling technique, fifty sample plots (20 m×20 m size) were laid in five transect lines for exploring *V. dainellii* species in Sirso moist evergreen Afromontane forest. In plots, where *V. dainellii* were found, vegetation data and stumped individuals (timber pieces resulting from the illegal cutting of trees) were recorded. Regeneration was recorded using sub-plots. *Vepris dainellii* is the first ranked woody species by recorded a higher number of bowdlerized stems. The regeneration of *V. dainellii* species was higher in disturbed sites compared to undisturbed sites. Besides, the regeneration of the species positively correlates with the intensity of clear-cuts or the number of stump individuals of the species (73.5%). Whereas, the species regeneration and forest canopy cover, altitude, slope and aspect were not correlated. *Vepris dainellii* is a disturbance resilient species with the presence of mother trees. Though, this study suggested detailed research on the threshold of clear-cut intensity and functional traits in response to disturbance in moist forest ecosystems.

S.102.5 Phyto-nutrient profiling of Amaranth species grown under the organic medium enclosed trough system

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Amaranth species are a highly popular group of indigenous leafy vegetables (ILV) consumed in South Africa as a relish. Amaranth is rarely cultivated due to lack of protocols for optimum production. Climate change impacts on vegetable production has mandated farmers to resort to and develop sustainable, effective and efficient environmentally friendly growing practices. The Organic Medium Enclosed Trough (OMET) system is a non-drainable vegetable growing technique. The aim of the study was to investigate the effects of the OMET system on primary and secondary metabolites of two Amaranth species: *A. caudatus* and *A. cruentus*. Primary metabolites of the two species determined after harvesting included %protein, macro- and micro-elements using AOAC methods. Secondary metabolites, targeted (total phenolics, flavonols and tannins) and untargeted metabolites were analysed using photometric assays and UHPLC-MS-Q-ToF techniques, respectively. *A. caudatus* and *A. cruentus* grown under OMET system exhibited higher contents of nutrients including %protein, Ca, Mg, P, K, Mn, Cu, Fe, Se, Zn compared to non-OMET grown *A. caudatus* and *A. cruentus*, respectively. In contrary, *A. caudatus* and *A. cruentus* grown under non-OMET system recorded the highest total phenolics, flavonols and tannins compared to the same Amaranth species, *A. caudatus* and *A. cruentus* grown under OMET. The use of unsupervised PCA showed less metabolic variation and the use of supervised OPLS-DA showed clear metabolic variation based on treatments, OMET and non-OMET. The use of OMET system can be recommended to mitigate the climate change impacts in vegetable production as well as to combat the crisis of malnutrition hence it eliminate water and nutrient seepage, especially in developing countries whereby irrigation water is the most scarcest agricultural commodity.

S.103 ADVANCES IN PHYLOGENOMICS AND SYSTEMATICS OF THE BRASSICACEAE. SESSION 2

S.103.1 The timing, placement, and impacts of the tribe Brassiceae mesohexaploidy

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Gene duplications are one mechanism that provides raw material for the emergence of novel traits. The two major mechanisms for duplicating genes are polyploidy events resulting in whole genome duplications/triplications (WGD, WGT) and small-scale duplications (SSD). The combination of these is an important force in plant evolution. Mustard crops like bok choy, broccoli, cabbage, and canola among others (Brassica) share a relatively recent WGT. Duplicated genes from this WGT have been shown to influence patterns of domestication and phenotypic plasticity in mustard crops. However, it is unclear when and where on the mustard phylogeny this event has occurred. In this study we combine sequence and fossil data to both date and place this WGT event on the mustard phylogeny. Further we explore how gene/genome duplications influence the abiotic stress tolerance of a crop wild relative of mustard crops that shares this WGT. Using a combination of ionomics, metabolomics, and comparative genomics, we characterize aspects of salt stress response in Cakile maritima and identify retained duplicate genes that have likely enabled adaptation to salt and mild levels of cadmium. These findings help to phylogenetically localize and date this WGT. In addition, we demonstrate the power of using crop wild relatives as they can provide understanding of the evolution of environmental adaptation and genetic targets/tools for developing resilient crops in the face of global/climate change.

S.103.2 The pathways of post-polyploid diploidization and descending dysploidy in Biscutella (Brassicaceae)

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In plants, whole-genome duplications (WGDs) are often followed by genome-wide diploidization including descending dysploidy, i.e., chromosomal rearrangements that reduce chromosome number and genome size. However, the genomic basis and evolutionary significance of chromosomal rearrangements are still poorly understood. Here, we report the consequences of the WGD event for infrageneric diversification using comparative genomic analyzes of eight *de novo* assembled *Biscutella* species (Buckler mustard) that differ in genome size (0.7 to 1.1 Gbp) and chromosome number (n=6, 8 or 9). The estimated 9 million-year rediploidization of the progenitor genome was marked by extensive reorganization of the parental subgenomes, genome downsizing, descending dysploidy (n=14 n=6, 8 or 9), and cladogenetic/speciation events in the genus *Biscutella*. We reconstructed the ancestral genome of *Biscutella* and analyzed two differently fractionated subgenomes, which have evolved at unequal rates during post-polyploid diploidization of the sequenced genomes. Although the dominant, less fractionated subgenome has retained more intact genes, the more fractionated subgenome has a more stable karyotype structure with fewer chromosomal breakpoints. In addition, duplicated syntenic genes and their extensive structural variation are associated with environmental adaptation. Our results provide new insights into the role of dysploid changes in plant genome evolution and speciation.

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S.103.3 Diversification and biogeography of yellowcress herbs (Rorippa, Brassicaceae)

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Yellowcress (*Rorippa* Scop.) is a Brassicaceae genus with an accepted 86 species and a worldwide distribution characterized by amphitropical disjunction. Most of *Rorippa* species have affinity for wet habitats, where migrating birds may transit their seeds or propagules far from local populations. They also have robust tolerance to whole-genomic changes, such as interspecific hybridization and polyploidization. About 70% of *Rorippa* are polyploids, and 90% of them are endemic to specific continents. *Rorippa* polyploids are globally distributed but more prevalent in the Southern Hemisphere (accounting for 91% of species). These observations highlight a potential role of long-distance dipsersal (LDD) in shaping the amphitropical disjunction of *Rorippa* and suggest that polyploidy may have promoted effective LDD. To test the polyploid role in LDD, we traced the biogeographic and speciation history for 17 diploids and 41 polyploids of *Rorippa* using variation from plastid genomes and multiple nuclear loci. The ploidy role in dispersal rate difference was demonstrated using trait-dependent biogeographic modeling. We demonstrate that polyploidy would be not only a driver but also a responder of LDD in *Rorippa*, highlighting a synergistic relationship between them. Our results provide a framework to uncover the biogeographic consequences of polyploidization and the joint roles of polyploidy and LDD in shaping the distribution of biodiversity.

S.103.4 Population genomic evidence of inter-ploidy introgression in natural plant populations of Arabidopsis arenosa

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Polyploidy, the presence of multiple genome copies as a result of whole-genome duplications (WGD), is an important speciation mechanism in plants. WGD has been traditionally assumed to cause immediate reproductive isolation due to strong genetic incompatibilities leading to sterility between polyploids and their diploid progenitors and/or inviability of inter-ploidy offspring. However, recent field surveys, cytological and population genetic studies have demonstrated that gene flow between plants with different ploidy levels can happen in natural populations. Yet, it remains unclear how common such inter-ploidy introgression is and to what degree it contributes to plant adaptation. Here we present new results on *Arabidopsis arenosa*, a natural plant system in which both diploids and autotetraploids are present. We focused on one primary and three secondary contact zones across Europe, where diploid and tetraploid individuals of *A. arenosa* are found coexisting in mixed-ploidy populations and/or in geographically closed diploid and tetraploid populations. We used whole-genome sequencing to test for inter-ploidy gene flow on both genome-wide as well as local genomic scales. We found significant evidence of introgressed genomic regions across contact zones. We also identified genomic regions that can be acting as barriers to introgression between different ploidy levels. We identified the genes localized in these regions and we performed GO enrichment in order to interpret how their functions could have contributed to adaptation of polyploids. Overall, our study provides further genomic evidence of inter-ploidy introgression across the genome and across different contact zones in a natural plant system and how this introgression may have an impact in the adaptation of polyploid lineages.

S.103.5 Testing the ‘snowball’ theory on intraspecific reproductive isolation in Arabidopsis lyrata

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The Bateson-Dobzhansky-Muller (BDM) model posits that the evolution of intrinsic postzygotic barriers occurs when independent mutations become fixed in diverging populations. If we assume that new mutations become fixed at rate *n*, then the number of pair of potentially interacting loci that could contribute to reproductive isolation between the populations accumulates at rate n^2. This is the ‘snowball’ theory, which so far only has been empirically tested in interspecific studies in *Solanum*, *Eucalyptus*, and *Drosophila.* In this project we aim to address whether a ‘snowball effect’ also can be detected within a species using the outcrossing species *Arabidopsis lyrata* as a model. We 1) identify the number of loci responsible for reproductive isolation between populations assumed to represent different divergence times, and 2) test for a correlation between the number of loci contributing to reproductive isolation and population divergence. We selected three populations, previously demonstrated to produce varying degrees of F1 sterility in experimental crossing studies. We produced three F_1 hybrid populations and crossed two individuals from each of them to produce three F_2 populations, each comprising 500 individuals. We currently perform quantitative trait loci (QTL) mapping of reproductive isolation (pollen fertility) in the F_2 populations using genotype data from restriction-site associated DNA sequencing. Preliminary results indicate a declining trend in fertility with respect to population divergence.

S.103.6 Identify potential cross-compatible CWRs in Brassicaceae using phylogenetic approaches

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Crop wild relatives (CWRs) hold a wealth of genetic diversity which can be used to improve and help adapt traditional crops to succeed under environmental changes, being of paramount importance for research and conservation. Characterising and understanding the cross-compatibility between CWRs and crops, is essential to direct breeding efforts and to prioritise conservation of CWRs and facilitate their accessibility for future sustainable use. Wild species in the Brassicaceae family host desirable agronomic traits, biotic and abiotic stress tolerance. We reviewed the current classifications of CWRs in the Brassicaceae with the aim of identifying new potential cross-compatible CWRs from a total of 1,242 species using phylogenetic approaches. These approaches were used to fill in gaps of species without genetic sequence data to estimate their evolutionary relationships with Brassicaceae crops. Gaps in *ex situ* conservation and characterisation of CWRs were reviewed by compiling globally available data. Around 70% of the wild Brassicaceae lacked genetic sequence data available, and chromosome numbers were available for only 40% of them. Generally, compatibility data between wild species and crops, and phenotype and genotype characterisation data were available for major crops and very limited for minor crops. Half of the species had no records of being conserved *ex situ* and 80% were not assessed for their conservation status. Generate more sequence data for more species is key to understanding the needs of the cultivated species and to identify new CWRs. Using phylogenetic distances, we proposed 103 new potential CWRs, which we recommend as priorities for cross compatibility tests with crops and for physiological and phenotypic characterisation, including 71 newly identified CWRs for 10 minor crops. Confirming the cross-compatibility of the new potential CWRs with the same chromosome number is critical, in addition to generating more DNA sequencing data to complete the genetic characterisation of the family.

S.104 PLANT CONSERVATION GENETICS: FROM IN-SITU AND EX-SITU CONSERVATION TO REINTRODUCTIONS AND RESTORATIONS. SESSION 4

S.104.1 Species delimitation and genetic conservation of the endangered firs Abies beshanzuensis and A. ziyuanensis

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Abies beshanzuensis is one of the most endangered species in the world, with only three individuals so far. The accuracy of endangered species delimitation largely determines the efficiency and conservation strategies. The taxonomy of *Abies beshanzuensis, A. ziyuanensis* and *A. dayuanensis,* have always been controversial. *A. dayuanensis* has been considered as the synonym of *A. ziyuanensis,* whereas *A. ziyuanensis* is currently treated as a variety of *A. beshanzuensis*. To test this classification hypothesis, we performed target enrichment sequencing on 23 individuals from eight extant populations and obtained 805 single nucleotide polymorphic sites from 60 single-copy nuclear genes for population genetic analyses. Results of population genetic structure and demographic history analyses showed that this endangered fir group has diverged into two lineages corresponding to *A. beshanzuensis* and *A. ziyuanensis*. *A. ziyuanensis* first diverged from the common ancestor of *A. beshanzuensis* and *A. dayuanensis,* the latter two split apart later and more closely related, forming the other lineage. The genetic diversity is low within these populations. Strong genetic differentiation was found among populations. Gene flow is not detected after lineages split, probably because of the fragmented habitats which blocked effective genetic exchanges among populations. Ecological niche comparison showed that the average annual temperature and the temperature of the coldest quarter were significantly higher in the habitats of these endangered firs compared to those of non-threatened firs in East Asia. Therefore, we inferred that global warming is likely to push this group of endangered firs to the edge of extinction. According to the significant population differentiation, we provide genetic evidence that *A. dayuanensis* is a synonym of *A. beshanzuensis* and resurrect *A. ziyuanensis* as a separate species. We also highlight the necessity to carry out *ex-situ* conservation in the Hengduan Mountains and the Qingling-Bashan Mountains and conduct *in-situ* regeneration.

S.104.2 Conserving the Florida ziziphus (Pseudoziziphus celata): integrating translocations, demography, and epigenetics

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Florida ziziphus (*Pseudoziziphus celata* (Judd & D.W. Hall) Hauenschild) is a critically endangered, clonal shrub, endemic to sandhill habitat within the Lake Wales Ridge of central peninsular Florida. It was once thought to be extinct but was rediscovered in the wild in 1987 and several locations since then. Several barriers to species recover exist, including a highly restricted range, low genetic diversity, slow growth, and the presence of mating types. Since the 1990s, our comprehensive efforts to rescue the species combine demographic monitoring, ex-situ conservation, genetics, propagation, and translocation to establish new populations on protected lands. In this presentation, we (1) report on the genetic diversity in the species and how this information is used in conservation translocation, (2) describe advances in understanding the epigenetic diversity in this species, (3) report on demographic success of the species' introduction efforts. We have documented 46 genotypes in existence, and only three S-locus mating types, which severely limits cross-compatibility. DNA methylation patterns suggest a potential epigenetic basis for mating types, though further research is required. Demographic monitoring on 18 translocations established between 2002-2023 shows that the Florida ziziphus has a high survival rate but very low recruitment rate, so maintaining viable, self-sustaining populations remains a challenge. Nevertheless, strides have been made in developing germination techniques, tissue culture propagation, and best land management practices for transplant survival, especially prescribed burn management. Overall, Florida ziziphus serves as an important case study for the preservation of a highly endangered clonal species, which was brought back from the brink of extinction.

S.104.3 Using genomic data to inform management decisions for augmentation of a rare San Diego endemic succulent

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San Diego County, USA is a hotspot of plant biological diversity. Many rare plant species are severely threatened by habitat fragmentation in this rapidly developing population center. Dudleya brevifolia is a diminutive, deciduous succulent that is an edaphic endemic with 6 known extant occurrences all located within a five-mile radius. The range of this species' genetic diversity, both within and between occurrences, the degree of inbreeding, and the possibility of outbreeding depression was not previously known. Our study set out to genotype representative individuals from five of six known occurrences in order to inform management practices. We sought to understand 1) whether the distinct occurrences were genetically similar or different from one another, and 2) whether there was evidence of inbreeding due to fragmentation between populations. This information will help land managers decide if seed from more robust populations might be appropriate for supplementing smaller populations in augmentation projects. Genomic data indicated that individuals separated into three distinct clusters corresponding closely with geographic localities. Further analysis showed moderate differentiation (Fst) exists between the more distant populations, while slightly higher than expected heterozygosity (He) and low inbreeding (Fis) were seen across all sites. Based on this data, we suggest managing the clusters as populations where seed from occurrences within each cluster might be used to augment each other as needed.

S.104.4 Conservation and population genetics of the federally endangered Florida torreya (Torreya taxifolia, Taxaceae).

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Florida torreya, or *Torreya taxifolia* (Taxaceae), is one of the most endangered conifers in North America and is endemic to the ravines east of the Apalachicola river in the Florida panhandle. In the last century, populations have declined from nearly 700,000 trees in the early 1900s to around 800 trees today. This dramatic decline is the result of an invasive fungal pathogen, *Fusarium torreyae*. For the last 30 years, staff at the Atlanta Botanical Garden have been collecting cuttings for safeguarding, caging trees to prevent deer browsing, and tagging and monitoring wild trees in Torreya State Park and the Nature Conservancy's Apalachicola Bluffs and Ravines Preserve. Recently, partnership with the Florida Native Plant Society has allowed outreach to private landowners to locate, tag, and collect cuttings of trees on private lands. Using the collection of trees from across its range, we are performing conservation genetic studies of *Torreya taxifolia* using target gene capture to assess the level of genetic diversity and population structure remaining in the wild. Conifers are notorious for having extremely large and highly repetitive nuclear genomes, making typical population genomic techniques such as Genotype-by-Sequencing (GBS), restriction site-associated DNA sequencing (RADseq), and genome skimming unfeasible. Gene capture, in contrast, allows for targeted sequencing of specific loci in the genome and allows us to overcome the problem of the large, repetitive genome structure. This method is a cost-effective way to obtain DNA sequence variation necessary to distinguish among closely related populations. Results suggest that the entire species range is consistent with a single panmictic population. In addition, private landowners hold significant genetic diversity in this species, highlighting the importance of landowner relationships. Together, these projects will advance conservation efforts for this critically imperiled conifer.

S.104.5 Genomics, morphology, and flow cytometry inform taxonomy and conservation of rare cacti in the genus Echinocereus

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Echinocereus is one of the most diverse genera of the Cactaceae family. Many *Echinocereus* species display wide variation in stem, spine and floral morphology within and among populations. Such variation has resulted in the description of over 70 taxa, with a number of these considered rare, threatened, or endangered. While detailed morphological, cytological, and distributional studies have contributed greatly to our knowledge of species, subspecies, and varieties within *Echinocereus*, the addition of genomic data are needed to enable understanding of evolutionary relationships and eliminate long-standing taxonomic confusion. Our recent work in *Echinocereus* has focused on three rare taxa: *E. arizonicus* subsp. *arizonicus*, *E. fendleri* subsp. *kuenzleri*, and *E. fitchii* subsp. *albertii*. For each of these taxa, population-level samples have been collected throughout the range and from a subset of close relatives. Population genetic and genomic, and flow cytometric data have been obtained and analyzed using standard population genetic, clustering, ordination, and phylogenetic approaches. Results indicate that genetic variation is high and typically geographically structured, sometimes supporting the rare taxon as a unique evolutionary lineage, but sometimes supporting stronger genetic affinity among geographically proximate populations and non-monophyly of the rare taxon. Detailed morphological studies for these same taxa have revealed that large sample sizes are critical for understanding the range of morphological variation within and among populations and reducing sampling error and phenological effects from environmental factors. Although most results from these genetic and morphological studies are in alignment with each other and support current taxonomy, some are not, which might be expected given the recent and rapid radiation of this genus and the potential for convergent evolution in characters that are typically used to define taxa. Information gained from these studies is actively being discussed with conservation managers to help prioritize and optimize conservation efforts.

S.105 PATTERNS AND PROCESSES DRIVING CLIFF PLANT COMMUNITIES: APPROACHES FOR THE CONSERVATION OF ENDEMIC CLIFF FLORA. SESSION 2

S.105.1 Is the current conservation management effective to protect at-risk cliff plant species against increased climbing pressure?

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Cliff flora constitutes one of the less studied biodiversity components worldwide. This is surprising since it shelters a huge amount of very endangered plant species, and also a high representation of very ancient lineages and relicts which have survived perched on the inaccessible rocks. Cliffs shelter low competitive taxa which are refuged up there, but also a complete guild of rupicoluous specialists which have developed morphological and physiological adaptations to occur there. Consequently, cliffs are natural labs to evaluate microevolutive mechanisms but also to have a complete perspective of the biological history of a territory. However, our knowledge on the ecological and evolutive determinants of these habitats is almost null, although botanists have systematically explored the cliffs to complete the checklists of every explored territory. Threats are putting at risk this biological treasure. Emergence and recent massification of climbing as a very popular outdoor activity together with the incidence of other drivers of Global Change such as warming are pushing most of these plants at the verge of extinction and make necessary to evaluate the impact of this increasing pressure on the viability of these plants. Here we evaluate the risk associated to the popularization of this sport and the effectivity of conservation measures taken to face this problem. Specifically, we evaluated if the measures taken within protected areas are effective and, also, if they leakage to the surrounding areas. Preliminary results suggest they are ineffective. A paradigmatic example of this pressure is the almost total extinction of the population of *Petrocoptis grandiflora* in the Enciña da Lastra Natural Park duto climbing.

S.105.2 Conservation of cliff plants with the aid of remote collecting drones

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Cliff ecosystems often host unique, narrowly endemic plants. Due to the terrain, it is difficult and dangerous to access these areas. Rapidly evolving drone technology has been helpful in developing a deeper understanding of these cliff taxa through efficient aerial survey. Here we present a high-resolution approach to exploration and documentation of plants growing on vertical surfaces. In addition, new drone-based remote collection hardware has been developed for collecting plants from these hard-to-reach areas. This combination of tools has had an amazing impact for the conservation of critically endangered Hawaiian cliff endemic taxa.

S.105.3 CLIMB TO CONSERVE. An innovative approach to managing and mitigating the impact of climbing by sharing responsibilities between scientists, administration and climbers.

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Climbing has seen a rapid increase in the number of people practising the sport that has led into a growth in the number of outdoors climbing areas, which challenges the conservation of endemic plants related to rocky habitats. This has propelled administrations to develop mechanisms to protect this endemic species through regulation or ban of the activity in certain areas, specially in legally protected environments. Scientific knowledge must provide tools to assess the adequacy of these measures as well as methods to undertake restoration and reinforcement interventions to improve the status of protected species. CLIMB TO CONSERVE aims to reinforce two populations of plants listed as ‘Vulnerable’ located in Bierzo region, Northwest area of Iberian Peninsula. In order to do that, a multidisciplinary team has been created, involving regional Administration, scientific community and climbers association. We work with *Petrocoptis grandiflora* Rothm. and *P. viscosa* (Rothm.) P.Monts. & Fern.Casas, two endemic species with a very restricted distribution that live in cracks, ledges and limestone overhangings. We focus on restoring one population of each specie that have been affected by non-regulated climbing activities, a challenge *per se* due to its lack of available water and its inaccessibility. The main contribution is the testing of restoration both in zones where climbing has been forbidden and is still taking place. We center our contribution on detailing the followed protocol and on discussing effects observed related to methods of sowing, sowing period and the effect of climbing in germination and survival of seedlings. CLIMB TO CONSERVE aims to join scientific criteria and the collaboration of climbers to restore affected plant populations. Furthermore, it sets a basis from where administration can implement regulations which help to create a conservation conscience and natural heritage custody in those who spend more time with these species, the climbers.

S.105.4 Anthropogenic threats and conservation status of coastal plants: the case of two endemic Azorean taxa

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Natural and anthropogenic threats are causing alteration of coastal areas worldwide. Most of the coastal biodiversity is endangered, taking a particular toll on island ecosystems, like the Azores. To better understand the biotic and abiotic factors constraining the distribution and conservation status of the two endemic plants, *Azorina vidalii* (Campanulaceae) and *Lotus azoricus* (Fabaceae), we performed a global survey of coastal plant communities in the archipelago, also covering environmental descriptors, natural and anthropogenic threats. Moreover, we revised their IUCN conservation status and estimated the population fractions within protected areas. Non-indigenous plants were commonly found in plots with or without the target endemics, contributing for the absence of well-defined coastal plant communities. Nonetheless, indigenous taxa commonly occurred at the plots with *L. azoricus*. With a larger area of occurrence, *A. vidalii* ecological niche differed from *L. azoricus*, the latter being restricted to dry and rocky sea cliffs, mostly in Santa Maria Island. Besides the presence of invasive plants, signs of habitat destruction, trampling and grazing, and of natural threats, such as coastal erosion were commonly observed. Occurrence data indicated an endangered status for both species, although this would change to critically endangered for *L. azoricus* when using smaller occurrence plots. Both species are threatened since their habitat is restricted to a very narrow vegetation belt, strongly limited by sea influence and human pressure, and with the frequent presence of invasive plants. While focusing on two endemic plants, our study allowed a broader view of the conservation status of coastal plant communities in the Azores.

S.105.5 Cliff species as indicators of dark diversity of an island habitat affected by invasive herbivores

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Widespread anthropic activities have left few well-preserved habitats in Europe, leading to a significant impoverishment in their ecosystems. This degradation has also occurred on oceanic islands, where, in addition, the introduction of invasive herbivores has resulted in many habitats being characterized by the least palatable species. Thus, there is a profound lack of knowledge about the original plant communities, as the ecosystems have been considerably impoverished, leaving most of the species richness restricted to cliffs inaccessible to herbivores. The Canary Islands have not been exempting from these problems, although still retain high endemicity. For many of their habitats, few well-preserved remnants of original vegetation remain. This has led to serious conservation problems as there are difficulties in restoring habitats without having suitable reference ecosystem. Some of the best species refuges are found on platforms and cliffs within Caldera de Taburiente National Park (La Palma island), which harbour an extensive representation of the Canarian pine forest. Traditionally, this ecosystem has been defined as poor in species, but high endemicity and richness rates are in the cliffs. On the other hand, the accessible areas barely preserve 10% of their potential richness. Here we present a comparative study of the diversity and composition of the flora in the pine forests of Caldera de Taburiente. Plots located on inaccessible platforms and cliffs, cliff base exclusion plots, restoration exclusion plots and their respective controls were used. The results obtained show that invasive herbivores density is the most important driver in determining gradients of diversity and species composition. The characteristic species of the pine forest in the presence of invasive herbivores are not dominant in inaccessible areas. The Canarian pine forest restoration must be aimed at a progressive enrichment in which the refugee species must be used to recover the diversity and structure of understory communities.

S.105.6 Specialist plants on vertical calcareous rock formations in the Pyrenees share common traits and strategies

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Among mountain environments, vertical rocky outcrops present especially extreme conditions for plant life. These outcrops are characterized by the strong effect of gravity, minimal soil presence, limited water and nutrients, and challenging seed dispersal. In response to these conditions, certain plant species have undergone evolutionary processes that have enabled them to adapt to life on rocks, but, is there any shared trait or common strategy between specialist rupicolous plants? This study aims to be a first step into addressing this question, focusing it in a more concrete field: calcareous mountain cliffs in the Pyrenees. For this purpose, 10 rupicolous species and 10 generalist plant species were selected, each paired between them, with a genetically closely related counterpart to control for phylogenetic factors. Various functional traits were measured for each species, including leaf area, specific leaf area (SLA), leaf dry matter content, leaf thickness, flower area, plant size and leaf nutrient concentration. Preliminary results indicate that rupicolous plants tend to exhibit a more compact trait niche, suggesting a narrower range of adaptations that allow them to survive in such harsh environments. Additionally, these plants seem to display smaller size, leaf area and SLA compared to their generalist counterparts. Further systematic studies in other vertical cliff environments are encouraged to enhance our understanding of the adaptations in rupicolous plants.

S.106 SYSTEMATICS AND EVOLUTION OF LAMIALES. SESSION 2

S.106.1 Pollen morphology of Indo-Chinese Clerodendrum (Lamiaceae) and its systematic implications

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Clerodendrum is a highly species-diverse genus belonging to the family Lamiaceae and comprises approximately 250 species distributed in Asia, Australia, and Africa. Systematic studies of the Indo-Chinese *Clerodendrum* have previously relied on morphological and molecular evidence, while pollen morphology is poorly understood. The palynological evidence has been reported as important for taxonomic resolution for delimiting taxa within Lamiaceae for decades. In this study, pollen morphology of 22 representative Indo-Chinese *Clerodendrum* were investigated using light and scanning electron microscopy. The results revealed that pollen grains are monad and isopolar or heteropolar in type, subspheroidal to prolate spheroidal in shape and the surface with microechinate ornamentation surrounded by perforations. The apertural types are tricolpate or hexacolpate arranged in two series (trizonocolpate and tricolpate on the proximal pole). The length of the polar axis ranges from 38.14 μm to 96.42 μm and the length of the equatorial axis is from 31.38 μm to 97.72 μm and the exine thickness varies from 1.41 μm to 3.71 μm. Palynological evidence provides insights into detailed micromorphology that can be support phylogenetic relationships of the infrageneric taxa especially species within *Clerodendrum* section *fortunata* and *Clerodendrum* section *Tridens*. In addition, the results support the distinction between morphologically similar species.

S.106.2 Karomia gigas (Lamiaceae - Ajugoideae): floral morphology, systematic position, genetic diversity, and rescue from extinction

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The tree species originally known as *Holmskioldia gigas* was first collected in a small patch of coastal forest on the coast of Kenya in 1977. Only one mature, fruiting tree and one sapling were observed, and by 1985, they were both found to have been cut down. Thus, when the species was formally described and named in 1988, it was considered "Feared Extinct". The species was transferred from the genus *Holmskioldia* (Lamiaceae subfamily Scutellarioideae) to *Karomia* (subfamily Ajugoideae) in 1992 with the caution that its generic placement would have to be confirmed by its then-undocumented floral morphology. The rediscovery of *Karomia gigas* in 2003-2011 in two Tanzanian coastal forests more than 600 km south of its original Kenyan locality demonstrated that the species is not extinct, but its flowers remained unknown. A large number of mature fruit with seeds were collected in 2017, but initial attempts to germinate and propagate the species were unsuccessful due to fungal infection of most of the wild-collected seeds. In 2018, a second attempt at germination after treating the seeds with a fungicide was successful, resulting in 30 healthy seedlings that grew into young saplings that produced flowers in early 2021. Analysis of its floral morphology confirms the current placement of this species in *Karomia*, and DNA sequencing will further elucidate its subfamilial and generic position. With only 46 known individuals in the wild, *Karomia gigas* is assessed as Critically Endangered on the IUCN Red List of Threatened Species. Genomic analysis of an ex-situ population has provided important insights into the conservation of genetic diversity *K. gigas*. With many threats and low population numbers in its native habitat, continued protection and propagation of this species is required to enable future population recovery in Tanzania and eventually repatriation to Kenya.

S.106.3 The study on phylogenetic position and character evolution of the genus Utricularia (Lentibulariaceae) in Thailand

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The genus *Utricularia* is a carnivorous plant in the Lentibulariaceae family, consisting of around 270 species divided into 35 sections, of which 27 species are native to Thailand (from 7 sections). This genus possesses bladder-like traps with appendages surrounding the entrance. Numerous species of this plant in Thailand have not been investigated using molecular techniques, hence this study aims to determine the phylogenetic position of *Utricularia* in Thailand in comparison to other species in the GenBank database, using the internal transcribed spacer (ITS) region, and then reconstruction the ancestral state to study some selected morphological characters (life form, presence of rosette leaves, twining inflorescence, floral color, and hairy seed. The results reveal that *Utricularia* in Thailand evolved from multiple clades within many sections. Furthermore, most morphological characters evolve multiple times throughout their evolutionary history.

S.106.4 Comparative phylogeography of mints in the California Floristic Province

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Mediterranean-like biomes across the globe are biodiversity hotspots for both animals and plants. However, because such climates have only existed since the mid-Miocene, lineages adapted to Mediterranean-like biomes have diverged relatively recently, making it difficult to make robust inferences of phylogenetic relationships. Moreover, apparent abiotic niche conservatism within these lineages often leads to high levels of range overlap among species, potentially obscuring their biogeographic history. In particular, it is possible that pulses of expansion and contraction of suitable habitat throughout the Pleistocene, especially contraction towards the present, mimics a scenario of sympatric speciation when in fact speciation was primarily allopatric. The California Floristic Province is the only area of Mediterranean-like biome in North America and is the center of diversity – and potentially the area of origin – for several clades of mints (Lamiaceae), including *Lepechinia* sect. *Calycinae* (5 species), *Salvia* subg. *Audibertia* (19 species), and *Monardella* (> 40 species). Prior studies have shown that all three clades have diversified since the mid-Miocene, although relationships within clades have been difficult to resolve. Using a phylogenomic hypothesis of relationships and a suite of biogeographic tools, including generating ecological niche models for all ancestors that originated in the last 5 million years, we test if all three clades (1) show similar temporal patterns of divergence, (2) show parallel patterns of area of origin and directionality of geographic spread, and/or (3) show evidence of sympatric speciation rather than allopatric speciation followed by secondary contact. Our results provide important insights into the origin and maintenance of species diversity within Mediterranean-like biomes.

S.106.5 The acualescent species of Henckelia (Gesneriaceae)

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The genus *Henckelia* Spreng. (Gesneriaceae, sub-family Didymocarpoideae) includes 82 species, distributed in Northeast and South India, Sri Lanka, Myanmar, Nepal, Bhutan, southern China, northern Vietnam, northern Laos and northern Thailand. The genus was treated earlier as a synonym of *Didymocarpus* Wall. until it was resurrected and remodeled by Weber and Burtt (1997). Weber *et al*. (2011) re-defined the genus based on molecular data and included species of *Henckelia* sect. *Henckelia*, *Chirita* sect. *Chirita* (excluding the species under *Damrongia* Kerr *ex* Craib), the monotypic genus *Hemiboeopsis* W.T.Wang and exclude the species of *Henckelia* sect. *Loxocarpus*, *Didymanthus*, *Heteroboea* and *Glossadenia*. *Henckelia* includes mainly perennial plants, sometimes with a woody base; caulescent to acualescent (rarely creeping) habits; infundibuliform to tubular corolla; geniculate or straight filaments; unilocular or bilocular ovary; chiritoid to (rarely) truncate stigma and capsules splitting into 2 valves, or only along the dorsal side. Species of *Henckelia* generally fall under two groups: (1) plants predominantly caulescent, with internodes and leaves in whorls of 2 or 3, and orthocarpic capsules dehiscing along both upper and lower suture; (2) plants predominantly acaulescent, with leaves in basal rosette and plagiocarpic capsules opening along the upper suture only. The former group includes 64 species, distributed throughout the distributional range of the genus except South India, while the latter group includes 18 species, found in South India as well as in Sri Lanka. All the 16 species of *Henkelia* found in South India are acualescent, whereas Sri Lanka has eight species of Henckelia of which three are acaulescent. *Henckelia humboldtiana* (Gardner) A.Weber & B.L.Burtt is the acaulescent species seen both in South India and Sri Lanka. The present paper discusses the taxonomy, ecology and endemism of the acaulescent *Henckelia*. A phylogenetic tree is also constructed from ITS and trn loci.

S.106.6 A left-right story: Understanding the function and evolution of enantiostyly in the genus Didymocarpus (Gesneriaceae)

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Enantiostyly is a type of stylar polymorphism in which either style and anther or style alone is deflected from the main axis of the flower to either right (R morph) or left (L morph). The floral design of enantiostylous flowers has been interpreted to promote insect-mediated cross-pollination, although, there are very few experimental examinations of this hypothesis. Therefore this study aims to understand the evolution and fitness consequences of enantiostyly in the genus *Didymocarpus* Wall. (Gesneriaceae) a narrow endemic herb distributed from the Himalayas to the Malay peninsula. To evaluate this we tested the following hypothesis: 1) enantiostyly is a synapomorphic character in the genus *Didymocarpus* and it evolved from a straight-styled ancestor, 2) floral morphology of enantiostylous flowers decreases autonomous self-pollination while maximizing pollen transfer between floral morphs thus increasing reproductive fitness. We collected morphometric data including the presence of enantiostyly for 43 *Didymocarpus* species from field surveys and literature. We mapped enantiostyly and a few other associated floral traits to the phylogenetic tree and estimated the ancestral states for these traits. All the above analysis was carried out in R using packages phytools, ape, and caper. Pollinator observations, pollen dye experiments, and hand pollination experiments were performed in four enantiostylous species and three non-enantiostylous species during the flowering period between July-September in the Northeastern states of India. Our analysis shows that enantiostyly is a synapomorphic character in the genus *Didymocarpus* and the evolution of this character and the degree of spatial separation between anther and stigma shows a significant correlation with corolla tube shape. Results from our field experiments indicate that enantiostylous floral morphology decreases autonomous self-pollination and increases the efficiency of inter-morph pollen transfer. Furthermore, enantiostylous species exhibited higher natural fitness in terms of fruit production compared to non-enantiostylous flowers.

S.107 SPATIAL MODELLING OF PLANT NICHES AND DISTRIBUTIONS IN THE ANTHROPOCENE. SESSION 2

S.107.1 Seagrasses on the move: tracing the multi-decades trends of lagoon meadows using Landsat series imagery.

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Lagoons globally provide crucial ecosystem services, harbouring a rich mosaic of fragile habitats. Among these, seagrass meadows play a vital role for this ecosystem and its biota, by sustaining trophic networks and influencing sediment and nutrient dynamics. Their distribution and functioning are closely tied to ecological disturbances, showing rapid shifts over time in relation to the ongoing global changes. Furthermore, lagoons often host multi-species meadows, where species interactions might complicate the understanding of the whole ecosystem responses to environmental changes. Long term monitoring of species and communities is, hence, important to understand the response to past and future global change scenarios. The availability of long term open-access satellite data (e.g. Landsat mission) offers a new remote sensing perspective for studying seagrass community dynamics in shallow waters, especially when combined with the power of machine learning algorithms. In this study, multispectral seasonal images were used with a Random Forest algorithm to map the trends of seagrass meadows and individual species in the vast Grado and Marano lagoon (Northern Adriatic) over two decades. Supervised classification models were built using a large field training dataset collected in 2010 (n = 426, accuracy of 92%) together with Landsat 5TM and 8OLI imagery and then applied from 1999 to 2019 images. The change detection analysis revealed a 14.16 km² expansion (+ 39 %) of the entire seagrass community at a rate of 1.59 km²* year⁻¹. Despite Landsat's low spatial resolution, discrimination of individual species achieved an accuracy of 76% allowing the tracing of relative species movements and shedding light on their complex dynamic over time. The observed expansion might underpin an increasing sea water influence that are radically modifying Adriatic brackish water bodies, emphasizing the connection between ongoing environmental changes and the rapid responses of seagrass meadows.

S.107.2 Classical metrics misguide the interpretation of species distribution models affected by sampling biases

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Species distribution models (SDMs) are a vast collection of techniques that predict species' likelihood of occurrence across spatial and temporal dimensions. These techniques barely require two inputs: presences (referred as only-presences when real absences of species are unavailable) and a set of relevant environmental variables for the niche of target species.

Thus, the recent expansion of open platforms offering massive georeferenced data on biodiversity has boosted the use of SDMs. Still, the employment of such data holds a major limitation: the profusion of sampling biases. The former implies that opportunistic presences are potentially affected by heterogeneous sampling efforts across study areas and species, which demands the implementation of adequate bias corrections. As well, modelers usually take advantage of classical metrics (namely AUC and TSS) to evaluate the overall quality of model predictions. However, AUC and TSS have been widely criticized given its poor capacity to assess the biological reality of predictions, and it would be alarming if such metrics are eventually unsensitive to sampling biases. In this study, we selected 31 fleshy-fruited plants as a study case to evaluate the sensitivity of classical metrics to sampling biases, as well as to compare the effect of three distinct bias corrections on the quality of predicted distributions. We run models on a (sub-)continental scale and used both classical and alternative, spatially explicit metrics of model performance. Our results suggest that bias corrections are imperative to improve predictions, whilst model performance depends on settings as the modelling algorithm or the method to generate pseudo-absences. Likewise, classical metrics were particularly weak to discern biased predictions, and eventually contradicted alternative metrics. Altogether reveals the convenience of implementing contrasting, spatially explicit validations when assessing predictions affected by sampling biases.

S.107.3 Spatial distribution of Annonaceae across biomes and anthromes: knowledge gaps in spatial and ecological data

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Covering approximately 7% of the terrestrial portion of the earth's surface, tropical rain forests harbour c. 45% of all terrestrial species, including approximately three fourth of all tree species. Although humans have impacted tropical forests long before modern times, they are currently at risk because of increasing anthropogenic activities. Especially during the last few decades, humans increasingly influenced the earth's surface to meet their needs. As a result, most natural biomes have changed into anthropogenic biomes, also called anthromes. Understanding how different taxa are affected by these changes is key in order to inform measures for conservation and protection, something especially important in this UN Decade on Ecosystem Restoration. Here, we investigate if this impact can be quantified for the globally-distributed tropical plant group Annonaceae (Soursop family) using spatial (distributional) data. Insight is gained in how Annonaceae are distributed over biomes and anthromes. We find that even for a taxonomically well-studied group such as Annonaceae, very little is known about the true distribution and ecological requirements of species. We urge to invest in 1) the exploration of ecological requirements of species in relation to their genetic patterns, in order to understand the impact of ecosystems changes, 2) research on distributional patterns in a temporal framework since the available data collected over decades might not reflect current distributions over biomes and anthromes well, and 3) high-quality spatial data collection that should adhere to the FAIR data principles, so that the quality of spatial analyses will increase. These data will also contribute to better base-line data for IUCN Red List assessments, which are a vital tool to assess the level of threat to a taxon.

S.107.4 A Species Distribution Model to elucidate the occurrence of an endemic species

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The presence of species in ecological communities mainly depends on abiotic factors, biotic factors, and their dispersal ability. Species Distribution Models serve as valuable statistical tools to clarify the distribution of a species considered the relationships among multiple species and their interaction with the environment. Our aim is to determine how biotic and abiotic factors influence the spatial distribution of *Crocus etruscus* Parl., an endemic geophyte of Central Italy. We constructed a hierarchical mixed-effects model using the "lme4" package in R programming language, with the presence of *C. etruscus* as the response variable. We conducted vegetation surveys to identify the dominant tree species coexisting with *C. etruscus*, considering them as biotic factors. Subsequently, we combined these factors with the classes of Corine Land Cover to incorporate random effects into our analysis. Functional leaf traits linked to the Leaf Economic Spectrum (leaf area, specific leaf area, leaf dry matter content) represented additional biotic variables. The leaf traits of *C. etruscus* were determined on samples collected during the vegetation surveys. Then the fixed-effect explanatory variables were the abiotic variables, sourced from the online databases WorldClim and SoilGrids, and the biotic variables, represented by the functional leaf traits of *C. etruscus*. This study provides an assessment of the influence of abiotic and biotic factors on the occurrence of *C. etruscus*. Such insights provide valuable guidance for the management of this species and aid in the identification of key areas for further exploration, thereby contributing to a comprehensive understanding of its distribution range.

S.107.5 Temperature and drought resistant species' past and future

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The Mediterranean region is utterly vulnerable to global change and provoked disturbances in Mediterranean plant species' distribution will be crucial for management and conservation design. Climate change impact in two well-adapted Mediterranean species, drought, and temperature-resistant, was studied (rockrose (*Cistus ladanifer* L.; CL) and strawberry tree (*Arbutus unedo* L.; AU)). The past, present, and future potential spatial distribution was unfolded, and the potential glacial refugia based on modeling, phylogeography, and fossil data was verified. Modeling was made based on real occurrences and environmental variables using machine learning and regression-based algorithms. The potential future distribution was projected for the years 2050 and 2070, considering a less and more severe climate scenario. The precipitation variables had decreasing importance in the obtained models, followed by the temperature variables, in the case of the CL, but conversely in the case of the AU, being the slope influential. For both species, the results of the Last Glacial Maximum (LGM) projection suggested the presence of refugia in the core of the Mediterranean Basin, particularly in the Iberian Peninsula (PI) southeast. Projections for the Mid-Holocene (MH) indicated increasing climatic suitability and expansion for the two species relative to the LGM. The past distribution projections modeled were congruent with the two independent approaches (fossil and genetics), validating the CL distribution modeling in the past, unlikely in the AU case, where very strong fossil signals were found in the IP borders, even in northern regions. Those species will be dramatically affected by global warming, despite drought and temperature resilience, particularly the CL. Contrarily to AU, CL northward future migration is unlikely to happen, but a westward collapse towards the Portuguese coast. The AU northern migration will depend on its ability to pace and adapt to environmental changes speed. Consequently, thermophilic Mediterranean species will probably be endangered.

S.107.6 What explains the high island endemicity of the threatened parasitic Rafflesia in the Philippines?

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Rafflesia are rare holoparasitic plants. In the Philippines, all but one species are found only on single islands. This study aimed to better understand the factors contributing to this distribution pattern. Specifically, we sought to determine whether narrow environmental tolerances of host and/or parasite species might explain their island endemicity. We used Maxent species distribution modeling to identify areas with suitable habitat for *R. lagascae*, *R. lobata*, and *R. speciosa* and their *Tetrastigma* host species. These analyses were carried out for current climate conditions and two future climate change scenarios. Although species distribution models indicated suitable environmental conditions for the *Tetrastigma* host species in many parts of the Philippines, considerably fewer areas are inferred to have suitable conditions for the three *Rafflesia* species. Some of these areas are found on islands from which they have not been reported. All three species will face significant threats as a result of climate change. Our results suggest that limited inter-island dispersal abilities and/or specific environmental requirements are likely responsible for the current pattern of island endemicity of the three *Rafflesia* species, rather than environmental requirements of their *Tetrastigma* host species.

S.108 PLANT DIVERSITY, BIOGEOGRAPHY AND EVOLUTION IN THE TROPICS FOR CONSERVATION, RESTORATION AND SUSTAINABLE USE. SESSION 3

S.108.1 Tree diversity and liana infestation predict acoustic diversity in logged tropical forests

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Logged tropical forests can retain a great deal of biodiversity, but there is substantial variation in the type and severity of habitat degradation caused by logging. Logging-induced habitat degradation can vary significantly at fine spatial scales, with differing effects on plant communities and the growth of lianas, which are woody, climbing vines that proliferate in degraded forests and infest trees by climbing onto them and competing for above and below ground resources. The impacts of such fine-scale variation in habitat structure on faunal diversity is relatively poorly known. We recorded soundscapes and variation in local-scale habitat structure in selectively logged and old-growth primary forests in Malaysian Borneo to examine how changes to logged forest structure predict variation in acoustic diversity indices that are known to correlate with biodiversity indices. We show that acoustic indices relating to higher soundscape diversity increase with liana prevalence but decline with tree species richness and are unaffected by the liana load of adult trees. Our results suggest that acoustic data represent a simple, practicable measure for detecting fine-scale patterns of biodiversity response to post-logging habitat structure. Our findings also suggest that retaining many trees lightly infested by lianas in logged forests is the optimal outcome for biodiversity. This emphasises the need for forest restoration that retains some climbers, rather than blanket-cutting of all stems in projects seeking to return post-logging forest communities towards their primary forest state.

S.108.2 Plant diversity and cultural specificity influence traditional knowledge on ecosystem services in western Amazonia

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Biodiversity and cultural idiosyncrasy shapes plant traditional knowledge in the Amazon basin. Yet, the factors that influence how different human groups gather knowledge for a certain purpose are not well understood. We aim to investigate: 1) the relationship between traditional knowledge (culture) and biodiversity and 2) the degree of floristic knowledge convergence among Indigenous communities. We inventoried 1907 species of woody plants in 115 0.1-ha plots in western Amazonia. The relationship between use diversity and species richness was analyzed per plot with generalized linear models, whereas the relationship between cultural and floristic distance was explored with beta regression models. The Euclidean distances between floristic and cultural distances were compared among Indigenous communities to analyze the degree of knowledge convergence. High plant diversity and heterogeneity of rainforests contribute significantly to the development of traditional knowledge within and between Indigenous communities. In most cases, the differences in knowledge across human groups are mainly due to floristic distances, showing the interrelation of these variables. However, in some cases, floristic distances were higher than cultural distances (36%), *i.e.,* knowledge convergence. In other cases (14%) floristic distances were lower than cultural, implying unique bodies of knowledge between communities. Biodiversity largely influences versatility of uses and traditional knowledge turnover both at local and regional scales. We highlight the importance of floristic composition in shaping knowledge for each Indigenous community, however different patterns of knowledge convergence among Indigenous communities were found. These findings highlight the importance of considering both cultural and biological factors in understanding Indigenous knowledge networks. Respecting and valuing the distinct bodies of knowledge requires an understanding of these factors and a commitment to supporting their autonomy and self-determination in preserving and transmitting knowledge systems.

S.108.3 Comparing taxonomic and phylogenetic diversity of woody plant communities in contrasting biogeographic regions of Colombia

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Biodiversity distribution in Neotropical regions, such as the Amazon, Tropical Andes, and Choco, continues to captivate scientists. This study contributes to the ongoing debate over Earth's most plant-diverse region, unraveling the interplay of geological history, climate, and evolution. Our primary objective was to compare taxonomic and phylogenetic diversity in woody plant communities across the Amazon, Northern Andes, and Choco, utilizing 48 permanent 1-ha plots. A secondary objective was to discern the relationship between species richness and phylogenetic diversity in these biogeographic regions, exploring its connection to the Museums and Cradles hypothesis and the role of these regions. We observed the highest species accumulation rate and species richness (SR) in the Amazon. Similarly, phylogenetic species richness was most pronounced

in the Amazon, followed by the Choco and Andes. Contrary to expectations, the Choco surpassed the Northern Andes in angiosperm SR and phylogenetic diversity (PD). Strong positive correlations between SR and PD were evident across regions. Our findings reveal distinctive taxonomic and phylogenetic diversity patterns. The Amazon, rooted in ancient geological history, exhibits higher SR and PD. In contrast, the Andes and Choco, with more recent origins, demonstrate higher speciation rates, evidenced by greater SR relative to PD. Residual analysis of our data suggests unexpected results, with the Amazon aligning with a cradle hypothesis, the Northern Andes resembling a museum, and the Choco displaying characteristics of both. This study challenges preconceived notions, offering insights into taxonomic and phylogenetic diversity in the Amazon, Andes, and Choco. By elucidating the relationships between geological history, climate, and evolution, our findings underscore the importance of considering both dimensions in biodiversity assessments. Effective conservation in these Neotropical regions requires accounting for their unique evolutionary dynamics and the implications of varying geological ages on plant community composition.

S.108.4 Functional traits in four tropical dry forest species in relation to soil water availability under nursery conditions (Colombia)

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During process of propagation and management of key plant species for ecological restoration (ER), it is necessary monitoring the growth and functional response before planting, because the nursery management influence the survival and success of plants in restoration areas. In this research, the response of four species of inter-Andean tropical dry forest (TDF) in Colombia was analyzed under different conditions of soil water availability (WA): 100%, 79.6%, 65.9% and without irrigation (main environmental filter). The species were selected by their successional preference, 120 plants were included in the experimental design, divided into four treatments per species: *Ochroma pyramidale* (pioneer), *Senna spectabilis* (pioneer), *Tabebuia rosea* (intermediate-advanced) and *Astronium graveolens* (intermediate-advanced). The experimental phase was carried out for seven consecutive weeks, then total harvest was performed to measure six traits: leaf area (cm^2), leaf thickness (mm), xylem vessel density ($\#/mm^2$), xylem vessel diameter (µm) and the proportion of secondary roots (% dry biomass). In *O. pyramidale* WA -response traits are related to stem and roots with an affinity towards the acquisitive strategy and resists drought, in *S. spectabilis* the response were leaf thickness and stem, with an affinity towards the acquisitive strategy and avoids drought. For *A. graveolens* and *T. rosea*, the response traits were stem and root, related to the conservative strategy, however *A. graveolens* tolerates drought as it remained evergreen, while *T. rosea* resists as leaf abscission occurs with prolonged drought (deciduous). In all species the relationship between traits was different, however under prolonged drought the proportion of secondary roots increased, as a strategy to search water. We conclude that these species require differential irrigation management to improve their response in growth, transplanting and survival in the nursery, this management guarantee a better response in the areas will be restored.

S.109 CRYOBIOTECHNOLOGY: BROADENING THE SCOPE OF PRESERVING PLANT BIODIVERSITY FOR THE FUTURE

S.109.1 Cryopreservation of Macadamia – a tough nut to crack

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The preservation of *Macadamia* diversity is important to conservation of species in the wild and the future of the world-wide macadamia industry. We aimed to determine whether standard seed banking or cryopreservation of whole seeds would be suitable for preserving these taxa. We first investigated the response of seeds of five taxa to desiccation and storage for 1 month at -20 and -192°C. All taxa tolerated drying but responded poorly to storage at both temperatures. Thermal analysis of dry seeds was then used to investigate energy transitions during freezing and thawing that might explain the observed response. Samples of cotyledonary tissue were sealed in aluminum pans then lowered from 20 to -150°C, and raised from -150 to 50°C, in a differential scanning calorimeter. The resulting thermograms showed a crystallisation transition between -10 and -20°C, and a broad melting transition from around -20 to 0°C, for all taxa. Based on these results, we compared the effect of storage at 4 and -5°C (avoiding the crystallisation transition zone) against storage at -20 and -192°C for seeds of *M. integrifolia* x *tetraphylla* 'Beaumont' and *M. jansenii*. Both taxa responded significantly better to storage at the higher temperatures than at -20 or -192°C. However, we expect the large seeds of some *Macadamia* taxa may still be short-lived under those conditions so have commenced research on cryopreservation of the much smaller embryonic axes. Preliminary experiments have shown that normal seedlings can be produced from fresh embryonic axes providing they have a small amount of cotyledon attached, are sterilised in 2% bleach for no more than 15 minutes and are sown on MS medium containing 2% activated charcoal and 250 ppm gibberellic acid. Experiments testing survival following drying and immersion in liquid nitrogen will be undertaken in the next fruiting season.

S.109.2 Bryophyte spore conservation: what do we know and what else can we learn?

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Bryophyte spores offer enormous potential for biological studies and conservation. As unicellular model for stress tolerance studies, they can provide essential information on how the land was conquered. Being key elements in reproduction and dispersal, they play important part in the biology and biogeography of the species. And for our efforts in preserving biodiversity, they can be used for efficient ex-situ conservation in spore banks. Bryophyte spores are usually unicellular, although some species produce multicellular spores because of an endosporic germination. Most bryophyte spores have fully developed chloroplasts at maturity, and our results show that they can be highly lipidic. This is a unique combination of characters in land plants' propagules, as seeds and fern spores containing chlorophyll often show low storage lipids. Bryophytes have proved to be long term survivors, growing from soil banks after a century (e.g., *Bruchia vogesiaca*, *Physcomitrium eurystomum*). However, our comparative studies suggest that they are generally short lived at room or experimentally controlled conditions. This may be related to the unique combination of spore characters mentioned above. To improve our knowledge on these structures we should learn about their physiology (e.g., type of storage lipids, contents of chlorophyll, other pigments, and antioxidants), ecology (e.g., relationship between desiccation tolerance and xerocastic/hygrochastic dispersal) and biogeographic implications (e.g., how differences concerning spore features justify differing distribution patterns in related taxa). Finally, for the purpose of ex-situ conservation, we should experimentally understand the storage conditions that preserve their maximum longevity. Moreover, we must decipher the parameters for the optimal spore germination and protonemal growth in a large and diverse number of species. We aim to offer a brief overview of current knowledge and future perspectives of this line of research because, despite their importance, our knowledge of bryophyte spores is still fragmentary and sometimes contradictory.

S.109.3 Phylogenetic diversity stored in seed banks: looking back and ahead

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With two in five plants facing extinction, identifying currently unsecured branches of the Tree of Life is key to prioritise future conservation efforts. Thus, phylogenetic diversity (PD) methods become crucial in designing cost-effective conservation planning for species' prioritisation and prevent lineages loss. Conventional seed banking (i.e., conservation of desiccation-tolerant seeds at below-zero temperatures) is the most efficient and effective ex-situ method for long-term conservation. However, the development of phylogenetically informed seed collecting programmes is difficult due to the insofar limited accessibility of biodiversity data represented in conservation facilities and to the lack of tailored methodological frameworks. Here, we used a comprehensive dataset spanning over 30 years conservation effort of 109 institutions across 29 European countries and provided a new flexible method to identify those species whose conservation would maximize the phylogenetic history representativeness should they become protected in conventional seed banks. Over one third (8,383 species) of the European angiosperm flora is currently secured in conventional seed banks, representing 60% of the total PD. However, this value is lower than the potential PD that could have been conserved because whole plant lineages are absent from banked seed lots. We show how securing further 4000 unsecured species selected from those lineages, would lead to protect 90% of total PD, as opposed to the 74% achieved from the same number of randomly selected unsecured species. Our method allows to prioritise among unsecured species using a stepwise-PD-maximisation procedure, adaptable to different resource availability scenarios. Nevertheless, for some of those species there are obstacles that prevent their seed collection and conservation. Thus, this study provides baseline data to promote better-grounded seed-based conservation policies and more generally, our new method will serve to prioritize among unsecured species of any taxonomic group so that the trade-off between secured evolutionary history and budget availability is maximised.

S.109.4 Conservation of oak species by biotechnological tools

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The genus *Quercus,* which includes more than 400 species of oak, is found throughout the northern hemisphere in a wide diversity of habitats. Oak forests play vital social, ecological and economic roles. However, the sustainability of oak populations is currently threatened by habitat loss caused by, among other factors, human-mediated disturbance, adverse environmental conditions, attack by pathogens and pests and in particular by a complex disease commonly known as "oak decline". The conservation of oak species is therefore of great importance. Biotechnological tools based on in vitro cultivation, such as micropropagation and cryopreservation, are considered good alternatives to other classic conservation strategies (i.e., in situ conservation or field collections). In vitro culture techniques enable conservation of the germplasm of woody species that undergo vegetative propagation or that produce recalcitrant seeds; they also enable the conservation of biotechnology-derived products. The present work revises the main advances in the conservation of oak genetic resources using biotechnological tools based in vitro techniques. Different strategies are reported for short- and medium-term (micropropagation) and also long-term conservation (cryopreservation in liquid nitrogen) of oak. In the first approach, shoot cultures and somatic embryos are maintained by periodic subculture (4-6 weeks), often indefinitely. In addition, the subculture period can be greatly extended (12 months or even longer) by subjecting the cultures to slow growth conditions (i.e., low temperature, illumination, or nutrients). Long-term conservation procedures have also been developed for different oak species by cryopreserving somatic embryos. Cryopreservation of somatic embryos was performed following vitrification- and desiccation-based procedures. Comparative studies of these methods clearly showed that the vitrification-based procedure yielded the highest recovery rates.

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S.109.5 The plant cryo phenotype

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Cryobiotechnology embraces three components of low temperature science: natural, physiological adaptation and capability; fundamental science of various stress tolerances; and innovative design for biobanking of various explants (cryopreservation). Even though cryo-based solutions are widely accepted as a critical part of a strategy to combat the risk of biodiversity loss, an understanding of species' cryobiotechnology is still patchy. Nonetheless, progress over the last 20 years has been made on the cryo responsivity of species' explants, leading to a better comprehension of cryo phenotypes, i.e., the functional traits that contribute to cryo success in the natural, experimental and biobanking setting. These traits relate to, *inter alia*, the extent or ease of cellular physiological adaptation (including elicitation) to cold and dehydration, the dimensional (physical) limits for tissue cryo and species' differences in cryoprotectant permeability, seed lipid composition and thermal properties, and inter-specific variation in somatic embryogenesis and regrowth of explants *in vitro*. We provide an overview of these multiple cryo phenotypes and identify gaps in knowledge that need to be addressed by a future research agenda.

S.110 WORLD FLORA ONLINE: DEVELOPING TAXONOMIC CONSENSUS FOR LAND PLANTS SUPPORTING SCIENCE, CONSERVATION AND SUSTAINABLE USE

S.110.1 Integrating taxonomic and floristic data into a global perspective: the case of the South African flora

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Taxonomy serves as the foundational framework essential for evaluating, monitoring, and safeguarding biodiversity. At the onset of the 21st century, acquiring taxonomic information for these endeavours presented challenges; however, recent advances in technology have considerably eased this process. The establishment of the World Flora Online (WFO) Consortium has garnered global support in the pursuit of a global Flora. In 2013, the South African National Biodiversity Institute (SANBI) joined the WFO Consortium and has since achieved notable success in creating the e-Flora of South Africa. Drawing from the 2024 release of the South African National Plant Checklist, the country has 22,158 indigenous taxa (20,202 indigenous species) of which 14,154 taxa (12,210 species) are endemic. As documented on the WFO website (April 2024), the global species count stands at 377,216, signifying that South Africa contributes approximately 5.4% to the global floral knowledge. Remarkably, 3.2% of this contribution is unique due to the high level of endemism in the country. Taxonomic information is harnessed from existing published information to populate the e-Flora of South Africa database. Starting from 2016, data from the South African National Plant Checklist and the e-Flora of South Africa have been integrated into the WFO, fulfilling the country's international obligations concerning the Global Strategy for Plant Conservation and WFO. By 2020, comprehensive coverage of all indigenous species was achieved within the e-Flora of South Africa culminating in its 2023 publication on SANBI's new Biodiversity Advisor platform. Looking ahead, the e-Flora of South Africa will be maintained in alignment with updates to the South African National Plant Checklist, accompanied by expansion to encompass descriptions of infraspecific taxa, genera, families, and naturalised taxa. An inclusive overview of the e-Flora of South Africa project will be presented to provide a comprehensive understanding of its scope and significance.

S.110.2 Consensus classifications are crucial for conservation: How CITES utilises checklists

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The Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) aims to ensure that international trade in wild animals and plants does not threaten their survival. To manage and regulate trade in endangered species, taxa are listed on one of three CITES Appendices. Many groups are included in the Appendices via higher classification listings. In such cases an entire genus will be listed, for instance '*Pachypodium* spp.' (i.e., all species of *Pachypodium*). As classifications change, genera can be split apart or lumped together. These changes in classification have dire implications for law enforcement officials who need to implement CITES regulations. The situation is further complicated when different resources provide different classifications for the same group of plants. Therefore CITES designates standard nomenclature references to use for certain listed taxa, especially those with higher classification listings. These standard references contain lists of names that are currently accepted in those taxa and forms the basis for updates to the CITES Checklist of Species and Species+ databases, which are regularly consulted by those who need to regulate international plant trade. Standard nomenclature references for CITES can take the form of published revisions or other taxonomic works, customised checklist publications produced specifically for this purpose, or time-stamped extracts from online data sources. The WFO Plant List can play an important role as a consensus classification source, curated by a global specialist-based community of experts, to be used for future CITES standard nomenclature references. Time-stamped extracts for a specific group from the WFO Plant List will be ideal to serve this purpose. Furthermore, the WFO Taxonomic Expert Networks (TENs) are ideally placed to produce customised CITES checklist publications. In fact, three such checklists based on the WFO Plant List are currently being produced for CITES by WFO TENs.

S.110.3 Electronic tools and social networks: resolving names and integrating new taxa in developing a global consensus classification

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The World Flora Online (WFO) was developed in response to the Global Strategy for Plant Conservation and the need for suitable floristic data to support conservation. WFO currently contains about 1.6 million plant names, with associated concepts, and over 600,000 pieces of descriptive content. WFO includes a global consensus plant classification, developed through merging and incorporating multiple data sources, augmented by input from WFO's Taxonomic Expert Networks (TENs). TENs are key to achieving a robust, curated, consensus classification. These social networks are open groups of taxonomic specialists providing relevant taxonomic and nomenclatural expertise to resolve issues and maintain the classification. TENs vary in size, structure, and function. Some are new while others are built on existing collaborations. The WFO classification is managed through Rhakhis, a standalone, web-based data management tool allowing curation of the data. Curator authentication is handled via a link to ORCiD. Authorisation for curators is delegated hierarchically down the taxonomic tree. This allows TENs, and the TEN Manager, to oversee and manage the live data directly and delegate curatorial authority to colleagues. The TEN Manager has additional tools to add newly published, historic names and edits from the International Plant Names Index (IPNI); incorporate structured classification files from sources like World Checklist of Vascular Plants (WCVP), BryoNames, and datasets provided by TENs stored in institutional taxonomic databases or in Catalogue of Life's ChecklistBank. The WFO classification is published 6-monthly as the WFO Plant List, and is provided in multiple formats with a CC-0 licence, including data archives on Zenodo and ChecklistBank with DOIs. Two R packages are available to match and resolve names to a WFO ID. Name matching is also available through an interactive online matching tool that accepts text lists and csv files. Machine to machine interfaces allow for integration with curatorial and other systems.

S.110.4 Catching up on plant diversity: the online flora of Mexico "eFloraMEX"

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Mexico is a megadiverse country with an elevated diversity of species of vascular plants. A comprehensive Flora that includes all of the vascular plants distributed in Mexico does not yet exist. Electronic Floras have demonstrated the value of a compendium based on existing knowledge and published Floras, checklists and revisions. The objective here is to summarize and evaluate the taxonomic and digital resources and the bioinformatic tools needed to develop an online Flora for the vascular plants of Mexico, as well as to discuss its content. Organization of this project will follow World Flora Online. It will be based on approximately 5.3 million specimens deposited in Mexican herbaria, with an inter-operational portal to other biodiversity platforms. The name assigned to this online flora is "eFloraMEX". The main challenges to completing this Flora are building the team, training taxonomists, digitizing the specimens for most of Mexican herbaria and obtaining the required long-term funding.

S.110.5 Bridging the phylogeny to classification gap at genus and species levels to obtain the best possible taxonomic knowledge in the Caryophyllales

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The order Caryophyllales constitutes a major clade of the angiosperms, encompassing about 13.500 species. Whereas the circumscription of families has been stable since a number of years, the circumscription of genera shows considerable turnover as the number of species included into phylogenetic analyses raises. From 749 genera accepted in 2015, the current state of knowledge justifies the monophyletic circumscription of >779 genera. The examples of the three speciose families Cactaceae, and in particular Caryophyllaceae and Plumbaginaceae show that large (>100 species) and widespread genera lack consistent taxonomic treatments. We have therefore developed a work-flow that aims at integrating the available knowledge: The basis forms a name source compiled from available electronic sources (WFO core data, WCVP, IPNI) with a preliminary assessment of the status as accepted name and synonym. As next steps protologue and type information is added as completely as possible, and published sources for taxon concepts matching the accepted species are assigned as secundum references with priority being given to phylogeny-based synopses or monographs. Further support to evaluate taxon concepts at species level comes from phylogenetic analyses which we are also directly implementing or facilitating within the TEN. The EDIT Platform is used to manage the taxonomic backbone (taxon concepts, names, references, associated data) what allows for an easy change of taxon circumscriptions once new knowledge become available and the generation of publication ready outputs of taxonomic treatments. The results show that the number of accepted species can differ considerably from previous estimates and hitherto available species lists. All together more than 50 botanists from 30 countries are so far involved in the Caryophyllales TEN.

S.110.6 Catalogue of Life and the need for a global consensus classification for plants

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Taxonomic name services are relevant in science to combine data from different sources. In fact, all information about a species is tied to its name. Usages extend beyond science to different domains, like legislation, health, nature management amongst others. A global consensus classification is also used for discovery and access to biodiversity data, such as in the Global Biodiversity Information Facility (https://gbif.org), and for measuring the progress of implementing targets from international policy initiatives like the Convention on Biological Diversity. In its 27 years of existence, Catalogue of Life (COL; https://catalogueoflife.org) has created a global index of described organisms (Bánki et al. 2023). But taxonomy is dynamic and ever changing. Continuous effort by taxonomic communities is essential to keep up with new scientific insights. COL is supported by a community of more than 500 experts, who are acknowledged in the COL Checklist citation. Together with the World Flora Online (https://worldfloraonline.org), COL is aspiring to get towards a global consensus classification for plants. Filling gaps in plant taxonomic data and ensuring the highest data quality are essential for meeting user needs. The ChecklistBank infrastructure (https://checklistbank.org), a publishing platform for taxonomic data, is a helpful tool in overcoming challenges. It offers open access to data sources, and tools for comparing species lists amongst others. We invite plant taxonomists to become part of the endeavour and help make the best possible taxonomic data available.

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S.111 NEW DIRECTIONS IN EARLY MODERN BOTANY COLLECTIONS AND ARCHIVES

S.111.1 Networks, maps and silences in the Sloane Herbarium, 1680-1753

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Understanding the history of early natural history collections is an essential prerequisite for almost any other research on them, though their histories can be challenging to reconstruct. Recent work in the history of science, history of knowledge, collection histories, and digital humanities offers productive methods for conceptualising and reinterpreting these fragile objects. The herbarium of Hans Sloane (1660-1753) comprises 265 volumes and about 125,000 specimens. As a collection it has been periodically studied especially since the 1880s, but it is difficult to access and to comprehend its scale, complexity, and limitations. My work combines archive-based research with a folio-by-folio review of all the volumes, and the creation and analysis of an enriched XML version of James Dandy's catalogue, *The Sloane Herbarium* (1958). Together, these approaches offer opportunities for researching plant knowledges and histories at scale, and reveal some of the gaps and silences in the way the collection has been mediated to us. Incorporating mapping and network analysis, my work explores the social and cultural relations of plant collecting as centred in Britain and Ireland, the geographical origin of specimens, and how that changed over time. In so doing, it examines the implications for understanding and constructing provenance for material from the seventeenth and eighteenth centuries and discusses the methodological insights arising from such approaches.

S.111.2 The lasting impact of Caspar Bauhin's (1560-1624) enormous herbarium: 40 years of assembly and 400 years of dissemination

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Caspar Bauhin (1560-1624) is one of the most influential botanists of all time. His publication Pinax Theatrum Botanicum (1623) represents approximately the first complete compendium of all ca. 6000 known plants, 130 years before Linnaeus' famous Species Plantarum (1753). By listing extensive synonymy, a somewhat "natural" classification, and a greatly improved naming system that included genus and species as explicit ranks, Bauhin shaped botany as a scientific discipline for centuries to come. Bauhin based his plant catalogue and descriptions on his herbarium, that by his own account contained ca. 4000 species. Of these, some 2700 survive. In this talk I sumarize the process of its assembly over 40 years, including through exchange with at least 70 contemporaries evidenced from Bauhin's Phytopinax (1596), Pinax (1623), letters, and herbarium labels. The following 400 years, the herbarium influenced directly and indirectly other key figures in the history of botany, including Albrecht von Haller, Carolus Linnaeus, and Augustin Pyramus de Candolle. I emphasize how the "biography" of the herbarium tracks changing concepts in herbarium based research from the late renaissance to current research, the latter exemplified by ongoing projects regarding comparative genomics of tomato domestication and progress in digitalization. I conclude that these developments necessitate closer collaboration between historians of science and natural-scientists.

S.111.3 Tracing the introduction history of Tulipa sylvestris in northern Europe in the 16th century

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Tulipa sylvestris is a small yellow tulip that was introduced in northern Europe during the 16th century by botanists. Unlike commercial ornamental tulips that came from Ottoman gardens, *T. sylvestris* came from the Mediterranean region. It subsequently escaped from gardens to become widely naturalized in Europe, where it is commonly known as the "wild tulip". Its introduction path is poorly understood and complex due to naturalization, polyploidization and a complex taxonomy. We combined historical research and population genomics to reconstruct the introduction history of *T. sylvestris* in Europe. Our historical search was restricted to original 16th-century sources, including herbarium specimens, botanical texts, illustrations and archives. We also performed genomic repeat profiling, and constructed median networks using rDNA and complete chloroplast genomes. DNA was sampled from native and naturalized *T. sylvestris* populations across Europe and historic herbarium material, including a 16th-century specimen from the Rauwolf herbarium collected in 1563. Our results show that the introduction of *T. syvlestris* was not a one-time event but happened through several routes in the period between ca. 1550 and 1580. Famous 16th-century botanists were involved, including Conrad Gessner, Ulisse Aldrovandi, Matthias de Lobel and Carolus Clusius. Seeds were introduced first from the garden of Padova in northern Italy to Zurich, Switzerland, in ca. 1554–1559. This material was most likely not further spread in Europe. Historical and DNA data point out that naturalized *T. sylvestris* in northern Europe originates from Bologna in northern Italy. Another introduction route via the west Mediterranean is historically connected with Montpellier in southern France. Our findings show that (ancient) DNA is of great value to fill gaps in historical sources. Moreover, we argue that a genetic approach on past crop movements can only reach its full potential when embedded in proper historical context.

S.111.4 Combining scientific archives, historical methods, and indigenous knowledge to reconstruct Oxford's du Bois Herbarium (1680-1740)

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The du Bois Herbarium, a collection of nearly 14,000 botanical specimens pristinely preserved within the Oxford University Herbaria, is a unique relic of early modern science. Compiled by English East India Company treasurer Charles du Bois between 1680 and 1740, the Herbarium is closely tied to leading figures of eighteenth-century botany, melding early British scientific and colonial histories into a single source. Despite the compendium's exciting potential, the du Bois Herbarium remains one of the least explored collections of its kind, largely neglected after it was dismantled from its original binding in the 19th century. While long deemed archaic, this project argues that the du Bois Herbarium should instead be considered a vibrant scientific archive, brimming with details about the inner workings of natural history and its ties with Britain's early colonial endeavours in India. Charles du Bois and his herbarium bring a fresh perspective to the histories of eighteenth-century botany, which have long been dominated by a historiographical hyper-fixation on the Atlantic world and more famous figures such as Hans Sloane and Joseph Banks. Furthermore, du Bois's unique interest in collecting and documenting South Asian plant names, allows for an unprecedented opportunity to trace the interest in, and treatment of, indigenous Indian knowledge within pre-Linnean taxonomical systems. Highlighting the accompanying manuscripts and materiality of the herbarium, this examination also shows how these now-discarded naming systems are central to reconstructing the herbarium's original form. Charles du Bois stood at a key crossroads between early modern structures of commerce, science, and empire, presenting an ideal entry to discussions of 'decolonising' natural history. The first to bring such a critical lens to the University of Oxford's historical collections, this project shows how centuries-old specimens provide deeper insight into early modern botany, and the larger scientific and colonial communities that underpinned its development.

S.111.5 The herbarium collections of the Moravian Church – network analysis with digital humanities methods

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The *Herbarium Dresdense* (DR), Germany, houses about 500.000 specimens of worldwide origin. One of the oldest and most valuable collections is the *Herbarium Barbiense* of the Moravian Church (in German: Herrnhuter Brüdergemeine) from the mid to the late 18th century. On their mission to spread Christianity, the Moravians settled on many continents and took the advantage of exploring culture and nature of their new home countries. Being excellent observers and documentarists, they left a barely explored corpus of objects and texts of tremendous importance for natural sciences and humanities. A current project, which uses Digital Humanities methods, aims to identify the historical contexts of their herbarium collections, i.e., through personal correspondences, itineraries, botanical manuscripts, and publications to reconstruct the names of the individual collectors, to clarify their manifold contributions to botany and finally to create an overview of their influence on the development of modern natural sciences. The scientific heritage of the Moravian Church members demonstrates that they were strongly integrated into the scientific community of the 18th and 19th century. Letters in the collections of the Linnean Society show, that they were in close contact with leading scientists, e.g. Carl v. Linné, discussing issues on plant taxonomy, exchanging specimens and presenting own fieldworks and floras. Using methods of the Text Encoding Initiative (TEI), Normed Data and Linked (Open) Data, we want to contextualise herbarium specimens, which often lack detailed collection information, with associated archive material (e.g. flora manuscripts, plant lists, field books) in order to enrich the specimens with botanical metadata and thus make them usable for research. First results are presented in our contribution.

S.112 MECHANICAL FORCES IN PLANT GROWTH AND DEVELOPMENT

S.112.1 How cell wall structure and mechanics affect plant organ function

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Plant tissue is a cellular solid material in which walls of adjacent plant cells form a complex network that is the main mechanical component of the tissue. Therefore, mechanical properties of cell walls are crucial for plant growth and for supportive or movement functions of plant organs. Protoplasts of growing cells are encapsulated in primary cell walls that are under tensile stress generated by turgor. These prestressed walls provide structural support to growing organs but at the same time are a direct growth regulating factor. The regulation acts via mechanical properties of primary walls that depend on their chemical composition and structural anisotropy. Secondary cell walls, in turn, are formed after growth cessation and ensure performance of specific organ functions even long after death of the encapsulated protoplasts. We investigate the complex relationships between cell walls and organ function and growth using trees as a model system. Trees are unique in providing opportunity to investigate both primary and specialized woody secondary walls in the same plant species. In our work we combine biochemical analyses with mechanical tests and deformation measurements. We address the question on how composition of primary cell walls affects elongation of hypocotyls and their stiffness, focusing on the hemicelluloses, which are the least extensively studied component of primary cell walls. We also introduce a scale of conifer (Abies sp.) cones as a new model to study the role of cell wall in movements of organs built of dead cells. Similar, albeit slower, movements are observed in reaction wood, which has major importance for the forestry sector.

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S.112.2 Transcriptomic profiling reveals early woody root responses to mechanical stress

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Plants are exposed to a variety of mechanical stresses including wind, herbivory, gravity, and belowground physical obstacles. These factors can have major economic impacts on crops, forests, and urban trees. Revealing the plant molecular responses to mechanical stress is crucial for understanding the mechanisms underlying their adaptive strategies. A lack of knowledge persists regarding the early root responses to mechanical impedance, especially in woody roots. We opted for RNA sequencing (RNA-seq) to investigate the early genetic response in the woody roots of *Populus nigra*. Mechanical stress over a temporal scale ranging from 1 to 6 hours was applied, adopting plant-adapted root bending approaches, after which root tissues were manually sectioned into concave (compressed zone) and convex (stretched zone) sides to discern spatially distinct gene expression patterns. The study constitutes the first characterization and comprehensive view of the early transcriptomic landscape in woody roots, emphasizing the role of spatial considerations in the plant responses to mechanical stress and the way in which the asymmetrical sensing is integrated into global root responses. The results provide new insights into the early molecular events associated with mechanical stress in woody roots reflecting the dynamic of time-dependent and side-specific transcriptomic shift. Key genes and pathways involved in stress perception, signal transduction, and the activation of defense mechanisms were identified. These genes and pathways could be perspective targets for further functional characterizations and enhancing plant resilience to mechanical perturbations and thus growth in forestry, urban and farming context.

S.112.3 How mechanical forces interact with heterochrony as a major force of floral evolution

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Heterochrony functions as a fundamental process in the evolution of organisms, as the event causing changes in the timing of initiation and in the duration of a developmental process. In flowers this process is linked to the early development of floral organs and their subsequent expansion. As organs develop in the confined space of the flower bud, they undergo spatial constraints which are intimately linked to heterochronic shifts. Mechanical pressure may be effective at different stages of development, at the onset of flower formation, when organs arise, and at flower maturation. Heterochronic shifts lead to a delay or acceleration of the development of neighbouring primordia, ultimately affecting the morphospace of the flower. The results of these shifts are altered organ positions and morphologies (heterotopy and homeosis), fusions, or organ reductions and loss, leading to major changes in floral evolution and diversification of flowers. A number of examples illustrate how delay and accelaration in the development are intimately linked to the effect of mechanical forces on developing organs. These affect the transition from inflorescence to flower through bract and bracteoles, the constraint caused by the perianth on stamens and carpels, and the centrifugal influence of stamens on petals, and carpels on stamens, respectively.

S.112.4 Bending in style: a bead-spring mechanical model for stylar deflection and development in flowers of Cyanella alba

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The widespread occurrence of left/right symmetry breaking in the biological realm underscores a pervasive yet not fully comprehended phenomenon. In particular, the molecular basis of handedness in helical plant growth and the mechanical forces driving asymmetric development in reproductive organs are central, unresolved questions in plant developmental biology. The mirror-image flowers of *Cyanella alba* serve as a striking example of the asymmetric development of plant reproductive organs. In these flowers, the style is deflected either to the left or right side of the floral axis, with a pollinating anther deflected in the opposite direction. Our microscopy imaging of *Cyanella alba* carpels revealed that stylar bending results from differential expansion in ovary wall regions. However, how mechanical forces influence such differential expansion remains unclear. Here, we combine data-driven modelling based on image recognition and biophysical modelling using a bead-spring formalism to investigate the mechanical forces guiding ovary wall growth and stylar bending. By optimising biophysical model parameters to best represent ovary morphological features identified through image recognition, we not only quantify the mechanical forces responsible for ovary expansion and style bending, but we also identify the stiffness of the style base as the primary factor driving stylar bending following differential expansion of the ovary walls. Our findings offer insights into the balance of forces necessary to break symmetry in plant organ development, shedding light on the mechanisms at play in symmetry breaking within biological systems.

S.112.5 Effects of mechanical forces on the flower development in Arabidopsis thaliana using a novel experimental system

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The mechanical forces have a key role in plant development, including the floral development in angiosperms. Our observation revealed that the phyllotactic variation in the staminate flower of *Ceratophyllum demersum* should be caused by the mechanical forces on the adaxial side of floral primordia, which may be a common mechanism in angiosperms. Based on this result, we have developed a novel experimental system for the analysis of the effects of mechanical forces on the floral meristem of *Arabidopsis thaliana*, aiming to induce morphological changes in flowers. A micromanipulator with a microdevice which is shaped to fit the contour of the abaxial side of young floral primordium is used to cause the contact pressure on floral primordia in this experimental system. We conducted contact experiments using this system, and successfully induced morphological changes in floral primordia during development. In several primordia, the tip of the abaxial sepal was divided into two or three lobes through their development. Another pressured floral primordium developed an additional sepal on the abaxial side (two abaxial sepals). On the other hand, we also found the fusion of sepals in some floral primordia. These results suggest that the mechanical forces have multiple effects on the floral development.

S.112.6 Glutamate in mechanosensing and mechanotransduction: a dynamic spatio-temporal integrator between mechanosensing and microtubule behaviour

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When responding to various stimuli plants couple cellular responses to intercellular ones, leading local stimuli to affect characteristics of tissues and organs. Upon wound and touch, for example, plants respond with increasing apoplastic glutamate levels and increasing cytoplasmic calcium levels travelling across tissues and organs in a wave-like manner. Intriguingly, it is unknown how glutamate is released upon mechanical stimulation and what the implications of this release are in the context of mechanosensing and mechanotransduction. Microtubules are key in defining tissue mechanical properties, and it is well documented that they can dynamically respond to changes in stress patterns. However, how microtubules reorient in response to mechanical stress it is not known. We hypothesise that glutamate could affect microtubule dynamics and properties via posttranslational modification (glutamylation) of tubulin, therefore representing the missing link between mechanosensing and microtubule behaviour. To test this, we investigate levels of tubulin glutamylation in plants, mechanisms of glutamate release upon touch and effects of glutamate on microtubule dynamics.

S.113 THE PAST, PRESENT, AND FUTURE OF PALMS (ARECACEAE)

S.113.1 The tumultuous past, glorious present, and troubled future of palms

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Palms (Arecaceae) have been studied for decades all around the world, yielding an ever-growing wealth of data on their geographical distribution, traits, fossils, genomes, and uses by people. The combined study of these datasets can help us understand how palms evolved, how they can be used and protected today, and how they may cope with future challenges. We illustrate this here with two examples from our past and current research. First, we show how combining genomic and paleontological data improves our understanding of the relationships, ages and early historical biogeography of palm genera. Up to 1255 nuclear genes were sequenced for each palm genus and the data were used to estimate their phylogeny. Affinities and ages of hundreds of palm fossils were then reviewed and some of the fossils were selected to inform the estimation of early divergence times and historical biogeography in the family. Second, we use machine learning based on occurrence data points to estimate the extinction risk of hundreds of species, and we combine these predictions with trait and ethnobotanical datasets to assess the impact that predicted extinctions could have on palm phylogenetic and functional diversity, and on palm uses around the world. We conclude by discussing how integrating ecological, morphological and genomic data could help to predict and improve palm resilience to global change, highlighting the urgent need and opportunity for collaborative international studies on this topic.

S.113.2 Palms in space and time: Progress towards a genomic species-level phylogeny

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Evolutionary and ecological studies rely on phylogenies to shed light on the patterns and processes that have shaped biodiversity through space and time. However, our understanding is often fragmented due to incomplete phylogenetic sampling. Here, we are moving towards having a complete phylogenetic framework for the palm family (Arecaceae) based on target enrichment sequencing data. Bioinformatic analyses are based on a "divide and conquer" approach where each palm subfamily is analyzed separately in order to minimize the effects of paralogous genes. Then, subfamilies are combined to understand their relationships and to reconstruct the backbone. Our sequencing database includes all five subfamilies, all 183 genera and 2,080 species (83% of accepted species). The extensive taxonomic sampling could only be achieved due to a massive joint effort of >40 researchers of the Palm Phylogeny Working Group (PPWG). Most of the deep relationships that we recovered with these data are consistent with our understanding of palm phylogeny from earlier studies. However, the majority of species-level relationships have never been tested before and are explored for the first time in this new genomic tree. The phylogeny tree was dated using the most recent revision of fossils available for the family and used as a framework to understand its historical biogeographic patterns through space and time, diversification and biome evolution.

S.113.3 Unravelling evolution in the date palm genus: phylogenomics and species delimitation of genus Phoenix.

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Palms are distributed along sub-tropical and tropical regions of the world and depended upon by millions of people. As such, ongoing aridification raises concerns for palm conservation and their supported livelihoods, and makes it critical that we gain a deeper understanding of drought adaptation in palms. Comparative studies including model crop species and their more variable wild relatives show great potential to progress the understanding of complex traits such as drought tolerance. A good model to perform such studies is the *Phoenix* genus, which includes the culturally and economically important date palm crop (*Phoenix dactylifera*), and thirteen wild species occurring in habitats that vary in aridity. However, the phylogenetic relationships and species barriers of *Phoenix* species have not been elucidated so far. This slows down understanding of *Phoenix* evolutionary history and prevents robust estimations of how wild species may suffer from future aridification. Accurate delimitation of species and the inferring of the species relationships in *Phoenix* has been impeded by morphological and genetic similarities among species, in some cases resulting from past or ongoing hybridisation. For instance, hybridisation among the Cretan date palm (*Phoenix theophrasti*) and west African date palm has been documented and is considered the reason for the increased genetic diversity among west African date palm populations. To build accurate phylogenies while solving the delimitation of species within the genus, multidisciplinary research looking at genetic, ecological and morphological information must be undertaken on well identified accessions, and genomic approaches must account for gene flow between species. Here, we infer well-supported phylogenetic relationships in genus *Phoenix* and clarify the taxonomic status of the Cape Verde date palm by using authoritatively-identified herbarium specimens and gene-flow aware approaches. This will improve our knowledge on the *Phoenix* system which will aid conservation efforts and in crop development.

S.113.4 Phylogeny and biogeography of Hispaniolan palms

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The Caribbean is a biodiversity hotspot and harbours 2% of the Earth's plant diversity. The region is comprised of more than 700 islands, one of the largest of which is Hispaniola. Hispaniola is home to two nations, Haiti and the Dominican Republic, and harbours approximately 38 palm species distributed among 16 genera. The impressive Caribbean palm diversity is poorly known, particularly on Hispaniola. Previous work on Caribbean palms will be reviewed to identify knowledge gaps and contextualize our work on the colonization history of Hispaniola. Using a dated phylogeny and historical biogeographic analysis, we discuss island diversification. From this, palm species delimitation and conservation action are discussed, with a focus on *Coccothrinax*. Recent monographic work on *Coccothrinax* is summarized in a preliminary phylogenetic framework. A multispecies coalescent inference with multiple samples for nearly all populations present on Hispaniola supports novelties in the genus, species limits, and conservation needs on the island.

S.113.5 Macroevolution and macroecology patterns in a changing world: insights from an iconic tropical clade

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Palms (Arecaceae) likely originated in TRF-like ecosystems of Laurasia in the mid-Cretaceous. While many palm lineages fail to colonize seasonally dry habitats, the evolution of drought-avoidance traits enables certain clades, like the tribe Cocoseae, to thrive. The acaulescence growth form, linked to outstanding cocosoid palm diversification in Latin America, involves an underground stem, enhancing survival during seasonal dry spells and fires. Acaulescence serves as a preadaptation allowing rainforest cocosoid lineages to colonize new fire-prone and drier zones. Indeed, geographic distribution patterns of palms seem closely tied to their traits, particularly in both seasonally dry habitats and islands. Insular habitats play a crucial role in shaping palm trait diversity, with island palms exhibiting higher evolutionary rates for height, fruit size, and predominantly being dioecious. Trait flexibility in sexual system evolution and the *in situ* radiation of dioecious lineages contribute to the outstanding distribution of palms on islands. As sessile organisms, plants respond to environmental change through reproductive traits. Spatial segregation and physiological specialization of sexes in dioicous plants create mismatches in individual responses to environmental change. Conversely, self-fertilization, linked to the dominance of hermaphrodites in drought-stressed habitats, circumvents the need for sexual partners. Different sexual systems of palms (dioecy, hermaphroditism, monoecy, and polygamy) respond similarly to climate change, with reductions in potential distribution expected for all systems. Climate change threats to global palm richness are ubiquitous but uneven geographically. Most species are expected to lose suitable areas, particularly in Latin America, where palm richness is concentrated. Sharp richness loss is projected for Amazonia and Cerrado, the sources of diversification of drought-avoidance traits like acaulescence. Our studies underscore the intricate interplay between evolutionary history, functional traits, and environmental change in shaping the fate of palm diversity.

S.113.6 Using Bayesian and deep learning models to infer the origin and evolutionary trajectory of palms

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Throughout the long evolutionary history of life, species of all kingdoms have undergone staggering diversification and faced countless environmental changes and extinction events. Since the great majority of species that lived on Earth have since gone extinct, it is difficult to infer how the evolution of biodiversity unfolded over billions of years. The fossil record provides the most direct evidence of past biodiversity. Yet, using fossils to understand the time of origination of major lineages and how their diversity changed over time is challenged by the inevitable incompleteness of the paleontological record, plagued by taxonomic, temporal, and spatial biases. Here we present a suite of supervised and unsupervised models based on Bayesian inference and deep learning to infer clade age and species richness dynamics in deep time. We compile a comprehensive global database of palm micro- and macro- fossils to evaluate the age of the clade independently of assumptions made under phylogenetic molecular clock models. We also infer the diversity dynamics of the clade after accounting for the biases in the fossil record. Our findings provide new insight into palm evolution across more that 100 million years and the basis for data-driven priors to improve the use of fossil information in phylogenetic inference.

S.114 FLORAL POLYMORPHISMS AS A RESEARCH TARGET FOR NATURAL SELECTION

S.114.1 Transitions between combined and separate sexes via natural selection on polymorphisms in sex allocation

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Transitions from hermaphroditism to dioecy have occurred numerous times in the diversification of angiosperms. While the role of inbreeding avoidance in driving these transitions has received substantial attention in both theoretical and empirical studies, we know much less about how transitions might evolve selection for sexual specialisation, despite the fact that sexually dimorphic specialization often accompanies the evolution of dioecy. In this presentation, I present new theoretical results that show how dioecy may evolve from hermaphroditism when there are advantages to sexual specialisation such as those associated with pollen or seed dispersal. The theory also predicts an association between the shape of 'gain curves', which relate fitness to sex allocation, and the evolution of XY versus ZW sex determination. I illustrate the process modelled with empirical results from a long-term experimental evolution study in which we observed, first, the breakdown of dioecy via loss of a Y chromosome and, subsequently, the early stages of a transition back towards separate sexes via selection on variation at sex-allocation loci unrelated to the original sex chromosomes. The study thus draws a theoretical link between sex-allocation and sex-chromosome evolution and draws on the remarkably rapid evolution of sex allocation under experimental conditions that shows how such a link may be manifest.

S.114.2 Genomic studies of the evolution and loss of distyly shed new light on convergent evolution

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Distyly is a floral polymorphism governed by a supergene, that has evolved repeatedly in independent flowering plant lineages, making it a prime example of convergent evolution. Distyly promotes outcrossing and efficient pollen transfer by pollinators via the presence of two floral morphs that differ reciprocally in the positions of their anthers and stigmas, coupled with a heteromorphic self-incompatibility system that reduces self- and intra-morph fertilization. While distyly has evolved multiple times, it has been lost far more frequently, often in association with convergent evolution of floral selfing syndromes. Studying the genetic basis of convergent evolution and loss of distyly therefore offers an excellent opportunity to investigate to what extent convergent phenotypic evolution is associated with repeated evolutionary changes at the molecular level, at the level of genetic architectures, regulation of molecular pathways, or in terms of selection at particular genes. Studying repeated losses of distyly further offers an opportunity to test theoretical predictions on the genetic causes of supergene breakdown, and the population genetic consequences of selfing. Here, I present our work on these topics in *Linum*, a plant system that is exceptionally well suited for this purpose. Harnessing high-quality genome assemblies, we have for the first time identified and characterized the distyly supergene in *Linum* at the molecular level. We have also tested theory on genetic causes of loss of distyly and documented pervasive population genomic consequences of this major evolutionary transition. Taken together, genomic studies of distyly have revealed striking similarities in hemizygous genetic architectures and molecular evolution of independently evolved distyly supergenes, contributed new insights into the genetic basis of floral morphs, and provide a foundation for further characterization of the genetic underpinnings and genomic consequences of convergent evolution and loss of distyly.

S.114.3 Is flower colour variation adaptive?

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The evolution of flower colour is argued to be driven by pollinators. While most flowering species are colour uniform, a minority exhibit within-population colour variation. This variation is hypothesized to result from balancing selection, assuming flower colour is an adaptive trait. Balancing selection is driven by multiple selection agents, driving balanced and equalized fitness of all colours. For example, differential pollinator behavior balances fitness of two colour morphs in *Linum pubescens*. Species with spatial pattern of variation suggest a more complex picture. For example, populations of *Anemone coronaria* in the arid climate region are red-monomorphic, while in the Mediterranean climate colour polymorphism is maintained through admixture due to partial partitioning of pollinators. Pollinators in polymorphic population of *Fritillaria persica* showed little discrimination among colour morphs due to lack of detection among continuous shades of flower colour. The wide range of continuous flower colour variation in *Iris petrana* is driven by differential expression levels of a few genes in the anthocyanin biosynthesis pathway, with no selection on flower colour likely because lack of discrimination by pollinators. These pieces of evidence suggest that flower colour variation is largely associated with either of three selection regimes: monomorphic populations are under directional selection, populations with discrete colour polymorphism are under balancing selection, and continuous colour variation is the hallmark of neutral or no selection on flower colour. Studying the rare cases of continuous flower colour variation can shed light on the evolution of flower colours and its role in communicating with pollinators.

S.114.4 Exploring the origin of a shared flower color polymorphism

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Polymorphisms are common in plant and animal species. However, the origin, maintenance and evolutionary forces acting on cases where the polymorphisms are shared between closely related species remains challenging. How is a shared polymorphism maintained across closely related species? Convergent evolution, introgression, and the maintenance of an ancestral polymorphism are the three main possible evolutionary pathways. Although shared neutral genomic variation is commonplace, very few examples of shared functional traits exist. Herein, we investigate a fascinating case that involves a blue-orange flower color polymorphism maintained across two closely related species, *Lysimachia monelli* and *L. arvensis*, using a multiscale approach. We performed UV-vis reflectance spectra, flavonoid biochemistry, and petal transcriptome comparisons followed by climate niche analysis, to explore different hypothetical evolutionary scenario of the polymorphism origin. The similarities in reflectance spectra, biochemistry, and transcriptomes suggest that a single shift from blue-to-orange shared by both species is possible. Transcriptomic analyses revealed two orange-specific genes are directly involved in both blue-orange color polymorphisms: *DFR-2* specificity redirects flux from malvidin to pelargonidin production while *BZ1-2* stabilizes it with glucose, producing the orange pelargonidin 3-glucoside. Interestingly, the different geographic distribution pattern between both species suggests that their environmental adaptations may transcend flower color variation and that both species experienced a different evolutionary history since their divergence, adding complexity to the maintenance of the polymorphisms to the present days. This persistent flower color polymorphism may represent an ancestrally polymorphic trait that has transcended speciation with some unique ecological effects.

S.114.5 An unusual supergene underlies the floral polymorphism in heterostylous Amsinckia (Boraginaceae)

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Heterostyly is a polymorphism where two or more discrete floral morphs are produced by different individuals in a population. The morphs have reciprocally different placements of their male and female reproductive organs, which promotes inter-morph pollen transfer, and thus enhances outcrossing rates. Although this morphological syndrome likely evolved hundreds of times independently in plants, it is unclear to what extent repeated evolution occurred at the developmental and genomic level. Here, we focus on the Boraginaceae, a family in which gains and losses of heterostyly were frequent. Using the example of *Amsinckia* (fiddlenecks), we build a chromosome-scale genome assembly and integrate genetic maps, cytogenetics, population genomics and functional molecular approaches. We characterise style development and functionally validate a candidate gene, which highlights remarkable parallel evolution of developmental mechanisms with other origins of heterostyly. As predicted by theory, we find that the efficacy of natural selection is enhanced in heterostylous populations as compared to predominantly selfing (homostylous) populations. However, the heterostyly supergene of *Amsinckia* differs fundamentally from the relatively small and hemizygous supergenes in other heterostylous plants, because both dominant and recessive alleles are present and they involve a large inversion which captured thousands of genes. The large size is unexpected and raises the question how this supergene could be viable over long times. The lack of meiotic recombination characteristic of supergenes should lead to the accumulation of deleterious mutations in proportion to their size. We present how *Amsinckia* exploits several complementary processes to mitigate and avoid the risk of maladaptive consequences of the adaptive floral polymorphism of heterostyly.

S.114.6 Pollinators and pollen fates in plants with stylar polymorphisms

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Plant species that are polymorphic for style length or orientation have evolved repeatedly in the angiosperms. Stylar polymorphisms are considered to promote efficient cross-pollination, but have rarely been considered in terms of floral adaptation to particular pollinators. Here I explore how polymorphisms involving length and orientation of styles (and also stamens) interact with pollinators to influence the fates of pollen. I compare the effectiveness of different flower visitors as pollinators of long-tubed distylous plants and consider the conditions under which stylar polymorphisms could be maintained through disassortative pollination. I also consider whether selection for traits that enable transfer of pollen on the wings of insects can explain the evolution of enantiostyly in some plant lineages. The evidence reviewed shows how stylar polymorphisms generally promote efficient pollen transfer via morphological fit with specific body parts of various animal pollinators.

S.115 POLYPLOIDY AND HOMOPLOID HYBRIDIZATION AS EVOLUTIONARY DRIVERS IN MEDITERRANEAN PLANTS. SESSION 1

S.115.1 Evolution of polyploid species complexes in the Mediterranean: phylogenomic studies in Brassicaceae genera

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Recently diversified and polyploid-rich plant lineages pose a challenge for both taxonomic and evolutionary studies. Recent speciation, recurrent polyploid formation, involving both auto- and allopolyploidy, and permeable reproductive barriers between species with historical and recent gene flow result in intricate species complexes. These are characterized by high diversity, but phylogenetic inferences often yield shallow, largely unresolved or conflicting phylogenetic structuring. Genome-scale data obtained by high-throughput DNA sequencing, as well as recent developments in phylogenetic approaches that account for reticulate and polyploidization events, provide excellent opportunities to improve phylogenetic inferences and gain insights into such evolutionarily challenging lineages. We illustrate these advances in our studies of polyploid species complexes in Brassicaceae genera by applying ddRADseq and target enrichment with genome skimming (Hyb-Seq). The studied species complexes show the highest diversity and concentration of polyploid endemics in southern Europe, which probably evolved through repeated cycles of glaciation-induced range shifts, isolation of populations in multiple refugia, followed by range expansions and secondary contacts. In *Alyssum*, we found evidence of introgression events between diploids both within and between clades and revealed a unique case of parallel polyploid speciation with eight sibling polyploids containing subgenomes from the same two diploid progenitors. In *Cardamine* and *Odontarrhena*, when specifically targeting the Eastern Mediterranean region, we detected both historical and recent interspecific gene flow and elucidated the origin of several auto- and allopolyploids. We identified diversity hotspots that may result from long-term species persistence and diversity accumulation in situ, but also arise as melting pots favoring species contacts and polyploid evolution. Overall, our studies highlight the evolutionary role of hybridization and polyploidy in stimulating plant speciation in southern Europe and demonstrate the power of thorough phylogenomic approaches when studying reticulate evolution in polyploid species complexes.

S.115.2 Species delimitation and evolutionary relationships in the Leucanthemum polyploid complex (Compositae, Anthemideae)

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Gene flow at the diploid and polyploid level, multiple formation of polyploid species, often under reciprocal parentage, and the young age of polyploid species radiations account for the taxonomy of polyploid complexes being the ultimate challenge for a DNA-based, phylogenetic species-delimitation approach. Additionally, reconstructions of the evolutionary history of polyploid complexes are still hampered by the lack of explicit methods for the reconstruction of reticulate (species) phylogenies. The present contribution summarizes the state-of-the-art of our project aiming at the establishment of a methodological pipeline for species delimitation and phylogenetic reconstructions in the polyploid complex of the genus *Leucanthemum* Mill. (ox-eye daisies; Compositae-Anthemideae), which comprises around 43 species with ploidy levels between 2*x* and 22*x*. At the diploid level, species discovery and validation methods based on genetic, ecological, geographical, and morphometric datasets were applied to test the currently accepted diploid morphospecies, i.e., hitherto morphologically delimited taxa. Novel approaches were taken in the analyses of RADseq data (consensus clustering), morphometrics of reconstructed leaf silhouettes from digitized herbarium specimens, and quantification of species-distribution overlaps. We show that 17 of the 20 *Leucanthemum* morphospecies are supported by genetic evidence. At the tetraploid level, the same methodological approach revealed the evolutionary relationships among additional eight morphospecies and resulted in an adequate taxonomic treatment of these taxa. Further results are presented for species-delimitation and phylogenetic studies in the *L. atratum*-group, which comprises diploid and hexaploid taxa, and in the decaploid *L. pachyphyllum*-group. While in the former double-digest Genotyping-by-Sequencing (ddGBS) was used for genetic fingerprinting, the latter study was based on a newly established Nanopore-based AFLPseq procedure and bioinformatic analysis pipeline.

S.115.3 Invasive Bermuda buttercup in the Mediterranean basin: What have I become?

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Biological invasions provide ideal scenarios for investigating evolutionary changes within contemporary timescales. Following long-distance dispersal, exotic species face significant mate limitations, which can potentially lead to shifts toward uniparental reproduction. However, the interplay of multiple introductions and natural selection in novel environments can induce transformative changes in well-established populations. Bermuda buttercup (*Oxalis pes-caprae* L.) is a polyploid tristylous plant native to South Africa and invasive in Mediterranean regions worldwide. While its native populations bear diploids or tetraploids with three flower morphs, facilitating sexual reproduction, invaded ranges display a reduced diversity, predominantly composed of pentaploid short-styled morph reproducing asexually. Nevertheless, new ploidies and floral morphs have been discovered in western Mediterranean basin, introducing new reproductive and, consequently, evolutionary contexts. This study aims to quantify shifts in ploidy and floral morph composition of Bermuda buttercup across the entire Mediterranean basin, exploring their implications for invasive species reproduction and evolution of reproductive systems. 'Finding Bermuda buttercup' team, comprising over 40 researchers and 12 countries, collected data on floral morph composition, ploidy and fitness variables in invasive populations across the Mediterranean basin. Ploidy was determined for the majority of populations using flow cytometry on fresh material, while selected populations underwent floral morphometric analyses and quantification of pollen loads. This extensive assessment unveils novel insights into the distribution of ploidy and floral morphs and two contrasting scenarios emerge after successful establishment in the Mediterranean basin: the transition to uniparental reproduction through clonality due to mate limitation, and the re-establishment of sexuality driven by multiple introductions of compatible mates and/or the breakdown of tristylous polymorphism in pentaploid short-styled plants. These findings underscore the dynamic nature of invasion processes, highlighting that ecological and genetic constraints inherent to the invasion process can give rise to distinct reproductive strategies, ultimately shaping the likelihood of invasion success.

S.115.4 Beyond the discovery of plant natural hybridization: lessons from Iberian groups on an often deceptive process of inquiry

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The complexity of natural hybridization and its corollary—the difficulty of unraveling hybridization scenarios and understanding their impact on the evolution of plant groups—are mainly due to two causes. Hybridization is an open process that can lead to different outcomes, from no effect in sterile of unfit hybrid offspring to hybrid speciation, or adaptive introgression. The dynamism of hybridized genomes is higher than that of non-hybridized genomes on short time scales after hybridization, and this may also be true on longer time scales (ancient hybridization). This dynamism, which obscures the initial traces of hybridization, is driven by the genetic adjustments required following the merger of two differentiated genomes, a process that involves coping with genic incompatibilities and purging the minority genome. In the medium and long term, however, it can be also fueled by standard evolutionary mechanisms such as adaptation in interaction with the environment. There is one consequence of this whole situation that has been insufficiently discussed: how complexity can deceive the researcher along the process of inquiry, and whether some steps can be anticipated whenever new cases of hybridization are unveiled. This presentation discusses how meandering investigations that aim to shed light on hybridization scenarios might actually be, using three Iberian angiosperm groups that represent contrasting cases. In *Armeria*, the benefits of bidirectional introgression for two species in a coastal southern Spanish hybrid zone were inferred after several phylogeographic studies. The Iberian endemic *Phalacrocarpum* illustrates the challenge of reconstructing hybridization occurring at different time scales. *Arenaria* sect. *Plinthine* epitomizes complexity resulting from polyploidy combined with hybridization. The incorporation of genomic data and new analytical techniques has led to a gradual improvement in this subject. However, the lack of universal models is a major obstacle to our advance in the elucidation of hybridization scenarios.

S.115.5 Allopolyploidization, inter-ploidy introgression and the evolution of sexual systems in the plant genus Mercurialis

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The annual lineage of the plant genus *Mercurialis* (Euphorbiaceae) is found in Europe and Northern Africa and shows a remarkable diversity in sexual systems and ploidy levels. While *M. annua* is diploid and dioecious (separate males and females) across large parts of Europe, hexaploid *M. annua*, which are found on the Iberian peninsula and in Northern Africa, are monoecious (male and female inflorescences on the same individual) or androdioecious (male and monoecious individuals in the same population). Here we present results concerning the evolutionary history of these polyploid *Mercurialis* lineages and discuss how it may be related to the variation in sexual systems. We show that polyploid *Mercurialis* lineages are the result of a complex series of allopolyploidization events. In addition, the presence of common male-specific DNA sequences suggests that maleness is based on an ancestrally shared XY system of sex determination in both dioecious and androdioecious lineages. Surprisingly, phylogenetic trees based on Y-linked sequences suggest that the Y chromosome in androdioecious hexaploid lineages has been introgressed from distantly related perennial lineages instead of more closely related annual lineages, which contributed to its allopolyploid subgenomes. Using additional population genomic datsets we test for further signatures of introgression genome-wide and propose the hypothesis that the strong outcrossing advantage of the male phenotype could have favored such inter-ploidy introgression specifically for the Y chromosome.

S.115.6 Can changes in ploidy drive the evolution to allogamy in a selfing species complex?

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The evolution of mating systems in plants is central to understanding the rise of their diversity on Earth. The transition towards self-fertilization is a well-known example of convergent evolution and, in fact, the opposite direction is expected to be forbidden according to evolutionary theories. The mating system is often shaped by the action of biotic drivers such as pollinators in outcrossing plants. Here, we suggest that the ploidy could also promote changes in the reproductive strategies through to its effect on traits related to pollination. To this end, we used several populations from the Erysimum incanum species complex which has been described as predominantly selfing. We performed over 7,000 controlled crosses to assess the inbreeding depression. In addition, we measured mating traits such as flower size, herkogamy, anther exertion and the relative investment between male and female reproductive investment (i.e., pollen-ovule ratio). We described three ploidy levels -the hexaploid level was previously unknown- and estimated the genomic diversity of each ploidy. We found significant differences in the self-pollination success among ploidies and, even, among populations within the same ploidy. A certain degree of inbreeding depression was present in higher ploidies, which were also accompanied by larger flowers with higher anther exposure, a more accentuated herkogamy and a higher allocation in pollen production related to the ovule amount. These findings suggest that ploidy could be promoting alternative reproductive strategies to selfing, driving mating system diversification within a selfing species, which has not been described in the wild before.

S.116 THE FUNCTIONAL ROLE OF NON-CHARISMATIC BIODIVERSITY IN THE FACE OF A CHANGING WORLD

S.116.1 Variation of surface thermal heterogeneity and water dynamic within nonvascular epiphytic communities during a dehydration cycle

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Nonvascular epiphytic communities include poikilohydric organisms, such as lichens and bryophytes which lack organs for active water uptake and regulation of thermal and gas exchange. Furthermore, they have no protective tissues, therefore they directly respond to fluctuations of ambient environment also for gas exchange and light. Shifting the perspective to the epiphytic scale, functional traits of lichens and bryophytes could act as effect traits influencing the surrounding temperature through the exchange of water and heat at the substrate-atmosphere interface. In this work, we hypothesised that the composition of nonvascular epiphytic community may affect the water availability and, consequently, the surface thermal pattern. We verified if i) in a dehydration process, the epiphytic water content and their thermal pattern co-varies following a trend linked to the community composition; and if ii) the greater thermal heterogeneity is linked to a more diverse epiphytic community. To test these hypotheses, we selected 32 different epiphytic community samples. Then, we monitored them during the dehydration process by regularly weighting the samples and capturing InfraRed images every 40 minutes. Using structural equation modelling, we evaluated the relationships between epiphytic communities, water-related variables and surface thermal pattern. The results confirmed our hypotheses: community composition showed both a direct effect on thermal patter and an indirect effect mediated by water content and dehydration dynamic. Community dominated by foliose lichens and bryophytes exhibited higher water content, less water loss, and lower temperatures pattern. Conversely, communities with a greater cover of crustose lichens showed a faster water loss and an higher temperatures pattern. Hence, a more diversified community will have greater thermal heterogeneity.

S.116.2 Are ephemeral streams early-stage soils or fluvial ecosystems? The role of biocrusts to maintain their functioning

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Understanding global change impact on biodiversity is crucial to conserve healthy ecosystems and the essential services they provide to people. However, our understanding of the functional role of biocrusts on ephemeral streams remains unexplored. Ephemeral streams are watercourses that flow episodically during periods of intense rainfall and dry up quickly. They are widely distributed in hyper-arid, arid and semi-arid regions where the current global drying trend will be more severe, and they play a crucial role on global carbon processing and greenhouse gas emissions. Although ephemeral streams are expected to support a unique fraction of biodiversity as they are transitional habitats between aquatic and terrestrial ecosystems, it remains unclear which organisms may inhabit these highly dynamic habitats. Biocrusts offer a promising avenue to address this challenge given their global occurrence and their functional importance in terrestrial water-limited ecosystems such as drylands. Besides, biocrusts play key roles in global carbon and nitrogen cycles and regulate the horizontal and vertical fluxes of water (i.e., water balance). Thus, this project aims to address these challenges by exploring the functional role of biocrusts for tracking the direct effect of climate change on biodiversity but also its impact on the functioning of Mediterranean ephemeral streams.

S.116.3 Effects of mycorrhizal fungi and the functional diversity of plants on ecosystem functioning: an experimental approach

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In exchange for the carbon assimilated by plants, mycorrhizal fungi increase plant nutrient supply, protect them against pathogens and drought, and influence soil formation and aggregation, among other benefits. These processes, in turn, affect the diversity of the vegetation and multiple ecosystem functions, including one of the most important, biomass production. The functional traits of the host plants dominating the vegetation can be used to estimate the responsiveness of plant communities to mycorrhizal fungi and their relevance to ecosystem multifunctionality, as plants vary in their responsiveness to mycorrhizal fungi and their carbon economics. Despite the potential relevance of plant functional diversity as mediator of mycorrhizal effects on dryland diversity and functioning, experimental tests of such effects are still missing. This study aims to evaluate, through an experimental approach, the effect of arbuscular mycorrhizal fungi (AMF) on plant biomass production. For doing so, we used simplified grassland communities two with functional groups, forbs and grasses, where varying dominance of one or another plant functional group is used as an indicator of plant functional diversity. Arbuscular mycorrhizal fungi increased plant biomass production, but no effect of functional diversity on biomass production was found. Furthermore, no interactive effects of functional diversity and mycorrhiza presence on biomass production were found. This study indicates that to fully understand the interactions between AMF and different plant species it is also essential to consider all the complexities of nutrient economy mechanisms. This work also underscores the importance of considering soil microorganisms and mycorrhizal-plant interactions in studies of ecosystem functioning, emphasizing the need for a comprehensive understanding of belowground processes.

S.116.4 The green side of the white continent: occult precipitation and terrestrial cryptogams in Antarctica.

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Maritime Antarctica (Antarctic Peninsula plus adjacent archipelagos) is one of the richest vegetated areas in Antarctica, with 189 and 59 species of lichen and of bryophytes respectively, but also one of the most fragile regions. After a period of decreasing temperature in the last 20y, in Maritime Antarctica this trend is currently shifting. Changes in air temperature induce variations in the type, frequency and timing of precipitation but predictions show high uncertainty regarding their direction and extent for this region. Furthermore, while "occult precipitation" (fog, snow, or rain with strong wind) is probably a key source of available water for the ecosystem, its occurrence and relevance are, so far, understudied. Thus, we aimed at evaluating how changes in water availability may affect the ecophysiological performance of some of the most prominent photosynthetic species of the antarctic tundra, with especial emphasis on horizontal precipitation and on lichen and moss flora. For this purpose, we have (i) monitored the potential contribution of occult precipitation to the ecosystem, (ii) studied anatomical and physicochemical properties of the thalli involved in the capture, absorption and retention of water and (iii) evaluated interspecific differences to deal with periods of water restriction, as well as biophysical and physiological traits involved on them. Our preliminary results reveal that (i) occult precipitation is potentially very relevant for terrestrial vegetation in Antarctica, particularly at moderated elevations (>200m asl); (ii) there are important interspecific differences in the wettability of thalli surfaces and in their capability to delay desiccation; (iii) there are significant interspecific differences in the longevity of thalli in the dry state.

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S.116.5 Mycorrhizal associations interact with stand development and climate to influence tree diversity patterns across tropical montane forests

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Symbiotic associations between trees and soil fungi – mycorrhizas – influence forest structure and diversity, with important differences between mycorrhizal types. It is thought that communities dominated by ectomycorrhizal associations exhibit weaker negative conspecific density dependence because of improved nutrient acquisition and protection against soil-borne pathogens to conspecifics, relative to arbuscular mycorrhizal associations. This mechanism should explain stand-level gradients of tree diversity, with low-diverse forest communities dominated by ectomycorrhizal trees and high-diverse communities dominated by arbuscular mycorrhizal trees. Here, we tested this hypothesis across tropical montane forests and found that, in general, tree species diversity was lower under the dominance of either ectomycorrhizal or arbuscular mycorrhizal trees, and higher in mixed communities of both mycorrhizal types. However, this pattern was dependent on forest stand development and climate, with ectomycorrhizal dominance differ-

entially influencing tree diversity between young and old-growth forests, from cold to warm climates. In particular, ectomycorrhizal dominance was associated to increased tree species richness but decreased tree species evenness across old-growth forests located in median- and warm conditions along the climatic gradient. Our findings indicate that mycorrhizal associations may represent an important factor shaping forest biodiversity in subtropical and tropical regions, the most species-rich and varied environments of the planet but currently at risk from the pressures of human-driven environmental changes.

S.116.6 Interspecific and intraspecific variability in functional traits of lichens communities from gypsum soils across a latitudinal gradient

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It is known that environmental variables affect functional diversity in terricolous lichen communities from gypsum soils. And although these observed responses of functional traits in relation to environmental changes may be due to species turnover and/or intraspecific trait variation (ITV) it is not known until what extent ITV and species turnover influence the observed trait variability. In order to understand how these communities survive under challenging conditions we aim to analyze the effect of environmental and soil variables on intraspecific trait variation (ITV) and species turnover and which is the contribution of both processes to functional variability. For this purpose, we quantified the relative contribution of species turnover and ITV determining the functional variation in lichen communities from gypsum soils in Spain and analyzed the relation with climate and edaphic predictors. We surveyed 35 plots along a latitudinal gradient and measured a set of eleven quantitative functional traits potentially affected by climatic and edaphic conditions and related to water use strategy, photosynthetic performance, and nutrient uptake. The results showed that ITV explained most of the functional changes in lichen communities along the latitudinal gradient except in the water holding capacity which had a similar relative contribution of both ITV and species turnover. Interestingly, climatic variables barely affected most traits except in the case of the nitrogen content and traits related with water use strategy were mostly affected by gypsum content. These results suggest that lichen communities confront environmental conditions (mostly gypsum content) by adjusting their trait values within the species rather than by the replacement of species.

S.117 PLANT DIVERSITY IN SPECIALIZED HABITATS - ECOLOGY TO EVOLUTION

S.117.1 Diversity of tree layer species along slope gradient of Moerolakop hill in Nylsvley Nature Reserve

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Slope gradients play an important role in distribution of species within the vegetation. Interesting vegetation distribution patterns are therefore more noticeable in mountainous regions which are set apart by steeper slopes. This study attempts to showcase species distribution patterns along Moroelakop hill located in Nylsvley Nature Reserve, Mokghoopong municipality, Limpopo Province. Point-Centred-Quarter (PCQ) method was used in data collected to achieve the purpose of the study which was to analyse and compare the vegetation structure of Moroelakop hill's north-facing slope. The parameters sampled through PCQ included the plant species height, basal stem diameter and canopy diameter. The relative density and relative frequencies were used to determine importance value index (IVI) of sampled species. Data collected from the North facing slope revealed the dominance of *Diplrorhynchus condylocarpon* and *Combretum molle*. Species like *Grewia bicolor*, *Dichrostachys cinerea* and *Combretum zeyheri* had low relative frequency and subsequent low IVI. Diversity was measured using Shannon-Weiner diversity index. Shannon diversity index for north facing was 2.20 (down-slope), 1.97 (mid-slope) and 1.77 (upslope). There is a significant difference in terms of species diversity recorded along the slope gradient. The study has flagged out species that need to be monitored in order to manage the vegetation well.

S.117.2 Clade-specific phylogenetic structure of boreal habitats suggests non-uniform assembly processes across phylogenetic scales

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Understanding how plant communities are assembled is critical to explaining the functioning of ecosystems and the maintenance of biodiversity. The phylogenetic distance among species in a community (i.e community phylogenetic structure) has been used to infer deterministic and stochastic assembly processes, albeit with criticisms. However, the effect of the phylogenetic scale (old versus young lineages) and spatial scale on measures of community phylogenetic structure are rarely tested, yet essential to unravel different assembly processes that might operate across species in a community. We examined clade-specific phylogenetic structure of different plant communities defined at the habitat scale, and the aggregated phylogenetic structure of communities defined at a smaller plot level scale. We obtained vascular plant species lists for six habitats in Newfoundland, Canada, and for 73 permanent 1m2 plots at Gros Morne National Park to estimate their mean pairwise phylogenetic distance standardized for sample size (SES-MPD). As expected, we found that the phylogenetic structure of plant habitats was clade-specific, with clustering at deep angiosperm nodes, overdispersion, and no pattern at both old and young lineages. Our results suggest that different lineages may exhibit different assembly processes within a habitat. As expected, at smaller spatial scales, communities showed strong phylogenetic overdispersion likely explained by processes like limiting similarity and competition.

S.117.3 First global assessment of an edaphic endemic flora: diversity, main features and conservation status of the world gypsum flora

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Plant species that grow only on unusual soils represent a significant proportion of plant diversity worldwide. These unique endemic communities are comprised of resilient and sometimes bizarre plants that thrive on difficult soils that most plant species cannot tolerate. One of the most widespread, yet understudied substrate-endemic floras of the world is that of gypsum soils. Gypsum ($CaSO_4 \cdot 2H_2O$) soils occur worldwide in arid and semiarid ecosystems, posing serious restrictions to plant life. Despite these limitations, gypsum soils host rich endemic floras that have evolved independently on five continents. Plant communities growing on gypsum represent an excellent opportunity to investigate soils as a driving force in plant evolution and ecology, offering key insights into such fundamental biological processes as adaptation, the formation of new species, and the factors controlling plant community composition. Here we present the first global assessment of an edaphic endemic flora, providing information on the diversity, functional traits and conservation status of plants restricted to gypsum soils worldwide. Over 1200 taxa are restricted to gypsum in the world. These taxa belong to 86 families grouped in 32 orders, ranging from recently diversified groups like Poales to ferns, indicating restriction to gypsum soils evolved separately in different lineages of the plants tree of life and occurs in very distantly related groups. Most species are small perennial woody plants and almost half of the taxa are local endemics, pointing at the rarity and potential vulnerability of gypsophilic floras worldwide. Notably, more than a third of the gypsum endemic taxa have been listed in conservation reports or red lists and one-fourth are under a certain degree of protection. Our study highlights the singularity of gypsum ecosystems globally and calls for urgent action to preserve these unique plant communities.

S.117.4 Mycoheterotrophy in orchids: a Himalayan perspective

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This study presents an analysis of mycoheterotrophy in orchids of the Himalayan region, Diversity of mycoheterotrophic orchids is highest in the eastern Himalaya while Nepal Himalaya also harbors considerable number of species. Owing to their unique genetic rearrangement, they exhibit anomalous feeding mechanism, which signifies a considerable evolutionary modification. However, due to their specific habitat requirements and regenerative potential, conservation of such species in the wild is becoming increasingly challenging. This paper aims to summarize the occurrence and conservation status of one of the enigmatic orchid groups in the Himalayan region to understand their diversity and facilitate their conservation efficiently.

S.117.5 Molecular ecology of endemic shrubs in isolated OCBIL populations

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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 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.

S.117.6 Pollinator-mediated frequency-dependent selection of floral colour polymorphism in a nocturnally pollinated ginger from Western Ghats of India

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Polymorphism refers to the presence of discrete forms within a population of taxonomically recognized species. Because species characteristics can be continuous, the idea of when to delineate each morph is highly controversial and becomes a statistical problem. Here we present a method of recognizing morphs versus inherent within species variants by extensively examining a trait or set of traits within a population and delimit them based on gaps in their frequency of occurrence. This method assumes that while there is a continuum in morphology, this continuum may not extend to other morphological, ecological, or physiological traits of the species. Here we present a complex geographic mosaic of traits of a highly polymorphic ginger, *Curcuma caulina* (Zingiberaceae), from the genus otherwise known for its polymorphic morphological traits. Here we describe the multifaceted nature of floral colour polymorphism in *C. caulina*, demonstrating that it extends beyond mere colour variation of the lateral bracts to encompass ecological and physiological traits of the species. Finally, we present that the pollinators, along with the plant's traits which are associated with floral colour, play a central role in governing the dynamics of selection regimes across populations to maintain floral polymorphism. This study highlights that our handicap in defining a species based on morphological characters has limited our understanding of how polymorphic a species can actually be. We offer a new perspective on floral polymorphism that integrates the eyes of taxonomists and ecologists.

S.118 SPEEDING UP OUR UNDERSTANDING OF ADAPTIVE EVOLUTION WITH GENOMICS

S.118.1 Adaptive evolution of Arabidopsis and its relatives in the new genomic era

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How organisms adapt to climate change is a fundamental biological question. High throughput genome sequencing of *A. thaliana* and its closely related species speed up the studies of plant adaptive evolution. Transposable elements (TEs) are a type of repetitive DNA sequence mobilizing across the genome, which consists of a large fraction of the genome size, and its mobilization could rapidly produce large-effect mutations. However, there are many questions about TEs, for example, how TEs insertion affect gene and phenotypic variation, what are the driving forces of TE load variation, and how did the genetic load of TEs vary during range expansion. Based on the genomics and genetics analyses of *Arabidopsis thaliana* and its relatives, we demonstrated that TEs are an important source of genetic variation that could account for high phenotypic diversity, and could plays important roles in the process of adaptive evolution. In addition, we revealed that effective population size, high transposition rate, and selective sweeps contributed to TE accumulation in the expanded populations. In particular, we genetically mapped and identified multiple candidate causal genes and TEs, and revealed the genetic architecture of TE load variation. Overall, our results highlight TEs could play a crucial role in the process of adaptation.

S.118.2 The Evolution of Splicing Specificity

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Splicing is an important gene regulatory process. Alternative splicing can lead to varied proteins being produced and can also alter gene expression levels. Alternative splicing can be seen during development and in response to changes in environmental cues, allowing plants to display developmental and phenotypic plasticity in response to abiotic stress. The regulation of alternative splicing evolved with increasing complexity as plants diversified, particularly as genomes duplicated. This has resulted in an amplification of splicing genes such as SR proteins. As a result, it is difficult to study splicing regulators due to functional redundancy. The bryophyte *Marchantia polymorpha* gives us a chance to untangle the regulatory mechanisms of alternative splicing, due to its low genomic duplication. We use the CRISPR Cas9 mutagenesis system and in-house bioinformatics tools of splicing measurements to uncover the targets of splicing factors and define splicing specificity. Comparisons of splicing in different species provides evolutionary insights on splicing specificity.

S.118.3 Mechanisms of trinucleotide repeat expansions in plants

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We identified an association between trinucleotide repeat expansion and phenotypic changes under elevated temperatures in the wild-type Arabidopsis strain. Trinucleotide repeats are part of microsatellite repeats, and their expansion has been linked to several human genetic disorders. However, the underlying mechanisms by which these repeats regulate gene expression remain unknown. Can we address this fundamental biological gap using Arabidopsis as a natural model for repeat expansion to investigate the molecular mechanisms associated with gene expression? Over the years, we have developed Arabidopsis as a natural model to uncover the molecular mechanisms associated with repeat expansion-induced gene silencing. Recently, we discovered two molecular mechanisms that induce epigenetic gene silencing at the repeat-expanded locus. I describe the novel genes and pathways we have uncovered. Our findings provide important insights into the molecular mechanisms underlying the association between trinucleotide repeat expansion and pathogenesis in Arabidopsis. Overall, our study has significant implications for understanding the underlying mechanisms of repeat-induced gene regulation and pathogenesis not only in plants but also in understanding the human genetic disorders associated with trinucleotide repeat expansions.

S.118.4 Unraveling carnation domestication: comparative genomics among wild and cultivated Dianthus species

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The *Dianthus* genus, native to Europe and Asia, presents one of the fastest diversification rates ever reported in flowering plants, with a high incidence of polyploidy and over 300 species. Carnation (*Dianthus caryophyllus*) is one of the most important ornamental flowers, that has been cultivated for centuries, overcoming an extensive domestication process which is largely understudied. Fragrance is an important property of marketable ornamental flowers, but modern carnation cultivars have weak fragrances in contrast to wild carnations. *Dianthus broteri* is a recently radiated polyploid complex with four cytotypes (2x, 4x, 6x and 12x) endemic to the Iberian Peninsula. This complex, which present a highly diverse scent composition, has been studied as an evolutionary model in the genus. With the objective of understanding the ongoing evolutionary processes of domestication, fragrance divergence and the impact of transposable elements (TEs), we assembled a chromosome-level genome of the diploid *Dianthus broteri* (876.17 Mb with scaffold N50 53 Mb and 43,817 protein coding genes). We performed comparative genome-wide analyses between the wild carnations *D. broteri* and *D. sylvestris* (assembly genome size 443.52 Mb), and cultivated *D. caryophyllus* "Francesco" (568.89 Mb) and "Aili" (584 Mb) varieties. We compared genome structure, gene families gain and losses and TE landscapes. Differences in genome sizes are not the result of the increase in gene content but can be explained due to increase of TEs in *D.broteri*, with a higher abundance of long terminal repeat-retrotransposons (LTR-RTs). LTRs highly impact the structure, function and evolution of the host genome, and might have an important role in domestication and the divergence between *Dianthus* species. Furthermore, using transcriptomic data, we have studied MYB transcription factors and terpene synthases to understand the importance of scent emission in wild carnations.

S.118.5 Population genomics of rapid weed adaptation in Amaranthus

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North America has experienced a massive increase in cropland use since 1800, accompanied more recently by the intensification of agricultural practices. Through genome analysis of present-day and historical samples spanning environments over the past two centuries, we studied the effect of these changes in farming on the extent and tempo of evolution across the native range of the common waterhemp (Amaranthus tuberculatus), a now pervasive agricultural weed. Modern agriculture has imposed strengths of selection rarely observed in the wild, with notable shifts in allele frequency trajectories since agricultural intensification in the 1960s. An evolutionary response to this extreme selection was facilitated by a concurrent human-mediated range shift. By reshaping genome-wide diversity across the landscape, agriculture has driven the success of this weed in the 21st century.

S.119 THE ROLE OF RESEARCH INFRASTRUCTURE TO ADVANCE BOTANICAL KNOWLEDGE AND RESEARCH

S.119.1 Biodiversity information standards: enabling data infrastructure

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Data standards are crucial for the efficient and effective sharing of biodiversity data for herbarium management, conservation, policy development and botanical research. They enable data to follow FAIR (findable, accessible, interoperable, reusable) and CARE (collective benefit, authority to control, responsibility, ethics) data principles. Data standards are essential for data infrastructure projects such as the Global Biodiversity Information Facility (GBIF). Biodiversity Information Standards (TDWG - https://www.tdwg.org/) is a not-for-profit, scientific and educational association that enables international collaboration among creators, managers and users of biodiversity information and promotes effective dissemination and sharing of knowledge about the world's biota. In collaboration with partner organizations, TDWG develops, maps and maintains standards, extensions and guidelines for documenting and exchanging data about geo- and bio-diversity, to guarantee data interoperability between communities. The most widely used of these is Darwin Core, which facilitates the sharing of information about the occurrence of taxa in nature as documented by observations, specimens, samples, and other related information. Also relevant to the botanical community are: Audiovisual Core - a set of vocabularies to represent metadata for biodiversity multimedia resources; Taxon Concept Schema – taxon concepts as defined in published taxonomic classifications, revisions and databases; the Humboldt Extension - an extension to Darwin Core for representing information about scope, method and completeness of observational inventories; and the MIxS (Minimum Information about any (x) Sequence) extension to Darwin Core to integrate genomic data. Information technology and scientific methods are not static, and data standards must be developed and maintained to keep pace with needs and expectations. Early TDWG standards relevant to botany have been reframed and absorbed into current standards. In addition, TDWG establishes new community-led interest groups to develop standards and vocabularies that cover new areas, such as People in Biodiversity Data, Collection Descriptions, and Plant Phenology.

S.119.2 Catalogue of Life, ChecklistBank and Taxonomic Data Services

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Catalogue of Life (COL; https://catalogueoflife.org) aims to list all described organisms covering all life on earth. COL contains more than 2,1 million described species (Bánki et al 2023). COL however needs to become more comprehensive, including more names and bridging over to genetic resources. Different approaches on how to speed up will need to be explored. COL could also benefit from new endeavours to support the online registration of names. To improve its processes and to scale up its effort, COL has teamed up with the Global Biodiversity Information Facility (GBIF; https://gbif.org) to build a new infrastructure, ChecklistBank (https://checklistbank.org). ChecklistBank is an open data publishing platform with a focus on taxonomic and nomenclatural datasets, as well as non-global taxonomic lists and policy relevant species lists. ChecklistBank is core infrastructure for both GBIF and COL. More than 50K taxonomic datasets are openly accessible for use. These also include well managed plant taxonomic data sources, as well as datasets from digitised literature. Data sets can be explored, published and downloaded through various data standards and data types. Since datasets are processed within ChecklistBank in a similar manner, datasets can be better compared to one another as to the taxonomic overlap and differences. Name matching services are available through an Application Programming Interface (API) and a user interface. COL is a prime user of ChecklistBank. A range of data services could support both scientific and broader societal use.

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S.119.3 Harmonizing dynamic botanical knowledge at the source: infrastructures for resolvable IDs and taxon concept subscriptions

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Botanical taxon names are vital for information accessibility across diverse systems, used locally in fields from systematics, forestry, agriculture, ecology, and conservation to government regulations and medicine. Traditionally, taxonomists played a crucial role in connecting and mediating knowledge from various sources. Nowadays, machines are often uncritically asked to perform this task online. However, scientific names may be ambiguous if used as the identifier, posing challenges due to the taxon's hypothesis-based circumscription and the existence of multiple name variants. Globally unique identifiers for botanical names, variants, and "designations" are provided by initiatives like WFO Plant List and IPNI. They can control machine interactions and help to conserve data cleaning results. Integrated into taxonomic systems like WFO's flora site or EU-Nomen (PESI), these identifiers can enable tracking of taxonomic and nomenclatural changes proposed by these sites. The EU TETTRIs project aims, inter alia, to document and enhance these processes, establishing functional workflows for mapping local taxonomies. Basic use cases, such as checking names against the normative EU-Nomen checklist, are already covered by existing mechanisms, often also used for data cleaning. But local data portals often link to aggregator databases, relying on name strings as the search parameter, which may be inaccurate. Integrating the resolvable ID improves data quality and opens further possibilities. Users who matched their names should have a "taxon concept subscription" option for automatic notifications of name usage changes. For this, target aggregators must monitor changes in taxon concepts, including alterations in status, nomenclatural status, and addition/removal of synonyms. Introducing this into infrastructures like the GBIF/CoL Checklist Bank would make it possible to subscribe to a multitude of versioned online treatments. TETTRIs aims to instigate this development. In the project's remaining period, we'll test and document aggregator services, promoting name ID usage for a linked data landscape in biodiversity information.

S.119.4 GBIF evolves to meet botanical research needs

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In collaboration with Index Herbariorum, GBIF has rebuilt and manages the Global Registry of Scientific Collections. GRSciColl contains collection information for over 5,500 herbaria and synchronizes weekly with Index Herbariorum. GBIF has aligned over 104 million plant and fungal specimen records to herbaria GRSCiColl records. Each herbarium that shares data with GBIF has a collection data page which, in addition to collection metadata, contains an informative dashboard summarizing data by taxon, IUCN threat status, collectors, identifiers, and origin of specimen. These statistics are also summarized across national and taxonomic groups in various GBIF hosted portals managed by the community. The specimen alignment to the collections is part of GBIF's work to update our Darwin Core based data model. GBIF runs a clustering algorithm weekly to identify potential relationship between records such as: types, duplicates, literature citations, DNA sequences, and phylogenies. The clustered records are viewable in the 'Related" tab on a hosted portal. GBIF is developing a material catalogue that integrates these related records into a single record. This record includes data shared by the specimen holder such taxonomic, spatial data and often images, as well as related data about the specimen that has been shared via GenBank (or ENA), BOLD, literature citations in taxonomic revisions, published phylogenetic trees, and trait datasets. To improve data quality GBIF encourages community curation of taxonomic, phylogenetic, and spatial data. As demonstrated in the Legume Portal, we invite taxonomic revisions to be published to ChecklistBank, a GBIF-Catalogue of Life collaboration. From ChecklistBank the taxonomic data can be viewed on a taxon specific data portal and be quickly integrated into GBIF's taxonomic backbone to improve the quality of the specimens shared with GBIF. A similar phylogenetic pipeline is available on the portal in partnership with Open Tree of Life.

S.119.5 Innovation leading to new ways of knowing in Australian botanical collections and the Atlas of Living Australia

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Once thought of as static, collections are being reframed as resources whose potential goes beyond the physical entities held in herbaria. In Australia, novel projects are being undertaken in botanical collections, and the results can often be accessed through the Australasian Virtual Herbarium (AVH) and the Atlas of Living Australia (ALA) (https://www.ala.org.au/). The collections, AVH and the ALA together represent critical infrastructure for understanding Australia's biodiversity. Many novel projects utilise advanced computing power, cloud-based storage, and analysis tools. For example, digitisation projects have been completed by organisations including the National Herbarium of NSW and the Australian National Herbarium, one of the CSIRO National Research Collections. These projects aim to go way beyond previous efforts in terms of sheer numbers and the scale of the operation required to deliver the result. Another activity is AusTraits, which compiles data across over 30,000 species and hundreds of traits. Collected data can be accessed on ALA species pages. Of particular interest in Australia is Indigenous knowledge recorded on herbarium sheets; unique and valuable information. Building community and collaborations to bring Indigenous knowledge and western science closer together is an active challenge for those working in Australian botany. The Atlas of Living Australia provides a conduit for new information to be published online and made accessible. The aggregated data then provide even more opportunities for new knowledge to be generated, with tools to view, download and visualise information. Areas of future development in the ALA include work in biosecurity, including weeds and plant pests; better data about interactions, such as between plants and pollinators; and inclusion of genomic data. Much that is new can be generated from specimens that may be old.

S.120 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 5

S.120.1 Unveiling the Hidden Harmony: exploring the mycobiome of the threatened Posidonia oceanica Seagrass in the Mediterranean Sea

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Posidonia oceanica (L.) Delile is a threatened endemic seagrass of the Mediterranean Sea. As a Mediterranean Climax community, *Posidonia* meadows hold high ecological relevance in primary productivity, food web support and nutrient cycling, also providing multiple ecosystem services as biodiversity hotspot, ecosystem engineering or carbon sink. Despite its recognised importance, *Posidonia* meadows are declining at an accelerating rate by global or local anthropogenic pressures. Like terrestrial plants, *P. oceanica* host a diverse community of microorganisms which may influence its ecophysiology and health, even regulating the biogeochemical dynamics of entire meadows. Among microorganisms, very little is known about *P. oceanica* mycobiome. Fungi in terrestrial ecosystems are known to confer benefits to the plant and could play a crucial role in functioning of the seagrass ecosystem, spanning from mutualism to parasitism. We performed a large-scale sampling at 3 localities in the Mediterranean Sea (France; Crete and Cyprus respectively) and a Next Generation Sequencing (NGS) study based on ITS2 and 5.8S rDNA sequence analyses, in order to investigate how the fungal communities' structure and composition associated with the *P. oceanica* environmental matrices (seawater column or sediment) and plant compartment (leaves, roots or rhizome) differ according to environmental variability and biometrics or physiological descriptors. A single species dominated the fungal community, *Posidoniomyces atricolor*, hitherto unknown from other hosts and supposed to be responsible for the putative dark septate endophyte (DSE) colonization pattern found in *P. oceanica*. Out of *P. atricolor*, the less dominant taxa showed a strong plant compartment specificity. The consistent occurrence of the DSE suggested a mutualistic relationship as with mycorrhizal fungi in terrestrial plants, representing an integrated approach for the monitoring of the *P. oceanica* meadows in an even more changing environmental condition.

S.120.2 The impact of fire regime shifts on plant species persistence

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Climate change is leading a shift in ecological processes, and fires are arguably one of the most spectacular examples of such shifts. Fire regimes are changing and recent megafires around the world are examples of the extremes that fire events can reach. Plant species are adapted to historic fire regimes, persisting within thresholds of fire frequency, seasonality, severity and extent. Developing an understanding of how shifting fire regime elements can impact persistence and recovery of plant species is therefore essential for conserving biodiversity. Seeds are key drivers of plant population dynamics and their study can allow us to predict the trajectories of functional groups of species. Seeds are also critical for applied restoration, where plant populations have been pushed past the limits for natural recovery. Drawing on the results from recent research, I look at how different elements of the fire regime, including extreme fire severity and out-of-season burns, interact with plant and seed ecological processes to determine which species may persist and which will struggle. While the reduction of climate change impacts requires a global effort, a clear understanding of local processes can help to provide informed conservation management, while local restoration efforts can help to minimise negative impacts for those species most at risk.

S.120.3 Continuous turning on stress genes stabilizes gene regulatory networks and benefits mangroves' adaptation to unstable environments

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When experiencing unstable environments, a major challenge for plants is the maintaining stability of gene regulatory networks (GRNs). How plants accumulate genetic changes to stabilize GRNs in the long-term adaptation to environmental fluctuations is rarely revealed. In this study, we proposed a possible strategy of continuously turning on stress-responsive genes, which may increase GRNs stability while increasing energy costs. We tested the hypothesis by comparing expression profiles in a typical mangrove plant *Rhizophora apiculata* and its inland relative *Carallia pectinifolia*. Mangroves inhabited intertidal zones with highly fluctuated salinity and other stressors. We found that the gene expression profiles of *R. apiculata* were more stable than that of *C. pectinifolia* under salinity changes. It is caused by the transitation of stress-induced expression to constitutive expression in >4,000 genes. The genes include the up-regulation by high salinity in inland plant meanwhile constitutively high-expressed in mangroves and the down-regulation in inland plant and always low-expressed in mangroves. The former are enriched in salt stress response, while the latter are concentrated in the metabolic and development processes such as photosynthesis. We reconstructed GRNs based on time-series expression data and identified 42 key transcription factors that may have dominated the gene expression profile transitation. We also identified genetic changes possiblely responsible for the evolution of mangrove GRNs. In summary, mangroves have undergone extensive changes in gene expression profiles compared to their inland relatives. In particular, many salt stress response genes have evolved from stress-type to constitutive expression, which may be caused by changes in the expression patterns of key genes on GRNs. The growth-defense trade-off, investing more energy in denfense at the cost of growth, may be an important strategy for mangroves to adapt to the fluctuating intertidal environments.

S.120.4 Exploring the capacity of rare species to acclimate to environmental change

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The enduring question of why some species are rare while others are common has important implications for the conservation of rare species and overall biodiversity. In the context of both current constraints to their ranges and their responses to rapid rates of contemporary environmental change, rare species can be limited in their capacities to adapt or migrate due to low genetic diversity and/or fitness as is suggested by previous research and our recent meta-analytic work. While the ability of rare species to acclimate also could influence their current rarity and responses to environmental change, this capacity has been relatively underexplored in rare species. To compare the capacity of rare versus common species to acclimate, we investigated the phenotypic plasticity of individuals of rare *Boechera perstellata* (Braun's rockcress) and *Pityopsis* ruthii (Ruth's golden aster) with their widespread congeners *B. laevigata and P. graminifolia* propagated from seed collected from several populations throughout their ranges in controlled-environment growth chamber experiments. In contrast to our predictions that rarity would be associated with acclimatory constraints, both rare species exhibited phenotypic plasticity in response to changes in light and water availability that were comparable or greater than that exhibited by their common congeners. However, rare species were comparably constrained in their ability to acclimate to temperature. Overall, our findings elucidate the narrow ranges and habitat specificities of these rare endemic species of the southeastern USA and their vulnerability to future environmental change. To further explore the potential role of acclimatory constraints in species rarity we offer recommendations for field-based transplant experiments of endemic rare species such as *B. perstellata* and *P. ruthii* beyond their natural ranges.

S.120.5 Riparian forest response to extreme drought: what do high water table forests reveal about forest resilience to drought?

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Droughts significantly impact forest ecosystems, reducing forest health and productivity. Droughts thus compromise key forest functions such as carbon sequestration and consequently nature-based solutions for climate change mitigation and adaptation. Riparian forests play key roles in the functioning of aquatic and terrestrial ecosystems. However, there is limited understanding of the response of riparian forests to drought. Here we investigate riparian forest drought responses and resilience to an extreme drought event at a regional scale. Specifically, we examined riparian forest drought response strategies and how drought event characteristics, average climate conditions, topography, soil and vegetation structure and functional composition shape the resilience of riparian forests to drought. We used a time series of Normalized Difference Vegetation Index (NDVI) and Normalized Difference Water Index (NDWI) derived from Sentinel-2 satellite imagery to calculate the resistance to and recovery after an extreme drought (2017-2018) in 49 sites across an Atlantic-Mediterranean climate gradient in North Portugal. We used generalized additive models and multi-model inference to understand which factors explained drought responses. We found a trade-off between drought resistance and recovery, as well as contrasting strategies across the climatic gradient of the study area. Riparian forests in Atlantic areas showed higher resistance, while those under Mediterranean influence showed a higher recovery than the former. Canopy structure and climate context were the most relevant predictors of drought response. However, three years after the extreme drought, median NDVI and NDWI across the study area had not returned to pre-drought levels. Our study shows that riparian forests present trade-offs between drought resistance and recovery and may be susceptible to extended drought legacies associated with extreme and/or recurring droughts, similarly to upland forests. This work highlights an underestimated component of riparian ecosystems vulnerability to climate change and emphasises the need for further understanding on long-term resilience to drought.

S.121 CAREX: THE EVOLUTION OF A MEGADIVERSE GENUS TACKLED FROM MULTIPLE APPROACHES. SESSION 2

S.121.1 Forces driving the divergence of Carex (Cyperaceae) lineages: the role of the biotic component

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Divergence between lineages and speciation may be attributed to both geographic isolation and adaptive ecological differentiation. *Carex elata* and *C. reuteriana* are two closely related species with very similar habit and ecological requirements, inhabiting river shores at medium-low altitudes, that display an allopatric distribution within the Iberian Peninsula. They conform an ideal system to study the relative importance of geographical versus ecological factors in differentiation and speciation. We employed a multidisciplinary approach integrating abiotic, biotic and geographical factors, with genomic data (genotyping-by-sequencing) to infer the relative role of different evolutionary drivers. Abiotic factors were assessed based on 38 bioclimatic variables. We characterised biotic factors using the community of co-occurring plant species as a proxy containing presences and absences of vascular plant taxa (using 1536 vegetation inventories). Geographical factors were evaluated with a distance matrix based on geographic coordinates. We used regularized generalized linear models to determine which variables contribute more to explain the observed allopatric distribution pattern. Furthermore, we examined the relationships between genetic distances (from SNPs) and abiotic environment, biotic and geographical factors. The genomic analysis revealed a clear geographic structure of the taxa. Interestingly, their distributions are better predicted by the presence of other species within their respective communities than by abiotic or geographical factors. This suggests that biotic factors have played an important role in the divergence of these taxa or act as a proxy for other unaccounted ecological factors. In addition, inter-population genetic distances of each taxon are significantly associated with all aforementioned factors, albeit with varying degrees of influence. However, biotic distances alone explain the highest proportion of genetic distance variance within *C. elata,* whereas abiotic or geographical factors have a greater effect in *C. reuteriana.* This study contributes to a deeper understanding of the evolutionary processes shaping the distribution and population dynamics of species.

S.121.2 Is the red leaf colour of Carex (Cyperaceae) in New Zealand an adaptation to browsing by the extinct moas? A study of the dissuasive effect on herbivory by extant ratite birds

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The moas were giant flightless birds (ratites) endemic to New Zealand, where they were the largest herbivores before their rapid extinction after colonization by maori people (c. 1440 AD). Moas' herbivory is considered a major force in the evolution of native vegetation, and their evolutionary legacy can still be seen in traits of different plant species. Colour-based plant defence has been proposed as a strategy to avoid herbivory. Genus Carex, which has a hotspot of diversity and endemicity in New Zealand, has red-leaved species in four different lineages. Despite this is a unique feature not found elsewhere in this megadiverse cosmopolitan genus, its evolution has not been investigated yet. In order to evaluate if red foliage could have helped Carex to escape from herbivores, a cafeteria-type experiment was conducted in a zoo using the moas' closely related extant species Dromaius novaehollandiae (emu) as a proxy. We exhibited green-leaved and red-leaved morphotypes of two Carex species (subgen. Carex, sect. Echinochlaenae) to evaluate emus' diet preference on the different colour morphotypes. We studied different growth parameters in control and bird-exposed plants (e.g., dry biomass, specific leaf area, root-shoot ratio, etc), and the interaction of birds with plants (time, peck number) through phototrapping, during three two-week cafeteria presentations. Our results show that emus clearly interacted and consumed the green plants over the red ones, which was also evident from several significant measured plant variables. This suggests that red-leaved plants could be less visually attractive and/or palatable to ratite birds. Our study supports the hypothesis that red-leaved Carex foliage could have adaptively evolved to avoid herbivory by moas in New Zealand.

S.121.3 The genus Carex (Cyperaceae) in New Zealand: a southern hemisphere hotspot in a boreotemperate genus

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Carex is a megadiverse genus with about 2000 species of cosmopolitan distribution, which is especially diversified in temperate and cold regions of the Northern Hemisphere. In New Zealand, however, it is remarkably the second largest angiosperm genus with 115 native species (c. 85% endemic), but its study has received comparatively little attention. We provide a general revision of the natural history of *Carex* in New Zealand, including systematic, biogeographic, ecological, morphological and evolutionary aspects. In the context of the latest dated phylogeny of *Carex*, New Zealand has been recurrently colonized by multiple lineages via long distance dispersal. Time of colonization seems to have a strong influence in the extent of lineage diversification, probably as a result of more ecological opportunity for diversification for earlier arriving lineages. Two lineages (sects. *Echinochlaenae* and *Uncinia*) which concentrate most species diversity (>70%) could have undergone evolutionary radiation processes, which is in agreement with molecular evidence, wide ecological and morphological diversity, and relatively uniform chromosome numbers. A wide array of disjunction patterns is revealed by the distribution of non-endemic taxa. On the other hand, restricted endemics shed light on putatively important areas for *Carex* speciation. Some morphological features are remarkable, including the unique presence of red-leaved species in four different lineages, a feature that could have evolved as a possible adaptation to escape herbivory by the extinct moas. Our revision remarks the extraordinary multidisciplinary interest of the study of New Zealand *Carex* and paves the road for future specific research on this group.

S.121.4 Population genomics and phylogeography in sedges: speciation, niche evolution and landscape genomics of Carex gr. furva

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The genus *Carex* L. (Cyperaceae), with about 2,000 species, is one of the most diversified genera among angiosperms. Previous studies, based on morphological and molecular data (plastid DNA regions and RADseq) from 10 populations across the Iberian Peninsula, recognised two different species within *C. furva* complex: *C. furva* and *C. lucennoiberica*. *Carex lucennoiberica* is a species endemic to high siliceous mountains in the Iberian Peninsula. In contrast, *C. furva* is only distributed in Sierra Nevada, a high Mediterranean mountain in Southern Spain. Both species only co-occur in Sierra Nevada, which is an excellent area to study genetic divergence and local adaptation in the presence of hybridization. Here, we aim to (i) verify the split of both species by means of phylogenomic analyses performed by RADseq markers and using morphological characters measurements, (ii) study the niche evolution of both species, with special focus in Sierra Nevada using dataloggers (Ibutton®) to record temperature data across their distribution in Sierra Nevada and (iii) correlate fine scale RADseq loci of this group with temperature records and microclimate layers. Morphological and molecular data suggests two main groups in Sierra Nevada, corresponding to *C. furva* and *C. lucennoiberica*, but also intermediate individuals are found, evidencing gene flow between species. Our results allow us to conclude that there are not significant climatic niche differences between *C. furva* and *C. lucennoiberica* populations but there are some other microhabitat differences. Finally, our preliminary landscape genomic results suggest that there is evidence of local adaptation in this group.

S.121.5 Carex sect. Racemosae (Cyperaceae): Insights into diversification and systematics of a taxonomically challenging group

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The mainly arctic-alpine *Carex* sect. *Racemosae* (>60 spp.) constitutes one of the larger, yet taxonomically most challenging groups within the megadiverse genus *Carex*. Previous molecular studies have been limited by incomplete sampling and have failed to disentangle the taxonomic delimitation and phylogenetic placement of several controversial, doubtful, or rare species. We achieved a more or less complete species sampling thanks to a global collaborative effort, including field campaigns and herbarium work as well as ongoing taxonomic revisions in Eurasia and the Neotropics, Divergence-time estimation and multispecies coalescent (MSC) analyses were conducted on a multi-accession Sanger-sequencing dataset (i.e., multiple samples per species) using nuclear (ITS, ETS) and plastid (*rps*16, *trn*K–*mat*K, *trn*L–*trn*F) DNA regions (ca. 6,000 bp). Biogeographic analyses suggest a Late Miocene (c. 10 Myr) origin within the forest and mountain-steppe belts of the Northern Hemisphere, followed by several, partly trans-continental range expansions, mainly during the early diversification process (10–5 Myr). A trans-Cordilleran disjunction is also evident. Overall patterns highlight the importance of Central Asia and Western North America for the group's diversification. Obtained clades are more congruent with biogeographic rather than by morphological patterns. Diversification rate analyses showed an unexpected, continuous and uniform slowdown in diversification rates across all major clades, suggesting niche conservatism coupled with niche filling. Finally, several taxonomic and nomenclatural changes are suggested, i.e., some regional taxa previously placed in synonymy of other widespread species require revalidation (e.g., *C. apodostachya*) or remain "orphan species" with no clear assignment to any specific clade (e.g., *C. serreana*). In conclusion, our collaborative study provides fundamental insights into the evolutionary dynamics of a significant high mountain plant group and lays the groundwork for a comprehensive global revision of *Carex* sect. *Racemosae*.

S.121.6 Carex phylogenomics (Cyperaceae) and MADS-box gene evolution

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With around 2,000 species, *Carex* (Cyperaceae) is the second-largest genus of monocots. Its great diversity means that extensive taxonomic sampling and genome-scale sequence data are necessary to unravel its detailed evolutionary history and evaluate its newly proposed infrageneric classification. In this study, we estimated both nuclear and plastid phylogenetic trees based on genome-scale data, incorporating 152 representative taxa. We recovered 490 single-copy nuclear gene loci using *Carex*-specific probes through the Hyb-Seq technique and sequenced 71 coding plastid genes through genome skimming. Results showed that four of the six subgenera proposed in the new classification system were highly supported (bootstrap support ≥ 95%) in nuclear and plastid trees. However, their positions in the plastid and nuclear trees differed for many taxa or clades, suggesting a putative hybrid origin, which was assessed by HyDe and GHDet analyses. We also obtained high-quality genome sequences from five *Carex* species (*C. siderosticta, C. paxii, C. dickinsii, C. breviculmis,* and *C. capricornis*) and analyzed them with two previously reported *Carex* genomes and representatives of other Poales lineages. The genome sequences from *Amborella trichopoda*, *Oryza sativa*, and *Arabidopsis thaliana* were employed as references to detect MADS-box genes in *Carex*. The maximum-likelihood tree, constructed using an amino-acid-aligned DNA matrix, showed unique duplication and deletion events in the evolutionary history of MADS-box genes in *Carex*. Furthermore, we generated transcriptomes for each floral organ from two *Carex* species and compared them with those from *Arabidopsis* and rice. Our findings 1) highlight conflicting phylogenetic relationships among some subgroups, possibly due to the different evolutionary histories of plastid and nuclear genomes, and 2) shed light on floral structure and genome evolution in *Carex*.

S.122 SOLANACEAE: BIOLOGY, SYSTEMATICS AND EVOLUTION. SESSION 2

S.122.1 Untangling the web of Solanum sections Herpystichum and Pteroidea

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Solanum sections Herpystichum and Pteroidea are small sections of ten species each within the Potato Clade of the enormous genus Solanum. Both sections range from Central America to the central Andes and are heterogeneous groups of species that include herbs and vines, and species with simple and compound leaves. Pteroidea is defined by inflorescences in an axillary position, unifoliate sympodial units, and rugose, conical fruits in most species. This combination of characters is unique in Solanum and lends support to the monophyly of Pteroidea. Herpystichum, on the other hand, is more heterogeneous, but can be characterized by onion-shaped floral buds and distinctly flattened fruits in some species. Phylogenetic analyses based on nuclear and plastid markers have shown that the two sections form a strongly supported clade, but an understanding of the relationship between the sections has remained elusive. Analysis of concatenated data supports the two sections as reciprocally monophyletic, or with Pteroidea nested within Herpystichum. Similarly, analysis of individual markers recovers Pteroidea as sister, in a polytomy with, or nested within Herpystichum. Our analyses of both nuclear and plastid markers, as well as nearly complete plastid sequence data suggest frequent shifts in leaf complexity in the entire clade and a single origin of sect. Pteroidea. Origins of the flattened fruits of Herpystichum, as well as the monophyly of the section itself, remain enigmatic. The additional data, however, reinforce the previous findings that the widespread species, S. anceps and S. mite are not monophyletic, and both morphology and molecular data suggest that there is at least one undescribed species in sect. Pteroidea. Additional sequence data using ddRAD-seq is underway, which may provide additional insights into the evolution and relationships among these groups.

S.122.2 Communities pulling together for 21st century taxonomy: the Solanum (Solanaceae) story

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There are only a handful of genera of angiosperms with more than 1,000 species, and they are often left aside by botanists studying plant diversity. Their sheer size frightens us away from beginning to tackle them; they don't fit into a three- or five- year funding cycle, and making progress, let alone finding a way to begin, can be daunting. But what if we looked at working together in different ways? Not as lone taxonomists working on a group but as a collective – let's call it a "meta-lab" where different sets of people come together for different types of analysis, all with the goal of understanding something a single botanist could never do in a lifetime. Solanum is one such giant genus, with more than 1,400 currently recognised species distributed on all continents but Antarctica. Solanum was last treated as a whole on a global basis in the 19th century; we know a lot more today about both species diversity and relationships. I describe how the Solanum "meta-lab" has approached working on such a monster and show how the community approach facilitates significant progress in taxonomy, phylogeny and the production of identification tools; I I also discuss some of our recent advances and where we are going next.

S.122.3 Distinct assembly patterns of Solanum: insights from the globe and Australia

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Solanum (Solanaceae) is one of the largest genera of angiosperms (containing more than 1,000 species) with worldwide distribution and great economic importance. However, few studies have been conducted on the global and continental distribution patterns of the genus. We here measured the diversity and endemism patterns of *Solanum* all over the world and using Australia as an example of the regional scale for its diverse species richness and insular geographical property. Around the globe, we found that Central America to South America has the highest species richness, species endemism, phylogenetic diversity, and phylogenetic endemism, whereas Australia has the second highest diversity and endemsim, especially in its eastern coast. The distributions of neo- and paleo- endemism centers are generally congruent with the local volcanic activities and orogenic movements. Within Australia, the hotspots were distributed mainly in the tropical or temperate forests and grasslands and generally congruent with the vegetation types. Based on the clustering analyses, we further identified a certain linkage among Africa, Asia, and Australia, especially the clustering in Asia-Australia showing a pattern of multiple clusters in Philippines and Indonesia, suggesting that *Solanum* in tropical Asia possibly have multiple origins. By investigating the diversity patterns of *Solanum* through global to regional scale, our study suggests that diversity patterns of *Solanum* at the global scale are more likely shaped by the local orogenic movements, while those at regional scale (e.g., Australia) are more likely affected by the vegetation heterogeneity. The possible connection among Africa, Asia, and Australia was figured out to help to reveal the complex and controversial origin of Asian *Solanum*.

S.122.4 Functional and ecological diversification of underground organs in Solanum

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The evolution of geophytes in response to different environmental stressors is poorly understood largely due to the great morphological variation in underground plant organs, which includes species with rhizomatous structures or underground storage organs (USOs). Here we compare the evolution and ecological niche patterns of different geophytic organs in *Solanum* L., classified based on a functional definition and using a clade-based approach with an expert-verified specimen occurrence dataset. Results from PERMANOVA and Phylogenetic ANOVAs indicate that geophytic species occupy drier areas, with rhizomatous species found in the hottest areas whereas species with USOs are restricted to cooler areas in the montane tropics. In addition, rhizomatous species appear to be adapted to fire-driven disturbance, in contrast to species with USOs that appear to be adapted to prolonged climatic disturbance such as unfavorable growing conditions due to drought and cold. We also show that the evolution of rhizome-like structures leads to changes in the relationship between range size and niche breadth. Ancestral state reconstruction shows that in *Solanum* rhizomatous species are evolutionarily more labile compared to species with USOs. Our results suggest that underground organs enable plants to shift their niches towards distinct extreme environmental conditions and have different evolutionary constraints.

S.122.5 Taming a monster: taxonomic revision of the Torva clade of Solanum (Solanaceae) in the Andes

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One third of *Solanum* species remain to be taxonomically revised (~250 of the total 1,200 species). The unrevised species are focused in five clades mostly Neotropical clades with highly plastic leaf morphology and indumentum that is difficult to understand without field observations, large number of specimens, and access to microscopic details. One of these clades is the Torva clade with ca. 68 species and 269 names and which includes the pea eggplant (*S. torvum*) used for its edible fruits. Regional accounts have helped to clarify taxonomy of the group (e.g., Costa Rica, Africa and Asia), but a set of poorly understood species complexes remain in the tropical Andes especially that have been used as a dumping ground for complex morphological variation that may represent several distinct species. This talk presents a taxonomic overview of the Torva clade in the Andes. Based on a detailed morphological study of herbarium specimens, fieldwork, and nomenclatural revision, we recognise 36 species of the Torva clade in the Andes, of which 7 species are new and 5 are newly resurrected. The clade is most diverse in Peru where 21 species are found. Reassessment of the morphological traits reveals that trichome structure on stem, leaves and flowers is key to species delimitation. Other key characters include floral bud shape, calyx lobe shape, and corolla shape. The morphological species concepts will now be tested using target capture bait sequence data.

S.122.6 Moving forward on Solanum (Solanaceae) systematics: phylogenomic insights from unarmed lineages

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Building robust phylogenetic frameworks is the basis to pose any evolutionary question. Nevertheless, understanding relationships among taxa can also benefit society in many other ways, for example, in crop improvement. The economically important genus *Solanum* (Solanaceae) has had significant advances on its systematics in the past decades, where recent works have revealed strong incongruence among phylogenomic datasets and reticulate diversification in deep nodes. We present genomic insights from two unarmed lineages of the genus (clades Brevantherum and Geminata). These lineages together represent >20% of species diversity in *Solanum*. We generated target capture data (353 Angiosperm bait set) for 140 species and retrieved these regions from publicly available genome skimming data from another 5 species. Our results show that the 353 bait set can be useful to resolve relationships within genera, but more variable regions are desired for recently diversified lineages like Geminata. The heterogeneous length of recovered target regions seems to influence the support of recovered clades and, as this heterogeneity is related to DNA quality and sample preservation, it might remain as a challenge to any speciose group. Incongruences were found within the 353 bait set alone, and we argue a gene genealogy interrogation method should be employed in these cases. Capturing 353 targeted regions from genome skimming data yielded satisfactory amounts of data for these lineages, and it is a promising approach to compare different datasets and reduce bench work time related to sequence capture. We conclude that universal probe sets such as the 353 can be useful for big genera like *Solanum*, considering specific baits can be less cost-effective.

S.123 EVOLUTION OF KEY INNOVATIONS IN LAND PLANTS REVEALED THROUGH THE LENS OF EVODEVO. SESSION 3

S.123.1 Genetic underpinnings of growth regulation, flowering and floral organ identity in the holoparasitic Apodanthaceae

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Plant-plant parasitism has independently evolved 12 times in angiosperms. The ca. 4750 parasitic plants constitute only 2% of all angiosperm diversity; however, they exhibit some of the most outstanding genome reductions and extraordinary modifications in terms of development, structural adaptations, and reproductive strategies. The most dramatic developmental reductions occur in the endoholoparasites, which grow completely inside of their hosts as parenchymatic cells, lack typical roots, shoots and leaves, and become visible only through emerging flowers and fruits. We have focused on documenting the atypical developmental transitions occurring in the Apodanthaceae, specifically in the Salicaceae parasite *Apodanthes* and the Fabaceae parasite *Pilostyles*. These plants have no root (RAM) or shoot (SAM) apical meristems; however, flowers initiate in contact to the host vascular tissue, completely inside the host, and emerge having completed organogenesis. Using comparative genomics, we are currently characterizing plastome reduction and are documenting extensive horizontal gene transfer in the mitogenomes. Using comparative transcriptomics (derived from the host, the parasite, and mixed tissues), we have addressed the mechanisms through which *Pilostyles* maintains stem cells in the absence of primary meristems, the signals perceived for reproductive transitions in the absence of typical photoperiod sensing leaves, and the endogenous capacity for organogenesis in the dark, fully embedded inside of the host. We present data on: 1) the substantial reduction in the SAMs genetic machinery; 2) the regulation of cell division during the endophytic phase until the completion of flower development, 3) potential recruitment of host flowering regulators by the holoparasites; and 4) expression analyses of endogenous *LEAFY* and MADS-box floral organ identity homologs in these atypical flowering plants. We discuss our results in comparison with emerging developmental data from other holoparasitic plants to determine convergent mechanisms in the evolution of parasitism.

S.123.2 How do ectopic cambia form? A case study from the legume family

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Secondary growth is a remarkable evolutionary innovation in vascular plants, representing a developmental process through which plants increase in thickness. Typically, secondary growth generates a core secondary xylem (wood) surrounded by a sheath of secondary phloem (inner bark), and this pattern is achieved through a delicate balance between cell initiation, proliferation, differentiation, and programmed cell death – all governed by a single stem-cell region called the vascular cambium. Thousands of seed plants share this conserved mode of radial growth, which is regulated by a common set of conserved genes. However, this typical modality of vascular radial growth has been disrupted in several lineages of gymnosperms and angiosperms that contain alternative vascular developmental pathways called 'vascular variants'. In certain lineages, the presence of vascular variants becomes especially intriguing when the stem produces supplementary vascular cambia in unconventional locations, in addition to the initially formed original vascular cambium. This phenomenon is called ectopic cambia and generates distinct anatomical patterns, most commonly 'successive cambia' where concentric rings of cambium and its products encircle the stem/root. This process results in the development of stems or roots with multiple cambia. In this study, we investigate the evolution and development of ectopic cambia, with a particular focus on the Fabaceae. By comparing *Phaseolus vulgaris* (typical secondary growth) to *Wisteria floribunda* (ectopic cambia), we combine anatomy with comparative transcriptomes to elucidate the developmental and molecular mechanisms underlying successive cambia formation. We generated seventeen transcriptomes to explore variations in gene expression within and between species, focusing on both typical and ectopic cambia. Moreover, we explore the molecular evolution of conserved genes related to vascular development (*WOX4, CLE41, PXY, ER*) to test for signatures of selection, gene duplication, and pseudogenization in lineages with and without successive cambia.

S.123.3 Comparative single nuclei sequencing of the monocot gynoecium reveal candidate genes underlying septal nectary development in banana

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Nectary function is central to many important ecological interactions. Across flowering plants, nectaries are diverse in positional location and morphology, yet few have used genomic approaches to examine how nectaries develop. Most monocot flowers form septal nectaries, which are located on the margins between the three fused carpels that comprise the gynoecium. While key transcription factors underlying nectary development in eudicots have been characterized, the genes driving monocot nectary development are virtually unknown. As a first step to identifying candidate genes, we are using single nuclei RNA sequencing to obtain cell-type specific expression profiles. We isolated and sequenced banana (*Musa* "Ice Cream") nuclei from two sets of tissues—one region enriched in nectary cells at the top of gynoecium (the "top") and the other that lacks nectary cells at the base of the gynoecium (the "base")—and asparagus (*Asparagus officinalis*) nuclei from whole gynoecia. We identified putative nectary cell clusters and genes, and a number of candidate genes will be spatially validated with fluorescence *in-situ* hybridization. These analyses will determine whether both species share a common core set of genes for nectary development. Results from this study will form the foundation for understanding how nectaries have been conserved in monocots.

S.123.4 A BLADE-ON-PETIOLE orthologue regulates corolla differentiation in the proximal region in Torenia fournieri

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The three-dimensional shape of a flower is integrated by morphogenesis along different independent axes. Differentiation along the petal proximodistal axis is tightly linked to the specification of pollinators; however, it is still unclear how a petal patterns its proximodistal axis. The corolla of *Torenia fournieri*, exhibits strong differentiation along the proximodistal axis, including a distal petal lobe region, an intermediate corolla tube, and a proximal corolla neck region that is controlled by an ALOG family homologue, TfALOG3. In this study, we report a floral-specific *BOP* gene, *TfBOP2*, which is predominantly expressed in the proximal region of the corolla. CRISPR knockout mutants of *TfBOP2* have shorter proximal corolla tubes and longer distal lobe regions, with ectopic growth of conical cells in the fusion boundaries of the corolla tube, consistent with its expression pattern as a proximal regulator. Mutants of BOP homologues in *Arabidopsis thaliana* also show developmental defects in the petal proximal region, favouring a shared role of BOPs among different species. Genetic analysis demonstrates the interaction between *TfBOP2* and *TfALOG3* in the control of corolla proximodistal differentiation since double mutants have the shortest proximal corolla tubes while exhibiting normal boundary fusion. We further found that TfALOG3 physically interacts with TfBOP2 and can recruit TfBOP2 to the nuclear region, indicating its possible function as a complex. Our study favours a hypothetical shared BOP-ALOG complex across the core eudicots that is recruited to regulate corolla differentiation in the proximal region axis of *T. fournieri*.

S.123.5 How do neotropical orchids bloom? a comparative transcriptomic approach in orchids with different habits and storage organs

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Flowering in angiosperms occurs when vegetative meristems (VM) that form leaves become inflorescence meristems (IM) that form bracts and flowers. This process has been comprehensively studied in monocots, such as Oryza sativa, where the genetic regulatory network (GRN) includes promoter genes such as FT, COL and FUL that activate floral meristem identity genes. There are also repressors involved in the maintenance of vegetative phases that include TFL1 and AGL24/SVP, in addition to FLC and VRN2 that are important in response to cold. In contrast, little is known about how flowering is genetically controlled in neotropical orchids with different habits that colonize different micro-niches and respond to subtle environmental changes. We performed an exhaustive analysis of the morpho-anatomical and transcriptomic changes from VM to IM in three orchids: Epidendrum fimbriatum (miniature terrestrial), Cattleya trianae (epiphytic with storage organs), and Elleanthus aurantiacus (a big size terrestrial). Our RNAseq results show a higher proportion of differentially expressed genes (DEGs) involved in flowering in terrestrial species compared to epiphytic taxa. Conversely, a greater number of genes related to the metabolism of sugars and lipids was found in the epiphytic species. The most important flowering transcription factors within the DEGs include the promoters FT2A, FD2A, FUL1B/1A, SOC1La, LFY and the repressors COL4A/4B, SVP2A, GHD7, AP2 and TFL1. We validated our results using spatiotemporal expression by ISH and by protein-protein interaction using Y2H. We found important differences between the flowering GRN in orchids and model crops in the Poaceae: 1) high duplication rates for flower integrators in orchids but a low percentage of transcriptionally active homologs; 2) the retention of canonical flowering integrators, at the expense of low expression, loss of key protein interactions, and possibly pseudogenization of some homologs; and 3) changes in transcriptomic profiles in different orchids according to their morphological adaptations and habits.

S.124 ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS. SESSION 3

S.124.1 Medicinal plants profile of the Mapulana people of Ehlanzeni District in Mpumalanga Province, South Africa

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South African government has declared public health care free for all citizens. Traditional medicine is preferred as supplement to avoid challenges faced by the public health care system; most people rely on both health-care systems. A semi-structured questionnaire was administered to participants who included elderly people, community adults and youths. Data was analysed by calculating the use value and informants' consensus factor. The study revealed that the elderly are custodians of traditional medicine. Hundred and six plant species were identified in treatment of 50 different ailments. The recorded medicinal plant species were distributed amongst 55 plant families with Fabaceae (20%), Crassulaceae (5%) and Cucurbitaceae (5%) as dominating families. Plant parts such as roots (48%), leaves (26%) and barks (15%) were collected from herbs (45%), trees (37%) and shrubs (18%). *Aloe zebrina* (0.38), *Aloe marlothii* (0.29), *Sclerocarya birrea* subsp. *caffra* (0.28) and *Siphonochilus aethiopicus* (0.28) use values were the highest. Gonorrhea (1.80), stomach cleansing (1.40) chicken diseases (1.19), bad luck (0.88), flu (0.84), and diarrhea (0.80) received the highest informants' consensus factor (ICF). Plant species with low use value and ICF were known by the elder and few community adults.

S.124.2 Ethnobotanical Exploration: Assessing antifeedant and phytochemical properties of selected plants against Spodoptera frugiperda

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Environmental and health hazards linked to synthetic pesticides have prompted a growing interest in botanical insecticides as safer and environmentally friendly alternatives for controlling insect pests in agriculture. Following the historical utilization of plants in folk remedies and their continued application in diverse communities, this study explores the insecticidal potential of nine traditionally recognized plants as insecticides against the *Spodoptera frugiperda* larvae. The feeding deterrence activity of methanol and hexane extracts was evaluated using a choice test bioassay where maize leaves were used as test food. *Podalyria sericea* and *Cassytha ciliolata* hexane extracts were the most toxic to the larvae, with LC_{50} values of 0.779 and 0.993 mg/ml, respectively, as compared to the methanol extracts LC_{50} values of 1.853 and 1.461 mg/ml, respectively. Subsequently, the most efficient insecticidal extracts underwent further chemical analysis for compound isolation, purification, and structural elucidation of secondary metabolites. The efficacy of the isolated compounds with insecticidal activity will be evaluated and compared with synthetic insecticides, paving the way for a comprehensive assessment of their potential use as sustainable alternatives in pest management.

S.124.3 Phase 5: Status of ethnobiology and study perspectives in Albania

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The science of ethnobiology has been influenced by theories and methods belonging to various scientific disciplines, giving it an interdisciplinary nature. In this article, we address the main trends and new directions in ethnobiology, focusing on the contribution of evolutionary theories that have altered the conceptual and interpretative framework of ethnobiology today. Additionally, we outline the main phases of ethnobiology in Albania, with a focus on ethnobotany, from its beginnings to the present day. From here on, in accordance with the theoretical development of contemporary ethnobiology in Europe and the USA, we attempt to create a local research framework and explore the ways in which ethnobiological studies may develop in the future in Albania.

S.124.4 In vitro culture and hairy root induction in Solanum virginianum: an important component of 'Dashamoola' an ayurvedic multi-ingred

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Solanum virginianum L. (Solanaceae) is one among the Dashamoola group of plants used in Ayurveda. Dasmul Asava and Dasmularishta are well known ayurvedic formulation used as analgesic and anti-inflammatory. The roots of *S. virginianum* are used in these formulations and therefore, there is a need to develop an efficient protocol for *in vitro* multiplication of this species so that roots can be obtained on a large scale within a short time span. Accordingly, we standardized the *in vitro* protocol for this species using nodal explants. MS (Murashige and Skoog) medium supplemented with different concentrations and combinations of cytokinins was used for shoot initiation. MS supplemented with 0.75 mg l^{-1} BA ideally yielded 31.7±1.33 shoots/explant ($p<0.05$) with a response of 95%. Combination of BA (0.75 mg l^{-1}) and TDZ (1 mg l^{-1}) produced the highest number of shoots (63.91±5.19 shoots/explant) with 90% response. Subculturing the shoots on different concentrations of BA led to 100% shoot multiplication with an average shoot number of 26.25±1.31 shoots/explant and average shoot length 4.43±0.26 cm. MS augmented with IBA (2.5 mg l^{-1}) and IAA (1.5 mg l^{-1}) was used for *in vitro* rooting of shoots that yielded 26.83±1.27 roots/shoot with 92% rooting response and the average root length 6.25±0.33 cm. *Agrobacterium rhizogenes* mediated hairy root induction was successfully done in leaf and stem explants of *S. virginianum* using ATCC 15834 strain. The transformation was confirmed by Polymerase Chain Reaction (PCR). Initiation of hairy roots from both leaf and stem explants was recorded but in varied frequencies (leaf 37.77%, 5.88±0.22 hairy roots/explant and stem-21.33% with 3.18±0.29 hairy roots/ explant). Proliferative growth of hairy roots was achieved in the 9th passage (188.94±3.65 hairy roots/leaf explant) and in 6th passage (115.77±6.62 hairy roots/stem explant).

S.124.5 The bitter chemicals in the tip shoots of Bambusa oldhamii Munro (Green bamboo)

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When the young bamboo shoots of Bambusa oldhamii have their best taste, they are rich in nutrition and widely used in traditional Chinese cuisines. But the shoots erupted out of the soil surface with sunlight for several days, the flavor would be changed to a little bitterness in the tip shoot which would decrease the price in the market. Our research was aimed at mining out the bitter chemicals that would influence the bitter flavor when the shoot of green bamboo grew from underground to above ground. In our previous research based on three developing bamboo shoot phases, we mined several bitter chemicals counting for the flavor transformation, such as Solanidine, Amygdalin, Salicin, Arbutin, and others from metabolome data, and the AP2/ERF transcription factor family and the pathway of Biosynthesis of phenylpropanoids might play a key role in the biological process based on the correlation analysis with gene expression data corresponded with each phases. To explain the biological question more comprehensively and with multiple perspectives, the design and experiment proposal was improved. The shoot development phases of Bambusa oldhamii were extended to seven phases, and the transcriptome data was assembled based on the genome reference, moreover, the detection of the metabolites has a different method, finally, we mined more than 30 bitter chemicals. The bitter chemicals were distributed in the family of Flavonoids, Terpenoids, Amino acids, Purines and derivatives, Carbohydrates, and others. With the correlation analysis between the data of metabolome and transcription factor expression data with corresponding phases, we found that bHLH and HB would be the major transcription factor family, AUX/IAA would be the major transcription regulation factor family, and Leucine Rich Repeat Kinase XI & XII would be the major protein kinase family participate in the biological process of flavor taste transition.

S.125 PLANT DIVERSITY, BIOGEOGRAPHY AND EVOLUTION IN THE TROPICS FOR CONSERVATION, RESTORATION AND SUSTAINABLE USE. SESSION 4

S.125.1 The key role of the seasonally inundated forest in the conservation of biodiversity in southeastern Mexico

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Wetlands are one of the most productive ecosystems in the world, supporting a large biodiversity. Tintal (seasonally inundated forest dominated by *Haematoxylum campechianum*) is a characteristic wetland of the Southeastern Mexico and have a long history of commercial exploitation. Due to its structural characteristics and the conditions of the areas where it develops, tintal could work as a critical habitat for many plants and animal species, and as a refuge, mainly in highly anthropized landscapes. Furthermore, as the tintal develops at sites where water disappears totally or partially during determined times of the year, and the characteristic vegetation favors the formation of open spaces, these areas can be easily accessed to carry out sampling. Therefore, the tintal is the ideal case study in order to demonstrate the impact of human activities on wetland ecosystems. We analyzed the variations in the richness and abundance of different plants (vascular epiphytes) and animals (macroinvertebrates, amphibians, reptiles and bats) between preserved and human-disturbed tintales. The study was carried out at 27 tintal sites in the Southeastern Mexico, 10 preserved and 17 human-disturbed, and for each group different sampling techniques were used. The species composition and structure differ between preserved and human-disturbed tintales. In the case of vascular epiphyte species, the richness and abundance were related to a degree of conservation, and the tintal can be an important reservoir of these plants. Most of the researched tintales were highly anthropized, but the tolerance of several animal and plant species to these landscape modifications has allowed them to make use of such areas. The function of tintales as islands and sources of diversity in degraded land matrices and *H. campechianum* must be considered as a key species. This allows as to value the importance of tintal from an ecological and biodiversity conservation point of view.

S.125.2 Epiphytic bryophytes as indicators of successional changes in tropical lowland rainforests in Sri Lanka

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Epiphytic bryophytes stand out as vital indicators of ecosystem transformations in rainforests due to their heightened sensitivity to environmental shifts. Succession, the gradual evolution of plant communities over time leading to the establishment of a mature and stable ecosystem, can be effectively monitored by tracking the presence and abundance of specific species. This study aims to investigate the response of epiphytic bryophytes to forest succession in three lowland rainforests in the Southern Province of Sri Lanka; Wilpita, Kottawa, and Pituwala. The assessment of bryophytes on 135 trees across three succession stages (early, intermediate, late) in each forest site was conducted, and the impacts of forest succession stage, tree species richness, and diameter at breast height on epiphytic bryophyte species richness per plot were analyzed using generalized linear mixed models. Results revealed the identification of 73 bryophyte species across the three forests. The diversity of epiphytic bryophytes exhibited a pattern, being highest in late succession stages and lowest in early succession stages across all three forest sites. The families Calymperaceae, Sematophyllaceae, and Jungermanniaceae emerged as the most abundant among bryophytes in the three lowland rainforests. A significant revelation of this study is the identification, for the first time, of the pivotal role played by tree species richness in influencing the richness of epiphytic bryophytes in the Kottawa, Pituwala, and Wilpita forests. Notably, higher tree species diversity in late succession forests is found to be a key factor contributing substantially to the conservation of epiphytic bryophytes in lowland rainforests. This study underscores the importance of exploring epiphytic bryophytes in tropical lowland rainforests in Sri Lanka, offering valuable insights into successional processes and ecosystem dynamics. The obtained information holds crucial implications for the formulation of effective conservation and management strategies, particularly in light of the persisting environmental changes.

S.125.3 Cascading effects of defaunation on vertebrate-dispersed plant communities in Madagascar

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Madagascar's biodiversity faces various threats leading to defaunation and biodiversity loss. However, how defaunation affects biotic interactions and hence ecosystem functions, such as seed dispersal of fleshy fruited plants by vertebrate (frugivory), remains unclear. We used structural equation modelling to test whether the loss of trait matching between fruit-eating and seed dispersing animals (frugivores) and fleshy-fruited vertebrate-dispersed plants (i.e., dysfunctional seed dispersal) has led to high plant extinction risk, and whether protected areas in Madagascar conserve seed dispersal interactions. We integrated distribution data, dispersal traits, and IUCN Red List status of 2,852 vertebrate-dispersed plant species and 129 frugivore species in 649 communities across Madagascar. We detected a loss of seed size to body size trait matching in non-protected areas, suggesting that many large-seeded plants do not co-occur with frugivores that are able to swallow and effectively disperse the seeds. Interestingly, such 'dysfunctional' communities also showed the largest proportion of threatened plants, but only when they were depleted of all large-bodied frugivorous lemurs, with birds or bats left as the largest seed dispersers. We also found that protected areas conserve lemur-dominated communities with the highest proportion of threatened plants, but not the highest seed dispersal dysfunctionality. In these communities higher dysfunctionality did not lead to higher threat. This suggests that increased plant extinction risk is linked to defaunation as well as other stressors. Our results highlight the importance of biotic interactions for ecosystem functioning and plant extinction risk in Madagascar, emphasizing how timely monitoring ecosystem functioning of degraded ecosystems may help conserve biodiversity.

S.125.4 Biodiversity of terrestrial chlorophytes in Yogyakarta Province, Indonesia

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Algae can be found in a variety of habitats, including terrestrial habitats. Chlorophytes are algae that are often found as the main component of terrestrial algal populations. Molecular data also explain that the diversity of terrestrial algae is much higher than the others. However, several problems in studying terrestrial algae make the study of terrestrial green algae challenging. As a result, it is difficult to find data on terrestrial green algae and their species diversity, especially in Indonesia. More research is needed on the diversity of terrestrial Chlorophyta species in Indonesia. Therefore, this research was conducted to determine the diversity of terrestrial Chlorophyta species in Indonesia, especially in the Yogyakarta Province. At the time of sampling, physicochemical parameters of the growth environment were also measured. The algae samples were examined under a light microscope and morphological identification was analysed. Diversity and Evenness Index were also calculated and presented. Species descriptions and identification keys of twenty-one species grouped into eleven families are reported here. This paper is the first report on terrestrial algae from Yogyakarta Province. The environmental factors such as temperature, humidity, wind speed and light intensity affect the growth and density of terrestrial algae. However, each species has different tolerance to these environmental factors.

S.125.5 Floristic wealth of North Eastern Region (NER) of India – an aura of nature

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North Eastern Region (NER) of India comprises eight States *viz.* Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura. The region covers an area of 2,62,179 sq. km, of which, about 66% is under forest cover. Occupying only 7.7% of the total geographical area of India, the region supports about 50% of the total flora of the country. Blessed with tropical humid climate, vast altitudinal variation, dynamic ecosystems and geographical isolation, the area serves as a rich repository of wild floras. Two important biodiversity hotspots, the Himalaya and the Indo Burma cover the region which contains a globally significant array of unique flora with high endemism. Diverse forest types ranging from tropical to sub-tropical broad-leaved forests, temperate, sub-alpine to alpine meadows host various plant species. These include gigantic trees and lianas in the foot hills of Himalayas to rhododendron scrubs at the high-altitude alpine region. Composition of about 8000 flowering plants with high percentage of endemic taxa has made the region an area of interest for the conservationists and nature lovers. The area has been identified as the home for a wide range of Orchids, Grasses and Bamboos, Gingers, Rhododendrons, Primulas, *Impatiens*, Begonias, *Pedicularis* and so many. Many commercially valuable hardwood trees, medicinal and aromatic species, ethno-medicinally important taxa used in the traditional systems are profusely found in the region. Still many areas are underexplored and even unexplored due to dense forests and tough terrain.

Exploration to the areas in future may open up new vistas for discovery of many new taxa. India has set up a wide network of conservation programmes for sustenance of biodiversity in the region along with prioritization of preserving ecosystems and their natural resources. In this paper, floristic diversity of the region is discussed with their challenges and opportunities of conservation.

S.125.6 Climatic determinants of Andean forests functional composition

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Trait composition of tropical forests are closely related to climatic factors. Andean forests are extremely diverse and occur over large areas with wide climatic variation. There is a general understanding of how trait composition of Andean forests varies across climatic gradients. However, detailed studies relating key plant functional traits -that could provide information about forest sensitivity to changing climatic conditions- are inexistent thus far. In this study, we used 86 permanent forest plots established in Ecuador, Perú and Bolivia. For each plot, we calculated community-weighted means (CWM) for the following traits: Leaf nitrogen, Specific Leaf Area (SLA) and Specific stem density (SSD). We used linear models to predict how trait varied in response to climatic variables obtained from extrapolated databases (i.e., mean annual temperature (MAT), mean annual precipitation (MAP), and vapor pressure deficit (VPD). Our results indicated that Andean forests trait expression is tightly linked to MAT and VPD, but the role of MAP was unclear. These findings confirm the critical role of climate on Andean forest's functional configuration.

S.126 ALPINE PLANT ECOLOGY AND DIVERSITY: FROM SPECIES TO ECOSYSTEMS. SESSION 3

S.126.1 Can alpine species take the heat?: Impacts of increased temperatures on early life stages

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Climate change threatens plant biodiversity worldwide. Alpine plant species are particularly vulnerable to climate change, as temperature fluctuations are projected to be most severe in high elevation areas. Even small shifts in climate can have major consequences on phenology, reproduction, fitness, and community composition. Early life stages (seed germination and seedling survival) are arguably the most important processes in not only the fitness of an individual plant, but also in the dynamics and persistence of plant populations. These initial developmental stages are expected to be more vulnerable to changes in climate than adult life stages and thereby represent a major bottleneck to recruitment and population responses as climate change increases in severity. To understand how the early life stages of alpine plant species will respond to warming temperatures, I used climate-controlled incubators at three different temperature regimes. Temperatures were based on current conditions and projected future conditions under moderate and severe scenarios. I found that two rare alpine species (endemic to the Rocky Mountains of the USA), *Physaria alpina* and *Townsendia rothrockii*, performed better under warmer temperatures as compared to control temperatures at both the germination and seedling stage. Germination proportion, number of leaves, and the length of the longest leaf were all higher on average under warm conditions for both species. The results show that early life stages of alpine plants may not be at high risk from warming temperatures, however there are many other shifting climatic factors resulting from climate change beyond temperature alone. Precipitation, snowpack, freeze/thaw cycles, and length/variability of seasons will all impact alpine species. Furthermore, it is important to understand the entire life cycle of the species and how conditions may impact plants at later life stages. Future studies aim to tease apart these considerations.

S.126.2 Daily functional dynamics of alpine plants at chloroplast level

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Alpine plants are exposed to very contrasting conditions of irradiance and UV radiation imposed by a day/night regime during the summer period. To maintain their photosynthetic efficiency under these conditions, alpine plants need to dissipate the excess energy and scavenge the reactive oxygen species (ROS) formed, via different photoprotective mechanisms. At chloroplast level, some carotenoids such as those involved in the xanthophyll cycle directly participate in the dissipation of excess energy. Some of them (such as zeaxanthin) are additionally strong antioxidants that act together with other antioxidant molecules (e.g. lutein, β-carotene and α-tocopherol). These lipophilic antioxidants are associated with plastoglobules, lipoprotein structures attached to thylakoid membranes that respond to stress conditions by changing their size and number. While daily modulation of some protective mechanisms such as the xanthophyll cycle are rather well known, daily oscillations in other molecules (tocopherols) and structures (plastoglobules) are virtually unexplored. In the present study, we aim at unravelling how the leaves of alpine plants are able to thrive under such strong diurnal oscillations, and in particular, what the role of those lipophilic antioxidants and their holding structures (plastoglobules) is on such responses. For this purpose, we studied five alpine species during a day/night cycle (*Ranunculus glacialis*, *Saxifraga oppositifolia*, *Veronica alpina*, *Geum reptans* and *Doronicum grandiflorum*) naturally growing in a talus field at 2630 m a.s.l. near Col du Galibier (French Alps). Combining physiological, biochemical and ultrastructural analyses our results show daily changes in plastoglobule size and number. The analysed antioxidants also presented oscillations, mainly the xanthophyll cycle. However, the changes were species-dependent, indicating possible different strategies among alpine plants living under similar conditions. We conclude that thylakoid membranes and their components present the ability to adapt according to daily changes of high irradiance in different species of alpine plants.

S.126.3 Adapting to extremes: cold stress tolerance mechanisms in montane plant communities of the Pyrenees

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Montane plant communities like those growing in the Pyrenees must face multiple and contrasting abiotic stresses throughout their life cycle. Particularly, during winter and cloudless sunny days, these species have to cope harsh low temperatures combined to high solar radiation, both promoting photo-oxidative damage. Extreme temperatures are a main factor limiting plant growth in montane habitats, besides the high risk of frost damage especially in open sites where wind may have a severe drying effect, often in snow-free sites. Here, we studied the cold stress tolerance mechanisms of four diverse perennial herbs inhabiting the Pyrenees: *Anthyllis vulneraria* L, *Leontodon hispidus* L, *Plantago lanceolata* L. and *Scabiosa columbaria*, with an emphasis on photoprotective and antioxidant, and their association with stress-related phytohormonal responses. The study was performed in a Pyrenean plant community located in a south-facing slope near Sispony (Andorra, Spain) at 1660 m.a.s.l., and a set of functional traits, including leaf gas exchange, photosynthetic pigments and photo- and antioxidant molecules (anthocyanins, carotenoids and a-tocopherol) were measured together with stress-related phytohormones (ABA, salicylic acid and jasmonates), during autumn (before), winter (during) and spring (after cold stress). All species studied were efficient in the prevention of photoinhibition during winter, as indicated by values of the maximum efficiency of PSII (F_v/F_m) above 0.75 during winter. However, they distinctly respond to cold-induced desiccation stress, as indicated by reductions in the relative water content (RWC), which could recover during spring in *A. vulneraria* and *L. hispidus*, but not in *P. lanceolata* and *S. columbaria*. ABA and jasmonates confirmed the differential behavior and increased stress sensitivity of *A. vulneraria* and *L. hispidus*. compared to that of *P. lanceolata* and *S. columbaria*. This knowledge is very valuable for predicting how global warming may impact the Pyrenean plant communities.

S.126.4 Phenotypic plasticity to warming and drought in a Sphagnum species

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Phenotypic plasticity enables species to adapt to fast environmental changes. Therefore, it may provide a fitness advantage at a short-term response and may evolve through natural selection at long-term scales. Studying phenotypic plasticity in a climate change simulation experiment would allow predicting the viability of populations in their current distribution limits facing global change. Mires are sensitive ecosystems and peat mosses growth determine the ecosystem functioning. In *Sphagnum* hummocks, maintaining moisture in the apical part of shoots compromises *Sphagnum* survival, growth, and sexual reproduction. Therefore, many anatomical and morphological traits are key to retain water from precipitation. We carried out a field experiment on *Sphagnum capillifolium* hummocks in the Pyrenees. We simulated global warming by transplanting *Sphagnum* shoots from two mires at high altitudes (2190 m and 2340 m a.s.l.) to a subalpine mire (1770 m). We simulated drought by placing transparent roofs and digging ditches around hummocks. After two growing seasons, we analysed the performance of nine anatomical functional traits of *Sphagnum* shoots from the experiment and of other *Sphagnum* samples from the donor populations. *Sphagnum* shoots showed significant changes under drought conditions: leaf hyaline cells were wider and longer, and they had more but smaller pores. These changes coincide with a greater water absorption, transport and retention capacity. Thus, they could be considered an adaptation to drought. Plasticity varied according to donor populations, suggesting a region-specific adaptive potential. However, we could not demonstrate phenotypic plasticity when transplanting samples to lower altitudes, but only to drought conditions. Extended warm and dry summers compromise *Sphagnum* hummocks in the climatic edge of distribution. The outcome of our study suggests that *Sphagnum capillifolium* would have the potential for adaptation to future climatic scenarios to some extent. Furthermore, the experiment showed how hummock restorations are feasible using near populations as donors.

S.126.5 Plant diversity survey and progress in the flora of Pan-Himalaya

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Pan-Himalaya covers the northeastern Hindu-Kush, Karakoram, Himalaya, and Hengduan mountains. These majestic mountain ranges form the highest region in the world, which is called 'the roof of the world'. Three biodiversity hotspots are wholly or partially included in Pan-Himalaya, i.e., Himalaya, Mountains of Southwest China, and Indo-Burma. However, although this region is an important and indispensable source of biodiversity, the plant diversity of Pan-Himalaya is poorly known. There is even no complete record of the flora for this most unique region. The aim of the Flora of Pan-Himalaya (FPH) project is to understand the plant diversity of Pan-Himalaya and present the first complete record of the flora of Pan-Himalaya. For the last ten years, the FPH project has organized 15 comprehensive expeditions (>10 taxonomists) and more than 400 teams (each consisting of 3–5 taxonomists) and has investigated nearly all areas of Pan-Himalaya (except those areas in Northeast Afghanistan). Members of these expeditions have collected more than 150, 000 specimens, and have taken more than 200, 000 pictures of vascular plants in Pan-Himalaya. Observation data, living seeds, and silica gel-dried leaves have been collected as well. New or updated illustrations have been drawn for more than 1, 000 representative species. Based on extensive field work and integrative phylogenetic analysis, one new family, 10 new genera, and more than 100 new species from Pan-Himalaya have been described. A sound knowledge of the plant diversity of Pan-Himalaya is the only way to achieve sustainability, and it is also essential for ecological civilization development, which is now an important national policy of China. The FPH project is the first and key step in improving our knowledge of the plant diversity in Pan-Himalaya.

S.126.6 Variable phenological responses of High Andean species to artificial warming in Antisana Volcano

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Climate warming globally affects plant communities, affecting their distribution, development, productivity and phenological patterns. However, studies of phenological responses to warming in species of equatorial regions are very scarce. In our investigation at Antisana Volcano, Ecuador, we characterized the reproductive phenophases (buds, flowering, and fruiting) of 12 selected plants in high altitude grasslands (páramo) under passive warming using Open Top Chambers (OTC). Objectives included assessing if reproductive seasons coincide among 12 selected páramo species with different growth forms, determining if artificial warming induces phenological shifts, and understanding its impact on reproductive structure abundance. We monitored the phenology of 12 species every 22 days over a year in 23 control plots, and 23 plots under passive warming. We used circular statistics to characterize and compare the phenology of the different species, and we used non-parametric variance analyses to assess if there is a significant phenological shift related to warming for the selected species. Results revealed diverse seasonality patterns, with seasonal, aseasonal, and species with mixed patterns. Seasonal species exhibited a higher abundance of reproductive structures between May and August, indicating a "reproductive season," independent of growth form. Contrary to temperate regions, where temperature increase led to earlier flowering and fruiting of many species, we found no significant phenological shift in plants under passive warming in comparison to control. However, significant differences in reproductive structure abundance emerged between control and warming treatments among species, with five producing more structures in control plots and three within chambers. This suggests that warming in equatorial regions may consistently affect the production of reproductive structures in páramo species, instead of their flowering and fruiting seasons, thus potentially altering community composition in the future. The heterogeneous response underscores the urgency of assessing a larger number of species for conservation measures in this highly endemic and diverse region.

Symposia Session 8 Thursday

S.127 FUNCTIONAL ASPECTS OF NECTAR-MEDIATED PLANT-POLLINATOR INTERACTIONS

S.127.1 Where the bee sips: the perception of nectar by eusocial bees

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Floral nectar and pollen are the currencies of the transactions that occur among flowering plants and their animal pollinators. The sense of taste allows pollinators to make rapid decisions about food quality. Specialist feeders like bees, however, that feed on nectar and pollen may have adaptations that permit them to have greater acuity for compounds like sugars that are relevant to their survival. We know surprisingly little about the way that the chemical composition of nectar influences floral choice by pollinators. In this talk, I review what we know about the bee's sense of taste. My lab has discovered that bees have specialized mechanisms for the perception and encoding of sugar molecules in food which make them capable of discriminating among sugar compounds. We have also found that bee species have specific preferences for nectar cocktails, indicating that bees may exert selective pressure on plants to produce nectar suited to their metabolic needs.

S.127.2 Geographic variation of nectar properties in generalist plants: pollinated-mediated selection or adaptive wandering?

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Nectar is one of the important floral characters that shape plant-pollinator interactions. Some nectar properties, e.g. sugar profiles, seem relatively conservative across different populations of the same species, whereas there is reported considerable variation in others. For instance, in some members of the supergeneralist family Apiaceae nectar of individual plants from certain populations includes amino acids (AAs) that are absent in representatives of other populations. In species of *Rhododendron* producing toxic nectar such variation was reported for toxic grayanotoxine I. Such divergence may be correlated with habitat properties but also may reflect pollinator-mediated selection exerted by local insect communities. The paper discusses plausible evolutionary scenarios that arise from the spatial variation of nectar characters in plants, with the special focus on generalist pollination systems.

S.127.3 Nectar thieves are costlier than robbers to animal-pollinated plants

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Mutualistic interactions are biological markets where different species exchange commodities to mutual benefit. Because of that, mutualisms are susceptible to exploitation, with individuals taking without reciprocating. While models predict fitness costs inflicted by exploiters, empirical knowledge is limited, highlighting the need for broader quantification. Pollination serves as a case study since animal-pollinated flowers are commonly exploited by larcenists—non-pollinating animals consuming flower rewards without reciprocating. The impact of larcenists on plant reproduction varies widely, indicating differing costs and factors influencing them. In the context of nectar flowers, the behavior of larcenists, classified as robbers or thieves, plays a crucial role. Robbers damage flowers while extracting nectar, potentially affecting flower attractiveness and female reproductive function. Thieves, though not damaging, can disrupt flower visitation patterns. Plant mating systems further mediate these costs, with self-incompatible or strongly selfing plants experiencing greater impacts. The study aims to fill gaps in understanding by employing a meta-analytical approach, focusing on primary nectar robbing and theft and considering different datasets capturing various pollination process steps. We found that both robbers and thieves negatively influence flower visitation patterns, but only thieves impact nectar quality and availability. Surprisingly, robbers have neutral effects on nectar traits and even improve male reproductive success. On the contrary, thieves consistently reduce male and female reproductive performance. Importantly, these effects remain consistent across plant mating systems, challenging previous generalizations. The study provides a comprehensive evaluation of larcenists' costs on animal-pollinated plants, revealing that nectar theft is more detrimental than robbing, regardless of the plant's mating system. This pioneering evidence enhances our understanding of the intricate dynamics of mutualistic interactions in ecological and evolutionary contexts.

S.127.4 Nectaries changes across the flower lifetime ensure multiple ecological interactions

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Nectar is an essential trophic resource for many animals, playing an important role in plant-animal interactions. *Amphilophium mansoanum* (DC.) L.G. Lohmann (Bignoniaceae) is a liana with extranuptial nectaries (ENN), at the calyces' margins, and nuptial annular nectariferous disk (NN) below the ovary, at the bottom of the floral tubes. The energetic content, the chemical composition, and the dynamics of nectar from both nectary types are different. These traits seem to be under selective pressure by the interacting animals since ENN is visited by ants, wasps, flies, and cockroaches, and the latter mainly by large-sized pollinating bees. The aim of this study was to understand the functioning of these nectaries based on ultrastructural evidences. The ENN released nectar since the bud stage, while the NN released nectar only during the anthesis. These patterns matched the changes in the cell's machinery: For ENN, in the young bud stage, amyloplasts were scarce and since the pre-anthesis bud, the starch grains presented degradation signs and became almost absent, while cytoplasmic oil bodies, mitochondria, endoplasmic reticulum, and leucoplasts became more evident. For the NN, in the young bud stage amyloplasts were also scarce, but there were lipophilic bodies in plastids and vacuoles. However, at pre-anthesis stage there was a massive increase in amyloplasts abundance, Golgi bodies (fewer than in ENN), mitochondria and plastids with different contents. At anthesis, we observed an increase in cytoplasmic oil bodies, protein in the cytosol and starch grain degradation. These ultrastructural changes in ENN, evince a transition from hydrophilic to lipophilic secretion. In NN, in contrast, the population and morphology of organelles were consistent with hydrophilic secretion during the whole flower's lifetime. These differences in nectaries functioning may be linked to nectar features that attract specific animal groups, acting on protection and pollination mutualism throughout the flower's lifetime.

S.127.5 Nectariferous and nectarless Prosthechea Knowles & Westc. (Laeliinae; Orchidaceae)

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In the flowers of *Prosthechea* Knowles & Westc. (Laeliinae; Orchidaceae), there is an internal spur or reservoir formed by the fusion of the labellum base and the column. This structure acts as a nectary in nectar-secreting species. However, not all species in this genus produce nectar. In order to determine the structural adaptations for secretory activity or any constraints leading to the cessation of nectar production, the inner floral spur (cuniculus) of selected nectar-secreting and nectarless flowers was examined at the anatomical and cellular level. Our results indicate that the presence of nectar in the studied species is unrelated to the structure and character of the epidermis that covers inside of the spur, e.g. occurrence of the trichomes or papillae, and cuticle surface. Additionally, the ultrastructure of epidermal and subepidermal cells, distribution of plasmodesmata and the occurrence of reserve materials are similar in both types of flowers. Nectar, if present, becomes visible during the late bud stage, one day prior to flower opening, and is solely accessible during the first day of anthesis. It is then likely reabsorbed. Limited amount of accessible nectar in the flowers of *Prosthechea* can represent a mechanism for pollinator manipulation, enabling plants to decrease the energetic costs of the interaction while still ensuring consistent pollinator visitation.

S.127.6 The evolution of nectary anatomy: structural and developmental modifications associated to pollinator switch in Malvaceae

Cristina R. Marinho[1], Lluís García-Mir[1], Lucía del Castillo[1], Elisa Román[1], Magui Olangua[2], Olga Fernández-Palacios[2], Rosa Febles[2], Yannick M. Staedler[3], Jürg Schönenberger[3], Javier Fuertes-Aguilar[1]

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The presence of floral nectaries (FN) composed of a carpet of multicellular secretory trichomes, is one of the most conspicuous features of Malvaceae. Although their location within the flowers is virtually constant in the Malvoideae subfamily, they display considerable morphological differences associated with specific pollination syndromes. Here, we aimed at understanding the evolution of the anatomy underlying the pollinator-mediated nectar secretion comparing the FN structure and development between three phylogenetically-related Malva species pollinated by insects (*Malva wigandii, Malva canariensis*) or birds (*Navaea phoenicea*). Buds and flowers were collected along seven developmental stages, from which FNs were dissected and processed for optical microscopy, SEM and CT-scan. Morphological parameters were digitally measured using ImageJ and analyzed with RStudio suite. We found changes in growth and differentiation patterns, anatomy, and starch metabolism relevant to nectar secretion. 1) Trichome inception developed synchronically among the five sepals in all species, but monocentrically in *M. canariensis* and *M. wigandii*, and polycentrically in *N. phoenicea*. 2) *N. phoenicea* FN takes longer to develop than other species, which may be related to its greater structural complexity. As a result, bird-pollinated *N. phoenicea* FN are much larger and show a nectariferous parenchyma that is more compact, thicker, and with abundant phloem vascularization. On the contrary, entomophilous species show smaller nectaries, with a parenchyma with intercellular spaces and few or no phloem terminations. 3) Trichomes have a similar shape, but they are shorter and tightly packed in ornitophilous *N. phoenicea*, which also accumulated more starch in the parenchyma over time than the other species. This study provides evidence for the intimate relationship between FN morphology and nectar production, showcasing the pivotal role of FN size and structure in determining nectar output across distinct pollination strategies.

S.128 PLANTS IN FOSSIL LAGERSTÄTTEN

S.128.1 The Umm Irna flora, a latest Paleozoic melting pot from the Dead Sea Region, Jordan

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With some 60 species the Umm Irna flora from the Dead Sea region in Jordan ranks among the most late Permian diverse floras known worldwide. During the latest Permian the present-day Dead Sea region was situated at a paleolatitude of c. 15ºS at the western end of the Paleotethys in a monsoonal floodplain setting with meandering rivers, abandoned channels, ephemeral lakes and backswamps of various size. The Umm Irna Formation, exposed on the eastern side of the Dead Sea, is characterized by rapid vertical and lateral facies changes. About a dozen localities have yielded a very diverse flora reflecting the different depositional settings. Not only the high diversity but also the excellent preservation, particularly the cuticles, and the composition make this flora unique. The Umm Irna flora comprises elements of at least three of the four major floral provinces, Euramerica, Cathaysia and Gondwana. Not only the mixed nature of this flora is of interest, but also the earliest appearances of extinct plant groups traditionally regarded as typically Mesozoic, i.e., corystosperms and bennettitaleans, and the still existing podocarpalean conifers, which became major, some even dominant constituents of early Mesozoic floras. Moreover, the Umm Irna flora includes the last appearances of long-ranging Paleozoic groups, including noeggerathialean progymnosperms, lepidodendrids, as well as lyginopteridalean, callistophytalean and gigantopteridalean pteridosperms, glossopterids, and walchian conifers. The Umm Irna flora contributes to a better understanding of evolution, distribution, extinction and survival patterns in a crucial period in life history, shortly before the largest mass extinction on Earth.

S.128.2 The Fossillagerstätte Kühwiesenkopf of the Middle Triassic of the Dolomites (N Italy)

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The Triassic was characterized by greenhouse conditions, but experienced major environmental changes linked to several short but severe climate shifts. It is in this climatic scenario that a vegetation turnover took place with the appearance and radiation of modern plant families and the rapid diversification of the gymnosperms, which then became ecologically dominant for most of the Mesozoic era. In 1999 a rich fossil horizon has been discovered within the Anisian terrigenous-carbonatic succession of Kühwiesenkopf / Monte Prà della Vacca (Dolomites, N-Italy). The fossil horizon yielded abundant marine fossils, such as brachiopods, bivalves, fishes, and ammonoids, but yielded also abundant terrestrial plant fossils and a small reptile skeleton called *Megachirella wachtleri* Renesto et Posenato, 2002, which represents the oldest known squamate. The main fossiliferous level represents a rapid burial event caused by submarine flows within a marine basin, triggered by heavy storm events in the terrestrial domain, but plant debris and scattered plant remains occur in other layers along the section as well. The flora is composed of both sterile (shoots, roots, stems, leaves) and fertile organs (fructifications, seeds, fertile fern leaves) attributed to at least 35 taxa. Among those are some of the oldest representants of the Caytoniales seed ferns as well as conifers that are more closely related to the Permian forms than to Mesozoic ones. This demonstrates how this period of time was important for the evolution of plants.

S.128.3 A snapshot into the exceptionally well-preserved Jurassic vegetation of the Mahajanga Basin, Madagascar

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Here we present results originating from a collaborative project involving paleontologists, geologists, and botanists from the Swedish Museum of Natural History and Mahajanga University, Madagascar. Madagascar's geological history is central to interpreting the origins of its flora and fauna as the island separated from continental Africa in the Jurassic ca. 165 Mya, leaving Madagascar and its biota to develop in isolation from other continental landmasses. Paleobotanical studies are few, most dating back to the 1960s and 1970s by Appert, who described Upper Jurassic (Oxfordian) assemblages from the Manamana massif (southwestern Madagascar). Dipteridaceous ferns, conifers belonging to the genera *Brachyphyllum*, *Elatocladus*, *Cupressinocladus.*, *Cyparissidium*, and *Araucarites*, as well as minor amounts of "seed ferns", make up the majority of these impression floras. Our palynological results from two outcrop sections within the Mahajanga Basin, reveal well-preserved palynological assemblages of entirely continental aspect. While the older assemblage is highly dominated by fern- and lycophyte spores, including *Cyathidites, Baculatisporites, Dictyophyllidites, Ceratosporites* and *Retritiletes,* the younger assemblage is dominated by gymnosperm pollen, which constitutes c. 70%. Within the gymnosperms *Classopol-*

lis, *Araucariacites*, *Perinopollenites,* and *Callialasporites* are the most abundant spore genera. Based on these taxa, we assign the studied assemblage to the Early Jurassic (Pliensbachian–early Toarcian) *Corollina torosa* Zone of Helby et al. (1987). The floras are very similar to the coeval floras of, e.g., Sweden and Australia, revealing a highly homogenous global vegetation pattern at the time growing in a stable ecosystem for many million years, as similar floras are present in the Late Jurassic, as outlined by Appert.

S.128.4 Paleoecophysiology of Early Cretaceous Crato Flora (Brazil)

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The Crato Formation of the Araripe Basin, northeast of Brazil is one of the best *Fossil Konservat Lagerstätte* to access Early Cretaceous paleoecosystems in equatorial regions of Gondwana. There, the apparent dominance of gymnosperms splits attention with the emerging group of angiosperms. Despite intensive geological and taxonomic studies made in this area, approaches to elucidate the paleoecophysiological aspects of fossil plants are still rare. Interestingly, the gnetaleans, a gymnosperm lineage, which convergently evolved similar features with many angiosperms, might have occurred the same environments together with some early angiosperms. Until now, it is still lacking clear evidence showing the reason for intense diversification and radiation of both angiosperms and gnetaleans in the early to middle Cretaceous. Both plant lineages may be functionally similar and then subjects to similar selective pressures. One of the big questions is what caused the subsequent success of angiosperms and the coeval decline of gnetaleans. Did gnetalean taxa already differ, in the Crato flora, from angiosperms in terms of ecophysiological adaptations and tolerance ranges? Could this have influenced on the subsequent success of the angiosperms? In addition, does the ecological role of these plants differ significantly? To address these questions, 35 specimens of 17 angiosperm taxa and 70 specimens of 20 gnetalean taxa were preliminarily selected to analyze their paleoecophysiological leaf traits. The functional types of fossils and living taxa were included in our analysis, as well as the type of fossil association according to the mode of transport. The leaf energy balance model was used to infer the leaf temperature and transpiration from measurements of vein density and leaf width. As a result, the ecological requirements of fossil taxa of angiosperms and gnetalean gymnosperms were estimated and compared with those of related living plants in different habitats.

S.128.5 How does fossilisation change the anatomy of wood: awareness and consequences?

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Fossil wood belongs to the most frequent and insightful records of ancient terrestrial life. Although cellular anatomical preservation often provides excellent detail, various alterations of organic matter occur during fossilisation and modify tissue properties. Due to manifold taphonomic pathways, plant tissues experience multiple changes, which may cause a tissue-volume reduction, including desiccation, microbial decay, charcoalification, coalification and mineralisation. A few case studies concerning different geological ages, preservational backgrounds and palaeogeographic occurrences offer evidence of widely distributed but vastly underestimated shrinkage phenomena in fossil woods. Samples from several Paleozoic to Cenozoic fossil lagerstätten representing diverse geologic settings are analysed to comprehend putative shrinkage reasons. As a result, volume reduction is more widespread in petrified wood than commonly thought and not easy to recognise. Unexpectedly, tissue contraction varies even in wood from the same fossil site, the same strata and reflecting the same taphonomy. Accordingly, quantitative data on cellular anatomy gained as a routine may be misleading, and cell size and shape modifications affect morphometric purposes, like the interpretation and identification of fossil species. Differences in preservation demonstrate the profound effects of microbial degradation, such as lack of tracheid secondary walls and decayed tissue constituents. Differential shrinkage of silicified wood and stromatolite encrustation help quantify shrinkage by providing graphically measurable, one- and two-dimensional parameters to assess percental volume loss during fossilisation. This study reveals essential shrinkage-related alterations independent of palaeoenvironment, plant material and host rock. The results demonstrate that shrinkage must be considered when comparing fossil and modern wood morphometric data.

S.128.6 The hyperdiverse conifer flora of the Baltic amber forest and its palaeoecological significance

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Late Eocene Baltic amber constitutes the largest amber deposit on Earth and one of the most important Cenozoic fossil lagerstätten worldwide, however, the picture of vegetation and habitat diversity of its source area has been very fragmentary. Notions concerning the Baltic amber flora were mainly based on palaeobotanical data published in the 19th century and the early 20th century, and conclusions concerning habitat types and palaeoclimate were predominantly drawn from the ecology of closest living extant relatives of fossil animals from Baltic amber. Here, we summarize our revision of historic monographic treatments and investigation of conifer inclusions from historic and newly discovered amber specimens, and show that the conifer flora of the source area of Baltic amber was hyperdiverse. Our study revealed five families, 17 genera and 26 fossil-species of conifers, including eight genera and 14 fossil-species of Cupressaceae (*Calocedrus*, aff. *Glyptostrobus*, *Cryptomeria*, *Cupressinanthus*, *Cupressinocladus*, *Quasisequoia*, *Sequoia, Taxodium*); six genera and nine fossil-species of Pinaceae (*Abies*, *Cathaya*, *Nothotsuga*, *Pinus*, *Pseudolarix*, aff.*Tsuga*), and one fossil-species each of the families Geinitziaceae (*Cupressospermum*), Cephalotaxaceae (*Cephalotaxus*), and Sciadopityaceae (*Sciadopitys*). Our data show that the Baltic amber conifer flora is unique and clearly distinct from both central European paratropical or subtropical floras and polar cool-temperate floras of the Eocene. Instead, assemblages from Neogene coastal lowland vegetation of mid-latitudinal Europe exhibit a similar conifer composition. Evaluation of the autecology of individual fossil-species unraveled a heterogeneous vegetation with a mosaic of forests and open habitats in alluvial plains, coastal swamps and mesic hinterland. Our data challenge previous notions that Baltic amber derives from tropical or 'subtropical' forests. Compilation of all currently available botanical data implicates a warm-temperate and humid palaeoclimate in the source area.

S.129 SYSTEMATICS, FLORISTICS, AND CONSERVATION: FACILITATING DATA INTEGRATION TO PROMOTE SOUND SCIENCE. SESSION 1

S.129.1 The intersection of taxonomy and conservation in the United States and Canada

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NatureServe is a conservation non-profit based out of Arlington, VA, USA that has a foundational role in North American conservation. NatureServe works with 60+ Member Programs (usually but not exclusively referred to as Natural Heritage Programs) to answer the three questions of conservation: What species exist, where are these species found, and how are these species doing?

NatureServe is a Red List partner but maintains a distinct ranking methodology that has been used to assess over 100,000 plants, animals, fungi, and natural communities. The NatureServe Network maintains a robust geospatial database that includes over 1,000,000 on-the-ground locations of rare species. NatureServe partners with numerous other organizations to maintain taxonomic currency (including but not limited to the Flora of North America committee, USDA-Plants, and Missouri Botanical Garden's Tropicos Database). NatureServe's ranking system of G-, N-, and S- ranks are integral to conservation as these ranks are a valuable prioritization complement to legal status designations assigned by government agencies such as the U.S. Fish and Wildlife Service and the National Marine Fisheries Service in administering the U.S. Endangered Species Act (ESA), and the Canadian Ministry of Environment and Climate Change in administering the Species At Risk Act (SARA). Integrating the best available taxonomy presents a pressing conservation challenge. The intersection of taxonomy and conservation is often misunderstood, difficult to understand, and confusing for the non-expert. This can lead to the misallocation of precious conservation resources, inappropriate decisions about what species should be conserved, and what natural communities should be restored or managed. Great conservation liabilities exist when there are taxonomic disagreements and misalignments. In this presentation, I give examples of how disagreements or misalignments have caused negative conservation impacts, discuss how NatureServe presents a multi-tiered taxonomy, and propose possible solutions to the botanical community.

S.129.2 The Flora of North America: a hard copy and online continental flora

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The *Flora of North America North of Mexico* (FNA) is a 30-volume work that includes taxonomic treatments for all the native and naturalized plants growing in the continental United States, Canada, Greenland, and St. Pierre and Miquelon. Treatments include accepted names and important synonyms, detailed morphological descriptions, dichotomous keys, phenology and habitat data, text- and map-based distributions, and line drawings of about 20% of the species. The project is a truly international effort involving a collaboration among about 1,000 artists, reviewers, and editors from throughout the world. FNA is a vital tool for those concerned with conserving the continent's flora for several reasons. For many groups, FNA provides the only comprehensive, modern North American treatments available anywhere. Although continental in scope, the treatments are reviewed by a team of about 75 botanists with expertise in their state or provincial floras, ensuring that important local variation and distributions are accurately reflected. The combination of keys and detailed technical descriptions improves plant identification. Furthermore, because taxonomic opinions vary, both among sources and over time, the included synonymy affords the opportunity for nomenclatural and taxonomic cross-walks. Because the treatments are made available online soon after they are published, they not only are widely accessible, but the finely parsed data are also made available in formats that improve data sharing and cross-linking. Efforts currently are underway to improve coordination among FNA, NatureServe, and the USDA-NRCS National Plant Data Team, organizations that play major roles in providing conservation data for North American plants. Looking to the future, we will be working to develop tools for moderated and versioned authoring and editing of treatments at FNA's website (floranorthamerica.org), allowing FNA to remain up-to-date by continuously incorporating results of new research.

S.129.3 Reinventing the "flora" as a 21st century tool for science and conservation

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The flora ("a treatise on or list of the plant life of a particular region") has been a centuries-old basic tool in understanding, studying, and using the plant biodiversity of a particular geographic area. The contents and format of floras have evolved through time, but typically include a list organized by taxonomy of the species native or naturalized in the region covered, with descriptions of the morphology, habitats, phenology, and synonyms of each, including keys for their identification, and sometimes including other information (illustrations, maps, synonyms, taxonomic discussion, chromosome numbers, etc.). Floras are difficult to develop, expensive to publish and purchase, often written for a limited and technical audience, and infrequently revised, hampering the utility and currency of this necessary resource. The Southeastern United States Flora project covers a biodiverse area of in southeastern North America, with about 11,000 vascular plant species. We are using modern technology to reinvent the flora as a dynamic, digital resource for modern biodiversity science and conservation by developing and maintaining a database, FloraManager. FloraManager supports easy revision by multiple, production of products in diverse platforms (traditional paper, web app, installable mobile app), and customization of those products. Digital flora products enable us to have nearly unlimited imagery, taxonomic concept-mapping to over 7000 other taxonomic sources, insertion of diagnostic illustrations as "popups" into keys, development of multiple-access graphic keys, geographic autosubsetting of keys, autocreation of "on-the-fly" dichotomous keys (decision trees) for any set of species in the flora, and inclusion of species-specific conservation information (imperilment status, wetland indicator status, heliophily, ecological conservatism, etc.). Goals include engaging a broader audience (general public, land managers, environmental consultants, etc.) for information on the plants of the region, using modern technology to make plant identification easier, and bringing current taxonomy to bear on locating and conserving plant biodiversity.

S.129.4 Taxonomic discovery from a regional perspective: current approaches and conservation implications

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Despite its long history of botanical exploration, the Southeastern United States still has much novel biodiversity to yield, as evidenced by the large number of new taxa described over the past 50 years – nearly 10% of the recognized native flora. Contemporary molecular tools, in conjunction with traditional systematic techniques, have made this continued advancement possible, particularly concerning difficult species complexes. Furthermore, many of these ongoing studies focus on long-recognized problematic groups, historically neglected due to the perceived need for extensive time and financial investments. As these rate-limiting factors lessen (e.g. NGS sequencing costs decrease), we are encouraged to pursue these "sidelined" studies with a collective evidence approach. This effort utilizes multiple data sources (molecular, cytogenetic, ecological, biogeographic, etc.) to help guide our ultimate taxonomic interpretations. While this approach is not conceptually novel, the power of current technologies to help aid this process is, and an approach that regionally targets known research needs is atypical in a world in which research funding tends to drive research by plant family. Our lab is actively pursuing resolution in a number of clades within taxonomic disparate genera including *Allium* (Alliaceae), *Astragalus* (Fabaceae), *Blephilia* (Lamiaceae), *Carex* (Cyperaceae), *Eryngium* (Apiaceae), *Helianthus*, *Marshallia*, and *Packera* (Asteraceae), *Micranthes* (Saxifragaceae), and *Thalictrum* (Ranunculaceae). We use select examples from these groups to illustrate the case-by-case nuances encountered during our systematic assessments, as well as discuss the regional and global implications of our findings.

S.129.5 Collaboration is the key to documenting and conserving biodiversity: A case study on Colorado's Front Range

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Conservation management requires time, personnel, and funding to accomplish effectively. However, these resources are often in short supply. It is therefore important for government agencies to efficiently spend their time, targeting the most vulnerable rare plant species and communities for protection. Additionally, which species agencies target for conservation relies on a foundation of accurate taxonomic classification. One taxon of conservation concern on the Front Range of Colorado is referred to as *Physaria* X1 by the Colorado Natural Heritage Program (CNHP). *Physaria* X1 is narrowly restricted in range and is hypothesized to be a hybrid between the rare *Physaria bellii* (G2S2) and more widespread *P. vitulifera* (G3S3). Previous research done nearly 30 years ago indicated that *Physaria* X1 may be genetically distinct and deserve recognition as a species. Based on these findings, *Physaria* X1 is tracked as a taxon of conservation concern, despite formal species recognition. However, designation at the species level would have significant management consequences for several agencies. A collaboration of researchers, government, and non-profit agencies determined if *Physaria* X1 deserved species recognition using population-level sampling and next-generation sequencing. Our results showed conclusively that *Physaria* X1 is not a unique species, but a phenotypically unusual *P. vitulifera*. However, surprisingly, one population of *P. vitulifera* was shown to be quite genetically distinct from other populations. Upon further investigation, we found populations of these *Physaria* to also be morphologically distinct from *P. vitulifera* and uniquely substrate specific. Therefore, we recommend that populations of this *Physaria* be treated as a new species, *Physaria pamsmithiae*, for the CNHP botanist who diligently tracked *Physaria* X1 and advocated for this project. These results highlight the importance of government and non-profit agencies working collaboratively with researchers to provide efficient, evidence-based conservation management strategies. Ultimately, these results also inform our understanding of regional biodiversity.

S.129.6 Using genomic data to inform taxonomy and conservation of rare plants

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Accurate taxonomic identification of rare plant species is essential for defining elements of biodiversity and directing conservation funding to protect that diversity. Recent advances in genetic data collection, particularly those utilizing next-generation DNA sequencing technologies, have increased the accuracy and speed of genetic studies, and has lowered the cost to generate robust genomic datasets. Genetic data provides a method to determine if species are distinct from close relatives, genetic structure of populations, and levels of genetic diversity within populations, independent of challenges associated with phenotypic plasticity, which can complicate analyses of plant morphology. However, many of these modern genetic tools remain focused on evolutionary studies and are not directly leveraged to support conservation. In this presentation, We discuss collaborations between the University of Northern Colorado, the U.S. Fish and Wildlife Service, and the Colorado Bureau of Land Management as a model to support the collection of conservation focused genetic data. Supported studies have examined taxonomic uncertainty, defined management units, and increased our understanding species life history. Examples will focus on how genetic data has improved the allocation of conservation resources in Colorado, with studies that determined that *Draba weberi* (Brassicaceae) is not a distinct species, that endangered *Sclerocactus glaucus* (Cactaceae) should be recognized as two species, and that *Erythranthe gemmipara* (Phrymaceae) is entirely clonal with a very uneven distribution of genetic diversity across the species range. Collectively, these results illustrate how agencies and researchers can collaborate to ensure that the taxonomy of plant species of concern is accurate and that conservation activities are targeted to species most in need.

S.130 MALVACEAE: PROGRESS & PROSPECTS IN EVOLUTIONARY RESEARCH IN THE COTTON & CACAO FAMILY

S.130.1 What have we learned from the Malvaceae fossil record?

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The Malvaceae is a family of flowering plants that consists of 244 genera and 4,225 species. This family is found on all vegetated continents and exhibits substantial morphological and habitat diversity. The fossil record has been abundant since the Cretaceous period, but many fossils, especially pollen and leaf remains, are ambiguous. As a result, some subfamilies, such as Malvoideae, may have a challenging-to-interpret fossil record. Nevertheless, Malvaceae fossils are distinguished by the variety of questions they have helped answer throughout the history of paleobotany. What have we learned from the fossil record of Malvaceae? This presentation highlights three focus of study that have been developed: (i) Origins: Although partial, Malvaceae fossils have helped clarify the temporal origin of the family and the diversification of its subfamilies, particularly by supporting molecular phylogenies. The study of new fossils has constantly made it possible to test the ages proposed by molecular analysis and has often extended the previously determined ages. (ii) Biogeography: Malvaceae serves as a model for the biogeography of subtropical floras. For instance, the genus *Craigia*, a relict group from East Asia, has an extensive fossil record that has helped elucidate the history of floras at various geographic levels in the Northern Hemisphere, especially exchanges between North America, Asia, and Europe. (iii) Morphological evolution: Fossils exhibit forms that are little or not documented in the present diversity, allowing us to understand the evolution of certain organs over time. Examples include the inflorescence bracts of the genus *Tilia* and the evolution of wood in the Sterculioideae subfamily, which have revealed morphological changes over time. From these three axes, it follows that the study of Malvaceae fossils addresses many key questions related to plant evolution. New fossils, for example, those from less explored regions, could refine both paleobotanical and neobotanical studies.

S.130.2 Reconstructing the phylogeny of Malvaceae

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The Malvaceae family outstands for its diversity in species richness, morphology, growth form, and geographic distribution. Unraveling the drivers behind such a high variation demands an integrative approach that leverages multiple data sources to yield a comprehensive picture of the evolution of this important family. It is known that numerous events of introgression occurred in the deep past of Malvaceae, which not only explains the pervasive phylogenetic discordance among genes trees, but also explains floral evolution in some subclades. However, the broader implications of introgression on floral evolution remain largely unexplored. This study aimed to quantify the extent of introgression among genera within Malvaceae and to assess its role in shaping floral morphologies. By examining a comprehensive molecular dataset of hundreds of single-copy nuclear genes across all nine subfamilies, we employed a maximum likelihood framework to ascertain introgression levels and direction. Floral evolution was examined applying a model that explicitly tests morphological evolution through introgression. This study illuminates the complex interplay between introgression and floral evolution, providing novel insights into the evolutionary processes that have shaped the phylogenetic relationships and diversity in Malvaceae.

S.130.3 Hibiscus sect. Lilibiscus: Expanding perspectives on the tempo and mode of extreme long-distance dispersal and rapid radiations on

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The last three decades have seen an explosion of studies showing long-distance dispersal to be a major force in determining the patterns of species distributions around the globe. The increasing prevalence of molecular phylogenies with widespread species sampling, coupled with improved dating methods, has revealed that dispersal and subsequent adaptive radiations are common and occur more rapidly than previously thought. Recent studies in the genus *Hibiscus* (Malvaceae) have demonstrated repeated dispersal events out of Madagascar alone, indicating that the island is not only a hotspot of biodiversity but also a source of colonizers to numerous continents. Perhaps most striking are the species in *Hibiscus* section *Lilibiscus*, a group that arose in Madagascar within the last ~2 million years. Members of *Lilibiscus* are largely endemic to oceanic islands, with 19 of the 30 species (63%) occurring on three volcanic archipelagos (Mascarene, Fijian, Hawaiian) spread across the globe. A parsimonious explanation for this distribution might be a single dispersal event out of Madagascar to the Mascarenes, from there to Fiji, and finally to Hawaii. We tested this hypothesis using a 2bRAD next-generation sequencing approach with over 700 samples and produced a phylogeny that includes every species in sect. *Lilibiscus* and closely related outgroups. The resulting species relationships revealed an unexpected colonization pattern, with at least three independent dispersal events out of Madagascar and two-way dispersal between islands in the Pacific and Indian Oceans. This suggests that we may still be underestimating the ability of species to regularly disperse across incredibly long distances and that species disjunctions could be much younger than expected. In addition, we uncovered a surprising biogeographical connection between volcanic archipelagos in the Pacific and Indian Oceans that requires further investigation.

S.130.4 Towards an updated classification of Malvales and Malvaceae: insights from phylogenomics and morphology

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The Malvales, a diverse order of flowering plants spanning various global biomes, boasts significant species diversity and morphological variability. Despite its ecological and economic importance, Malvales classification has been largely neglected since the late 1990s. This study addresses this gap by revisiting Malvales classification, emphasizing its largest family Malvaceae. By integrating molecular and morphological datasets, our primary goal is to map key traits for classification onto an extensive phylogeny and reassess taxonomic boundaries as necessary. This investigation enhances our evolutionary understanding of Malvales, bringing providing valuable insights for a more contemporary taxonomy. We generated a molecular dataset based on 196 nuclear genes for 188 genera within Malvales, including genera from all recognized families and subfamilies, almost all tribes, and all subtribes. Phylogenetic trees were inferred using maximum-likelihood and a coalescence approach to reconcile conflicts. A morphological matrix with 52 characters relevant for to supra-generic classification was compiled to identify diagnostic features within specific clades. Character state distributions were mapped onto the final phylogenetic topology to aid the search of for diagnostic features for of suprageneric taxa. Phylogenetic relationships and monophyly for most groups aligned with prior research. Significant variations in diagnostic morphological traits were observed across clades, including growth forms, leaf structures, pollen types, flower floral attributes, and fruit/seeds. Incongruities in relationships among some Malvales families and within well-supported Malvaceae clades were attributed to discrepancies observed in gene trees. For Malvaceae, uncertainties in basal Malvoideae were resolved. Incongruities among nuclear loci, while not impacting clade definitions, suggest caution in interpreting the current Malvaceae classification. We propose maintaining Malvaceae *sensu lato* and introducing two new subfamilies (Matisioideae and Durionoideae) for several tropical genera. Pollen characteristics define Malvoideae as a monophyletic subfamily. Four new tribes within Malvoideae improve taxonomic placement for genera previously of uncertain classification, aligning with updated findings.

S.130.5 A new phylogeny and classification for tribe Hibisceae (Malvaceae)

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Tribe Hibisceae represents a very iconic group of plants with extraordinary horticultural, agricultural and cultural significance. No studies, however, have broadly sampled across the dozens of taxa within the tribe, leading to uncertainty in the relationships among genera. The non-monophyly of the genus *Hibiscus* is infamous and challenging, whereas the monophyly of most other genera in the tribe has yet to be assessed, including the large genus *Pavonia.* We significantly increase taxon sampling and assess monophyly of most currently recognized genera in the tribe. We also include many newly sampled species and sections of *Hibiscus* and *Pavonia*. Our phylogenetic trees demonstrate that *Hibiscus*, as traditionally defined, encompasses at least 20 additional genera. The status of *Pavonia* emerges as comparable in complexity to *Hibiscus*. Our phylogeny offers clarity in the phylogenetic placement of several taxa of uncertain affinity (e.g., *Helicteropsis*, *Hibiscadelphus*, *Jumelleanthus*, and *Wercklea*). We introduce a new classification for the tribe and clarify the boundaries of *Hibiscus* and *Pavonia*.

S.131 THE ROLE OF AGMATOPLOIDY AND SYMPLOIDY FOR DIVERSIFICATION OF FLOWERING PLANTS WITH HOLOCENTRIC CHROMOSOMES

S.131.1 Evolutionary significance of holocentric chromosomes

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Holocentric chromosomes, in contrast to the commonly known monocentric ones, exhibit a remarkable tolerance for fragmentation. They have independently evolved multiple times in both plants and animals. Despite their rarity, holocentrics might have significantly influenced the colonization of land half a billion years ago, while also gaining relevance as significant agricultural pests in contemporary times. Furthermore, these chromosomes are increasingly becoming focal points in studying chromosomal speciation and comprehending the impact of recombination on species' success within dynamic or stable environments.

S.131.2 The architecture of chromosome fission and fusion in holocentrics

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Chromosome evolution is a major driver of diversification in angiosperms. Whereas polyploidy has been investigated at a great deal in angiosperms, dysploidy (chromosome number changes by fission/ agmatoploidy and fusion/symploidy without a significant change in DNA content) has been, in comparison, mostly ignored. The clade of family Cyperaceae, with holocentric chromosomes -kinetochoric activity is distributed along the whole chromosome-, and consequently a large range of chromosome number vatiation, is an ideal study system to investigate the consequences of chromosome fission and fusion. By fitting models of chromosome evolution in the phylogeny of the Cyperaceae, we have inferred that the rate of dysploidy, and also polyploidy, is not homogeneous across Cyperaceae, instead there are clades where rates of chromosome evolution accelerates or decelerates. Using comparative genomics of closely and distantly related species, we have also observed the pull of the present for chromosome evolution. The same way that the rates of molecular, morphological, fossil and speciation seem to accelerate towards the present in the tree of life, we have also found how the rates of fission and fusion seem to be much faster at microevolutionary scale than at macroevolutionary scale. Comparative genomics suggest that there is a strong genomic constraint that limits where fission and fusion may occur which results in parallel events of fission and fusion across different lineages and leads to underestimate the rates of dysploidy at the macroevolutionary scale. The inferred hotspots of dysploidy are very rich in repeat DNA, that is, the repeat landscape may determine the rates of fission and fusion and their location in the genome. Finally, at microevolutionary scale, we shed light into the crucial question of how new karyotypes become established. New chromosome variants may become fixed in the populations by both, stochastic processes like drift or selection of locally adapted karyotypes.

S.131.3 Cryptic evolution and diversification of agmatoploid-polyploid Luzula sect. Luzula (Juncaceae) in the Eastern Alps

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The diversification of flowering plants has been influenced by changes in the number and structure of chromosomes. While the evolutionary consequences of chromosome duplications (polyploidy) are well documented, much less is known about the effects of chromosome fragmentations (agmatoploidy). *Luzula* (Juncaceae) is a genus with common incidence of both phenomena, leading to a variety of cytotypes. The most variable and taxonomically intricate group within the genus is *Luzula* sect. *Luzula*, of which eight species with six karyotypes, including di-, tetra- and hexaploids, have been reported for the Eastern Alps. However, due to weak morphological differentiation among taxa, their distributions and phylogenetic relationships are insufficiently known. By using an integrated approach employing extensive vegetation surveys, relative genome size estimations, chromosome counts, RAD- and plastome sequencing, we aim at disentangling the evolutionary history and ecological niche segregation within this species complex. Combining a variety of different methods will allow us to reconstruct phylogenetic relationships among species as well as unravel the roles of chromosome duplication and fragmentation for speciation and ecological divergence in *Luzula*. In this talk we present preliminary results of ecological and genomic data. Our findings include common co-occurrence of cytotypes at the same locality and a varying degree of ecological differentiation among taxa. In the (sub)alpine belt, we found tetraploid species to be more common on silicates while diploid *L. exspectata* occurs mostly on calcareous bedrock and *L. sudetica* is restricted to humid habitats.

S.131.4 Initial insights about mono- and holocentromeres in carnivorous Drosera species

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Sundews are carnivorous plants that grow in nutrient-poor habitats, such as bogs, swamps, and sand dunes. They are distributed globally, with more than 200 species described. In addition to carnivory, sundews are reported to have great diversity of genomic and chromosomal features. The chromosomes of sundews have been studied for over a century revealing extraordinary variability in chromosome number and ploidy across species. But perhaps, one of the most fascinating features of sundews chromosomes is the fact that several species analyzed within the genus *Drosera* lack a visible primary constriction, leading to the assumption that holocentricity is common in the genus. This is very exciting as it points to the occurrence of both monocentric and holocentric species in a single genus. Combining genomics and cytogenetics we are analyzing the genome of *Drosera* species differing in centromere organization. We assembled the genome of 5 selected species from the main clades using a combination of long-read sequencing technologies. In addition we made use of low-coverage Illumina short reads for the characterization of the repetitive fraction of the genome in additional species. Our preliminary data reveals the different genome architecture of mono- and holocentric *Drosera* and suggest that satellite repeats are associated with centromeres in both types. However, satDNAs are rarely conserved among *Drosera* species contrary to other reported holocentric species. Moreover, the development of specific centromere markers allowed us to verify the centromere type of our set of species. In addition our data gives insights into the evolution of the karyotypes of *Drosera* species. Synteny analyses among *Drosera* and its sister clade such as *Nepenthes* showed that events of fission and fusion are common in the group. This work could provide the bases for the understanding of the genomic changes associated with holocentricity as well as the drivers of this transition.

S.131.5 Combining chromosome evolution models and phylogenomic data to disentangle polyploidy and single chromosome evolution in Drosera

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Drosera L. (Droseraceae, Caryophyllales) has been long thought to exhibit large amounts of chromosome evolution due to both single chromosome number change and polyploidy. We used the BiChrom model to test whether rates of single chromosome number increase and decrease, and chromosome number doubling differed between *D.* subg. *Ergaleium* and the other subgenera and between self-compatible and self-incompatible lineages. The best model for chromosome evolution among subgenera had equal rates of chromosome number doubling but higher rates of single chromosome number change in *D.* subg. *Ergaleium* than in the other subgenera. Contrary to expectation, self-incompatible lineages had a significantly higher rate of single chromosome loss than self-compatible lineages. The findings of different rates in different subgenera were further supported by phylogenomic analyses not finding evidence for any polyploid events in the *D.* subg. *Ergaleium* while finding evidence of polyploidy in the other subgenera. We found no evidence for an association between differences in single chromosome number changes and diploidization after polyploidy or centromere type. This study highlights the complexity of factors influencing rates of chromosome number evolution. Further work should explore whether meiotic and specifically holocentric drive might explain heterogeneity in chromosome number evolution in *Drosera*. This work is in part published in Evolution at https://doi.org/10.1093/evolut/qpad153.

S.131.6 Detecting shifts in the mode of chromosomal speciation across the cosmopolitan plant lineage Carex

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Recent studies of angiosperm diversification have focused on the role of polyploidy as a driver of diversification. However, we know far less about the effects of single changes in chromosome number—dysploidy, which can mediate lineage diversification by affecting recombination rates, linkage, and/or reproductive isolation. Modeling the effects of dysploidy on diversification is mathematically and computationally challenging because many states and parameters are required to track changes in individual chromosomes, especially in lineages that have high variability in chromosome number. Additionally, we expect the processes of diversification and dysploidy to vary across clades, which requires modeling process variation to disentangle the effects of the observed trait (chromosome number) from the effects of unobserved traits on diversification. In this work, we propose a new state-dependent diversification model of chromosome evolution that includes numerous character states and explicitly models heterogeneity in the diversification process. Our model includes parameters that functionally link diversification rates to dysploidy rates and differentiate between anagenetic and cladogenetic changes. We apply this model to *Carex* (Cyperaceae), a model lineage for understanding dysploidy and diversification, leveraging chromosome number information and the most recent time-calibrated phylogenetic tree for over 700 species and subspecies. We recover distinct modes of chromosomal speciation across *Carex*. In one mode, dysploidy occurs very frequently and drives faster diversification rates. In the other mode, dysploidy is rare and diversification is driven by other factors, unmeasured in our analysis. This study is the first to demonstrate that dysploidy drives diversification in plants while considering unmeasured factors affecting diversification.

S.132 BIOGEOGRAPHIC AND EVOLUTIONARY PATTERNS AND PROCESSES OF THE TROPICAL - TEMPERATE BIOME TRANSITION

S.132.1 Taxonomy, biogeography, and sectional boundaries of the tropical blueberries (Vaccinieae, Ericaceae) of Malesia

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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.

S.132.2 The tropical-temperate transition in a World without clear-cut climatic boundaries: evolutionary implications

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The so-called latitudinal diversity pattern has often been explained invoking the clear-cut climatic differences between tropical-temperate latitudes. However, this hypothesis assumes that moving from the tropics to the temperate latitudes implies drastic changes in the climatic preferences of the species. Yet the climatic transitions between regions are often gradual and overlooking their importance can deeply affect how we perceive the impact of climate on evolutionary patterns. We examined the nature and distribution of the transitions between climatic regions worldwide and evaluated their impact for inferring the past and present climatic preferences in the Asian Palmates, a highly diverse and climatically complex lineage of Araliaceae. We find consistent geographic patterns in the climatic transitions worldwide. Particularly, we detect a consistent higher extent and spatial complexity of the transitions between tropical-temperate climates in the Old World. By considering climatic transitions we identified that the early ancestors of the Asian Palmates had strong affinities for the subtropical-temperate transitions suggesting an initial diversification under such climate. This leads us to propose that the Asian Palmates diversified under these transitional climates and its evolution was interspersed with occasional shifts towards more pronounced tropical or temperate climates. Such results emphasized the significance of transitional climates in understanding niche diversity and evolutionary patterns and calls for a (re) evaluation of the role of transitional areas in promoting biodiversity across the Tree of Life.

S.132.3 A diversification-transition model between tropical and temperate biomes explains the Northern Hemisphere biodiversity

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The evolutionary patterns and processes driving ecological transition and diversification between tropical and north temperate biomes are complex and remain poorly understood in the Northern Hemisphere flora. Moreover, it is becoming clear that introgression is an important driving force of speciation in plant diversity. Here, we applied phylogenetic and biogeographic analyses to account for both introgression and incomplete lineage sorting based on genomic data from two charismatic lineages of the Northern Hemisphere, the tribe Viteae (the *Ampelocissus-Vitis* group) of Vitaceae and *Magnolia* of Magnoliaceae. Biogeographic inference and fossil evidence suggest that the ancestors of Viteae were widely distributed from North America to Europe during the Paleocene to the Eocene, followed by widespread extinction and survival of relicts in the tropical New World. During the climate warming in the early Miocene, an ancestor migrated northward from the refugia with subsequent diversification in North America and Eurasia. Similarly, *Magnolia* had once been widely distributed in the Northern Hemisphere in the early Palaeogene followed with extensive extinction and southward retreat to the low-latitude regions during the middle to late Eocene cooling climate. Magnoliaceae had been well diversified in the tropical regions with less development during the transition back to the temperate regions. Meanwhile, we found strong evidence for widespread incongruence and reticulate evolution among nuclear genes within both recent and ancient lineages in the *Ampelocissus-Vitis* clade and *Magnolia* during their biome transitions and diversification in the Northern Hemisphere. The scenario we report here may represent a transition model between tropical and temperate regions in general for flowering plants that adapted to the global climate cooling and fluctuation in the Northern Hemisphere.

S.132.4 The modernization of plant diversity on the Qinghai-Tibetan Plateau associated with the late Eocene climate transition

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The modernization of plant diversity, which means the floristic assemblage in deep time being similar to nowadays, is a milestone for the evolution of global plant diversity; however, little is known about when did this process occur. Recent paleobotanical investigation on the Qinghai-Tibetan Plateau (QTP) sheds new lights on this topic. The late Paleocene Liuqu flora (~59 Ma) from southern QTP mainly consists of Annonaceae, Fabaceae, Moraceae and Palmae, suggesting a tropical forest. The middle Eocene Jianglang flora (~47 Ma) from central QTP is composed of Apocynaceae, Araceae, Menispermaceae, Sapindaceae and Simaroubaceae, there is no dominant species in this subtropic flora. The Dayu flora (~39 Ma) from central QTP consists of both woody plants and herbs, indicating the vegetation of open woodland. The floristic components of all these floras mentioned above are quite different from modern vegetations. It is not until the latest Eocene that the floristic components are similar to nowadays, which is evidenced by the Markam flora from eastern QTP with Fagaceae and Betulaceae as the most abundant taxa. This kind of evergreen deciduous broad-leaved mixed forest still survives in southeastern margin of the QTP nowadays. During the latest Eocene, the growth of the QTP and the associated climate change from dry to wet condition may contribute to the modernization of plant diversity on the QTP and regions nearby, and gradually shaped the rich plant diversity in this large area.

S.132.5 Terrestrial plant evolution driven by the global cooling during the Eocene-Oligocene transition-examples from three tribes of Leguminosae

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An abrupt, dramatic global cooling event occurred during the short period of the Eocene-Oligocene transition (EOT). This paleoclimatic event drove a large-scale aridification and increasingly seasonality, which drastically influenced the evolution of plants and distribution of global vegetation, especially, the great retreating of boreotropical flora. However so far, previous biogeographic studies have not well interpreted the molecular mechanism of the influence on terrestrial plants. The leguminous tribes Glycyrrhizeae (the liquorice tribe), Adinobotryeae and Wisterieae (the *Wisteria* tribe) formed a clade, widely distributed in every continent except for Antarctica. Based on the data of orthologous nuclear genes and chloroplast genomes from deep next-generation sequencing, and using the interdisciplinary analyses of historical biogeography, molecular ecology and phylogenomics, our study revealed that the common ancestor of the three-tribe clade existed in boreotropical region during the Eocene, and experienced inter-tribal divergence, rapid niche evolution and biome shift from humid tropical forest to drier grassland or desert at the EOT. Subsequently, adaptive evolution occurred to many taxa of the clade, especially those of Glycyrrhizeae, to survive the changing habitats. On the other hand, the EOT global cooling differentiated the plant habits among the three tribes: herbs for Glycyrrhizeae, trees for Adinobotryeae and woody lianas for Wisterieae. To better investigate the noticeable point, with the annotated whole genomes obtained from the third-generation sequencing of representatives for each of the tribes, this study assessed the genome structure change and the evolution of the key gene families, whose function was to regulate the trait of habits by influencing the biosyntheses of cellulose and lignin. With the three tribes as a model, our results can provide a reference to the studies on plant evolution under the present background of global environmental changes.

S.132.6 Machine learning analyses of herbarium specimens identify morphological features characterizing tropical to temperate transitions

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The phylogenomic age has revealed that the number of plant lineages that can successfully transition between temperate and tropical biomes is surprisingly low. One explanation for this trend invokes the difficulty of tropical lineages acquiring the necessary traits to tolerate the cooler, drier, and more seasonal temperate zone. Nevertheless, in rare cases, some lineages have been able to successfully migrate from the tropics to temperate zones during their evolutionary history. Presumably, these transitions were facilitated by the acquisition of morphological characters enabling adaptation to novel habitats (i.e., temperate environments). Synthesis of biogeographic studies of many plant lineages improved our understanding of the frequency of tropical-temperate transitions, but our understanding of associated trait evolution lags behind. Here, we use novel approaches for quantifying phenotype—machine learning algorithms that can classify and extract leaf, flower, and fruit features from digitized herbarium specimen images—to infer the morphological characters that were important for enabling transitions from tropical to temperate biomes. Specifically, we used the machine learning package LeafMachine2 to extract leaf, flower, and fruit traits from tens of thousands of specimens in targeted groups. We used the plum/cherry genus (*Prunus*, Rosaceae) and the grape genus (*Vitis*, Vitaceae) because they represent rare lineages that successfully transitioned from tropical to temperate biomes. We used morphological data from tens of thousands of digitized specimens representing hundreds of species to trace continuous character evolution on time-calibrated phylogenies. This approach was selected so that the effects of both evolutionary history and past environmental conditions on observed phenotype could be considered. We measured leaf and reproductive characters and assessed phenology to identify features associated with biome shifts. Additionally, for comparative purposes, we investigated morphological variation within extant widespread species. The workflow developed for connecting morphological data with phylogenetic and environmental data is available as a user-customizable pipeline.

S.133 THE SPECIAL AND ENDURING VALUE OF MODEL CLADES IN EVOLUTION AND ECOLOGY

S.133.1 What is a model clade? Viburnum as an example

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What makes a clade a model clade? In our view it is not because it provides a good example of some particular phenomenon or process. This, we think, is true of every clade. Likewise, it is not because it is a clade that includes a model species such as *Arabidopsis thaliana*. Nor is it because it somehow represents a microcosm of the variety manifested by a more inclusive clade. Instead, we adopt the view that a model clade is simply one that has been studied intensively and from many different angles, leading naturally to a more holistic understanding. The expectation is that this concerted, integrative attention to a group of organisms will yield insights that would not otherwise be attainable, and this accumulation of context will invariably improve our interpretation of any one study in isolation. We view this context as critical in evaluating macro-evolutionary data and predict that studies of model clades will continue to provide the most compelling explanations of organismal evolution. Although there are no rules for the development of a model clade, there are some things that are foundational in providing a platform for diverse studies. One key element is the development of a firm understanding of phylogenetic relationships and of a phylogenetic classification system to support unambiguous communication across labs and generations. An additional consideration is clade size. There are distinct advantages to clades of moderate size – large enough to support convincing statistical analysis, but not so large that comprehensive surveys become too challenging. *Viburnum* (Adoxaceae) provides an example of a model clade in the sense that we have outlined here, and we provide concrete examples of novel insights that have emerged as a consequence of having carried out a diverse set of studies of *Viburnum* over multiple decades.

S.133.2 The tribe Bignonieae (Bignoniaceae) as a model for understanding evolution, ecology, and biogeography in the Neotropics

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The tribe Bignonieae (Bignoniaceae) comprise ca. 20 genera and 400 species that are broadly distributed through the Neotropics, representing the largest and most successful clade of lianas in this part of the World. Species of Bignonieae show diverse morphology, ecology, and distribution, occurring in all major ecological zones (dry to wet) and providing an excellent opportunity to further understand habitat movements, niche transitions, and adaptations to dry/wet environments. The comprehensive phylogenetic, morphological, distribution, fossil, and ecological datasets gathered during the past three decades allow us to test hypotheses on the evolution of morphology, ecology, and biogeography of this important plant clade. Some of this work involved detailed studies of traits associated with the climbing habit (e.g., wood anatomy, tendrils), insect-plant interactions (e.g., nectaries, mitedomatia, trichomes), pollination systems (e.g., traits associated with different flower whorls), and dispersal (i.e., seeds). While Bignoniaceae is a model system, our exhaustive exploration of the Neotropical Bignoniaceae established the basis for cross-taxonomic and multi-disciplinary studies that combine similar datasets for other organisms. The understanding of species' movements to dry environments across clades is allowing us to gain a deeper appreciation of clade-specific differences in the ability to adapt to climate change. Information of this nature is crucial to manage biodiversity, design sound policy, and establish conservation priorities.

S.133.3 Hydnophytinae as a model clade

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Widespread in nature, mutualistic associations –cooperative interactions between unrelated species– are pivotal for the generation and maintenance of biodiversity. These partnerships vary from loose, facultative interactions between large guilds to tight, obligate interactions on which species depend for reproduction or survival. The Hydnophytinae is a clade of 105 species of epiphytic Rubiaceae, most of which form symbiotic mutualisms with ants. Despite its size, the Hydnophytinae have a higher rate of evolutionary transitions in mutualistic dependence magnitudes than mycorrhizal, pollination and seed dispersal mutualisms, making them an ideal model clade to study the evolution of mutualisms. I synthesize a decade of work and show how integrative, phylogenetically-informed studies of Hydnophytinae ant/plant symbioses have shed major insights on our understanding of mutualisms as a whole. Using phylogenetic comparative methods, field experiments, comparative genomics and transcriptomics, 3D imaging, microbiology and modelling, I show how mutualistic dependence is critical for determining the evolutionary stability of the partnership, its efficiency in trading resources, and show how it mediates trait evolution within and beyond those involved in the interaction. I also show how the Hydnophytinae can help us resolve the paradox of multi-species mutualisms and share new insights on mechanisms promoting obligate dependence between 'macro' partners.

S.133.4 The where, when, and why of pulsed trait evolution in an explosive plant radiation, Lupinus (Fabaceae)

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We present an overview of why the genus *Lupinus* L. (Fabaceae) has emerged as a model clade for studying rapid recent plant radiations providing potent insights into the drives rapid ecological and phenotypic plant diversification. The Western New World *Lupinus* clade with more than 200 species, comprises a series of nested and parallel radiations, including the recent rapid Andean radiation. Previous work has shown that a combination of biome shifts and life form changes underpin accelerated species diversification, but detailed understanding of the interactions between environmental and phenotypic evolution is lacking. Moreover, while multiple drivers of high rates of species diversification have been proposed, the drivers of rapid ecological and morphological trait evolution remain unclear. Here we leverage taxonomic, morphological, biogeographic, and environmental data to ask what environmental factors drove the apparently differential rates of trait evolution among western New World *Lupinus* lineages. Specifically, we test which model classes, including models of incremental or pulsed change (i.e., Lévy processes), best describe evolution across eight traits, and whether life forms, climatic niches, and biographic realms affect the tempo and mode of trait evolution. We demonstrate a radically expanded trait space occupancy by the Andean clade. We reveal support for pulsed evolution in three of eight plant traits and identify five nested branches in the Andean clade that are congruent with "evolutionary jumps", rather than a single shift to an overall higher rate of incremental evolution. We find that these shifts are associated with perennials occupying aseasonal temperature niches, but not all such lineages experience "jumps", suggesting that longer life spans and longer growing seasons are prerequisites but, alone are insufficient to drive episodes of pulsed trait evolution. Our findings demonstrate the existence of rapid bursts of trait evolution and suggest that pulsed evolution may be a common feature of plant radiations.

S.133.5 Sarraceniaceae as a model clade

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Sarraceniaceae is the *Drosophila* of community ecology. The fluid-filled leaves of these carnivorous plants have, over the course of centuries, captivated professional and amateur botanists alike, and — owing to their unique phytotelmic habit — have been used by ecologists, entomologists, and microbiologists as miniature models for lakes, island chains, and animal digestive systems. The balance between tractability and realism in Sarraceniaceae microcosm studies has produced many key insights into the functioning and dynamics of communities and ecosystems that would otherwise be impossible in larger systems. Sarraceniaceae are similarly important from botanical and evolutionary perspectives. Captivating as these plants are, however, many aspects of their evolution and biology remain shrouded in mystery. While their phylogenetic placement is becoming clear, far less is known about their landscape genetic structuring, trait-environment relationships, and mechanisms of prey attraction, capture, digestion, and dispersal. Furthermore, major questions remain concernning the evolutionary history of the group, as well as mechanisms contributing to their local-scale diversification in the Southeastern United States and Guiana Highlands. In this talk, I discuss my research history with Sarraceniace and *Darlingtonia californica*, in particular. I show how an integration of ecological, genetic, and biomechanical studies focusing almost entirely on this single clade has, perhaps paradoxically, helped me become a more interdisciplinary scientist and more effective advisor and collaborator. I also introduce a brief history of the use of the Sarraceniaceae model system in community ecology — highlighting the groundwork of both established and early career researchers — and conclude by outlining areas which would further help enshrine the family as a model system that can effectively integrate many fields of science.

S.133.6 Cuscuta (dodders; Convolvulaceae) as a model-system to study biology of heterotrophic plants

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Among several dozen independently evolved groups of heterotrophs, *Cuscuta* is emerging as a model clade for understanding different aspects of heterotrophic plant biology due to the convergence of several factors. First, *Cuscuta* is one of the largest and most economically important lineages of heterotrophic plants. Second, phylogenetic relationships within this species-rich group are well-resolved and strongly supported. Third, the shallow phylogenetic level that encapsulates substantial diversity observed in this genus makes the system tractable. We are now interested to use this system to explore in-depth three particular venues of heterotrophic plant biology: *Cuscuta* is one of only two clades of haustorial parasites known to span the trophic continuum from photosynthetic hemiparasites to non-photosynthetic, obligate holoparasites. Most of its lineages are "cryptically photosynthetic" and capable of limited and localized photosynthesis. However, we were unable to recover any plastome sequences from section *Subulatae*, suggesting that plastomes of its species are likely entirely lost, a condition encountered only once before in the angiosperm evolution (Rafflesiaceae). Furthermore, *Cuscuta* may represent a genus with the broadest karyotypic and genome size diversity among all of angiosperms. This group includes species not only with regular monocentric but also with holocentric chromosomes, a feature found in a very few phylogenetically scattered groups of plants. In addition, the genus has diverse karyotypes, with enormous variation reported for chromosome numbers, chromosome size, and variation in nuclear DNA content as well as presence of symmetrical and asymmetrical karyotypes. Discordances between phylogenies derived from different data sources suggest that reticulation and polyploidy have likely played a significant role in *Cuscuta* species diversification, with potentially 10% of its species being of hybrid origin. Some of these cases are consistent with more ancient hybridization events while represent relatively recent reticulations. Our current progress in these three areas of *Cuscuta* biology will be discussed.

S.134 TELLING PLANT SPECIES APART WITH DNA. SESSION 1

S.134.1 Molecular barcoding identification of invasive species dispersed by wind and in the soil seed bank of South Georgia using phylogen

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Climate change and invasive species are major causes of biodiversity loss. Invasive species are highly competitive in ecosystems due to their ability to germinate and grow in a wide range of conditions, their capacity to produce high reproductive outputs and their effective dispersal strategies. Climate change has already severely impacted several ecosystems across the planet, such as sub-Antarctic regions with temperatures rising there fastest in recent decades. The effects of climate change can exacerbate the impacts of invasive species by enhancing features that favour invasiveness, such as tolerance to a broad range of environments. Islands are particularly vulnerable to the effects of climate change due to reduced habitable space, small populations, and low functional redundancy. The remote sub-Antarctic island of South Georgia is 160 km in length with a vegetated area of approximately 30,000 ha predominantly confined to near coastal regions due to snow and ice being prominently present inland. South Georgia has a history of use as a land base for extraction of natural biotic resources from the surrounding coasts and ocean. Due to human occupation, non-native flora and fauna were inadvertently and/or intentionally introduced. Today, the introduced flora with 41 species outnumbers the native flora with 24 species. To mitigate this problem, the South Georgia Non-Native Plant Management Strategy was implemented during 2016-2020 to reduce the population size of non-native species on the island. We evaluate the efficacy of this eradication programme by quantifying the incidence of invasive species seeds in the soil seed bank. We designed a molecular barcoding approach to enable accurate identification of seedlings by evaluating the resolution of traditional barcoding markers (i.e., *rbc*L and *mat*K) and optimising a high-throughput sequencing molecular barcoding method. We applied this method to identify seedlings that emerged from soil samples collected at key areas on the island.

S.134.2 An evaluation of the taxonomic status of Musa viridis, Musa splendida, and Musa paracoccinea using high-throughput sequencing data

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The delimitation of species based on morphological traits can be challenging due to overlapping trait variation. The taxonomic identity of closely related sympatric species with individuals displaying intermediate phenotypes is particularly questionable. However, thorough morphological assessments or traditional molecular analyses often lack resolution to clarify if two species are truly separate taxonomic entities or should be merged. Interestingly, advances in high-throughput sequencing methods and data processing during the last decades enable the use of high-resolution data to tackle taxonomic problems. Several species with an unclear taxonomic status are found in the banana family (Musaceae). In Vietnam, the *Musa* species *M. viridis*, *M. splendida*, and *M. paracoccinea* have very similar morphological trait characteristics. The main difference between *M. splendida* and the two other *Musa* species is the colour of the male flower bud: *M. splendida* has red flower buds, whereas *M. viridis* and *M. paracoccinea* have pink flower buds. All three species occur sympatrically, and individuals with red and pink male flower buds are found together in some populations. In this study, we used high-throughput (DArT) sequencing data from plants of nine populations to investigate the taxonomic status of these *Musa* species. Maximum likelihood phylogenetic trees were reconstructed for over 12,000 loci (< 120 base pairs) and one ASTRAL consensus tree was created from all locus trees. The individuals in the ASTRAL phylogenetic tree did not cluster by species identity, but by population, having individuals from different species in the same cluster. Consequently, we propose to merge the species *M. viridis*, *M. splendida,* and *M. paracoccinea* into one species named *M. splendida* according to nomenclatural conventions.

S.134.3 Precision of molecular plant identification of plants in the coastal dunes in Thy National Park, Denmark

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Coastal sand dunes are highly dynamic landscapes shaped by wind, water and salt. In Europe they are mainly distributed along the Atlantic coastlines. In Denmark sand dunes are widespread and are characterized by a rapid turnover of the constituent habitat types. In this project we address the need for novel and efficient ways of monitoring dunes dynamics. Traditionally, a trained botanist identify plants either by recognizing them or using a scientific flora. However, this procedure is constricted to the flowering season and often requires complete plant specimens. Molecular plant identification is a tool that may prolong the monitoring season, can identify plants based on fragments, and can add to the quality of plant identification. To test the precision of molecular plant identification we collected four individuals from each of 100 plant species common to or characteristic of the sand dunes in Thy National Park. For each individual we sampled a herbarium voucher specimen and leaf material dried and preserved in silica gel. From the leaf material the DNA barcode genes *rbcL* and *matK* were sequenced. We used *rbcL* sequences to probe into the ability of the international databases, Genbank and BOLD to retrieve the correct identifications. Less than 50% of the individuals were unambiguously identified to the correct species. However, a barcode gap existed between all species, except for a few hybrids of *Juncus*. A Neighbour Joining analysis clustered individuals of each species and was congruent with the current APGIV classification. We conclude that caution should be exercised when basing plant identification purely on BOLD and GenBank. The most important sources of error in the online databases were mismatch between the sequence uploaded and the underlying herbarium voucher specimen, wrong identification of herbarium specimens, and mismatch between the length of the sequence in the database and the sequence submitted.

S.134.4 Next-generation DNA barcoding using phylogenomic data

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DNA barcoding has the potential to enable and speed up plant identification, but traditional barcoding using single to few genes is limited by insufficient discriminatory power in plants. Novel sequencing technologies can routinely generate hundreds of genes even from degraded plant material, promising to overcome the current limitations and unlock a new era of next-generation DNA barcoding. Despite this potential, no barcoding tools exist that can handle dozens or hundreds of genes. To address this methodological gap, we have developed a novel approach to DNA barcoding that can take the information content of hundreds of genes into account. Here, we present our DNA identification toolkit and illustrate its potential to revolutionise plant identification using a case study of rattan furniture authentication. By comparison with traditional barcoding markers, we demonstrate a substantial increase in both accuracy and interpretability of our approach compared to existing methods. The toolkit is publicly and freely available (https://github.com/BenKuhnhaeuser/RattanID).

S.134.5 Towards a nuclear DNA barcode for land plants

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Accurate and rapid identification of plant species is of fundamental importance for understanding global biodiversity, monitoring change, and managing biodiversity. Yet plant species identification can be challenging in many situations. To address this challenge, a substantial body of data has been generated using standard plant barcodes such as *rbcL, matK, trnH-psbA* and ITS for telling plant species apart. These barcode markers are useful for many applications, but do not provide universal species-level discrimination. There is thus considerable interest in developing new standardised plant barcoding methods. In this presentation we (1) review the strengths and limitations of the standard barcoding approach; (2) explore the potential for gains in discriminatory power by using complete plastid genomes as plant barcodes; and (3) explore recent work considering options for utilisation of nuclear loci for plant DNA barcoding. In the exploration of nuclear loci for species identification we cover the frequency with which plant species resolve as monophyletic based on studies to-date, the number of randomly selected nuclear loci required to give maximal species discrimination, and whether there are individual loci that show any exceptional species discrimination performance. We conclude by outlining a roadmap for further developing nuclear DNA barcoding approaches for plants.

S.134.6 Plant DNA barcode library for native flowering plants in the arid region of northwestern China

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DNA barcoding is a well-established tool for rapid species identification and biodiversity monitoring. A reliable and traceable DNA barcode reference library with extensive coverage is necessary but unavailable for many geographical regions. The arid region in northwestern China, with a vast area of about 2.5 million km^2, is ecologically fragile and often overlooked in biodiversity studies. In particular, DNA barcode data from the arid region of China is lacking. We develop and evaluate the efficacy of an extensive DNA barcode library for native flowering plants in the arid region of northwestern China. Plant specimens were collected, identified and vouchered for this purpose. The database utilized four DNA barcode markers, namely *rbcL*, *matK*, ITS and ITS2, for 1816 accessions (representing 890 species from 385 genera and 72 families), and consisted of 5196 barcode sequences. Individual barcodes varied in resolution rates: species- and genus-level rates for *rbcL*, *matK*, ITS and ITS2 were 79.9%–51.1%/76.1%, 79.9%–67.2%/88.9%, 85.0%–72.0%/88.2% and 81.0%–67.4%/84.9%, respectively. The three-barcode combination of *rbcL*+*matK*+ITS (RMI) revealed a higher species- and genus-level resolution (75.5%/92.1%, respectively). A total of 110 plastomes were newly generated as super-barcodes to increase species resolution for seven species-rich genera, namely *Astragalus*, *Caragana*, *Lactuca*, *Lappula*, *Lepidium*, *Silene* and *Zygophyllum*. Plastomes revealed higher species resolution compared to standard DNA barcodes and their combination. We suggest future databases include super-barcodes, especially for species-rich and complex genera. The plant DNA barcode library in the current study provides a valuable resource for future biological investigations in the arid regions of China.

S.135 EVOLUTION AND FUNCTION OF CONVERGENT FLORAL PHENOTYPES. SESSION 1

S.135.1 Trade-off mitigation: a key concept to understand the evolution and function of convergent floral phenotypes

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Flowers are often thought to have adapted to pollination by specific animals due to the trade-off that one flower cannot adapt to diverse pollinators. If this is true, why do most flowers harbor various visitors, while maintaining distinct phenotypes among ecotypes, subspecies, and congeners? Because strong phenotypic trade-offs leading to disruptive selection have only been observed in highly specialized systems, we proposed a hypothesis that flowers can adapt to diverse pollinators simultaneously by evolutionarily mitigating trade-offs (Ohashi et al. 2021). In this talk, we explore three ideas about how floral phenotypic convergence evolves and functions from the perspective of trade-off mitigation. First, we demonstrate that certain phenotypic convergence in flowers—floral color change, compact inflorescences, and nocturnal anthesis—could have resulted from adaptive generalization for particular pollinator communities rather than adaptive specialization for specific pollinators. Next, based on the fact that even specialist flowers are often visited by minor pollinators, we discuss that any pollination system can be positioned along a continuum of “generalized systems for specific sets of pollinator groups.” With this in mind, we propose three types of functional traits that constitute a floral syndrome: those that *improve* pollination by primary visitors, those that *exclude* flower visitors that act as conditional parasites, and those that *modify* trait-fitness relationships to mitigate trade-offs among pollinators. Finally, we suggest that the concept of trade-off mitigation may provide an explanation for the uniformity of floral phenotypes in some clades. Flowers attracting a wide range of pollinators, such as compact inflorescences in Apiaceae, may have achieved "super-mitigating" phenotypes that could eliminate fitness valleys among all types of pollinators. In such flowers, any local shift in pollinator composition will not exert disruptive selection pressure but rather result in a slight change of the adaptive peak.

S.135.2 Andromonoecy as a convergent resolution to intra-locus sexual conflict in bisexual flowers

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Andromonoecy, the production of male and bisexual flowers by the same hermaphroditic individual, has evolved numerous times independently across flowering plants and is found in 7% of species. Despite its repeated evolution, its function remains poorly studied. Here, we consider the convergent evolution of andromonoecy as a resolution to sexual antagonism, drawing on data from the alpine plant *Pulsatilla alpina* that shares common features with many andromonoecious species. *Hypothesis*: We expected to detect evidence for strong sexual conflict on female allocation but not male allocation traits in bisexual flowers, i.e., female and male functions have different fitness optima only in the female allocation trait, thus favoring the production of unisexual male and bisexual flowers. We analyzed and compared selection gradients via female and male functions for five floral traits, including sex allocation, phenology, and display traits, in bisexual flowers of *P. alpina* using a paternity analysis. Our results indicate strong sexual conflict in the number of pistils and flowering date but not in the number of stamens in bisexual flowers. Specifically, we found evidence for disruptive selection on pistil number within flowers, such that flowers with many or no pistils contributed more to fitness than those with an intermediate number of pistils. By abandoning the female function, unisexual male flowers possess phenotypes that approach the male optimum of different floral traits. We show that the unisexual male flowers of andromonoecious species may allow hermaphrodites to resolve sexual conflict because modules with different genders can promote fitness through their specialized sexual functions. We discuss the extent to which modular variation in sex allocation in species with other sexual systems involving unisexuality and bisexuality (e.g., monoecy and gynomonoecy) may be explained similarly.

S.135.3 Plasticity-mediated floral convergence triggers the exploration of new generalist pollinaton niches

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Phenotypic convergence is a ubiquitous phenomenon that reveals the multiple evolutionary constraints that face the organisms and illustrates the ability of natural selection to find similar solutions to similar ecological problems. Uncovering the possible mechanisms behind the origin of convergence remains a fundamental goal in biology. Evolutionary theory shows that convergent phenotypes emerge through independent genetic changes selected over long periods of time. Here we show that convergence can also arise through phenotypic plasticity. By compiling the multidimensional floral phenotype, the phylogenetic relationships, and the pollination niche of more than 3000 Brassicaceae species, we demonstrated that the mustard species *Moricandia arvensis* exhibits a plastic-mediated intra-individual floral disparity greater than that found not only between species but also between higher taxonomical levels such as genera and tribes. As a consequence of this floral divergence, *M. arvensis* moves outside the morphospace region occupied by its recent ancestors and close relatives, crosses into a new region where it encounters a different pollination niche and converges phenotypically with distant Brassicaceae lineages. We suggests that, by inducing several phenotypes that explore simultaneously different regions of the morphological space, plasticity may not only promote the evolution of novelties but also trigger rapid phenotypic convergence.

S.135.4 Convergent evolution of sexual deception in Gorteria diffusa (Asteraceae)

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Gorteria diffusa is endemic to South Africa, but its floral morphology varies extensively across its range. Geographically distinct populations produce capitula with no petal spots, with simple petal spots and with highly complex petal spots that mimic female bee flies. These last forms attract pollinators through sexual deception. We have studied the development of these complex petal spots and their evolution within the species, and find that sexual deception has emerged at least twice in the system. I describe our work to understand the genetic and genomic changes that underlie the repeated evolution of this novel trait.

S.135.5 Convergent evolution of hummingbird pollination in the Neotropical spiral gingers: traits, genetics, and the selective environment

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The evolution of hummingbird pollination is common across angiosperms throughout the Americas, presenting an opportunity to examine convergence in traits, genetics, and selective environments to better understand how complex phenotypes arise. We examine many independent shifts from bee to hummingbird pollination in the Neotropical spiral gingers (*Costus*; Costaceae) and address common explanations for the prevalence of these transitions. We reconstruct ancestral pollination states on a well-resolved phylogeny and examine variation in traits and environmental correlates across independent shifts. Using a phylogenomic approach, we assess historical introgression events to determine if convergence could involve the sharing of alleles across species. We further dissect the genetic basis of a recent bee-to-bird shift and compare those findings to genetic changes underlying floral traits in other *Costus* species. We also test the hypothesis that hummingbird pollination is adaptive in high-elevation pollination environments relative to bee pollination by translocating flowering plants of both types across an elevational gradient in Costa Rica. A consistent set of traits predict hummingbird pollination, but not the stereotypical 'hummingbird' traits of long, red flowers. We find many shifts to hummingbird pollination, no reversals, a single shared phenotypic optimum across hummingbird flowers, and little evidence of introgression. Our genetic investigations find large effect color and scent loci, small effect morphology loci, and some overlap in loci across independent floral transitions. In contrast to other clades, we find no association between pollination and climate, and mixed evidence that hummingbird pollination is adaptive in montane environments. Evolutionary shifts to hummingbird pollination in *Costus* are highly convergent and directional, involve a surprising set of traits when compared with other plants with analogous transitions, and refute the generality of several common explanations for the prevalence of transitions from bee to hummingbird pollination.

S.135.6 Convergence and divergence: specialization and generalization in the most diverse poricidal flowered plant lineage

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Buzz-pollinated flowers represent some of the most iconic examples of evolutionary convergence in angiosperms. Typically, buzz-pollinated flowers exhibit a syndrome of convergently evolved traits including poricidal anthers, dimorphic stamens, and pollen as the sole floral reward. This suite of floral traits is thought to have evolved together in ca. 25 angiosperm families. However, at finer taxonomic levels, these traits are not always associated with one another. For example, stamen dimorphism appears to be context-dependent within the Melastomataceae (the most diverse plant lineage with poricidal flowers): dimorphic stamens tend to be associated with pollinator dependence, whereas pollinator-independent species are more likely to have monomorphic stamens. Furthermore, some melastomes have acquired divergent traits which are associated with increased pollinator specialization. For example, independent evolutionary origins of oils by the stamens appear to have made melastome pollen unpalatable to many bees, so that unrelated oil-producing flowers are almost entirely visited by a small subset of buzzing bees – those that also collect oil. On the other side of the specialization spectrum, some nectar-producing melastomes have increased pore size, allowing them to be visited by a more diverse range of insects. Together, the shifts towards more specialized or generalized systems suggest a complex pattern of both diverging and converging traits within paraphyletic melastome lineages.

S.136 BRYOPHYTE DIVERSITY, ENVIRONMENT AND CONSERVATION IN MEDITERRANEAN CLIMATE AREAS

S.136.1 California bryophytes: evolution and conservation in a biodiversity hotspot

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California is one of the world's biodiversity hotspots. It is also one of the places where biodiversity is most threatened, because of habitat loss, invasive species, and climate change. There is an urgent need to understand conservation priorities on the landscape of California for all groups of organisms, yet no such study has been made for mosses or liverworts. Bryophytes are indicators of ecosystem health, and contribute significantly to nutrient and water cycles. Therefore, we carried out spatial phylogenetic analyses for both groups. For mosses we pruned a larger spatial dataset of geo-referenced herbarium records for North America, plus matching phylogenetic data matrix, from Carter et al. (2022, *Journal of Biogeography*, 10.1111/jbi.14385) to make a California subset. For liverworts we assembled a new spatial data set from GBIF and mined molecular data from Genbank. A maximum likelihood phylogeny was constructed for both groups and used along with newly produced species niche models to find regions of significant phylogenetic diversity and phylogenetic endemism within California, employing a spatial randomization. We also carried out phylogenetic complementarity analyses to identify conservation priorities on the landscape that optimally increase protected biodiversity, using an algorithm that considers current land protection status and data on landscape intactness to identify priority sites containing concentrations of lineages that are evolutionarily unique, vulnerable due to small range size, and poorly protected across their ranges. We evaluated priorities using three different dimensions of phylodiversity): a phylogram (i.e., genetic divergence), a chronogram (i.e., evolutionary time), or a cladogram (i.e., speciation events). These metrics yielded conservation priorities that agreed in many places but differed in others. We compare these results to those previously published for vascular plants of California (Kling et al. 2018, *Phil. Trans. Roy. Soc. B*, 374: 20170397). Several top priority regions of the state emerged from these comparisons.

S.136.2 Orthotrichaceae (Bryophyta) in Mediterranean climate areas: unveiling an unexpected diversity in Central Chile

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The five global regions with Mediterranean climates harbor high and unique biodiversity, hence all being part of recognized hotspots. A climate characterized by a prolonged period of drought coinciding with the hottest time of the year may not seem, at first glance, favorable for bryophytes. However, several groups of mosses and liverworts are widely diversified in this environment. The representation of Orthotrichaceae in the different Mediterranean floristic regions is highly unequal, both in terms of the genera present, and in the overall specific diversity. The Mediterranean Basin and the California Floristic Province boast a notable diversity of species distributed among few genera, all belonging to the subfamily Orthotrichoideae. Conversely, in the Cape Floristic Province and Southwest Australia, there are relatively few species, but there is a significative presence of Macromitrioideae genera. In contrast to this, in Central Chile the diversity reported so far is very low, both in number of genera and species, with all taxa belonging to Orthotrichoideae. But, to what extent is this diversity scenery realistic for the southern hemisphere Mediterranean areas? Our studies in Central Chile indicate that there is indeed a considerable hidden diversity of Orthotrichaceae there. Specifically, our results unveil that there is a high number of previously unknown species belonging to the genera *Orthotrichum* and *Lewinskya*. Most are species restricted to the Chilean Mediterranean biome. However, two particularly diverse environments, sharing few species among them, can be distinguished: the fog oases of the coastal hills and the high elevation zones of the inland Mediterranean mountains. We provide data on the adaptive morphological characteristics of the new species, their distribution patterns, and their phylogenetic relationships, considering a broad framework that integrates species from other South American areas and the remaining Mediterranean regions worldwide.

S.136.3 Achievements, failures, and challenges in bryophyte conservation in Spain

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The conservation of bryophytes in Spain is at a considerable standstill. Despite notable initiatives in the field of regulation, such as the elaboration of the standard list, the improvement of some regional protection catalogues and the process initiated to extend national catalogues, the number of protected species is insufficient and centred on species protected at the European level. Improvements in the legislative field do not necessarily mean an improvement in the protection of bryophyte species because the legally established management mechanisms are not developed. The decentralisation of the Spanish state, while improving the distribution of funds, limits the control mechanisms over the autonomous communities. The level of non-compliance, generally high in our administrations, is aggravated by the fact that it is a small group of species that does not justify the administrations' investment in specialised training for their technicians. The improvement of the administrative situation will hopefully lead to an improvement in investment in research and monitoring projects, as the current situation means that there is a lack of demand for such studies. Generating a need in the administration may increase the number of research projects, both requested and granted, on bryophyte conservation and stimulate interest in training staff in charge of the management of natural areas and protected species. A review of the current situation is presented, with its achievements and shortcomings, and the most relevant scientific, technical, and administrative needs are analysed.

S.136.4 Resilient nature of cosmopolitan mosses in the Mediterranean Basin: insights into climate-driven molecular adaptation

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Across Mediterranean mountainous regions and surrounding lowlands, the ecological resilience of cosmopolitan mosses, *Bryum argenteum* Hedw., *Ceratodon purpureus* (Hedw.) Brid, and *Funaria hygrometrica* Hedw. delineated distinct clades. Our research story provides insights into the interaction between landscape diversity, climate change, and molecular adaptation in mosses. The genetic analyses of *B. argenteum* along the gradient surface of the Sierra Nevada Mountains compared to Tenerife Island unveiled a story of recurrent colonization spanning over millennia. Despite indications of native status, shared haplotypes with continental areas suggest recent introductions. Clade distinctions among genotypes mirrored enduring climatic barriers between the highlands and lowlands of the Sierra Nevada Mountains, influencing migration dynamics. In *C. purpureus*, morphological variations posed challenges in taxonomic delineation. The evolutionary trajectory and the emergence of a new *Ceratodon* species through peripatric speciation, genome expansion, and skewed sex ratios within the Mediterranean landscape. These genetic insights led to the identification of *Ceratodon amazonum* Nieto-Lugilde, O. Werner, S.F. McDaniel & Ros and the consideration of *Ceratodon conicus* (Hampe ex Mull. Hal.) Lindb., as a nothospecies, emphasizes the delicate impact of environmental factors on moss taxonomy amidst changing landscapes. Exploration of *F. hygrometrica* across the Sierra Nevada Mountains highlighted the correlation between landscape diversity and genetic makeup. Diverse landscapes harbored higher genetic diversity, possibly linked to spore establishment challenges in unsuitable environments. Altitudinal gradients influenced genetic structures, while precipitation and temperature shaped specific genetic markers, underscoring the pivotal role of environmental heterogeneity in shaping genetic diversity. Our ongoing investigation into the Heat-Shock Factor gene family aims to unravel mosses' molecular responses to climatic shifts, using *F. hygrometrica* as a model. Deciphering genetic variations and expression dynamics among genotypes will illuminate how these molecular mechanisms orchestrate adaptive responses to high temperatures and dehydration, offering insights into mosses' adaptive strategies amidst climate change challenges.

S.136.5 Bryophytes of Australian Mediterranean climate areas: Species diversity, adaptation, distribution and conservation

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Bryophytes that occur in the Australian Mediterranean biome have been the subject of many studies: regional checklists, taxonomic revisions, ecological studies of biocrust species and flora surveys of various locations across the biome. However, no cohesive study of the bryophytes which occur there has ever been attempted. We are presenting our observations and studies of targeted groups of bryophytes which are particularly diverse and/or particularly adapted to this biome as a first step to address this broader knowledge gap. Complex thalloid liverworts are well suited to this habitat type and the genus Riccia is the largest and most diversified group. South Africa and Australia both have over 50 species, half of the known diversity for the genus. Other families that have been successful in this biome include the Aytoniaceae, comprised of cosmopolitan species such as Reboulia, Plagiochasma and Asterella. The highly diverse genus Fossombronia has also developed adaptations to survive in extreme conditions, allowing it to thrive in Mediterranean conditions. However, it is the discovery of elusive and rare members of the Sphaerocarpales that has opened up the habitat of salt marshes, rarely visited by bryologists leading to the discovery and hitherto unknown diversity and range for these taxa. Many moss taxa are also well adapted to the extremes of this area, in particular tiny mosses such as Phascum, Stonea and Phascopsis, which thrive in biocrusts. We present the varied ways in which these bryophytes successfully survive in the harsh conditions in which they grow. While studies are continuing, progress is slow, and due to the decline in the number of active Australian bryologists, conservation of rare, threatened, or vulnerable species is well behind that for other plant groups. We conclude by summarising the conservation efforts that are currently being undertaken in Australia in the Mediterranean biome.

S.136.6 Green Canopies and Cityscapes: Decoding Urban Epiphytic Bryophyte Diversity in Novi Sad, Serbia – A Phorophyte Puzzle

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There is a notable gap in our understanding of the primary factors influencing epiphytic bryophyte diversity in urban areas. This study aims to provide fresh insights into the intricate web of epiphytic diversity within urban landscapes, specifically investigating whether phorophyte type exerts a predominant influence on bryophyte diversity compared to other tree characteristics. The survey encompassed seven locations in Novi Sad City, including three city parks and four main boulevards. All epiphytic bryophyte species were meticulously recorded across these sites, revealing a total of 35 species. To quantify bryophyte abundance, we utilized the microplot sampling method, employing microplots (10×10 cm) at a 20 cm distance on all four sides of each tree, from the base up to the 2 m heigh. Alpha-diversity measures included species richness, the Shannon diversity index, and the Pielou evenness index. The Sörensen similarity index served as a non-parametric beta diversity measure to assess the similarity between different locations. Environmental drivers, such as bark pH, tree diameter at breast height, bark structure, tree height, and phorophyte type, were incorporated. Multivariate analysis, specifically Canonical Correspondence Analysis (CCA) and Variation Partitioning, were employed to test the impact of environmental variables on epiphytic bryophyte diversity. he highest Shannon diversity index was observed on *Celtis occidentalis* and *Populus alba* trees, while *Betula pendula* and *Styphnolobium japonicum* exhibited the highest evenness index. CCA analysis indicated that the most influential explanatory variable was phorophyte type, explaining approximately 30% of the total variability. Tree height, tree diameter, bark pH, and structure significantly influenced the Shannon diversity index of epiphytic bryophytes, accounting for approximately 5% of the total variability. While this study underscores the predominant influence of phorophyte type on epiphytic bryophyte diversity, further research is warranted to unravel unexplained variations, possibly attributable to microclimatic conditions.

S.136.7 Bryo-ecological patterns in Mediterranean temporary ponds: a highly sensitive proxy for habitat monitoring

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This study contributes to the knowledge and understanding of Annex I priority habitat 3170*, where bryophytes play an essential role in the ecological patterns and are a significant indicator, especially concerning habitat monitoring, assessment, and management. In this paper, we analyze the bryological component of Mediterranean temporary ponds in two different areas in the Mediterranean Biogeographic Region, such as the “Pauli” of Giara di Gesturi in Sardinia (a Mediterranean island), and the Piana di Ferretto in Umbria (inland Central Italy), comparing the rate of bryophytes occurrence. The detected species are described in terms of their functional characteristics using Ellenberg values adapted for bryophytes. More specifically, the following parameters are considered: life strategy, life macroform, light and moisture preferences, chorological elements and humidity Belt. We focused on the distribution of bryophytes along concentric areas of the pools according to their humidity gradient. On this ground, the bryological flora of the studied Mediterranean temporary ponds was characterized from an ecological point of view. To account for ecological variability, data from the two areas were compared. Temporary Mediterranean ponds represent vulnerable niches where climate change is exerting its influence. The approach used in this study could be extended to comparable Mediterranean habitats, focusing on bryological ecology as an effective proxy for habitat monitoring under a scenario of unpredictable climate change.

S.137 USING HIGH-THROUGHPUT SEQUENCING TO UNDERSTAND PLANT EVOLUTION ON ISLANDS IN A DATA-RICH ERA: NEW INSIGHTS FOR NEW CHALLENGES. SESSION 1

S.137.1 Genome-wide data provide new insights into the phylogenetic relationships within the woody Sonchus alliance (Asteraceae)

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Numerous unique plant groups have made the Macaronesian Islands an exceptional area for studying evolution and speciation. Of several iconic angiosperm groups, the woody *Sonchus* alliance, which includes approximately 31 species in the Canaries, Madeira, and Cape Verde, represents one of the best-known examples of adaptive radiations. It has been difficult to unravel rapidly radiated interspecific relationships using conventional molecular markers (e.g., nrDNA ITS and chloroplast noncoding regions) due to the insufficient resolution and support. In order to clarify the biogeographic and evolutionary history of the alliance, we used the complete chloroplast genome and double-digest restriction site-associated DNA sequence (ddRAD-seq) data based on the thorough species coverage and multiple populations per species. The complete plastome sequences of 135 accessions provided well resolved strongly supported phylogenetic relationships but revealed non-monophyly of numerous species and unusual species relationships, suggesting rampant chloroplast polymorphisms. As previously suggested, the early divergence of segregate genera, *Sventenia*, *Chrysoprenanthes*, *Babcockia*, and *Lactucosonchus*, was supported. With 95 accessions, ddRAD-seq data also provided a fully resolved and highly supported phylogenetic framework for the alliance, while better reflecting species morphological and biogeographic relationships and revealing monophyly in most species. Newly inferred species relationships, timing of lineage divergence, and biogeographic history of the alliance based on the genome-wide nuclear data will be presented.

S.137.2 Great speciators of the plant world: Island biogeography of Asteraceae on Hawai'i and the Mascarenes

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Macroevolutionary models of island biogeography applied to high-throughput DNA sequencing data on island species are promising tools for inferring the processes governing biota assembly for entire communities over evolutionary time scales. However, to date, phylogenetic trees of island plant lineages that can be used for studying island biogeography have mostly been reconstructed using a limited number of loci, often leading to poor resolution, particularly in rapidly evolving insular radiations. Asteraceae - the largest plant family in the world - provides an excellent model system for looking at diversity dynamics on islands, due to this group's high diversity, endemism, and number of radiations across islands globally. In particular, the Asteraceae floras of two remote oceanic archipelagos - Hawai'i and the Mascarenes - are remarkably diverse. The Hawaiian Islands have 99 native Asteraceae species of which 98 are endemic, and are home to the iconic silversword alliance, a textbook example of adaptive radiation. The Mascarenes also have a high proportion of Asteraceae endemism (89%), but until now most of the native Asteraceae lineages on the Mascarenes have not been studied in a phylogenetic context. Here, we compile and build new dated phylogenies with target capture sequencing (Hyb-Seq) using both the Angiosperm-353 and the Compositae-1061 kits for all the native Asteraceae lineages that have colonized these two isolated oceanic archipelagos. We then use a macroevolutionary island biogeography model (DAISIE) to analyze and reconstruct the build-up of the diversity for the entire native Asteraceae assemblage on Hawai'i and the Mascarenes. Our approach using target-capture sequencing allows us to infer the number of colonization and radiation events with increased precision, estimate macroevolutionary rates of colonization, speciation and extinction, and to test whether these systems are at equilibrium.

S.137.3 The Paradox of Insular Diversification: How Can Lineages Depleted of Genetic Variation Radiate on Islands? Insights from the Galáp

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Despite the constraints imposed by founder events, small population sizes, and inbreeding, some oceanic lineages exhibit an astonishing degree of ecological and phenotypic diversity. This intriguing paradox raises a fundamental question: how do isolated lineages generate and maintain genetic diversity? While *de novo* mutation, the traditional source of genetic variation, is widely considered too slow to account for the observed levels of ecological differentiation and divergence in these lineages, alternative mechanisms remain elusive. In this work, we explore the role of diverse genomic architectures in fostering genetic diversity. With a focus on the adaptive radiation of *Scalesia*, we investigate the contribution of transposable elements and polyploidization to the generation of genetic variation. Our findings reveal an even distribution of transposable elements across subgenomes and a lack of association between ecological niche, phylogeny, and transposable element accumulation. Collectively, these results suggest that transposable elements may not have played a significant role in shaping this adaptive radiation.

S.137.4 Genomic dissection of island syngameons: arborescent Asteraceae from St Helena (South Atlantic Ocean) “

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The genera *Commidendrum* (4 spp.) and *Melanodendron* (1 sp.) from St Helena (South Atlantic Ocean) form a single clade whose ancestor reached the island in the early Pliocene. All species have highly divergent morphologies linked to ecology. *Commidendrum* and *Melanodendron* are known to form an intergeneric hybrid and *Commidendrum* is known to form interspecific hybrids. Plant genomics can untangle evolutionary history as well as complex histories of hybridization on islands. Genomic evidence is presented that hybridization has occurred in the *Commidendrum/Melanodendron* clade due to recent conservation efforts due to planting species in proximity. Furthermore, there is genomic evidence that hybridization events may be ancient, with the species forming a syngameon, so raising the genetic effective population sizes (N_e) of species. A syngameon is here defined as: "a group of otherwise distinct species interconnected by limited gene exchange, i.e., the most inclusive interbreeding evolutionary unit" (Suarez-Gonzalez et al., "Adaptive introgression: a plant perspective" Biology Letters 2017). Such hybridization events are postulated to be a continual source of background 'evolutionary rescue' of species from any small population size impacts over geological time, a phenomenon of particular importance and impact on islands. Genomic studies are an essential tool for the study of plant evolution on islands, and for endemic plant conservation.

S.137.6 Phylogenomics of the hyperdiverse Asteraceae family in an oceanic archipelago: unveiling insights into the mechanisms of evolution

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Invasive species pose a significant threat to biodiversity, particularly on oceanic islands. The native biota of oceanic islands is both fragile and unique, rendering these ecological systems especially susceptible to biological invasions and other anthropogenic disturbances. Despite this recognition, the mechanisms driving the success of invasive species remain uncertain. Charles Darwin proposed two competing hypotheses, collectively known as Darwin's Naturalization Conundrum (DNC), to predict a species' invasive potential. The first hypothesis, termed the "Pre-adaptation Hypothesis," posits that species closely related to the native community are more likely to invade successfully. This is attributed to their possession of similar life-history traits that pre-adapt them to establish and thrive under the local environmental conditions (environmental filtering). Conversely, the "Naturalization Hypothesis" suggests that species distantly related to native species can exploit empty ecological niches, avoiding competitive exclusion and thus exhibiting a higher potential for invasion (biotic filtering). Herein, we present the findings of a long-term project, **ASTERALIEN**, focused on testing the DNC within the Compositae family across the Canary Islands. We explored the DNC by examining two dimensions of relatedness between species: phylogenetic and functional distance. Utilizing a comprehensive phylogenomic approach to infer a super-tree encompassing all genera and a majority of species in the archipelago, we assessed the phylogenetic relatedness between alien and native species. This super-tree is constructed using hybrid capture-based target enrichment of the angiosperm-wide 353 and the Asteraceae family-specific 1061 probe sets for approximately 300 species. The integration of measured functional traits of all species collected in the field allow us to estimate functional distances between these two (naive vs. exotic) distinct functional groupings. By integrating both phylogenomic and functional approaches at unprecedent resolution, our study explicitly evaluates the mechanisms of evolution and invasion in alien species on oceanic islands within the framework of the DNC.

S.138 PHYLOGENOMICS AND EVOLUTION OF GYMNOSPERM

S.138.1 Phylogenomics shed new light on the evolutionary history of Cupressaceae

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As one of the largest families of gymnosperms, Cupressaceae comprises above 162 species (32 genera, seven subfamilies), and is the only gymnosperm group occurring on all continents except Antarctica. The world-wild distribution and high species diversity make this family an ideal example for exploring evolutionary history of the global intercontinental floras. Here we conducted a comprehensive phylogenomic study of Cupressaceae using more than 2000 single copy nuclear genes with a nearly complete sampling of species. Species tree reconstruction suggest that all genera and subfamilies were well-supported monophylies. Unexpectedly, we found the subfamily Athrotaxidoideae, which was sister to the remaining four subfamilies except Cunninghamioideae and Taiwanioideae in previous studies, was clustered with Sequoiodeae. Results of concordance analysis showed a high level of gene tree conflict of the ancestral node of Athrotaxidoideae and Sequoiodeae, suggesting it might have experience rapid speciation event and/or hybridization. PhyloNet analyses suggested three reticulation events within Cupressaceae at subfamily level. Molecular clock estimation revealed that two diverse evolutionary lineages (the tribe Cupresseae and *Callitris*), which together comprise ~70% of the species of Cupressaceae, underwent rapid diversification around the Cretaceous-Paleogene (K-Pg) boundary. A diversification rate shift was also detected along the ancestral branch of the tribe Cupresseae, corresponding a rate shift in phenotypic evolution. Biogeographical analyses suggest that the current distribution pattern of Cupressioideae and Callitroideae is largely associated with the breakup of Pangea, yet the detailed spatiotemporal evolutionary history is different from previous studies. In short, our phylogenomic survey suggest that the evolutionary history of Cupressaceae is more complex than previously thought.

S.138.2 Of signals and synthesis: the evolutionary implications of chemical signal divergence and its relationship to biosynthetic pathways in

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The staggering diversity of mutualistic interactions found in nature, has long been a topic of fascination to science, with studies of chemically-mediated ecological interactions contributing great strides in our understanding. Investigations on the chemical ecology of ancient insect-pollinated plant lineages provides critical insight into the myriad ways such mutualistic diversity could evolve. Brood-site pollination mutualism of cycads, an early-diverging lineage of gymnosperms, is the most ancient pollination mechanism yet documented; pre-dating even the rise and dominance of flowering plants. Cycad pollination is a classic example of a brood-site pollination mutualism, wherein pollinators develop within the reproductive tissue of their host plant, relying on them for shelter, food, and in this case, breeding site. Cycads' chemically mediated 'push-pull' mechanism ensures pollinators visit both pollen and ovulate cones through thermogenically driven increases in the concentration of cone volatiles (scent) that results in a mass exodus of pollinators from pollen cones and simultaneous attraction to conspecific ovulate cones. *Zamia,* a genus of cycads found widely dispersed across the Americas and the Caribbean, are pollinated by a group of specialist brood-site mutualists, the cycad weevils (Subtribe: Allocorynina). The Caribbean *Zamia* clade, shows remarkable diversity in cone volatile composition that appears to be both species-specific and rapidly evolving under positive selection suggesting that plant chemistry is integral for maintaining species boundaries, yet we remain woefully unaware of how plant volatile chemistry related to pollination evolves across a lineage. In this study we conduct a deep exploration of the chemical communication across the Caribbean *Zamia* clade by characterizing the quantitative patterns of cone volatile chemical composition in a phylogenetic and biogeographic context. We discuss the biosynthetic origins of biologically relevant compounds and the evolutionary implications of diverging signals.

S.138.3 Multidisciplinary approaches reveal the spatiotemporal evolution of gymnosperms

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Reconstructing the phylogenetic history of organisms and understanding what determines the distribution of species diversity remain challenging in evolutionary biology and ecology. This is particularly true for gymnosperms, which comprise only 13 families and a little more than 1,000 species. Although greatly outnumbered by the species of angiosperms, gymnosperms have huge ecological and economic value, of which conifers (about 615 species) constitute approximately 39% of the world's forests. In addition, the Northern Hemisphere conifers do not follow a latitudinal diversity gradient and show a unique distribution pattern, i.e., most species are distributed in mountainous areas at middle latitudes. It is of great interest to investigate the spatiotemporal evolution of gymnosperms, especially conifers. In recent rears, we have used phylotranscriptomics to robustly reconstruct the phylogeny of gymnosperms at both higher (interfamilial and intergeneric) and lower (interspecific) taxonomic levels, and employed multidisciplinary approaches to reveal the mechanisms underlying diversification and global distribution of conifers, including Gnetales. Our studies indicate: (1) Podocarpaceae originated in Gondwana in the late Triassic, and both vicariance and dispersal contributed to its current biogeographic patterns; (2) Cupressaceae very likely originated in Asia in the Triassic, and geographic isolation caused by continental separation drove the vicariant evolution of the two subfamilies Cupressoideae and Callitroideae in the northern and southern hemispheres, respectively; (3) The mid-latitude region has provided an evolutionary museum for global pines, topography played a primary role in pine diversification, and the aridity index was decisive for the niche rate shift; and (4) *Ephedra* very likely originated in the Tethys coast during the late Cretaceous, and the South American *Ephedra* species have a single origin by dispersal from Mexico or North America. Our study highlights the importance of integrating phylogenomic and ecological approaches to address evolution of biological groups at the global scale.

S.138.4 Sex chromosome evolution of Ginkgo biloba with implication for dioecy evolution of gymnosperms

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Sex determination genes of dioecy, which refers to male and female reproductive organs present in separate individuals, have been uncovered in a few angiosperms, while there is a contrasting gap in gymnosperms. Ginkgo biloba L., representing one of the five extant gymnosperm lineages, is a well-known dioecious tree species in which sex determination genes remain unknown. Here, anatomical observation, transcriptomic analyses, and evolutionary analyses strongly support that two B-class MADS-box genes at the non-recombination region of the Y chromosome acted as the sex determination genes of ginkgo. Functional transgenic analysis in Arabidopsis thaliana indicated that they were related to the male reproductive organ identity specification. Moreover, the spatial enhanced resolution omics sequencing (Stereo-seq) revealed that the highest expression level of the two sex determination genes were present in the male reproductive primordium, i.e., microsporophyll primordium, of male strobilus buds at the sex determination stage. Collectively, these results not only systematically verified the hypothesis that B-class MADS-box genes determine the sex of dioecy in gymnosperms for the first time, but also pioneered the construction of the spatial transcriptome atlas of male strobilus buds in ginkgo. In light of the present discovery, we discussed the repeated evolution of dioecy and sex chromosomes in gymnosperm as well as its time course in seed plants.

S.138.5 Reconstructing polyploid histories in Ephedra using target sequence capture

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The gymnosperm genus *Ephedra* (Gnetales) is widely distributed in New and Old World arid and subtropical regions and has featured prominently in elucidating the phylogenetic interrelationships of seed plants. Reconstructing the evolutionary history of *Ephedra* has been hampered by fast rates of molecular evolution and extensive polyploidization, with 80% of the c. 54 species known to be polyploids, mostly tetraploids of allopolyploid origin. Recent advances in generating large sequencing datasets and new methodological advances for inferring complex histories from genomic data provide new promise for resolving previously intractable phylogenetic problems. Here we used target sequence capture data, generated using the GoFlag 408 flagellate land plant probe set, to infer the evolutionary history across 139 samples representing nearly all species of *Ephedra*. We discuss some of the challenges of using target capture data for *Ephedra*, and explore the value of assembling off-target plastid loci and new methods for phasing polyploid taxa using short read sequences and network inference on our ability to infer the reticulate history of *Ephedra* and identify putative progenitors of polyploid species. While numerous questions about the evolution of *Ephedra* remain, our analyses using targeted capture data and comprehensive sampling across the genus present new insights into the complex history of *Ephedra* as well as the challenges that remain.

S.138.6 Perspectives on a comprehensive gymnosperm phylogeny from targeted enrichment sequencing

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The gymnosperms represent one of the two major lineages of seed plants and are critically important to the biodiversity of many ecosystems. While decades of molecular phylogenetic analyses have resolved many relationships within extant gymnosperms (c. 1080 species), some parts of the tree remain contentious, and there is a need for a comprehensive resource that highlights the complexities of evolution that can be illuminated with genomic data. We generated a phylogenomic dataset using targeted enrichment with the GoFlag 408 flagellate plant probe set, which covers 408 exons from 229 single or low copy nuclear genes, and sampled approximately 1060 taxa, representing all families and genera, and approximately 95% of all extant species. The resulting phylogeny is strongly supported, although some areas of the tree have weaker support and/or high levels of intragenomic conflict. Our analyses also highlight some of the challenges and limitations of targeted enrichment data from a universal probe set. We compare the tree inferred from targeted enrichment data with trees from plastid and transcriptome data. The targeted capture dataset provides new perspectives on some classic questions in gymnosperm phylogenetics and highlights areas where further research is needed, and it provides a resource of comparable and combinable data that can help illuminate future studies of evolutionary processes across the gymnosperms.

S.139 GLOBAL CHANGE AND EVOLUTIONARY ADAPTATION OF PLANTS IN COASTAL AREAS

S.139.1 Evolution and patterns of epimutation rates in stress

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DNA methylation plays an important role in plant response to environmental stress whereas its contribution to long-term adaptation remains elusive. Here we estimate evolutionary rates of methylation gain and loss in mangroves and the potential role of natural selection using population epigenomic analysis. Mangroves exhibit a high ratio of gain over loss of CG methylation. Cytosine sites in CG context, particularly in the promoter regions, are under significant selection to remain methylated in mangroves but not in non-mangroves. We also analyzed available expression profiling data of mangroves and found that gains of CG DNA methylation in both promoter and coding regions are associated with reduced expression variation in stress. Our results suggest that DNA methylation is favored by selection in plants under stress adaptation, perhaps due to its impact on maintaining transcriptional homeostasis.

S.139.2 Peripatric speciation of pantropical coastal plants in East Asia

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Pantropical plants with sea-drifted seeds (PPSS) expanded globally through long-distance seed dispersal by sea. These plants, representing individual species or closely related species, thrive globally in tropical littoral areas. Notable examples include *Ipomoea pes-caprae* subsp. *brasiliensis* (Convolvulaceae), *Canavalia rosea* (Leguminosae), and *Hibiscus tiliaceus* (Malvaceae). Closely related species are found in marginal areas of PPSS distribution, such as *Ipomoea pes-caprae* subsp. *per-caprae* (northern Indian Oceanic region), *Canavalia* subgenus *Maunaloa* (Hawaiian Islands), and *Hibiscus hamabo* (temperate East Asia) and *H. glaber* (Bonin Islands). Despite PPSS's extensive distribution, the species cohesion breaks down in peripatric areas due to limited gene flow, fostering differentiation through alternative allele fixation, local adaptation, and genetic drift. However, the spatiotemporal processes of peripatric speciation in PPSS remain unclear. To address this gap, we conducted phylogenomic analyses using plastome and genome-wide nuclear SNP data of *H. tiliaceus* and its East Asian relatives *H. hamabo* and *H. glaber*. Our dated phylogeny suggests that global expansion began around four million years ago, and species diversification began approximately one million years ago. Plastome phylogeny revealed that *H. hamabo* haplotypes were fully nested within *H. tiliaceus* haplotypes, supporting a peripatric speciation process involving migration to temperate zones. In contrast, *H. glaber* haplotypes showed diversification at the basal position in the plastome phylogeny. Genome-wide nuclear SNP phylogenies highlight distinct genetic segregations among species and geographical regions. *Hibiscus hamabo* exhibited low genetic diversity, whereas *H. glaber* displayed relatively high genetic diversity in both plastome and genome-wide SNPs. This study provides insights into the divergent genetic backgrounds of *H. hamabo* and *H. glaber*, both of which are undergoing peripatric speciation in East Asia. Discussions will focus on the factors contributing to these distinct genetic patterns in these peripatrically derived species.

S.139.3 Assessing the conservation of terrestrial HCIs in the Alboran Sea: Coast of Málaga and Granada

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The coastal regions of the Alboran Sea in southern Spain, bathed by the Mediterranean Sea, are celebrated for their remarkable biodiversity and contain several Habitats of Community Interest (HCI), a designation under the European Union Council Directive. Although those HCIs host various ecosystems and numerous endemic species whose conservation is the shared responsibility of EU member states, many of them face significant risks. In our study, we analysed the degree of conservation (DC) of terrestrial habitats along the coasts of Málaga and Granada, in order to provide key information for prioritising conservation measures. To that end, vegetation inventories were conducted to assess the DC of HCIs, current coverage, the presence of typical species from a phytosociological perspective, and the invasion of non-native species. Our findings suggest that HCI Groups 1 and 2 (i.e., 1150, 1210, 1240, and 2210), including dunes, halonitrophilous vegetation, and cliffs, were the most impacted due to displaying diminished plant coverage and a proliferation of invasive species. Enhanced management is therefore urgently needed to ensure the preservation and protection of those unique ecosystems. We also propose that the comprehensive evaluation method used in our study and the creation of a conservation index have the potential for extrapolation to other HCIs across Europe.

S.139.4 Genomic evidence for rediploidization and adaptive evolution following the whole-genome triplication

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Whole-genome duplication (WGD), or polyploidy, events are widespread and significant in the evolutionary history of angiosperms. However, empirical evidence for rediploidization, the major process where polyploids give rise to diploid descendants, is still lacking at the genomic level. Here we present chromosome-scale genomes of the mangrove tree *Sonneratia alba* and the related inland plant *Lagerstroemia speciosa*. Their common ancestor has experienced a whole-genome triplication (WGT) approximately 64 Mya coinciding with a period of dramatic global climate change. *Sonneratia*, adapting mangrove habitats, experienced extensive chromosome rearrangements post-WGT. We observe the WGT retentions display sequence and expression divergence, suggesting potential neo- and subfunctionalization. Strong selection acting on three-copy retentions indicates adaptive value in response to new environments. To elucidate the role of ploidy changes in genome evolution, we improve a model of the polyploidization–rediploidization process based on genomic evidence, contributing to the understanding of adaptive evolution during climate change.

S.139.5 Ecology and evolution of invasive salt marsh grass Spartina alterniflora

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Coastal saltmarsh wetlands provide high levels of ecosystem services. Many of these services stem from the vegetation of coastal saltmarsh systems. However, global change has posed a serious threat to coastal salt marshes in recent years. Therefore, it is critical to determine the spatio-temporal patterns, ecological processes and adaptation mechanisms of coastal saltmarsh vegetation. In this study, the global invasive salt marsh plant *Spartina alterniflora* was taken as the model salt marsh plant, and studied at the individual, population, and community levels. In particular, we studied the spatial and temporal dynamics, ecological processes and adaptation mechanisms of different levels of vegetation in coastal saltmarshes in response to multi-scale environmental gradients. Our study identified three key findings: 1) we clarified that the spatio-temporal allometric patterns in *S. alterniflora* followed self-thinning and life-history theory, suggesting that salt marsh plants may serve as simple, model systems for studies of plant life history. 2) Intraspecific hybridization and rapid evolution drive different latitudinal clines in *S. alterniflora* in the native and introduced ranges, indicating the importance of phenotypic plasticity and genetic control of change during the invasion process. 3) Community composition, distance, and latitude alter the synchrony and stability of *S. alterniflora* biomass, suggesting that managers should identify the most sensitive habitat to abiotic variation as a priority for monitoring. In summary, the above multi-level and multi-scale studies clarified the pattern, process, and mechanism of coastal salt marsh wetlands, and provided new methods, perspectives, and ideas for establishing salt marsh model system, understanding its ecological service value, and protecting habitat and species diversity. Furthermore, it also provides decision support for the adaptive scientific management of coastal wetlands under global change.

S.139.6 Leaf pattern in Colombian Caribbean mangroves

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The biotypological foliar pattern was characterized in the mangrove vegetation (39 inventories or surveys) of the Caribbean region of Colombia, in localities of the departments La Guajira (arid), Magdalena (semiarid), Sucre (semihumid), Córdoba (humid), defined by three phytosociological formations or alliances: Lagunculario racemosae - Avicennion germinantis especially the association Avicennion germinantis-Rhizophoretum manglis (Magdalena, Sucre); Laguncularia racemosae-Rhizophorion manglis with the association Lagunculario racemosae-Conocarpodetum erecti (La Guajira, Magdalena P. N.N. Tayrona) and Fico dendrocidae - Rhizophorion manglis especially the association Priorio copaiferae-Rhizophoretum manglis (Córdoba). 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 812 samples were processed, from 14 families, 19 genera and 21 species. The general pattern corresponds to simple, notophyll leaves (31-53 cm^2), with elliptic and oblong shapes, entire margin, obtuse apex and base, coriaceous consistency, unprotected and lamina thickness B (0.16-0.35mm). As the aridity condition increases (arid and semi-arid zones La Guajira, Tayrona N.N.P.), there is a tendency to increase the values of specific weight and succulence (gr/dm2), dry mass (%), leaf thickness (mm) and wood density (gr/ml), conditions that are related to higher salinity. Leaf area increases in the semi-humid and humid zones (moderate relationship with precipitation, R2 = 0.62**), a condition associated with lower salinity and/or greater influence of continental water. The results illustrate the differential responses related to the type of mangrove vegetation (floristic composition and structure-architecture aspects), furthermore the strategies species for to control salinity regulation and transpiration.

S.140 IAPT EARLY CAREER INVESTIGATOR SYMPOSIUM: THE EDGE OF THE UNKNOWN IN PLANT, ALGAE, AND FUNGAL SYSTEMATICS. SESSION 1

S.140.1 The rapid radiation of Bomarea (Alstroemeriaceae: Liliales), driven by the rise of the Andes

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Geological events such as mountain uplift affect how, when, and where species diversify, but measuring those effects is a longstanding challenge. Andean orogeny impacted the evolution of regional biota by creating barriers to gene flow, opening new habitats, and changing local climate. *Bomarea* (Alstroemeriaceae) are tropical plants with (often) small, isolated ranges; in total, *Bomarea* species occur from central Mexico to central Chile. This genus appears to have evolved rapidly and quite recently, and rapid radiations are often challenging to resolve with traditional phylogenetic inference. In this study, we apply phylogenomics—with hundreds of loci, gene-tree-based data curation, and a multispecies-coalescent approach—to infer the phylogeny of *Bomarea*. We used this phylogeny to untangle the potential drivers of diversification and biogeographic history. In particular, we test if Andean orogeny contributed to the diversification of *Bomarea*. We find that *Bomarea* originated in the central Andes during the mid-Miocene, then spread north, following the trajectory of mountain uplift. Furthermore, Andean lineages diversified faster than non-Andean relatives. *Bomarea* thus demonstrates that—at least in some cases—geological change rather than environmental stability has driven high species diversity in a tropical biodiversity hotspot. These results also demonstrate the utility (and danger) of genome-scale data for making macroevolutionary inferences.

S.140.2 On the origin and complex convergent evolution of fleshy cones in Podocarpaceae

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Conifers are economically and ecologically important and form extensive forests in both the Southern and Northern Hemispheres. The Podocarpaceae have evolved distinctive seed cones, most of which are fleshy. The detailed diversity and evolution of seed cones is poorly known in this family. We undertook a comparative analysis of Podocarpaceae seed cone morpho-anatomical traits and used ancestral state reconstruction to interpret their evolution. The family exhibits great diversity in functional structures and five distinct structures (free epimatium, fused epimatium, fleshy bracts, arils, and the receptaculum) are involved in the formation of their fleshy cones. Each of these structures has distinct evolutionary patterns, involving multiple origins and/or losses of fleshiness, with a minimum of 24 independent evolutionary changes either from non-fleshy to fleshy or fleshy to non-fleshy structures. The pathways of fleshy seed cone production vary among genera and sometimes within a genus. The Podocarpaceae show great evolutionary lability in seed cone morphology and especially in the production of fleshy seed cones, which are associated with the pollination mechanism (by assisting ovule inversion), protection of the ovule/seed and seed dispersal. The reconstruction of the ancestral Podocarpaceae seed cone is complicated by extinction, convergent evolution, and the relatively few fossil seed cone records.

S.140.3 Pteridophyte Phylogeny Group II and beyond: an updated, community-driven, and open classification for ferns and lycophytes

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We live in an era of big data, when no single person can manually digest all the information required to make optimal decisions. This fact extends to the field of systematic biology, which is being revolutionized by rapid improvements in genomic sequencing and phylogenetic analysis. One approach to handling this data deluge is to move beyond the traditional system whereby a single "expert" publishes their view on the most logical taxonomic system for a particular group, to one where a community of scientists work collaboratively to reach taxonomic decisions. This approach was successfully applied to ferns and lycophytes by the Pteridophyte Phylogeny Group (PPG) in 2016, resulting in the landmark PPG I classification. Since then, systematic research has continued apace, resulting in a need to update PPG I. Here, we report on the methodologies and progress to date of PPG II, with a focus on how such a community-driven, open approach to taxonomy can be employed by systematists studying other groups. In particular, in formulating PPG II we utilize GitHub as an open online platform to solicit and discuss taxonomic proposals and then, with the assistance of custom, open-source R scripts, to adopt those proposals, ensuring that taxonomic interdependencies are fully accounted for (see https://pteridogroup.github.io/).

S.140.4 Integrative taxon-omics and deep learning in Ranunculus

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Integrative taxon-omics aims to combine genomics with a multitude of different complementary datasets such as morphology, ploidy level, information on hybridization and/or apomixis, geography, or ecology. Here, the goal is to advance species delimitation and to achieve a more reliable species classification. Machine learning (ML) encompasses a range of methods that autonomously learn to map a given input to a desired output. ML is rapidly gaining attention in the biological and botanical community for its ability to process highly multi-dimensional, large-scale datasets. However, there have been few attempts so far to combine an integrative approach with ML methodologies. We explore the potential of ML to classify species in the highly reticulate evolving *Ranunculus auricomus* complex, in which taxonomically challenging processes such as apomixis, hybridization, and polyploidy are prevalent. In our previous work, we assessed different fusion techniques with the integration of morphological data and genetic markers using convolutional neural networks (CNNs) that now serve as a basis for the fusion of extensive genetic data, morphology, ecology, and ploidy as well as reproductive information. We show that an integrative approach in ML species classification is not only feasible but that it increases the performance of the neural network. We hope to encourage a more holistic perspective of future ML models.

S.140.5 Epiphyllous fungi from Early Cretaceous swamp forests: exploring multiple techniques for recovering fungal remains from lignites

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A preliminary report of fungal remains associated with leaves of different gymnosperm taxa is presented in this study. The fossils were recovered from lignites collected at the Early Cretaceous Tevshiingovi Formation (~120 Ma – Aptian-Albian) in Central Mongolia. This contribution also explores the different techniques used for recovering the fungal remains from the lignites. Around 450 specimens of leaves of several gymnosperm lineages (*i.e.*, ginkgophytes, corystosperms, conifers) were analyzed using multiple complementary techniques (*i.e.*, light microscopy, epifluorescence, SEM, and X-ray computer microtomography). For observations under light microscopy, most of the samples were previously bleached, applying a modified protocol for chemical treatment of fossil cuticles (with both H_2O_2 and KOH). Staining of the fungal remains with different stains (*e.g.*, safranin, cotton blue, congo red) for enhancing critical features was also explored. Abundant nonreproductive and reproductive remains of epiphyllous fungi are associated with the cuticular surface of around 70% of the specimens. The most conspicuous and abundant structures are scattered to densely distributed thyriothecium-like ascomata, which are mostly associated with the leaves of ginkgophytes and corystosperms. Additional remains include septate hyphae, often with appressoria, 1-3 septate phragmospores, scolecospores, and perithecia with associated filamentous mycelium. These fungal remains are attributable to epiphyllous, probably saprobic, fungi within different lineages of Ascomycota (*e.g.*, Dothideomycetes, Sordariomycetes) and other *incertae sedis* taxa. This report represents the first steps in documenting the fungal diversity associated with the leaves of gymnosperms and in the characterization of the ecological relationships between different organisms from the Early Cretaceous swamp forests of Mongolia. Exploring different complementary techniques demonstrates an improvement in recovering fungal remains from lignite samples. More importantly, the abundance and well preservation of the fossil fungi will help recognize different developmental structures and features of the epiphyllous community.

S.140.6 Bryophytes of the high mountains of Madagascar: a comparative analysis of diversity and distribution patterns

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Madagascar is a global biodiversity hotspot, with some of the highest levels of diversity and endemism on the planet. Its high mountain massifs are remarkable for having a higher degree of regional endemism, often localized to an individual massif. Madagascar's exceptional biodiversity has motivated many studies; however, they have not been evenly distributed and many groups of organisms remain poorly studied. Bryophytes are among the least documented of the Malagasy biodiversity. We conducted detailed analyses of bryophyte communities along elevational gradients in three high mountains in Madagascar to describe the hidden but important biodiversity of bryophyte and understand bryophyte community structure along elevational gradients. We explored Tsaratanana Integral reserve, North-western Madagascar (2888m), Andohahela national park, South-eastern Madagascar (1956m) and Marojejy National Park North-eastern Madagascar (2130m). Preliminary observation shows a diverse and abundant community of bryophytes. Overall, species richness is exhibiting a hump-shaped pattern along elevation gradients, peaking at mid-elevation. Preliminary analyses of the bryophyte community indicate that most species have a narrow range of elevational distribution and are specialized to a particular microhabitat. At higher taxonomic rank, many genera and families also have a narrow range of elevational distribution and microhabitat preferences. This implies that microhabitat preferences are taxonomically structured. This investigation constitutes a significant biodiversity resource that will be used in a range of contexts such as taxonomic revision of the many understudied and likely to be misidentified group of bryophytes. And given that there are no existing molecular databases on the bryophytes of Madagascar, new bryophytes collections from those unique sites have been considered for molecular analysis, especially leveraging next-generation sequencing technologies.

S.141 TRANSPOSON TAKEOVER: TRANSPOSABLE ELMENTS IN PLANT GENOME EVOLUTION, ADAPTATION AND REGULATION

S.141.1 Transposon dynamics in plant genomes

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Transposable Elements (TEs) are major components of eukaryote genomes and in particular of that of plants. The relationship between TEs and the host genome is often seen as a conflict with genomes tightly controlling TEs which transiently scape control by horizontal transfer or during stress situations, producing bursts of transposition and amplification, until the genome re-establishes the control and silence them. However, the dynamics of TEs is highly diverse and depends on the type and family of the TEs and the genome they inhabit. In our laboratory we are studying the dynamics of TEs in a wide range of plant genomes including rice, almond and peach, cotton, and *P. patens*. In this communication I present recent data illustrating different strategies followed by plant TEs to be maintained in the genome ecosystem. On the other hand, the long lasting presence of TEs in genomes has endowed the latter with a high plasticity during evolution. Our laboratory, among many others, has shown that TEs have generated genome variability linked to phenotype diversity selected during plant domestication and breeding. In particular, our recent data points to an important role of TE in generating subtle transcriptional variability of transcription factors and regulatory proteins, that has been selected accompanying domestication and local adaptation of crops. In this communication I also show recent data on the capacity of TEs to generate phenotypic diversity selected during crop domestication and local adaptation.

S.141.2 Dynamics of centromeric retrotransposons and their consequences for chromosomal evolution

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Beyond their fundamental importance for the segregation of chromosomes, centromeres and their evolution remain elusive. In plants, flanking (pericentromeric) segments are characterized by low recombination and chiefly constituted of gypsy retrotransposons. Although such distribution expectedly results from an equilibrium between the insertion of new copies and their removal by purifying selection in high-recombining segments away from the centromere, empirical evidence remains scarce. Chromosome-scale assemblies characterizing the gene space and repetitive fraction of three diploids within the highly-polymorphic species *Biscutella leavigata* and one outgroup species were used to assess the evolution of retrotransposons around centromeres. Despite high synteny within the species, we find large variability in the non-coding part of the genome and particularly high sequence turnover among pericentromeric segments of the genome from the smallest population. By comparing retrotransposons actively targeting pericentromeric regions such as CRM elements to similarly-distributed retrotransposons that are unknown to present biased insertion such as ATHILA elements, we infer their dynamics of transposition vs deletion and highlight the role of specialized retrotransposons during a centromere shift. We further show that they disperse towards the distal part of nucleolar chromosomes and invade intervening gene-rich regions, increasing the methylation of nearby gene and decreasing their expression. Accordingly, bursts of retrotransposon activity associated with the rapid evolution of centromeres are not only affecting the formation and maintenance of heterochromatin and chromocenters, but also result in considerable changes across the gene space.

S.141.3 Repeat turnover meets stable chromosomes: repetitive DNA sequences mark speciation and gene pool boundaries in beets

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Sugar beet and its wild relatives share a base chromosome number of nine and similar chromosome morphologies. Yet, interspecific breeding is impeded by chromosome and sequence divergence that is still not fully understood. Since repetitive DNAs are among the fastest evolving parts of the genome, we investigated, if repeatome innovations and losses are linked to chromosomal differentiation and speciation. We traced genome and chromosome-wide evolution across thirteen beet species comprising all sections of the genera *Beta* and *Patellifolia*. For this, we combined short and long read sequencing, flow cytometry, and cytogenetics to build a comprehensive framework that spans the complete scale from DNA to chromosome to genome. Genome sizes and repeat profiles reflect the separation into three gene pools with contrasting evolutionary patterns. Among all repeats, satellite DNAs harbor most genomic variability, leading to fundamentally different centromere architectures, ranging from chromosomal uniformity in *Beta* and *Patellifolia* to the formation of patchwork chromosomes in *Corollinae/Nanae*. We show that repetitive DNAs are causal for the genome expansions and contractions across the beet genera, providing insights into the genomic underpinnings of beet speciation. Satellite DNAs in particular vary considerably between beet genomes, leading to the evolution of distinct chromosomal setups in the three gene pools, likely contributing to the barriers in beet breeding. Thus, with their isokaryotypic chromosome sets, beet genomes present an ideal system for studying the link between repeats, genomic variability, and chromosomal differentiation and provide a theoretical fundament for understanding barriers in any crop breeding effort.

S.141.4 Role of transposable elements in the domestication of fruit trees: insights from the apple trees

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Transposable elements (TEs) are major components of eukaryotic genomes and are supposed to be evolutionary catalyzers. Unlike the extensive information available for annual crops, the role of TEs in the adaptation of perennial crops, such as fruit trees, has been studied in less depth. Yet, the domestication of perennials is expected to follow different processes than annuals, with distinct genetic outcomes. I present results on TE copy number variation and TE polymorphism insertions in crop-wild population pairs of the apple trees based on the joint study of SNPs and TEs and ongoing experiments. This research will add to our understanding of the role of TEs in the evolution of genetic diversity and innovation in perennials and, ultimately, in the adaptation of populations to recent environmental changes, together with the applied consequences of the findings.

S.141.5 Endogenous pararetroviruses (EPRVs): their evolution, diversity, and regulation

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Pararetroviruses (PRVs) share a common origin with retroviruses and LTR retrotransposons employing reverse transcription for genome replication. In plants, both episomal and chromosomal (endogenous; EPRVs) forms are present. Pararetrovirus evolution most likely occurred through recombination of an ancestral genomic retroelement with exogenous RNA viruses and resulted in horizontal gene transfer. Illegitimate recombination probably also facilitated pararetrovirus integration into the host genomes using virus sequences instead of homologous host genomic sequences on the sister chromatid (during mitosis) or homologous chromosome (during meiosis). RNA interference initiated in the host, regulates episomal and chromosomal pararetrovirus forms, while pararetroviruses themselves have evolved suppressors against this plant defense. Analysing genome and raw read sequences as well as small (sm)RNA databases revealed three types of EPRV clusters comprising petuvirus-, florendovirus- and caulimovirus-like sequences along with two distinct variants of Petunia vein clearing virus (ePVCV-1 and -2) in wild and hybrid petunia. Both ePVCV variants increased in copy number in *P. hybrida,* a diploid hybrid of *P. axillaris* and *P. inflata*, while exhibiting differences in sequences, organization and activity patterns. ePVCV-1 shared 99% sequence identity with the known episomal PVCV and host smRNAs mapped throughout its genome, likely serving as template for initiating episomal PVCV replication in *P. hybrida*. ePVCV-2, with only 74% similarity, lacked some regulatory elements and homologous smRNAs, rendering it replication incompetent. In the permissive genomes *P. axillaris* and *P. hybrida,* we found the pericentromeric regions to be hot spots for EPRV integration. In PVCV infected *P. parodii*, with no detectable ePVCV but episomally replicating PVCV, *de novo* integration of PVCV in the telomeric regions of a single chromosome was identified. We postulate that the pericentromeric insertions are older and silenced while telomeric ePVCV localizations of some *P. hybrida* lines indicate recent, transient activation of ePVCV-1 and *de novo* integration.

S.141.6 What is the contribution of transposable elements to adaptive evolution? A case study using the Persimmon genus Diospyros

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New Caledonia, a biodiversity hotspot with a mosaic of altitudinal, climatic and edaphic environments, was colonized by the Persimmon genus *Diospyros* four times. While three of the New Caledonian *Diospyros* clades have few species, one clade underwent an explosive burst of speciation over a period of ca. 1000 generations, today numbering over 30 species which have repeatedly colonized almost all habitat types on the peninsula. The genome sizes of the radiating clade are roughly double that of their non-radiating counterparts, driven largely by transposable element (TE) expansion rather than polyploidy, prompting speculation that transposable element dynamics underlie the success of the radiating clade through rapid generation of genetic diversity, ameliorating the founder effects which often follow long distance dispersal events. To investigate the origins of the adaptive variation required for *Diospyros* to so successfully colonize New Caledonia, we ask how TE dynamics may have contributed to the adaptive potential of radiating *Diospyros* species. Using long read PacBio sequencing data, we compare the TE landscapes of adaptively radiating *Diospyros* species to an outgroup of the radiation, asking which TE families have undergone expansion, when expansion occurred, and whether repetitive element proliferation pre-dated the burst of speciation in New Caledonian *Diospyros* or occurred after dispersal to the archipelago. By analysing the TE landscape of adaptively radiating and outgroup species within a comparative genomic framework, we can begin to answer questions about the interplay of the mobile genome, shifting ecological circumstances, and the drivers of biodiversity.

S.142 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 6

S.142.1 Integrating functional traits for predicting the response of flowering phenology to change in a diverse Mediterranean community

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Flowering time plays a key role in the reproductive success of plants. It is subject to natural selection and we now know that climate change is shifting flowering phenologies in the Northern Hemisphere, favouring early flowering. However, due to the scarcity of studies of natural communities with long data series, the traits involved in the response of flowering time to climate change are poorly known, especially non-vegetative traits (reproductive, phenological and phylogenetic traits). 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 overall flowering phenology of a species-rich community comprising 270 plant species from the Southwest of the Iberian Peninsula has changed over the last 35 years (1980 and 2020 decades) in response to climate change, and how functional traits conditioned this change. We built models combining vegetative, reproductive and phenological traits (flowering season), as well as phylogenetic information as a covariant. Preliminary results indicate that the advance in the flowering date is generalised across the community and that flowering season plays a significant role in the response of flowering to climate change, with winter/early spring flowering species showing a stronger phenological shift. Our results show that mismatches resulting from changes in the co-flowering neighbourhood may lead to new competitive or facilitative interactions regarding plant reproduction. This study will allow us to predict the phenological response of Mediterranean communities and the reassembly of species according to functional traits, increasing our capacity to design conservation strategies for natural areas in the face of climate change.

S.142.2 Historical forest uses constrain tree growth responses to climate change: a case on resin tapped maritime pines (Pinus pinaster)

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Resin extraction from pine trees was an important economic activity for most of the 20th century in forested countries such as Spain. However, the decrease in resin prices and massive rural migration to cities led to their abandonment in the 1960s-1970s. Reduced tree growth is often observed after long periods of resin tapping, but it is unknown how these formerly tapped stands would respond to recent climate warming and aridification. In Spain, maritime pine (*Pinus pinaster*) was extensively exploited for resin extraction in several regions subjected to increasing drought stress. To understand the differential growth and their responses to climate between resin tapped and non-resin tapped trees, we sampled three historically tapped maritime pine stands in Teruel, eastern Spain, where tapping finished in the 1970s. We extracted and measured cores from 51 resin-tapped and 47 non-resin tapped trees, and compared their growth trends and responses to climate variables and a drought index. Basal area increment was used to measure annual growth. We performed linear mixed regression models to understand the differential responses of resin tapped and non-resin tapped trees to climate variables, including as covariates tree size, age and the resin tapped status. In the study area, climate has progressively warmer and dried since the 1970s. Tree growth was higher in resin tapped trees compared to non-resin tapped trees, which were generally younger. Formerly tapped trees responded more to drought severity than non-tapped trees and were also more negatively impacted by warmer summer temperature. Our results suggest that the legacy effects of previous management can constrain tree responses to climate change.

S.142.3 Rate of phenology advance in boreal conifers in Canada

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The emergence of buds marks a critical phase in the life cycle of plants, signifying an essential response to seasonal shifts in weather patterns. Within boreal forests, distinct species display unique phenological behaviors, and their responsiveness to warming conditions can vary significantly. This study focuses on examining the budburst timing across Canada within three coniferous species, Balsam fir (*Abies balsamea*), black spruce (*Picea mariana*), and white spruce (*Picea glauca*) (Pinaceae). Our study encompasses 2839 locations spanning from 1980 to 2021. Our analysis involved identifying the triggers for budburst, assessing its acceleration rate, and discerning the spatiotemporal patterns in relation to climate. We developed response functions between budburst and climate (air temperature, precipitation, and solar radiation), and used the strongest correlations to test their effect on budburst. Employing spatially constrained multivariate clustering techniques, we discerned distinct budburst patterns across Canada territory. Our findings revealed a baseline disparity of 17 days between black spruce and balsam fir/white spruce budburst timings. Additionally, we observed a negative correlation between the mean minimum May temperature and budburst date. Black spruce exhibited a notable advancement in budburst at a rate of -3.33 days °C^{-1}, twice the rate of balsam fir and white spruce (-1.53 and -1.27 days °C^{-1}, respectively). Notably, the clustering of budburst timings corresponded closely with Canada's ecoprovince distribution, aligning with temperature gradients across the nation. May's mean minimum temperature emerged as the primary driver for budburst in northern tree species. Our projections suggest an earlier budburst in a warmer spring, with black spruce displaying the most pronounced rate of change. Intriguingly, the identified clustering patterns remained consistent despite the longitudinal precipitation gradient across Canada. This study underscores the intricate relationship between climate, geography, and the timing of budburst in boreal tree species.

S.142.4 Molecular mechanisms of seed persistence during the extreme heat of a wildfire

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Fire is a key ecological driver and many plant species have evolved to persist in fire-prone regions. During fire, different life stages of plants, including seeds, are exposed to temperatures as high as 150°C, yet are able to persist. This suggests that molecular processes within the seed provide a mechanism for survival. In this study, we sought to understand the molecular aspects of seed persistence during the extreme heat of wildfire. We focused on Acacia pycnantha, a species native to fire-prone southeastern Australia, which has heat-triggered germination cues and recruits prolifically post-fire, and therefore has a life-cycle tightly linked with fire. We explored the physiology of Acacia pycantha under heat stress through pairing molecular biology with traditional seed biology methods. To examine seed survival under extreme heat, we subjected seeds to 10-minute heat shock treatments ranging from 25ºC to 150ºC, and subsequently conducted germination trials. Seed water-content isotherms were constructed to determine seed hydration profiles post-heat stress, and mRNA extracted to create gene expression profiles. Gene expression was examined at different seed hydration levels after heating at the optimum temperature (92 ºC) for dormancy-break to understand the mechanisms that support persistence during the extreme heat from fires. We report on the genes, and thus mechanisms, that are expressed during extreme temperatures and the role these may have in enabling species persistence. This work is essential for ecological understanding and informing conservation efforts as fire regimes shift under a changing climate.

S.142.5 Unveiling the molecular mechanisms of drought stress response in cigar tobacco: insights from transcriptome and metabolome analysis

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Cigar tobacco is sensitive to water stress and can serve as an ideal material for investigating the molecular mechanisms of drought resistance. In this study, we examined the response of Cigar tobacco to drought stress through physiological, transcriptomic and metabolic analyses. Cigar tobacco seedlings were subjected to 20 (DR) days of drought stress. Compared to control (CK), the results indicated that drought stress inhibited plant growth, physiological traits and enzyme activities. Transcriptome analysis showed that a total of 6446 differentially expressed genes (DEGs) in DR/CK were identified. These DEGs were found to be involved in tryptophan and α-linolenic acid metabolism, flavonoid and phenylpropanoid biosynthesis and the mitogen-activated protein kinase (MAPK) signaling pathway. Furthermore, most alkaloids and lipid content were reduced, amino acids and their derivatives, lignans, flavonoids and coumarins were increased under drought stress. This change can be attributed to the upregulation of type III polyketide synthase B (PKSB), flavonol synthase/flavanone 3-hydroxylase (FLS), and UDP-glycosyltransferases (UGTs), as well as the significant downregulation of R2R3MYB and lipid metabolism-related genes. The regulation of cutin, suberine and wax biosynthesis, the flavonoid pathway and α-linolenic acid metabolism contributes to Cigar tobacco' s response to drought stress and provides valuable data for understanding the regulatory mechanisms underlying drought tolerance in Cigar tobacco.

S.143 ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS. SESSION 4

S.143.1 Ethnobotanical applications to treat snakebite in Colombia

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Colombia harbors a vast cultural and biological diversity, including a great richness of snakes. Most species are harmless to humans, although a few constitute a relevant public health problem as they induce severe envenomations and aftermaths. This pathology primarily affects rural regions in poor conditions. In Colombia, over 5.000 cases of snake envenoming, with

530 deaths, are reported yearly. Local communities use a vast number of botanic alternatives to treat snakebite due to the precariousness of public health. We performed a literature review from the last 50 years about plants used against snakebite in Colombia, including information from interviews with local communities in Mutatá town at Northwest Antioquia. More than 300 plant species useful for snakebite were compiled after this review, while local communities from Mutatá use 131 medicinal plants, including 31 for snakebite. From these, 21 species had not been included in any ethnobotanical study or report, highlighting that traditional knowledge keeps providing valuable information in plant use and management. Laboratory tests were then carried out using ethanolic extracts of five species. We did not find antivenom bioactivity but found no differences between extracts from four plant species and ibuprofen, suggesting analgesic activity. In addition, the anti-inflammatory activity of these plants and the amount of polyphenols in their ethanol extract were tested. Information on the biological activity of plant extracts used by the communities is an important source to find bioactive molecules and promote adequate plant use to which the communities have access. Therefore, we encourage local communities to conserve these traditions as a parallel treatment to public health programs focused on distributing and using antivenoms. Ancestral knowledge must be respected and conserved while public health is guaranteed.

S.143.2 Wealth of knowledge of medicinal plants used by three populations of the community of the urban area of the municipality of Neiva

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The loss of ethnobotanical knowledge for medicinal purposes has increased in recent decades due to the appearance of technologies or other factors that reduce the importance of the acquisition and dissemination of this knowledge in new generations, causing acculturation processes in the young people of the current societies. Therefore, in this study, the richness of ethnobotanical knowledge present in three populations of different ages (young people ≤19 years, adults between 20 and 39 years and older adults ≥40 years) in the urban area of the city of Neiva, was determined. through semi-structured interviews and the collection of data such as the species used, their parts used, the ways of preparation and consumption. Thus, older adults presented a greater wealth of knowledge (RQZ = 100%), reporting peppermint (Mentha spicata L.), calendula (Calendula officinalis L.) and aloe vera (Aloe vera Burm) as the most used to treat gastrointestinal conditions. neurological, musculoskeletal, or other types, using the leaves in greater proportion, due to their great capacity to store secondary metabolites responsible for the relieving effect of different symptoms and pathologies; This part was also used in the preparation of infusions, because it is the most intuitive way of preparing for oral administration. In conclusion, ethnobotanical knowledge is detrimental as populations become younger or very old, due to the growth of acculturation and memory loss due to old age, in addition, the use of plant resources is limited by the lack of vertical transmission of information, accentuated by the loss of biological wealth because of anthropogenic activities mostly related to local urbanization that fuels the degradation of ecosystems.

S.143.3 Ethnobotanical inventory of plants belonging to the categories of use: aromatic and medicinal distributed in the metropolitan area

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The flora species belonging to the categories of aromatic and medicinal use commercialized in the urban area of the city of Neiva were characterized, with 73 plant species, 61 genera and 38 families reported. The reported taxa were: Lamiaceae, Asteraceae and Myrtaceae families, these represented by more than 3 genera. It was evident that the most used plant resources are the leaves, inflorescences and stems as the most commonly used parts. Therapeutic actions mentioned to a greater extent were antispasmodic, antidiarrheal, antitussive, bronchodilator, diuretic, expectorant and hepatoprotective actions. In addition to, decoction and infusion technique of the fresh plant material were highlighted as the method of use most applied by the population. About 63% of the reported species are grown and obtained in the district of "Ulloa" province of "Rivera", 10% of the plant species are grown in district of "Cerro-Neiva" province of "Neiva" in the same department of Huila, and 27% of the plant species must be imported from the departments of Cundinamarca, Boyacá, Tolima and Cauca, showing that 70% of the interviewed people commercialize plants as their main socioeconomic activity, 24% commercialize plants due to lack of job opportunities, and 6% as an indirect economic resource.

S.143.4 Quantitative Phytochemical Analyses of the Fruit and Propagation of Amomum dealbatum Roxb. (Zingiberaceae)

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Amomum dealbatum Roxb. is an indigenous wild ginger of the Philippines of which its fruits are eaten by the local people to treat stomach upsets. It's leaf sheaths were also reported to be utilized in making hats and other handicraft products. Despite its uses, no propagation efforts are done by the local people for this species. The study was conducted to determine the quantitative phytochemical components of the fruits and propagate *A. dealbatum* utilizing indigenous growing media. Phytochemical analyses revealed that the fruits of *A. dealbatum* possess antioxidant property which was determined using the phosphomolybdenum method, while total phenolic content was determined through the folin-ciocalteu method and flavonoids were determined using aluminum chloride colorimetric method. Analyses of the fruits revealed total antioxidant activity (TAA) of 32.66 +- 1.80 mg AAE/g dried sample, total phenolic content (TPC) has a value of 4.33 +- 2.45 mg GAE/g dried sample and total flavonoid content (TFC) of 6.38 +- 81.22 mg QE/g dried sample. In comparison to other other studies, TAA and TFC are relatively higher, while TPC is relatively lower. Thus, the fruit extract of *A. dealbatum* contained flavonoid compounds which are higher in quantity compared with other plants which imply that the fruits of *A. dealbatum* possess high antioxidant potentials which has many benefits for health. Trial propagation of the species using the seeds were also conducted. Boiling the seeds before sowing and covering the pots with plastic improved the chance of the seeds to germinate. T1 (garden soil + rice hull, 1:1) and T2 (garden soil + sawdust, 1:1) are the best growing media which resulted to higher germination and growth rate of young shoots, respectively. Hence, *A. dealbatum* has high TAA and TFC and that propagation utilizing the indigenous growing media is feasible.

S.143.5 Ethnomedicinal appraisal of plants used for the treatment of gastrointestinal complaints by tribal communities of Western Himalaya

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Most of the mountain dwelling communities living in the Himalayas rely on traditional herbal medicines for primary healthcare needs. Present study was conducted in fairy meadows and allied valleys in District Diamir, Gilgit Baltistan autonomous territory in northern Pakistan. Documentation of traditional medicinal knowledge of local communities for the treatment of gastrointestinal disorders was carried out as a component of a wider medico-botanical expedition conducted in the entire base camp of the great Nanga Parbat peak during 2016–19. Various ethnobotanical parameters i.e., use value (UV), informant consensus factor (ICF), Fidelity level (FL), direct matrix ranking test (DMRT) and preference ranking (PR) were applied to evaluate the data collected during field surveys. The plants were also subjected to a comparative review for novelty assessment. A total of 61 medicinal plant species belonging to 55 genera and 35 families are reported here for the treatment of GIDs. Compositae was the leading family with 8 (13%) species. Fourteen gastrointestinal disorders were cured with 32% taxon reported for stomachic followed by diarrhea (15%) and constipation (14%). Highest use reports (5) and use citations (207) were reported for Mentha longifolia L. while highest UV (1.79) was obtained for Artemisia maritima L. Hylotelephium telephioides, A. maritima,

M. longifolia, M. piperita L., Allium cepa L., and A. annua L. exhibited 100% FL. Highest ICF was calculated against dysentery and flatulence. DMRT ranked Prunus persica L. first for its multipurpose uses. Taking constipation as a reference gastrointestinal disease, PR for ten plant species was calculated where H. telephioides was ranked first followed by A. maritima. Present study concluded that 19 out of 61 plant species were documented for the first time with novel medicinal uses to cure GIDs. These plant species could act as potential reservoirs of novel lead compounds for the treatment of gastrointestinal disorders.

S.144 POLYPLOIDY AND HOMOPLOID HYBRIDIZATION AS EVOLUTIONARY DRIVERS IN MEDITERRANEAN PLANTS. SESSION 2

S.144.1 Polyploid hybridization in Kalanchoe: Understanding a new invasive complex in the Mediterranean basin

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Invasive alien species pose a significant threat to global biodiversity, and ornamental plant trade is one of the primary causes of introducing alien plants. One such plant is *Kalanchoe ×houghtonii*, a purpoted artificial hybrid created from the crossing between *K. daigremontiana* and *K. tubiflora*. The two parental species are native to Madagascar, but together with the hybrid have become naturalised and a threat in several regions worldwide, particularly in Mediterranean climate areas. *Kalanchoe ×houghtonii* has four morphotypes, two of which are of known synthetic origin, and the other two which may occur naturally and could be derived from spontaneous gene flow between sympatric populations of the parentals. Reproduction is primarily promoted by propagules produced by the plant. From the cytogenetic point of view, *K. tubiflora* is tetraploid ($2n=4x=68$), while *K. daigremontiana* is diploid ($2n=2x=34$). For the hybrids, there are at least two cytotypes, a triploid ($2n=3x=51$) and a tetraploid ($2n=4x=68$). This study aims to elucidate the interplay between invasiveness, cytotype, and genetic diversity in *Kalanchoe xhoughtonii*. We sampled individuals from several wild locations of the Mediterranean basin, and we complemented the sampling with herbarium and cultivar samples from different regions of the globe. We performed whole genome sequencing and analysed the plastid and nuclear genomes – including the repetitive DNA content and the diversity of ribosomal DNAs – to infer the genomic composition of the hybrid complex. To better understand the contribution of each parental species in the different hybrid cytotypes, we enhanced the study with fluorescent in situ hybridisation (FISH) using 18S and 5S ribosomal DNA probes. Combining genomics, molecular data, and cytogenetics, we aim to provide a holistic understanding of the evolutionary history and the invasiveness of this new and aggressive hybrid complex in the Mediterranean habitats.

S.144.2 The role of homoploid and polyploid hybridization in the evolutionary success of wild wheats

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Polyploidization, or whole-genome doubling, appears to be widespread across plants, particularly in angiosperms. However, it is known to induce sudden drastic changes in nascent polyploid species at both genomic and physiological levels. Allopolyploidy combines polyploidization and hybridization, which additionally causes epigenetic instabilities between genetically divergent maternal and paternal subgenomes that trigger bursts of transposable elements. Nevertheless, allopolyploid species are frequent and generally have a larger geographical distribution than their diploid progenitors. This suggests that successful species might have evolved evolutionary advantages pertaining to their allopolyploid state. To investigate the long-term impact of allopolyploidy on species evolution and adaptation, we used the wild wheat *Aegilops* L. species as model species, a well-known diploid-allopolyploid system in which half of the species are allopolyploids. We collected ~400 samples from four allopolyploid species and their four diploid progenitor species. Based on chloroplast data and amplicon sequencing of 30 low-copy nuclear genes, we inferred a dated phylogeny that confirmed the homoploid hybrid origin of the *Aegilops* genus as well as the multiple maternal and paternal origins of the polyploid species. In addition, by jointly analysing our genomic data with geographical and climatic data, we found that allopolyploids combine both their diploid progenitors' niches. This likely promoted faster recolonization of available suitable niches after the Last Glacial Maximum in allopolyploids as compared to their diploid progenitors. Moreover, this also confer higher adaptability potential to colonize new ecological niches.

S.144.3 Ecological niches in the polyploid complex Linum suffruticosum s.l.

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The prevalence of polyploidy in the evolutionary history of angiosperms within the Mediterranean region appears intricately linked to the region's dynamic paleogeography and climatic oscillations. Polyploids often possess distinctive traits, enabling them to circumvent exclusion by the minority cytotype. These traits may enable polyploid individuals to thrive in habitats divergent from their progenitors, thereby expanding into new places and promoting spatial segregation. This study delves into the role of environmental variables to explain current distribution patterns of the five main cytotypes of *Linum suffruticosum* s.l. (diploids, tetraploids, hexaploids, octoploids and decaploids) across its distribution range. Employing maximum entropy modelling alongside niche equivalency and similarity tests, we discerned the realised environmental niche of each cytotype. Discrepancies in environmental conditions among *L. suffruticosum* s.l. cytotypes were evident, with polyploids demonstrating an affinity for habitats characterised by elevated drought and soil pH levels, lower temperature ranges, and diminished soil water and cation exchange capacities. Diploids exhibited the broadest environmental niche, while polyploids occupied a subset of diploid niche. Although some polyploids exhibited ecologically equivalent niches, they did not coexist naturally. Furthermore, the ecological niche of this polyploid complex diverged between continents, with North African habitats featuring distinctions in soil texture, higher pH, lower cation exchange capacity, precipitation, and soil water capacity, as well as higher temperatures compared to habitats in southwest Europe. While these ecological conditions played a pivotal role in cytotype distribution, the mosaic pattern remained incompletely explained by environmental variables alone. Other factors, such as reproductive isolation and competitive interactions among cytotypes, likely contributed to the extant diversity and distribution patterns. This study yields pertinent insights into the niche requirements of each cytotype, laying the groundwork for subsequent competition and reciprocal transplant experiments.

S.144.4 Intraspecific competitive performance of cytotypes is context-dependence over a latitudinal gradient

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Polyploidization, a common mutation observed throughout the evolutionary history of flowering plants, has played a pivotal role in shaping current plant diversity. While only a small fraction of neopolyploids (newly formed polyploids) successfully establish and spread, several factors contribute to this process. Crucially, neopolyploids must possess certain advantages over their diploid progenitors to gain a foothold, such as enhanced competitive ability. To investigate this competitive advantage, we compared the developmental and physiological responses of natural diploids, tetraploids, and synthetic neotetraploids of *Jasione maritima* var. *maritima* to intraspecific competition in controlled conditions. We also examined whether competitive abilities differed among populations within and beyond the contact zone. Diploids grown without competition exhibited superior developmental traits compared to the other cytotypes, such as increased size. Competition differentially impacted cytotypes, with neotetraploids demonstrating the least susceptibility and tetraploids the most significant negative effects. Notably, an asymmetric competitive response emerged across the latitudinal gradient. Populations outside the contact zone were most adversely affected, with tetraploid populations in the south experiencing the strongest negative impact compared to diploid populations in the north. The higher biomass and intermediate competitive capacity of diploids likely contribute to their persistence in northern distribution areas, while the dominance of neotetraploids under intraspecific competition would enable their establishment. Therefore, the asymmetric competitive abilities of cytotypes across their distribution range, potentially linked to environmental gradient adaptations, likely underlie the observed geographical patterns. Conversely, the similar competitive abilities of diploids and tetraploids within the contact zone may contribute to the maintenance of a dynamic and stable contact zone.

S.144.5 Long-term climatic stability and hybridization as drivers of the endemic diversity of Picris in the Eastern Mediterranean

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The Mediterranean basin emerges as a biodiversity hotspot, housing an exceptionally high number of endemic entities. This biodiversity stems primarily from the region's long-term climatic stability, coupled with extreme geomorphological heterogeneity, including myriad island systems and high mountain ranges with diverse bedrock. Despite climatic stability, oscillations during the Pleistocene triggered contractions and expansions in the majority of organisms. These fluctuations led to recurrent contact between previously allopatric lineages or species, fostering both within and between species hybridization and introgression. The resultant extensive and recurring gene flow significantly contributed to the evolution of numerous hybridogenous lineages and speciation events. This study delves into the evolutionary history of the genus Picris L. (Compositae), serving as an exemplary model to investigate the impact of hybridization on the diversification and speciation processes. The genus Picris originated in the Mediterranean, featuring two major lineages—one evolving in Northern Africa and the other arising in the eastern Mediterranean, specifically in the southern region of Asia Minor and the Near East. Both regions host the highest diversity of the genus, with pronounced species diversity, particularly in the latter region. Previous studies suggested that, beyond allopatric speciation, hybridization and introgression likely play a significant role in this eastern Mediterranean lineage. Employing target enrichment with genome skimming (Hyb-Seq) and inferring both nuclear and plastome phylogenies, our investigation scrutinized the extent to which gene flow contributed to endemic diversity in the genus Picris in this region. Our findings indicate that secondary contacts and gene flow between species and their lineages occurred recurrently across several time horizons. The evolution of many endemics, particularly those from Asia Minor, was notably influenced by hybridization and introgression events.

S.144.6 Hybridization processes and genetic structure in Western Mediterranean Tamarix gallica populations

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The genus *Tamarix* comprises trees and shrubs that grow mainly in saline habitats. In the Western Mediterranean region, three different species naturally occur: *T. africana*, *T. boveana* and *T. gallica*. These three species do not form a monophyletic group and some morphological intermediate samples have been mentioned. The species *T. gallica* is the most common one, and due to its complex morphology, it has been misidentified with *T. canariensis*, an endemic species from the Canary Islands. The aim of this work is to study the phylogeographic history and genetic diversity of the *T. gallica* populations in the Western Mediterranean, and to understand the natural hybridization processes between *T. gallica* and different co-occurring species. For this purpose, fourteen polymorphic nuclear microsatellite markers were analyzed, and two different plastid regions were sequenced for 377 individuals of *T. gallica* from its complete natural distribution and some individuals from other related species. Our results show that current hybridization processes between co-existing species are much more common than previously reported, even between phylogenetically distant species. The three Western Mediterranean species *T. africana*, *T. boveana* and *T. gallica* hybridize between them with different degrees of introgression in natural populations that do not always involve morphological variability. Besides, *T. gallica* has a genetically complex relationship with other species, since it shares haplotypes with other geographically distant species from the Eastern Mediterranean region. Nonetheless, the genetic structure of *T. gallica* population reveals certain clear geographic patterns. In addition, African populations showed a higher genetic diversity, and it diminished towards the north of the Mediterranean Basin. Our results show that incomplete lineage sorting and reticulate evolution have been crucial in the evolution of the genus, and all these processes might be the underlying cause for the morphological confusion between species.

Symposia Session 9

S.145 GENOMICS OF LOCAL ADAPTATION. SESSION 1

S.145.1 Multiple domestications of Asian rice: evidence from domestication genes across the genome

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Asian rice (*Oryza sativa* L.) is not only one of the world's most important crops but also serves as a model for studying crop evolution and understanding the progression of human civilization. However, the origin of Asian rice remains controversial for more than half a century. The controversy arises from four main factors: (i) the ambiguous population structure and genetic relationship of rice progenitors; (ii) poorly annotated samples that do not represent the gene pools of cultivated rice and especially wild rice; (iii) substantial gene flow and introgression among cultivar groups; and (iv) the lack of an effective approach to test for alternative hypotheses about domestication history. Of various speculations and opinions, two leading hypotheses stand out with empirical evidence: a single domestication event in China or multiple domestication events in geographically separate areas. These two hypotheses differ in their predicted history of genes/alleles selected during domestication. Here we amassed a dataset of 459 newly resequenced and 1119 publicly available genomes of wild and cultivated accessions that cover entire geographic range of wild rice and all known cultivar groups. With this large dataset, we developed a strategy to test for single vs. multiple domestication events; this strategy differs from previous studies by analyzing the selective sweep regions/selected genes that have single-origins across domesticated germplasm. We identified 993 selected genes that generated phylogenetic trees on which *japonica* and *indica* formed a monophyletic group, suggesting that the domestication alleles of these genes originated only once in either *japonica* or *indica*. Importantly, the domestication alleles of most selected genes (~80%) stemmed from wild rice in China, but the domestication alleles of a substantial minority of selected genes (~20%) originated from wild rice in South and Southeast Asia, demonstrating separate domestication events of Asian rice.

S.145.2 Genomic assessment of climate adaptation in an annual legume via artificial selection and assisted gene flow

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In response to global warming, early flowering in temperate plants may provide adaptive advantages. This research delves into the utilization of artificial selection (AS) and assisted gene flow (AGF) to increase the adaptive potential of *Lupinus angustifolius* L. populations, particularly in flowering onset. Common garden experiments and genomic studies on diverse populations unveiled marked genomic distinctions between northern and southern counterparts. AS was effective in advancing flowering in northern populations but not in southern ones, suggesting prior natural selection for this trait. Importantly, the advancement of flowering brought about consequential alterations in various vegetative and reproductive traits. Several divergent SNPs between control and AS lines within each population were identified. This number was higher in northern populations compared to their southern counterparts. Southern populations, with limited genomic diversity and diminished responsiveness to selection, may have a reduced capacity for evolution and adaptation to climate change. However, their genotypes favor early flowering, proving advantageous in AGF initiatives in northern populations. To validate this hypothesis, AGF was performed by using pollen from southern individuals to pollinate northern plants. This resulted in a marked advance of flowering onset, accompanied by heavier seed production and reduced above-ground growth, highlighting the influence of AGF extending beyond the flowering phase, as observed for AS. Genomic analysis identified 36 highly divergent SNPs between the control and AGF lines, a validation reinforced by genotype-phenotype associations with flowering onset, seed weight, and above-ground growth. This dual validation robustly reinforces the impact of AGF on these traits on both genetic and phenotypic levels. Overall, our findings underscore the pivotal role of genomics in comprehending genetic modifications induced by AS and AGF, providing detailed information on underlying molecular changes that may be essential for climate change adaptation through early flowering.

S.145.3 The adaptive potential of wild Coffee from Uganda in response to climate change

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Understanding how organisms respond to their environment by altering physiological processes will increase our capacity to make predictions about adaptation to global climate change. Adaptive clines have been increasingly studied in plant species within temperate zones to understand adaptation of organism in natural populations. However, they are still poorly understood in tropical environments. *Coffea canephora,* cultivated as Robusta, is an interesting tropical tree model to investigate adaptation in the tropics, as it is largely distributed within the range of the lowland tropical rain forests of Africa. In particular, modifications occurring in genes related to abiotic stress tolerance make these genes candidate for enhanced resilience to future climate change. We combined the use of both captured regions sequenced for a set of candidate genes related to drought tolerance (de Aquino 2022) and whole genome SNP markers (Tournebize 2022). We provided a comprehensive map of selection signals in the genome of the *C. canephora* (Salojarvi 2023) both at the species level and within its major genetic groups. The genotype-environment association suggests regional adaptation to spatially varying environments of the recent past, with a special focus on the Eastern edge of the distribution, in Uganda (Kiwuka 2021). More specifically, we found signals of selection tightly linked to several genes involved in response to biotic and abiotic stress and in caffeine biosynthesis. We also observed variation of wild Uganda accessions in both growth and drought tolerance (Kiwuka 2023) that can be utilised for optimizing breeding programs initiatives to develop drought-tolerant varieties with adequate yield capacity. Our results support the hypothesis of present ecological gradient contributing to the structure of the genetic diversity with variation in adaptive traits. Moreover, assessing the adaptive capacities of the present populations will help to predict their response to future environmental changes.

S.145.4 Nucleotide and structural adaptive variation facilitate the colonization of stressful habitats in a wild tomato species

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Species distributed across broad environmental gradients are ideal models for unraveling the intricate signals of demographic and adaptive variation in genome dynamics. *Solanum chilense*, a wild tomato relative, thrives in narrow valleys along steep altitudinal gradients in the Andes and has recently colonized isolated areas in highland and coastal regions around the Atacama desert. Utilizing whole-genome sequencing, we correlated climatic changes with demographic shifts and the emergence of adaptive variations. Selective sweeps at 112 genes associated with flowering time and other abiotic response networks, indicate concerted adaptation during colonization to new regions. Complementary, integrating transcriptomic data in response to water deprivation revealed two distinct drought-response networks: cell cycle and fundamental metabolic processes. Interestingly, genes with older selective sweeps exhibit greater network connectivity, illustrating the importance of network rewiring to improve the species' ability to colonize new niches. To gain a more comprehensive understanding of gene network evolution in response to colonization of new habitats, we investigated gene copy number variation (CNVs), identifying 212,207 CNVs that reflect the species' demographic history and reveal candidate genes associated with stress response and, intriguingly, flowering time regulation. Environmental associations link CNV dynamics to climatic variables, pointing to natural selection's role in shaping genome structural variation. These findings provide insights into CNV-driven adaptation in marginal populations, enriching our comprehension of plant evolutionary responses to changing environments. Lastly, we comprehensively examine pathogen resistance genes (NLRs) in *S. chilense*. A refined genome and target-capture approach reveal larger within-population than between-population Presence-Absence Variation (PAV) of NLR loci. Contrary to abiotic-stress response networks, PAV in NLRs is linked to demographic history rather than environmental gradients, challenging prevailing notions about NLR diversity maintenance. This study enhances our understanding of evolutionary processes shaping genome diversity and structure in an outcrossing plant with high nucleotide diversity.

S.145.5 Adaptive hybridization in Western European grapevine varieties

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Grapevine (*Vitis vinifera* L.) diversity richness results from a complex domestication history over multiple historical periods, which culminated in the creation of thousands of modern varieties with extensive phenotypic diversity. Unfortunately, the recent favoring of specific varieties/clones, climate change and the globalization-driven exposure to pathogens, has led to extensive genetic erosion in this widely cultivated and economically significant crop. Fighting this genetic erosion whilst addressing issues of resilience to climate change, yield and other traits, requires a crucial understanding of the genetic basis of grapevine variation. Such studies have been significantly enabled by the use of genomics approaches based on Next Generation Sequencing (NGS). Here, NGS-driven whole genome resequencing of individual genotypes has been used to tackle the extant genetic diversity present in grapevine germplasm, including a clarification of different features of its recent evolutionary path. Our results supported a model in which a central domestication event in grapevine was followed by post-domestication hybridization with local wild genotypes. This lead to the presence of an introgression signature in modern wine varieties across Western Europe, in which the Iberian Peninsula may have played a meaningful role. Furthermore, the examination of underlying genes suggests that environmental adaptation played a fundamental role in both the evolution of wild genotypes and the outcome of hybridization with cultivated varieties, supporting a case of adaptive introgression in grapevine. Acknowledgments: Fundação para a Ciência e Tecnologia (FCT/MCTES) for project GrapeVision (PTDC/BIA-FBT/2389/2020); FCT/MCTES and POCH/NORTE2020/FSE for support to S.F. (SFRH/BD/120020/2016); FCT/MCTES and POPH-QREN/FSE for support to M.C. (CEECINST/00014/2018/CP1512/CT0002).

S.145.6 The accumulation of deleterious mutations has a detrimental effect on tree growth in Pinus pinaster Aiton

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Genetic load, *i.e.*, the accumulation of deleterious mutations in the genome, is predicted to cause a reduction in individual fitness. In plants, an increased number of deleterious mutations has been documented as a consequence of population bottlenecks, for instance in small or recently colonised populations at the margin of species ranges, or in cultivated plants as a negative outcome of domestication. However, the actual adverse effect of genetic load on plant phenotypes remains virtually uncharacterised. We estimated genetic load in populations of the Atlantic-Mediterranean conifer maritime pine, *Pinus pinaster* Aiton, to examine its association with phenotypic traits related to growth and phenology (budburst) measured under common garden conditions. We observed a strong negative correlation between genetic load and tree height on the island of Corsica based on two different datasets (including 133,656 SNPs in 393 individuals and 10,185 SNPs in 334 individuals), thus suggesting a negative effect of the accumulation of deleterious alleles on tree growth on the regional scale. This association was further confirmed by a wide-range analysis including 464 individuals from 34 populations across the entire range of maritime pine in the western Mediterranean, Atlantic Europe and North Africa. Our study is one of the first to experimentally demonstrate adverse phenotypic effects of genetic load in a long-lived plant.

S.146 NEW INSIGHTS INTO PHYLOGENOMICS, SYSTEMATICS AND EVOLUTION OF SALICACEAE

S.146.1 Ecological gradients in various types of stress support different dimensions of plant chemical diversity: Salicaceae as a model

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Plants produce hundreds of thousands of specialized metabolites and many more probably remain to be discovered. There are currently multiple competing explanations for the origins and roles of chemical diversity in plants. We propose that to understand the origins and functions of chemical diversity, we need to decompose it into its various dimensions and link these to prevailing types of environmental stress. From this perspective, the willow family (Salicaceae) represents an ideal model system as the family is diverse from lowlands to highlands and from warm to cold climates. Our results from elevational gradients suggest that changes in the relative importance of stress by specialized insect herbivores and abiotic conditions drive differential phylogenetic trends in willow chemistry that, in turn, support increase in different dimensions of chemical diversity. Abiotic stress promotes directional phylogenetic increase in the concentration of metabolites such as flavonoids that protect plants from abiotic conditions. Abiotic pressures also act as a filter that selects for similar responses, which results

in convergent chemical traits in plants growing under similar conditions. Contrastingly, divergent chemistry can improve plant fitness under strong pressure by specialized insect herbivores. Under prevailing pressure by specialized enemies, plants can thus be selected to switch to a completely different form of defence rather than invest in high concentration or richness of their current metabolites. The resulting divergence should allow for a 'chemical niche' partitioning and promote chemical variation among plant species. We suggest that similar gradients in the relative importance of various types of stress can underlay global trends in the diversity of metabolites. Specifically, we propose that the elevational clines may be analogous to latitudinal patterns of herbivory, host specialization, and quantitative investment in chemical defence, due to similar underlying gradients in the relative importance of abiotic stress and biotic interactions.

S.146.2 Molecular evidence for sectional classification and spatio-temporal evolution of shrub willows (Salix L. subg. Chamaetia/Vetrix)

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Genus *Salix* is the largest genus of family Salicaceae with about 450 species of woody plants predominantly inhabiting the Northern Hemisphere. A large portion of the genus, about 300 species organized in 40 sections, is represented by the so called "shrub willows" belonging to subgenera *Chamaetia* and *Vetrix* that form a monophyletic clade. Several traditional molecular markers could not resolve the relationships within this clade. Traditional, morphology-based taxonomical classification continues to be under question due to vast inter- and intra-specific phenotypic variation and a lack of informative characters. The processes of hybridization, introgression and polyploidization played an important role in the evolution of willows and further complicated research of this genus. Thus, shrub willows remain a hard challenge that fascinates biologists to this day. In our project, we selected a RAD sequencing approach to generate a huge number of SNPs to disentangle the interrelations of shrub willows. This way we wanted to find evidence to justify or refute the current sectional classification. We were able to sequence more than 400 individuals of over 120 species of shrub willows collected worldwide. Using a maximum likelihood estimation, we built a well resolved phylogeny. Our data revealed that most of the species form monophyletic clades, though some exceptions show polyphyly. Morphological traits have evolved multiple times in shrub willows and current sectional classification does not reflect true biological relationships. Polyploidy evolved numerous times as a result of allo- and auto-polyploidization events. Patterns of species radiation could be observed in regions such as North America and Chinese Hengduan mountains. Migration and long distance dispersal further shaped the diversity of shrub willows. Our research presents a strong backbone for future studies on shrub willows regarding taxonomy, hybridization, polyploidization, ecology and many more.

S.146.3 A multi-method genomic approach to phylogenetic reconstruction of the Salicaceae

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With over 1,400 species, the Salicaceae exhibit broad distribution across tropical and temperate forests. Despite ongoing efforts in genome-based approaches, the family lacks a comprehensive phylogeny due to high rates of hybridization and polyploidy. With a sampling of 75 species, our study aimed to reconstruct an extensive Salicaceae phylogeny using whole-genome sequence (WGS) data. We utilized a set of 23,393 RAD-Seq loci from *Salix* as an initial reference library for mapping. The resulting matrix was then used in a second round of mapping, thereby extending the reads recovered from the main WGS dataset. Additionally, we extracted two targeted-capture subsets from our WGS data: the Angiosperms353 and a Salicaceae-specific gene sets.Applying various quality-trimming parameters, we compared phylogenetic informativeness across datasets. We performed ML-based phylogenetic reconstructions using supermatrix and coalescent-based supertree approaches. The length and the number of loci recovered from the WGS data varied between different filtering schemes. Compared to the WGS datasets, both targeted-capture datasets have longer loci with more parsimony informative sites. For both targeted-capture datasets, locus recovery rates were higher for the ingroup samples than the outgroups. Overall, phylogenetic reconstructions revealed consistent family-level topologies, highlighting the monophyly of the family and detailed relationships within. In contrast, the relationships within *Salix* showed lower support and some incongruence across different methods and datasets. In most phylogenies, the subgenera *Chamaetia* and *Vetrix* were recovered as monophyletic, but monophyly of the subgenus *Salix* was not supported in any of the phylogenies. Our study provides a thorough comparison of various genome-based sequencing datasets and phylogenetic reconstruction methods, while enhancing our understanding of the Salicaceae evolution by providing valuable insights into the complex relationships within the family.

S.146.4 Challenges for dating divergence times in the Salicaceae: hybridization and fossil calibration

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Understanding divergence times in the Salicaceae (poplars, willows, and relatives) are crucial for understanding environmental impacts on trait evolution such as sex chromosomes, pollination type, stature, and cold hardiness. Two factors underlie the challenges to estimation of divergence times: 1) the impact of hybridization on estimation of the species tree and 2) accurate placement of fossils onto the tree for calibrating the molecular clock. We used sequence capture protocols to investigate the intricate gene histories in both *Populus* and *Salix*. These histories often conflict with the overall species tree of the Salicaceae family. The diverse gene histories are linked to evidence of gene flow resulting from hybridization, dating back to the earliest divergence events in these genera. Current coalescent dating methods demand extensive computational resources and are feasible only when a limited number of genes are used. We show that variations in gene tree histories can significantly affect estimates of divergence times. Furthermore, despite the abundance of Salicaceae fossils, their limited morphological characteristics make it challenging to confidently place them within the family tree. Our findings demonstrate that calibrating the molecular clock using the most reliable fossils of the origins of subgenera within Salix and Populus leads to a substantial alteration in estimated divergence times compared to calibrating the clock based on the most reliable assessment of the Populus+Salix clade's origin time.

S.146.5 Evolution of sexual systems in poplars and its relatives

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Although hundreds of plant lineages have independently evolved dioecy, i.e., separation of the sexes, the underlying genetic basis has been resolved only in a small subset of species. Additionally, transitions between sexual systems, such as monoecy and dioecy, remain largely elusive. Here we show that diverse poplar species carry partial duplicates of an *ARABIDOPSIS RESPONSE REGULATOR 17* (*ARR17*)-like gene in the male-specific region of the Y chromosome. These duplicates give rise to small RNAs apparently causing male-specific DNA methylation and silencing of the *ARR17* gene. Excitingly, CRISPR/Cas9-induced mutations demonstrate that ARR17 functions as a single-gene sex switch triggering female development when 'on' and male development when 'off'. Despite repeated turnovers, including transitions between XY and ZW systems, sex-specific regulation of ARR17 is conserved across the *Populus* genus. Interestingly, ARR17 appears to be involved in sex determination in the sister genus *Salix* as well. To address the question of when ARR17 evolved its sex-determining function in the Salicaceae family and whether the same gene may control monoecy and dioecy, we analyzed *Poliothyrsis sinensis*, the closest monoecious relative of poplars and willows. We present first functional genomics results of *Poliothyrsis* and discuss their implications for the evolution of sexual systems in the Salicaceae. In summary, our work illustrates how single-gene sex determination in combination with minimal sexual conflict can facilitate repeated turnovers and prevent expanding recombination suppression and sex chromosome degeneration.

S.146.6 Sex chromosome evolution in Salix

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Sex chromosomes have been hypothesized to be drivers of speciation, however, they are difficult to study due to their complex and dynamic evolutionary trajectories. The species-rich, dioecious genus *Salix* (willows) has homomorphic sex chromosomes and is an ideal model system for the evolution of sex chromosomes. We de-novo assembled a chromosome-level genome of the dwarf willow *S. herbacea* using Pacbio HiFi and HiC sequencing. We detected a female heterogametic sex determination system and resolved both Z and W haplotypes on chromosome 15. Two sex-associated regions were located at both ends of a ~5Mb inversion: a 1.8Mb female-specific region (missing from males) and a 0.5Mb region with high sequence divergence between sexes. This suggests stepwise evolution of the sex chromosomes. The sex-associated regions of *S. herbaeca* show only partial synteny with the closely related *S. purpurea* indicating that the region expanded and evolved recently. We currently explore the evolutionary mechanisms that gave rise to the sex-associated regions in *S. herbacea* using whole genome re-sequencing of two *S. herbacea* populations and populations of eight further *Salix* species from the *Vetrix* section. We analyze signatures of selection as well as differentiation between populations and species in ZW homologous regions. With this study, we contribute to the understanding of fast-evolving sex chromosomes with possible consequences for lineage divergence and speciation.

S.147 SPEEDING UP CONSERVATION IN POORLY KNOWN ORGANISM GROUPS – NEW APPROACHES TO BRYOPHYTE CONSERVATION. SESSION 1

S.147.1 Bryophytes and lichens become increasingly visible through remote sensing data: new avenues for research and conservation

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Bryophytes and lichens are ubiquitous taxa contributing significatively to total biodiversity and ecosystem functioning worldwide. Conservation of these ecologically important and sensitive species is however hampered by current knowledge gaps on their diversity, ecology and distribution. Remote sensing (RS) can significantly aid to fill these gaps through its direct and indirect approaches. The direct approach consists in detecting the target species or specific attributes by directly capturing their spectral information, while the indirect approach focusses on the characterization of any habitat factor related to any aspect of the species, allowing for the quantification and eventual specialisation of their relationship across the landscape. Here, we provide a systematic review on the application of RS for the study of bryophyte and lichens, whose potential, as an emerging research area, remains largely unexplored. We identified a total of 101 articles on this topic, of which 55 and 46 followed a direct and indirect approach, with bryophytes and lichens being relatively well represented across them. Both approaches have used very diverse RS information, from purely spectral to indicative of topography, geology, vegetation, wetness, presence of snow, land uses or natural disturbances. They have been derived from a wide variety of airborne and satellite sensors (either optical or active). The direct approach has mainly focused on cover, health and vegetation types, while the indirect approach on α- and β-diversity, distribution, cover and abundance. By synthetizing the results and performances obtained in the reviewed articles across RS approaches, sensors, spatial resolutions and target aspects, we provide discussion on the limitations, knowledge gaps and new opportunities on the use of this technology for bryophyte and lichen research, as well as on the promising role that RS can play for improving their representation in conservation planning.

S.147.2 Cryopreservation of gametophytes as a tool for ex-situ conservation

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Between 2000-2016 a collection of UK threatened bryophytes was established at the Royal Botanic Gardens, Kew as part of the UK's conservation commitments. The majority of accessions were initiated from leafy gametophore material with dried and encapsulated protonemal material subsequently cryopreserved for long-term storage. Regeneration success rates after removing material from short-term cryo-storage were high, with all species able to regrow and 100% regeneration success for 50% of the species tested. However, viability after long-term storage remained unknown. In 2020 and 2021, after at least 14 years in the deep freeze, two species of ongoing conservation interest (*Ditrichum cornubicum* and *Orthodontium gracile*) were removed from the collection. Both successfully regenerated and were re-established into tissue culture, where they have been growing in protonemal form and producing leafy gametophores. Experiments are underway at the University of Plymouth to test weaning methodologies to enable growth in more natural environments. The impacts of long-term cryopreservation and the feasibility of using such material for reintroductions will be presented and discussed. The Kew collection contains over 20 species and the successful regeneration of two mosses is a hopeful sign that cryopreservation could be a useful tool for long term storage of bryophytes. This work forms part of a programme to develop standard methods for the reintroduction of bryophytes from cryopreserved collections and the removal and regeneration of additional species is planned.

S.147.3 Bryophytes as the canaries in the coal mine – using eDNA from 35 years of air samples to analyse changes in bryophyte phenology

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Bryophytes are physiologically highly dependent on climatic conditions, making them useful as early indicators of ongoing changes in biological communities. However, monitoring bryophytes is highly work-intensive, rarely carried out over extensive periods and even less frequent at temporal scales that allow detection of changes in phenology. eDNA approaches are surging in biodiversity monitoring, but bryophyte applications are still in their infancy. We explore a unique eDNA dataset (from the project Swe-BITS) based on airborne particles originally collected from Kiruna, northern Sweden, by FOI (Swedish Defence Research Agency) to detect radioactive downfall. Biological material, that had accumulated on glass fibre filters exchanged weekly during 35 years, was analysed for total DNA and matched against genetic data. As much as ten percent of the generated reads originated from wind-dispersed bryophyte spores. We selected 16 taxonomic groups based on information about local presence, available genomic data for discrimination and level of phylogenetic isolation. We found substantial changes in onset of spore dispersal in spring throughout the time series, with most bryophyte taxa advancing their spore dispersal a whole month, extending the entire season a month or more. The end-of-season timing remained largely the same. Phenological shifts may predate population changes, and both occurrence and phenology data from eDNA may inform conservation planning and efforts. At present, the taxonomic precision of the method is limited by the genomic resources available, but the possibilities are steadily increasing. The proportional nature of the data, with varying relative abundances of different kinds of airborne biological matter between sampling events, makes the analyses computationally challenging. We conclude that eDNA from air samples is a promising and potentially cost-efficient way to monitor changes in bryophyte communities.

S.147.4 Extinction risk of European bryophytes predicted by bioclimate and traits

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Extinction risk is not randomly distributed among species but depends on species traits, their relationship to environmental factors such as climate and land use, and corresponding threats by global change. While knowledge of which factors influence extinction risk is increasingly available for some taxonomic groups, this is still largely lacking for mosses, liverworts and hornworts. Here, we used random forest models to study which biological and ecological traits and bioclimatic variables are important predictors for extinction risk in European bryophytes. We found that bioclimatic variables were the most important predictors for extinction risk, most notably precipitation and precipitation seasonality. Important biological traits were plant size, life strategy and reproductive traits while important ecological traits were continentality and elevational range of species distributions. In general, species living at climatic extremes and/or those with a narrow environmental range are more likely to be threatened with extinction. In addition, small-sized species and/or species with low sexual or asexual reproductive effort and/or larger spore size are more likely to be threatened. Our findings indicate that future climate change will be an important driver of bryophytes' extinction risk, while biological and ecological traits will likely become most relevant for species in coping with future threats.

S.147.5 Project «Searching for the 'Brillófito'»: enhancing knowledge of the intriguing and rare luminous moss Schistostega pennata in th

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The luminous moss, Schistostega pennata (Hedw.) F.Weber & D.Mohr, is a Holarctic moss known for its unique green-emerald glowing protonema when exposed to sunlight. This distinctive feature has inspired several stories surrounding this intriguing feature. The distribution in the Iberian Peninsula represents the westernmost extent in Europe, with only 73 confirmed locations to date. It thrivs primarily in challenging environments such as caves, mines, and crevices, making the discovery of new populations a complex task. Despite its uniqueness, S. pennata faces conservation concerns and is categorised as Vulnerable or near Threatened in several Iberian Red Lists. Yet, the criteria for such designations remain unclear. To enhance understanding and contribute to the conservation efforts of this species, the «Searching for the 'Brillófito'» project was initiated. This project leverages citizen science to gather data on the distribution, ecology, and conservation status of the luminous moss. A comprehensive scientific communication campaign through newspapers, social media, and lectures was also launched to raise awareness and engage the public in moss-related initiatives. The response exceeded expectations, with citizens locating more than 15 new populations across the Iberian Peninsula. Some of these populations revealed new habitats not previously described for the Iberian populations. Interestingly, some were discovered in areas not predicted as optimal by the first species distribution model for the species, highlighting the complexity of understanding the ecological requirements of the species. Many questions remain regarding its ecology and biology in the Iberian Peninsula. These include the scarcity of populations, the mechanisms of dispersal and connectivity between them, the relationship with other non-Iberian populations, and whether luminescence could have an associated function not previously described. Unravelling these mysteries will require further research and an understanding of the role of the moss in its unique ecosystems.

S.147.6 Neglected plants: towards a comprehensive extinction risk assessment of the Brazilian bryophytes

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Over the last 50 years, escalating biodiversity losses, coupled with persistent and intensifying pressures, have resulted in the extinction of species before their scientific description. The Brazil stands out as a country with a vast diversity of bryophytes, with consistent progress done in past years towards a complete assessment of its flora. However, major gaps still exist, making the conservation of this group challenging. In this scenario, automated tools that assist in species extinction risk detection emerges as crucial alternatives to accelerate the process of biodiversity protection. Thus, we highlight the initiative of the Brazilian conservation community to optimize and automate processes for calculating criteria and parameters needed to assess species' extinction risk. Aiming to expedite the risk assessment and direct efforts towards truly threatened species, a list of endemics was created, with names accepted and validated by the backbone taxonomic of the Flora of Brazil 2020, and of broad occurrence, using the rapidLC method, totalling 100 species. The acquisition of occurrence records relied on databases such as Splink, JABOT, and GBIF. For a complete assessment, various biological data were extracted from available online databases, covering biomes, habitats, incident threats, among others. A web application development system was elaborated through the Shiny package of the R software, enabling the delivery of datasets to experts who validated determinations, confirming species distributions, and compiling biological data. The bryophytes were then assessed following the IUCN criteria, resulting in 48 species immediately assessed as Least Concern, while the remaining 52 were forwarded for continuous assessment, evaluated by the National Centre for Flora Conservation, Brazil's National and Global Red List Authority. The use of these tools represents crucial steps in the creation of a consistent red list for Brazilian bryophytes, emphasizing the importance of expediting risk assessments, especially in megadiverse tropical regions like Brazil.

S.148 SYSTEMATICS, FLORISTICS, AND CONSERVATION: FACILITATING DATA INTEGRATION TO PROMOTE SOUND SCIENCE. SESSION 2

S.148.1 Bringing plants to the table: Assessing bias to build a subsample of plants that represents global diversity patterns

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More than 40% of the world's plant species are rare and threatened by extinction. While destruction of the natural world has accelerated dramatically over the past decades, our knowledge of global plant biodiversity patterns has not accelerated at similar rates, with only 20% of the species having their extinction risk formally assessed by now. As our knowledge of plant biodiversity is incomplete, all global studies of plant diversity patterns are based upon subset of species. The included species and the amount of data available for those species are the result of >300 years of biased plant collecting. So, while studying diversity patterns based upon all available distribution data has its merits, it can also lead to a severely distorted view of global biodiversity patterns. It is thus necessary to identify and reduce these biases or find alternatives to better estimate extinction risk and biodiversity patterns from incomplete data. Determining the number of species needed to accurately represent different aspects of plant biodiversity patterns at a global scale thus has important implications for the validity of previous studies but can also be incorporated in future studies. We aim to identify the number of species needed to represent different aspects of global vascular plant biodiversity patterns including species, phylogenetic, floristic, and functional diversity using the World Checklist of Vascular Plants (WCVP) as a baseline. We use this information to determine how well datasets such as the IUCN Red List of Threatened Species, the Species Red List Index, and openly available plant occurrence data incorporate different aspects of plant biodiversity. The outputs will be of interest for biodiversity conservationists and macroecologists.

S.148.2 The evolutionary building up of a biodiversity hotspot: new insights of Andalusian Flora diversity from phylofloristic perspective

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Southern Spain, recognized as a plant biodiversity hotspot, boasts remarkable species diversity, notable endemism, and relictness, by its high environmental variability and dynamic geomorphological history. These factors have acted as drivers of migration and diversification in this region, contributing to the richness of its plant landscape. The three National Parks in Andalusia (Doñana, Sierra Nevada, Sierra de las Nieves) are considered the jewels of the crown, thought to exemplify the majority of ecological and evolutionary processes underlying the region's diversity. The flora of these natural reserves comprises a notably high percentage of species of the entire Andalusian flora. This, in turn, offers an assurance for preserving not only individual species but also populations and communities. The fields of phylofloristics and spatial phylogenetics open new avenues for understanding how evolutionary processes shape phylogenetic relationships of species in a region, elucidating their evolutionary patterns, which is particularly insightful when applied to biodiversity hotspots. Therefore, leveraging this new perspective, we used a megaphylogenomic approach (HybSeq, based on angiosperm353) to study the woody flora in these parks. Particularly, we explored the historical effects on biodiversity in these megadiverse areas and compare the patterns within and among territories. The phylogenomic results enabled us to calculate the phylogenetic diversity and signal associated with life-history traits (pollination, dispersal, flowering), ecological factors (habitat, substrate, altitude), and distribution within representative species ensembles of these biodiversity enclaves. Indeed, life-history traits displayed a strong phylogenetic signal and a pronounced overdispersal pattern. Interestingly, many ecological specialized character states, as a proxy of niche space, exhibited notable phylogenetic clustering, indicating their dominance within closely related species. These findings will provide new insights into the integration of evolutionary history into the criteria of management of protected areas and lineages.

S.148.3 Techniques for managing biodiversity information overload: some examples with bryophytes

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Our collective ability to effectively curate, summarize, and visualize biodiversity data has broader implications beyond botany into the disciplines of conservation science and policy. It is vitally important that decisions made in those areas are based on the best available science, and that starts with the data we create and manage. However, the increasing pace of digitization of biodiversity data threatens to overwhelm our capacity to capture, curate, and use these data. Direct access to the raw data upon which traditional floras, checklists, monographs, etc. are built, would seem to be a boon to both scientific research and policy development. However, in actual practice the results are mixed. End users often struggle to use these data effectively because they are provided 'as is', flaws and all. Moreover, significant effort is wasted as these data are downloaded separately by multiple parties and 'cleaned' for different use cases. In most cases, improvements made to these data externally never find their way back upstream to the original source and in turn, to other end users. Such duplication of effort generally results in reduced productivity without any significant increase in data quality. Moreover, the problem of curating these digital and online representations of botanical data has often fallen to botanists who are already overloaded and has been exacerbated by the lack of available tools for doing this efficiently. Here we illustrate some common problems and use cases using a dataset developed for bryophytes. While many of these problems are not new, practical solutions either remain elusive or are at best poorly implemented. Our aim is to provoke thoughtful discussion about potential strategies for overcoming these challenges.

S.148.4 From the extended specimen to conservation assessment: predicting species Red List status from publicly available information

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The IUCN Red List of threatened species (RL) is the most authoritative global quantification of extinction risk, and widely used in ecological research and applied conservation. Yet, due to the time-consuming assessment process, the RL is taxonomically and geographically biased, in particular towards the global North and charismatic taxa. One promising approach to speed up RL assessments and overcome these biases is the use of AI to predict extinction risk based on the combination of information from digitized collection specimens and citizen science data with remote sensing information on the environment. Here, we present IUCNN, an approach using deep learning models to predict species RL status from publicly available geographic occurrence records (and other data, such as traits if available). We show that AI methods can reach accuracies up to 95% in identifying threatened species and use the results from three recently published case studies -on the orchid family, global tree species and the biota of Madagascar- to illustrate the potential and caveats on using AI and collection specimen to predict species extinction risk.

S.148.5 Identifying gaps in the ex situ conservation of native plant diversity in China

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Due to intensified human pressure and climate change, *ex situ* conservation measures have become essential for conserving Earth's remaining biodiversity, but the development of targeted *ex situ* conservation strategies based on conservation gaps analysis is often a major challenge. Here, we used a dated phylogeny including 95.70 % of the Chinese vascular genera and 1,540,695 species distribution records to identify *ex situ* conservation gaps in the tree of life and geographic space in China. We found that at least 41.70 % (12,716 species) of all vascular plant species (30,494 species), including 49.31 % (1715 species) of Chinese endangered species, are conserved in the botanic gardens. The results show that most species in *ex situ* collections are from eastern China and have been housed in botanic gardens in this region, whereas several plant diversity hotpots in the southwestern and northwestern regions are not well represented in *ex situ* conservation; only 12.67 % of the collection capacity of the Chinese botanic gardens is allocated to endangered species; there are 18 phylogenetic clusters of genera absent from the *ex situ* collections and the missing species are mostly from alpine or desert, mainly distributed in the Himalaya-Hengduan Mountains and northern Xinjiang. Therefore, we suggest that more collection capacity of China be devoted to endangered species particularly in the southwestern and northwestern regions. Our study provides quantified resources of targeted inventory and area for future *ex situ* conservation in China, and a fundamental protocol to invest the future achievement of local or global *ex situ* conservation.

S.148.6 Conservation status assessments of species-rich tropical taxa in the face of data availability limitations: Insights from Sulawesi Begonia

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The feasibility of conservation and extinction risk assessments of plant species using the criteria outlined by The International Union for the Conservation of Nature (IUCN) Red List can be severely compromised by the limited availability of crucial underlying data. This is particularly true for species-rich, tropical plant taxa with a preponderance of microendemics, whose species are often represented by only a few collections in herbaria worldwide. *Begonia*, a megadiverse, pantropical genus (> 2100 species) and characteristic element in the herb layer of tropical forests, is a prominent example. The *Begonia* flora of the Indonesian island of Sulawesi, for example, is comprised of 65 species, 62 of which are endemic to the island, and 51 of which are represented by less than 10 collections in herbaria worldwide. Here we discuss how, despite of these data limitations, meaningful conservation assessments can be achieved by integrating (i) extensive fieldwork and field observations; (ii) herbarium collection locality data; (iii) data primarily based on remote sensing approaches including forest landscape integrity, forest cover loss and land cover categories; (iv) locality number estimates by evaluating the impact range of plausible threats (e.g. concession sizes for palm oil plantations and logging, or the size of large-scale forest fires), and (v) area of habitat estimations using overlap analyses of elevational ranges, forest landscape integrity and limestone karst distributions. The results indicate that most Sulawesi *Begonia* species are narrow endemics whose rainforest and limestone karst habitats have substantially deteriorated in the last two decades: 28 species are assessed as Critically Endangered, 24 as Endangered, six as Vulnerable, five as Least Concern and two species were considered Data Deficient. Conservation assessments of species-rich taxa such as *Begonia*, which include numerous narrow endemics, are important for the formulation of effective national-level action to prevent further extinction.

S.148.7 Integrating data for conservation: a use case for monitoring plant species on a European scale

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Human activities are exerting an increasingly profound impact on global biodiversity. There is a pressing need for a substantial improvement in our understanding of biodiversity to assist land managers, and decision-makers in formulating effective day-to-day strategies for preserving species and habitats. At the European level, significant efforts are underway to harness and leverage the vast corpus of floristic, environmental, and remote sensing data to refine our understanding of vegetation. The Pl@ntNet platform has been set up to meet this challenge, based on a workflow at the intersection of citizen science, botany, and data science. It now enables the automated identification of over 45,000 plant species using state-of-the-art deep learning algorithms. The millions of produced plant observations have contributed to numerous research and conservation projects, positioning Pl@ntNet in 2022 as a top-5 data provider to the GBIF international platform. In this presentation, we introduce the innovative methods currently being developed by the Pl@ntNet team to assist field botanists. Specifically, we discuss how today’s AI technologies allow us to establish contextualized summaries of plant biodiversity in specific areas. We discuss advancements in the analysis of multi-species images commonly generated during floristic inventories. Additionally, we showcase results obtained through DeepSDMs (Species Distribution Models based on deep learning) for predicting the distribution of species and indicators characterizing plant biodiversity at very high resolution. These results are disseminated through free online maps and services for managers, assisting in the identification of key conservation areas. Notably, this work has enabled map production from local to regional scale, at 50 m resolution. We provide a brief overview of identified and implemented uses of these results, demonstrating the various contexts in which these research findings can be impactful, whether for education, management, monitoring, or promotion of natural heritage.

S.149 SYSTEMATICS AND EVOLUTION OF EUPHORBIACEAE

S.149.1 New insights in the evolutionary relationships of Euphorbiaceae: Implications for classification and understanding character evolution

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Resolving relationships among Euphorbiaceae, the largest and least understood family of Malpighiales, is challenging due to the family's morphological diversity, ancient origins, and pantropical distribution. Molecular phylogenetic studies from the early 2000's discovered (but could not resolve among) seven major lineages of uniovulate Euphorbiaceae and identified widespread conflicts with existing suprageneric classifications. Our phylogenomic results from the Plant and Fungal Trees of Life (PAFTOL) project, which sampled 150 of the ca. 230 genera of Euphorbiaceae using Angiosperms353 target sequence capture, are largely congruent with the prior few-gene studies and offer improved backbone resolution. They support four subfamily-level clades including the previously unclear monophyly of Acalyphoideae, with Erismantheae as its first-diverging lineage. The monophyly of Crotonoideae is also strongly supported, with four major lineages plus a novel, isolated placement for monotypic *Klaineanthus*. The resolution of several critical deep nodes remains problematic, including among subfamily clades, which limits our understanding of the early evolution of major traits such as latex/laticifers, petals, and pollen types. In addition, the relationships within Malpighiales of hard-to-place parasitic Rafflesiaceae remain unclear and affect whether Peraceae could be reunited with Euphorbiaceae (as Peroideae). Hippomaneae s.l., the greatest remaining tribal systematics problem, represents a gap in our taxonomic sampling, with only nine of ca. 40 genera sampled. Striking variations in diagnostic morphological traits were observed across clades, including contrasting life history strategies, plant defenses, floral attributes, and specialized reproductive biology (e.g., changes in seed size and dispersal mode). The advances presented here are major steps towards a well-resolved generic phylogeny that would underlie a new classification for Euphorbiaceae and support future studies on the evolution of the astonishing diversity of the family and its biogeographic history.

S.149.2 Deciphering the drivers behind the "Odd Man Out" pattern using continental African Euphorbiaceae as a case of study

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The "Odd-Man-Out" pattern describes the lower plant diversity observed in continental tropical Africa compared to other tropical regions. We examine long-standing hypotheses behind this pattern by adopting a model-clade approach that combines in-depth knowledge of small-scale clade studies with the power of family-wide meta-analysis. We focus on 31 genera of Euphorbiaceae (~550 species), grouped into 19 clades. Our workflow involves the revision of each genus' alpha-taxonomy and the compilation of information about species traits, distribution, and ecology; the generation of phylogenetically informative sequence data from 431 low-copy nuclear genes, obtained using target sequencing (Hyb-Seq) and a taxon-specific bait kit; and finally, the integration of the assembled trait, ecological, biogeographic, and phylogenomic data to explore biological processes working at the clade-level, and general drivers acting clade-wide on Afrotropical lineages. Based on ~78% of the target species and all focal genera, we produced the first phylogenomic time-tree for the African Euphorbiaceae, including representatives of the three subfamilies Acalyphoideae, Crotonoideae, and Euphorbioideae. An ancient stem age (54-26 Ma) was inferred for the smallest genera (less than 10 species), predating the global climate cooling that followed the Paleogene. Diversification rate analyses using episodic birth-death models and an empirical strategy to account for missing species revealed a negative diversification rate between 23 and 5 Ma, which corresponds with a period of severe aridification in Africa. Paleoclimate niche projections showed climatically suitable areas across southern and eastern Africa for many genera, which disappeared after the Pliocene. Taken together, this evidence points to climate-driven extinction as the most likely process to explain the Odd-Man-Out pattern in African Euphorbiaceae. Frequent dispersal from Madagascar was an additional process involved in shaping diversification patterns, as revealed by an 80%-complete species tree for the mega-diverse genus *Croton*.

S.149.3 Inflorescence and floral morphology in the tribe Crotoneae: Implications for the systematics and evolution

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The tribe Crotoneae comprises six genera *Sandwithia*, *Sagotia*, *Acidocroton*, *Astraea*, *Brasiliocroton* and the mega-diverse *Croton*. However, there is no prior study compares floral morphology across all six genera except in few species of *Astraea* and *Croton*. To understand the floral diversity in this tribe, inflorescences and flowers from at least one species from each genus were examined with various techniques, e.g., light microscopy, scanning electron microscopy, resin sectioning and micro-CT. Our investigation revealed significant floral diversity among all genera. Our investigation further identified several synapomorphies across the Crotoneae tribe, including the exclusive presence of staminate flowers on the upper portion of the inflorescence, the presence of more than 10 stamens in staminate flowers, and the reduction of petals in pistillate flowers. Furthermore, synapomorphies of each subclade within the Crotoneae were identified. The *Sagotia*-*Sandwithia* clade members have botryoid inflorescences, simple trichomes, petals exceeding the size of sepals at the anthesis, and outermost stamens alternating with petals. In contrast, the *Acidocroton*-*Astraea*-*Brasiliocroton*-*Croton*clade exhibits racemose inflorescence, stellate trichomes with diverse forms, and outermost stamens positioning opposite petals. Notably, *Acidocroton*, despite belonging to this clade, exhibits some unusual characters that diverge from the typical patterns observed within the group. Our investigation also explored and discussed the inflorescence and floral morphologies of the Crotoneae compare to the tribe Jatropheae and others groups in the subfamily Crotonoideae. Therefore, our study highlights the remarkable heterogeneity present among members of this tribe and provides valuable insights into the key morphological features that define the entire group. Further research is needed to fully elucidate the complex evolutionary relationships and adaptive significance of floral characteristics within the Crotoneae.

S.149.4 A revised generic classification of Tragiinae including the subdivision of Tragia (Euphorbiaceae tribe Plukenetieae)

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Plukenetieae subtribe Tragiinae (Acalyphoideae) is a pantropical and subtropical lineage of ~14 genera and ~200 species of primarily twining vines characterized by their small unisexual flowers with diverse pistillate and androecial morphology, exceptional pollen morphology (including trends towards aperture reduction and loss), and stinging hair defenses. *Tragia* (~160 species) is one of the larger genera of Euphorbiaceae and has a complex sectional classification that until recently included several small genera that are now recognized as distinct (e.g., *Bia*, *Ctenomeria*, *Monadelpha*, *Zuckertia*). It was hypothesized that several more of the sections of *Tragia* could be resurrected as genera but only upon the careful assessment of molecular and morphological data. Using Bayesian phylogenetics on a concatenated dataset of nuclear ribosomal (ETS, ITS), nuclear low-copy (*TEB*), and plastid (*matK*, *ndhF*) DNA, we produced a robust and well-resolved phylogeny for Tragiinae. *Tragia* is strongly supported as paraphyletic with many subclades that could be recognized as distinct genera. Here, we outline our revised generic classification for Tragiinae, which circumscribes genera by a combination of floral morphology (specifically pistillate and androecial morphology), inflorescence structure, well-defined biogeographic distributions, and palynological evidence.

S.149.5 Shining light on a Boreotropical clade: evolution and diversification of Euphorbia subgenus Esula

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Euphorbia subgenus *Esula* Pers. is one of the four lineages of the megadiverse genus *Euphorbia*, and comprises over 485 annuals or perennials, including dendroid shrubs and pencil-stemmed succulents. While the group is primarily a northern temperate radiation it is most diverse in the Irano-Turanian and Mediterranean regions, but taxa also occur in Africa, Asia, and the temperate New World. We assembled the largest taxon sampling of *E.* subg. *Esula* to date (322 spp.), representing its entire geographic range. We updated previous phylogenetic analyses, which confirmed the current sectional classification of the group. We also estimated divergence times and reconstructed ancestral ranges using Bayesian methods. This framework allowed us to characterize the magnitude of extinction and speciation events that have shaped the extant diversity and present distribution of this subgenus. We also explored the influence of changes in life form/history in the diversification and the present altitudinal ranges of *E.* subg. *Esula*. Our results show the divergence of *E.* subg. *Esula* from its sister clade (the three other subgenera) c. 47 Mya, and diversification within this group ca. 41 Mya Biogeographic analyses suggest an ancient origin of the group in the Western Palearctic, where it steadily diversified over millions of years, before the subgenus dispersed to other regions recently. The group underwent parallel events of recent radiations coupled with life history changes, from annual to perennial. Our findings suggest a positive correlation between perenniality and high elevations. These results support that the recent rapid diversification of *E.* subg. *Esula* is associated with the evolutionary shift to perennial life forms, which allowed colonization of montane habitats and global range expansion beyond the Western Palearctic.

S.149.6 The almighty Ricinus: a phylogenomic study sheds new light on the historical domestication and invasive potential of castor bean

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Ricinus communis is an economically and culturally important species. Today, it is used in the automotive, cosmetic, and pharmaceutical industries, as well as an ornamental plant. In the last decades, the species has become an exotic invasive species in many areas of the world. We aimed to characterize the genetic structure of *R. communis* in its native and invaded areas using genomic data. Our sampling included specimens worldwide, with a special focus on naturalized populations, and also whole-genome data from previously published studies. Capture success using HybSeq was high in samples collected in the early twentieth century. We also managed to sequence one of the oldest specimens ever included in a phylogenomic analysis, a sample collected by A.J. Cavanilles in Valencia (Spain) in 1792. Introgression of populations was detected, although unique genotypes were found in the putative native range of *Ricinus* (Ethiopia and Somalia). Our results revealed frequent events of admixture and introgression between regions of the world that are supported by historical herbarium records in Europe. This demonstrates the cultivation and naturalization of *Ricinus* in Europe at least during the Great Age of Exploration. Herbariomics and sampling of naturalized populations have uncovered a wide genomic breath, unseen in previous studies. *Ricinus* climatic niche shows that it occupies areas with novel climates, not present in its native range, indicating a wide ecological plasticity that might have facilitated its naturalization in all continents.

S.150 POALES: FROM ADDRESSING GLOBAL SCALE QUESTIONS TO UNRAVELING THE EVOLUTIONARY SECRETS OF NEGLECTED FAMILIES

S.150.1 Cyperus margaritaceus and its relatives: How many species are there?

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The *Cyperus margaritaceus-niveus* complex (Cyperaceae) is a group of ten tropical species (*C. karlschumanii, C. kibweanus, C. ledermannii, C. margaritaceus, C. niveus, C. nduru, C. obtusiflorus, C. somaliensis, C, sphaerocephalus* & *C. tisserantii*) from sub-Saharan Africa & Madagascar united by the combination of a capitate inflorescence, white-yellow glumes and swollen bulb-like bases. Recent molecular studies in the C4 *Cyperus* clade, have shown that some members of the complex form a monophyletic group sister to the rest of the C4 *Cyperus* species, however regional floras have been unable to reach a consensus on inter-species relationships, presenting differing opinions on the circumscriptions of these taxa. In this study, we use multivariate morphometric analyses - Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA) and Classification and Regression Tree Analysis (CART) - to test the robustness of the species circumscriptions presented in these floras. Unlike flora accounts which only use a partial subset of the taxa, we use all species represented in the complex from across their entire geographical range. *Cyperus kibweanus* was not considered due to lack of material. The analyses show that eight morphospecies are recognised for the LDA, and six morphospecies are recognised for CART. Both PCA and LDA showed varying degrees of overlap in nine of the ten taxa, with no single group clearly separating in multivariate space. Notable results include: 1) the LDA cross-validation showing *C. margaritaceus* to form a robust entity despite its overlapping with the other taxa, and 2) the failure of *C. niveus* to form a distinct entity in both LDA cross-validation and CART. The computational approach attempted here is a useful tool to add to traditional taxonomic methods in resolving other species complexes in the Cyperaceae.

S.150.2 Unprecedented variation pattern of plastid genomes and the potential role in adaptive evolution in Poales

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The plastid is the photosynthetic organelle in plant cell, and the plastid genomes (plastomes) are generally conserved in evolution. As one of the most economically and ecologically important order of angiosperms, Poales was previously documented to exhibit great plastomic variation as an order of photoautotrophic plants. We acquired 93 plastomes, representing all the 16 families and five major clades of Poales to reveal the extent of their variation and evolutionary pattern. Extensive variation including the largest one in monocots with 225,293 bp in size, heterogeneous GC content, and a wide variety of gene duplication and loss, were revealed. Moreover, rare occurrences of three inverted repeat (IR) copies in angiosperms and one IR loss were observed, accompanied by short IR (sIR) and small direct repeat (DR). Widespread structural heteroplasmy, diversified inversions and unusual genomic rearrangements all appeared in Poales, occasionally within a single species. Extensive repeats in the plastomes were found to be positively correlated with the observed inversions and rearrangements. The variation all showed a 'small-large-moderate' trend along the evolution of Poales, as well as for the sequence substitution rate. Finally, we found some positively selected genes, mainly in C4 lineages, while the closely related lineages of those experiencing gene loss have already undergone more relaxed purifying selection. The variation of plastomes in Poales may be related to its successful diversification into diverse habitats and multiple photosynthetic pathway transitions. Our order-scale analyses revealed unusual evolutionary scenarios for plastomes in the photoautotrophic order of Poales and provided new insights into the plastome evolution in angiosperms as a whole.

S.150.3 Global dominance in open and closed habitats is driven by unique traits in the Poales

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Poales, one of the most species-rich orders of plants, often characterise open habitats, enabled by unique suites of traits. We test the hypothesis that key life form traits (photosynthetic system, annual/perennial, insect/animal pollination, epiphyte/non-epiphyte, presence of silica) diverge in different lineages at distinct times and places, leading to spatiotemporal heterogeneity in the diversification of families and the assembly of open habitats. We sampled 42% of Poales species and obtained taxonomic and biogeographic data from the World Checklist of Vascular Plants database, which was combined with trait data scored by taxonomic experts. A dated phylogeny of Poales was constructed using phylogenomic and phylogenetic data. We integrated spatial phylogenetics with regionalization analyses, historical biogeography, ancestral state estimations and models of contingent evolution. Diversification in Poales and assembly of open and closed habitats results from dynamic evolutionary processes that vary across lineages, time, space and traits. Parallel patterns of habitat and trait transitions are evident in the species-rich Poaceae and Cyperaceae families, yet other smaller families display unique evolutionary trajectories. Our results suggest that flexibility in key traits, which is displayed in the most species-rich lineages of Poales, might be an important adaptation allowing transitions between open and closed habitats.

S.150.4 Evolution of holocentricity in cyperids

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While most species have monocentric chromosomes with a regionally restricted centromere, holocentromeres show centromere activity along the entire chromosome. Holocentromeres evolved independently at least 14 times across plant and animal groups. Among plants, the cyperid clade (Poales) comprises the highest number of species with holocentric chromosomes. However, based on recent findings, the transition from mono-to-holocentricity occurred in this clade multiple times, because lineages with mono- or holocentric chromosomes exist. Independent transitions to holocentricity resulted in different adaptations of the centromere and genome structures in these different groups of species, giving insights into variable centromere plasticity and function. We review our recent findings regarding the centromere organization and the role of different classes of repeats in chromosome evolution in monocentric and holocentric Thurniaceae, Juncaceae and Cyperaceae species, and discuss the diversification of this group from a cytogenomic perspective.

S.150.5 Homology-based approach in assessing morphological diversity of Restionaceae

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Despite great taxonomic diversity and a significant role in the vegetation of Australia and South Africa, Restionaceae remain quite difficult in genus and species identification for non-specialists. The problem is at least partly caused by the insufficient amount of morphological data on Restionaceae based on homology instead of a descriptive approach. Well-defined morphological characters can indicate the accurate similarities and differences of taxa and are especially significant for systematics. Restionaceae are well-known for their commonly short and inconsipuous leaf lamina. To date, identification of Restionaceae commonly ignores some leaf characters, e.g., fusion of sheath edges, details of leaf sheath to lamina transition, and lamina morphology. Our analysis of the leaf charters of Australian Restionanceae indicates the taxonomical significance of foliar morphology. For example, we used the occurrence of a long leaf ligule (up to 1.5 cm) as a new character to distinguish species in *Anarthria* (a genus with unusually well-developed leaf lamina). We revealed, also using molecular data and micromorphology, that the commonly accepted species, *Anarthria gracilis,* represents a species complex comprising three distinct species. We present and analyse a new data set on key characters of leaf morphology, including fine details of sheath to lamina transition, for all genera of Australian Resionaceae. A case study of *Leptocarpus denmarkicus* provides an example of new knowledge on inflorescence morphology. We show that the female inflorescence unit in *L. denmarkicus* is a double rather than a simple spike. Spirally arranged glumes represent pherophylls bearing reduced lateral spikelets. Each true spikelet has two bracts, of which one is fertile and subtends a flower. Analogous situations may occur in other Restionaceae. Our aim is to produce a homology-based compendium of morphological character evolution in Restionaceae and to assess the adaptive value of taxonomic characters.

S.151 EVOLUTION AND FUNCTION OF CONVERGENT FLORAL PHENOTYPES. SESSION 2

S.151.1 Selection surfaces driven by different pollinators

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Pollinators are important drivers of floral divergence and speciation in plants. Indeed, *Tritoniopsis revoluta* populations appear to have diverged in response to different long proboscid fly pollinators, as evidenced by closely matched floral tube lengths and pollinator proboscis lengths. But in addition to long proboscid flies, most populations are also visited by solitary bees with short proboscides. Here we investigate how different functional pollinator groups affect pollen receipt across a wide range of floral tube length phenotypes. We experimentally increased floral tube length variance in two populations by translocating short and long tubed plants from elsewhere. We then counted the number of pollen grains deposited on virgin stigmas after single visits by either bees or long proboscid flies. We demonstrate that these distinct functional groups of pollinators have very different effects on pollen movement. More specifically, although bees may be important pollinators in these systems, they are unlikely to impose strong selection on floral tube length. In contrast, the morphological fit between the proboscides of long tongued flies and the corolla tubes of *T. revoluta* flowers appears to be a key feature affecting pollen transfer. This study explains why the tube lengths of *T. revoluta* are apparently adapted to flies rather than bees, even when both are present.

S.151.2 Convergent evolution of floral visual signals via different optical mechanisms

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Flower colour is a key enabler for plants to attract animal pollinators. The colours of flowers are generated by two basic optical principles: wavelength-specific absorption of light by floral pigments and reflection/scattering of incident light by floral structures (e.g., cell walls, starch granules, epidermal surface). We study the evolution of flower colouration using optics, anatomical methods and behavioural experiments with insects. Sampling different Angiosperm groups that are characterised by independent transitions between pollinators with different visual systems, we found that the optical properties of flowers evolve to maximise visibility to pollinators in four complementary ways. First, the type of pigment, which determines a flower's overall hue, is tuned to the spectral sensitivity of pollinators. For example, reflection of ultraviolet, blue, yellow or red light is linked to whether the prime pollinator can perceive this colour. Second, the amount of pigment, which determines the spectral filtering of the scattered light, is optimised to yield high colour contrast. Low pigment amounts yield pale colours, intermediate amounts vivid colours, and high amounts dull colours. Third, the amount of scattering ("brightness") of flowers is determined by the number and inhomogeneity of cell layers. Flower brightness increases upon a switch from diurnal to nocturnal pollination, and this is caused by modifications of both flower thickness and cell structure. Fourth, the epidermal surface determines the glossiness (specularity) of a flower. In specific taxa, such as sexually deceptive orchids and buttercups, very flat and specular surfaces create a brilliant visual effect. Behavioural experiments confirm that bees use surface gloss as a visual cue. In most species, however, cone-shaped epidermal cells annihilate surface gloss and so increase the absorption by pigments and enhance a flower's visibility. Together, our findings show that floral visual signals converge via different, complementary optical mechanisms to maximise visibility to their pollinators.

S.151.3 Exploring the role of local bee diversity on the evolution and spatial distribution of floral uniformity in tropical trees

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Floral phenotypes, as any other plant trait, may present geographical structuring based on biotic and abiotic conditions that favor certain traits to occur more often in sympatry due to convergence. Recently, it has been suggested that angiosperms and their main pollinators, the bees, may present a spatial mismatch in their patterns of diversity, with areas where bee species richness peak being areas where angiosperm species richness is relatively low and vice versa. We here explore how this spatial mismatch may impact the geographical distribution of floral phenotypes of bee pollinated plant lineages. First, we describe the spatial mismatch and explore whether this pattern leads to a decrease in the proportion of bee pollinated angiosperms in areas where bees are less diverse. Second, we investigate how local floral phenotype diversity in bee pollinated plants may be impacted by a less diverse, but not necessarily less abundant, pollinator community, specifically testing whether floral phenotypes would tend to be more morphologically uniform through time in these lineages. We discuss the results in the context of coevolution between bees and angiosperms and how this relationship has modulated the convergent and divergent evolution of floral traits across time and space.

S.151.5 Plant quantitative genetics to understand floral trait diversity

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Plants can evolve rapidly after changes in their pollinators and this is believed to be an important force behind the evolution of floral diversity. Both floral morphological and nectar traits can be expected to play important adaptive roles, with nectar being offered as a reward that varies depending on pollinator preference, and morphology optimizing the mechanical aspects of pollen transfer and access to rewards. Yet the response of different floral traits to novel natural selection can vary. Floral morphology is often expected to show high phenotypic integration to maintain pollination accuracy, while nectar traits can be environmentally sensitive. Genetic correlations and phenotypic plasticity can therefore play important roles that are not fully understood, particularly for nectar traits. We explored this in the context of recent pollinator change, using *Digitalis purpurea* to study the potential to respond to selection of traits that often show convergent patterns of evolution in response to pollination-mediated selection. *D. purpurea* shows rapid recent convergent evolution of corolla morphology but not nectar traits after a range expansion with hummingbirds added as pollinators. We studied phenotypic plasticity, heritability, evolvability, and integration of morphology and nectar in wild populations and in a multi-population common garden. Morphological traits showed higher heritable variation than nectar traits, and the proximal section of the corolla, which regulates access to nectar and shows rapid change in introduced populations, presented higher evolvability and lower integration than all other traits. Nectar was more plastic than morphology, driven by highly plastic sugar concentration. Nectar production rate showed high evolvability and potential to respond to selection. Our results explain patterns of rapid evolution in this species and provide novel insights on the causes and constraints in the evolution behind the extraordinary diversity of flowers.

S.151.6 Genetic mechanisms of convergent floral color evolution in Pedicularis

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Floral color, one of the conspicuous phenotypic traits in plants, exhibits a wide spectrum of variations. Color variations are mainly determined by the types, combinations and concentrations of different pigments. The underlying genetic pathways of pigment production have been well-studied and are relatively conserved across species. However, the evolutionary and genetic mechanisms driving the interspecific floral color variations, particularly in lineages such as *Pedicualris*, remain elusive. *Pedicularis* has over 500 species worldwide and over two-thirds are distributed in Hengduan Mountain, a recognized biodiversity hotspot. This plant genus has an exceptional diversity in floral color with a range encompassing white, yellow, red, purple and their combinations. A particular intriguing aspect of this genus is its floral color convergence, where similar color patterns recur in multiple independent lineages. It is unclear how independent mutations (genetic convergence), inheritance of ancestral polymorphisms and introgressions contribute to the observed convergence. Moreover, if genetic convergence is a major factor, its scale and scope is uncertain - occurring at a specific site, within a particular gene, along a pathway or in a genetic network. In our study, we analyzed transcriptome data of 83 samples across 57 *Pedicularis* species to build a phylogenetic tree using both coalescent-based and concatenated-based methods. We reconstructed ancestral colors in internal nodes using different MK-based models. We investigated gene tree-species tree discordances and the prevalence of hemiplasy in floral color evolution. By applying diverse phylogenetic comparative methods, we aim to detect potential evolutionary and genetic mechanisms underlying floral color evolution. This study will contribute to our understanding of the evolution and function of convergent floral phenotypes.

S.152 MOUNTAIN BIODIVERSITY AND EVOLUTION. SESSION 1

S.152.1 Applications of spatial phylogenetic to unravel biodiversity patterns and evolutionary history of the Himalayan flora

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Mountainous ecosystems are prime biodiversity reservoirs and also serve as hub of raw materials and minerals. Various factors such as climate, landscape, ecological gradients and topographic factors play role in maintaining biodiversity in mountainous regions such as Himalaya. Himalaya is one the world highest mountains range and known as biodiversity hot spot. The region is affected by strong elevational gradients, drastic altitudinal climate variations over very short distances which generate various environmental niches that leads to simple geometric constraints on species distribution boundaries resulting in divergence and speciation. This study focused on general trends and recent advances in highlighting biodiversity hotspots and its evolutionary history. Our study observed that use of species richness, phylogenetic diversity, phylogenetic endemism, and weighted endemism can help to understand biodiversity hotspots in the study area. On the other hand, phylogenetic patterns such as use of net related index and nearest taxon index revealed phylogenetic clustering and over dispersion within study region. Furthermore, our study highlighted that spatial distribution and phylogenetic tree by using β diversity metrics, help to understand phytoregions, indicator species and evolutionary distinctions within the Himalayan flora. Based on these factors, our study recommends that integrative, multifacteted and policy backed approaches are required for understanding of the Himalayan flora. Our study will be helpful in examining ecosystem drivers and provide novel insights into the maintenance and conservation of other mountain regions.

S.152.2 Floristic and evolution of the "sky islands" of East Africa

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The East African mountains are one of the world's crucial biodiversity hotspots, and their distinctive "sky island" structure makes them a Garden of Eden for the evolution of plant diversity. Long-term studies have focused on the diversity and evolution of the Afroalpine flora, and there is a lack of research on the floristic history of the entire montane system. Recent plant catalogs from East African mountains reveal the extremely high diversity of plants here, with about 7,000 species in 193 families and 1,544 genera, of which more than 15% are endemic to East Africa. The spatial and temporal phylogenetic patterns of the mountain flora reveal that the East African mountains are a convergence of ancient and young plants, serving as a museum and cradle of plant diversity in East Africa. Habitat disturbances caused by Pleistocene climate oscillations have led to colonization, dispersion, extinction, and evolution of species. Especially the dispersal of habitats of montane forest species to intervening lowlands during the Pleistocene glacial period facilitated species exchange between mountains. Meanwhile, the temporal differences in mountainous geological dynamics, such as volcanism and uplift, coupled with the island effect, intensify the differentiation of populations among mountains. Our research shows that the East African mountains are experiencing a gradual upward trend in the number of exotic plants, which poses a serious problem of homogenization of native plants. Plant diversity in the East African mountains faces vulnerability and urgently needs more conservation and research attention.

S.152.3 Mountain radiation across the Andes and the Himalaya-Hengduan Mts. driven by evolutionary confluence in a shrub clade, Berberis

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The high-altitude regions of the Andes and the Hengduan-Himalaya Mts. are home to some of the world's most remarkable plant radiations. However, little is known whether these radiations are experienced similar or different diversification history.The high-altitude regions of the Andes and the Hengduan-Himalaya Mts. are home to some of the world's most remarkable plant radiations. However, little is known whether these radiations are experienced similar or different diversification histories. In this study, we investigated the origin of the radiation of *Berberis*, an Andes and Hengduan-Himalaya Mts. (HHM) centered shrub clade. Our results revealed that the net diversification rate of the HHM steadily rised since the Miocene, whilethe rate of net diversification in the Andes remained relatively flat during the same period. We recognized multiple trait-environment matchings evolved from the HHM unlike the Andes, and found such relationships were stepwise evolved along the diversification history of an alpine deciduous clade. Here, we unraveled a distinct but little-tested scenario for mountain radiation, in which sequential assembly of multiple enablers (i.e., key trait evolution, mountain uplift, and paleo-climate change) synergistically function as a trigger to maintain and promote the radiation.

S.152.4 Different levels of competition explain species richness differences between two biodiversity hotspots

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Niche packing and niche specialisation are two central factors modulating biodiversity patterns across latitudes and altitudes. Niche packing is when species niches are finely packed in a multi-dimensional niche space while occurring in the same geographic space. Specialised species on the contrary should have narrow, separate niches and are highly adapted to certain environmental conditions. Both phenomena enable species to coexist by avoiding competition via resource partitioning. Here, we combine phylogenomics of six plant lineages, with occurrence records to compare niche and range metrics - size and overlap - of species between the highly diverse tropical alpine habitats of the South American Andes and the less species-rich alpine habitats on the eastern African mountains. Comparing species niche sizes between both continents using a multidimensional climate space, we found that overall niche size is larger in the Andes than in the mountains of eastern Africa. Additionally, range-overlapping species in the Andes showed generally less overlap in niche space than in Africa. Taken together, we hypothesise that biodiversity differences between the two tropical alpine ecosystems might be caused by different degrees of competition.

S.152.5 From the Andes to the Cascades—biogeography and evolution across western South and North American mountain ranges in Cistantheae

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The plant family Montiaceae (Caryophyllales) has an affinity for desert or alpine habitats and exhibits significant evolutionary lability in life history and climate niche. Lability in life history traits has been shown to cluster especially in one South and North American sublineage, the Cistantheae; this clade is distributed in desert and mountain regions from the Andes to the Cascade mountains, but is absent from equatorial regions (amphitropic distribution). Exploring evolutionary patterns in this lineage has been stymied thus far by unresolved phylogenies, exacerbated by decades of taxonomic confusion due to the presence of intraspecific variation in morphology. We aimed to clarify phylogenetic relationships within Cistantheae and delimiting species using various next-generation sequencing techniques, with the ultimate goal of understanding its biogeographical history and biome transitions. We sequenced 460 plant specimens involving 103 putative species (including outgroup taxa) collected largely from Chile, Argentina, Peru, and USA; the sequencing reads were assembled using a whole-genome reference of the species *Cistanthe longiscapa*. The consequent phylogeny supported genus-level relationships in the Cistantheae, and clarified species relationships in its subsections. Phylogenomic and population genomic approaches showed signatures of gene flow between select populations in smaller geographical ranges; we also inferred multiple long-distance dispersals between continents, with South America acting as the source pool for movements into North America. These analyses support several phylogenetic hypotheses from previous studies and reveal instances where species have been over-split and need taxonomic revision. The phylogeny also raises interesting implications about life history strategies and climate niche evolution, and their role in desert and mountain radiations. Finally, Cistantheae includes multiple rare and highly distinctive species that are vulnerable to extinction––highlighting the necessity for the conservation of their montane habitats and the importance of describing the clade's biodiversity.

S.152.6 Phylogenomic analysis of "quinas" and "pseudoquinas" (Cinchoneae - Rubiaceae) from Peru

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In its current circumscription, the Cinchoneae tribe includes 9 genera of neotropical distribution. Its species occur mostly in the Andes in South America, with few reaching Central America. Preliminary phylogenetic studies have suggested the monophyly of Cinchoneae but intrageneric relationships are still debatable. In this study, we sampled 8 genera of Cinchoneae (with ca. 50% of species for *Cinchona* and *Laden-*

bergia) and obtained multiple single-copy nuclear loci (ca. 207 genes) by using the "Angiosperm353 universal probe set", which was complemented with a taxonomic review of Cinchoneae. Phylogenetic inferences were realized with multispecies pseudo-coalescent (ASTRAL III) and gene concatenation analysis (ML). Our results strongly support the monophyly of the tribe and most of the genera, except for *Ladenbergia*. Furthermore, *Ciliosemina*, *Ladenbergia* and *Remijia* formed a clade, although the position of *Ciliosemina* (=*Remijia pedunculata*) and *Ladenbergia muzonensis* is still elusive. The position of *Ladenbergia muzonensis* is intriguing due to its intermediate floral morphology, which resembles both *Remijia* and *Ladenbergia* species. Additionally, our phylogeny also supports the recognition of a new species in *Cinchona*. Finally, our results show that sequencing data using the probe set designed for multiple gene capture is a useful tool for phylogenetic reconstructions in taxonomically complex groups.

S.153 USING HIGH-THROUGHPUT SEQUENCING TO UNDERSTAND PLANT EVOLUTION ON ISLANDS IN A DATA-RICH ERA: NEW INSIGHTS FOR NEW CHALLENGES. SESSION 2

S.153.1 Do we have enough data yet? Phylogenomics of a rapid island species radiation: an example from New Zealand Myosotis (Boraginaceae)

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Island systems represent natural laboratories for studies of species radiations, but they often present several challenges for species delimitation. New Zealand forget-me-nots (*Myosotis,* Boraginaceae) are a typical example where the c. 50 species are morphologically divergent but often lack sufficient genetic diversity to distinguish among the identifiable lineages. Many of these *Myosotis* species are geographically restricted in alpine areas, uncommon, threatened, and have high taxonomic and conservation priority. Several previous studies have attempted to identify species boundaries and groups using numerous data sources, including single-gene sequences (ITS, ETS, and plastid markers), AFLPs, and microsatellites. Here we present phylogenomic results based on Angiosperms353 baits, whole plastomes, and nrDNA to address long-standing questions in the southern hemisphere lineage of *Myosotis*. We sampled 300 individuals distributed across New Zealand representing all species and subspecies, and included representatives from the two native Australian species. Specifically, we address whether these genomic-level datasets identify taxonomically useful groups (subgeneric, species, subspecies) that are recognized by morphological attributes, including vegetative and reproductive characteristics and pollen. Additional questions we aim to address using these datasets include: Do species form monophyletic groups? Do geographic patterns exist? Can the data be used to delimit species as well as place individuals whose identity was uncertain based on their morphological characteristics? Overall, the phylogenomic data reflect earlier studies that show a recent, rapid species radiation of *Myosotis* in New Zealand. Although the backbone of the phylogenies generally have short branches with low support, collectively the phylogenomic data presented here are more useful than previous studies in identifying species groups. Finally, although this phylogenomic study does not fully overcome all of the challenges regarding species delimitation of rapid island species radiations, it nevertheless makes an important contribution to an integrative taxonomic revision of the southern hemisphere species of *Myosotis*.

S.153.2 Evolution in isolation: sympatric and hybrid speciation on a remote oceanic island

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Speciation with gene flow – sympatric speciation – has often been considered improbable. Recent evidence, which is becoming more readily available with next generation sequencing data, has revealed that it can occur and, in some scenarios, may be relatively common. The flora of Lord Howe Island (LHI) provides a unique system to study this process due to its isolation and small size, enabling us to rule out allopatry in many cases. A putative example of sympatric speciation on LHI is a small radiation of *Coprosma* (Rubiaceae), which has produced up to seven species across two independent colonisations. Alongside producing an integrated taxonomic revision of this genus, we are using a transcriptomic data to test the hypotheses that these species evolved in sympatry and that hybrid speciation has produced at least two of the (putative) species. The latter could provide some of the first substantial evidence for the syngameon hypothesis, the proposed role of elevated levels of hybridisation upon colonisation of a new environment in enabling rapid adaptive diversification under disruptive/divergent selection. This phylotranscriptomic approach involves constructing reference transcriptomes for each species, mapping RNA-seq reads from samples across each species' range, and producing a phylogenetic tree and network of the genus on LHI. This is complimented by a range of population genetic analyses to determine the stage of speciation and transcriptomic regions associated with differentiation in this radiation. Given the strong evidence for sympatric speciation among other genera on LHI (*Howea* and *Metrosideros*), further study into *Coprosma* allows us to determine how general sympatric speciation is across the island and thus how relevant this process is generating biodiversity on LHI and beyond.

S.153.3 Repeated dispersals and in-situ radiations shaped cactus diversity of the Antilles

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Cactaceae are a diverse subset (ca. 1800 spp.) of the arid flora of the Americas. Major diversity centers exist in Mexico, Andean South America and eastern Brazil. The Caribbean biodiversity hotspot, including the Bahamas, and the Greater and Lesser Antilles also houses substantial diversity of the family, especially species of seasonally dry tropical forest, with around 110 species of cacti found there. Most of those species (ca. 91) are endemic to the islands, thus providing a model system for studying island biogeography and the origins of Caribbean biodiversity. Previous work has provided insight into the possible ways in which this diversity was generated, however, no broadly sampled phylogeny is yet available to test these patterns. We generated a near comprehensive dataset of Antillean species of Cactaceae, as well as close relatives based on chloroplast genomes, to test the age and origin of Caribbean cacti. Numerous putative dispersals from the continent occurred during the late Pliocene and throughout the Pleistocene, which led to the tremendous diversity of cacti we now see in the islands. In-situ radiations were most prominent on the larger islands of Cuba and Hispaniola, and those two islands also were the most influential for the further spread of cacti across the rest of the Antilles. Cactaceae provide an intriguing piece to the puzzle for understanding Caribbean biogeography, and Pleistocene climatic events appear to have played a major role in their diversification, a pattern comparable to parts of the mainland distribution of the family.

S.153.4 Historical biogeography of two Caribbean clades of bromeliads

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Pitcairnia (Pitcairnioideae) and *Wittmackia* (Bromelioideae) are two genera in Bromeliaceae with high Caribbean endemism. *Pitcairnia* is the second largest genus in the family, distributed from Mexico to northern Argentina and the only one with presence in Africa. There are approximately 15 species reported in the Caribbean islands. *Wittmackia* is distributed in Brazil and the Caribbean with two separate radiations into the islands, one to the Grater Antilles that diversified into 17 different species, and another to the Lesser Antilles that resulted in one species with widespread distribution. Using a target Sequence Capture approach with the Bromeliad 1776 baits set we analyze the relationships within the Caribbean group and discuss biogeographic implication. Our analysis indicate that *Pitcairnia* colonized the Caribbean from northern South America in one single successful event and later diversified and that species diversity has been overestimated likely because of high phenotypic plasticity in the group. The colonization of the Grater Antilles by *Wittmackia* is also the result of a single event, in this case from Brazil, that resulted in a Puerto Rican and a (mostly) Jamaican clade.

S.153.5 Correlates of inter- and intra-island speciation in Aeonium (Crassulaceae), a species-rich Macaronesian radiation

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The *Aeonium* alliance (Crassulaceae) is the most species-rich and ecologically diverse plant radiation on the Canary Islands. In such radiations, speciation can take place either within islands or following dispersal between islands. By quantifying intra- and inter-island speciation events in the evolution of *Aeonium* and exploring their correlates, we hypothesized that (1) intra-island diversification resulted in stronger ecological divergence of sister lineages, and that (2) taxa on islands with a longer history of habitation by *Aeonium* show stronger ecological differentiation and produce fewer natural hybrids. We studied the biogeographical and ecological setting of diversification processes in *Aeonium* with a fully sampled and dated phylogeny inferred using a ddRADseq approach. Ancestral areas and biogeographical events were reconstructed in BioGeoBEARS. Eleven morphological characters and three habitat characteristics were taken into account to quantify the morphological and ecological divergence between sister lineages. In lineages that diversified within single islands, morphological and ecological divergence was stronger than in lineages derived from inter-island diversification, but only the difference in morphological divergence was significant. Those islands with the longest history of habitation by *Aeonium* had the lowest percentages of co-occurring and hybridizing taxon pairs compared to islands colonized by *Aeonium* more recently. Our findings illustrate the importance of both inter- and intra-island speciation in island radiations, of which only the latter is potentially sympatric speciation.

S.153.6 The draft genome of the cucumber tree (Dendrosicyos socotranus, Cucurbitaceae) as a genomic basis of adaptive evolution on islands

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The island syndrome is a recurring pattern in ecological and morphological differences between insular species and their continental relatives, typically involving loss of defensive structures, increased woodiness, and modifications in floral and reproductive traits. Although this phenomenon has long been treated as a textbook example of adaptive evolution, the underlying genetic mechanisms remain largely unknown. The cucumber tree (*Dendrosicyos socotranus* Balf.f.) is endemic to Socotra island, Yemen, and the only arborescent species among ~1,000 Cucurbitaceae species. Its anatomical features demonstrate adaptation to Socotra's seasonally dry habitat by storing water in the parenchyma of its swollen stems, allowing extended photosynthesis during the dry season. Moreover, the species attracts additional attention due to its vulnerable status on the IUCN Red List and its cultural significance for local communities as a source of fodder and medicine. Here, we report the first genomic exploration of *D. socotranus*. Based on *k*-mer spectrum analyses, the species is estimated to be diploid, with a ~400 Mb genome. Using a combination of Nanopore long-reads and Illumina short-reads, the genome was assembled into 181 contigs, totaling 405.9 Mb with an N50 of 4.9 Mb, and 97.7% BUSCO completeness. Genome annotation revealed that 65.4% of the genome consists of repeats and contains 19,241 protein-coding genes. Comparative genomics with 22 other cucurbits identified 7,592 gene families conserved across all examined cucurbits, as well as 19 gene families unique to *D. socotranus*. Functional annotation of these 19 gene families found one gene family presumably associated with self-incompatibility, suggesting a potential shift in the reproductive manner as observed in other insular species. Further analyses of this genome and comparison with its closest continental relatives will provide valuable insights into the genetic mechanisms that make *D. socotranus* outstanding in the family and facilitate our understanding of adaptive evolution on islands.

S.154 CYCADS AS EMERGING MODELS IN EVOLUTIONARY BIOLOGY AND SYMBIOSIS

S.154.1 The Cycas genome and the early evolution of seed plants

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Cycads represent one of the most ancient lineages of living seed plants. Identifying genomic features uniquely shared by cycads and other extant seed plants, but not non-seed-producing plants, may shed light on the origin of key innovations, as well as the early diversification of seed plants. Here, we report the 10.5-Gb reference genome of Cycas panzhihuaensis, complemented by the transcriptomes of 339 cycad species. Nuclear and plastid phylogenomic analyses strongly suggest that cycads and Ginkgo form a clade sister to all other living gymnosperms, in contrast to mitochondrial data, which place cycads alone in this position. We found evidence for an ancient whole-genome duplication in the common ancestor of extant gymnosperms. The Cycas genome contains four homologues of the fitD gene family that were likely acquired via horizontal gene transfer from fungi, and these genes confer herbivore resistance in cycads. The male-specific region of the Y chromosome of C. panzhihuaensis contains a MADS-box transcription factor expressed exclusively in male cones that is similar to a system reported in Ginkgo, suggesting that a sex determination mechanism controlled by MADS-box genes may have originated in the common ancestor of cycads and Ginkgo. The C. panzhihuaensis genome provides an important new resource of broad utility for biologists.

S.154.2 Paleogenomic data on karyotype evolution in the gymnosperms support Ginkgo and cycads as sisters and both as sister to Pinaceae

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Chromosome-scale genomes provide a basis for inferring ancestral linkage groups and processes of karyotype evolution. We have reconstructed the karyotypes of nine representatives of the major groups of gymnosperms, using an approach that starts from retained intact chromosomes and syntenic blocks. The results show that the most recent common ancestor of the gymnosperms had 24 unique protochromosomes and that their fusion can be traced from the Pinales ancestor to extant species of (((*Pinus*, *Cycas*, *Ginkgo*), ((*Cupressus*, *Metasequoia*), (*Taxus*, and *Torreya*))). The karyotypes of *Gnetum* and *Welwitschia*, by contrast, are extremely modified. Recent assessments of cycad and *Ginkgo* male and female reproductive organ development, pollen ontogeny and germination as well as ovule development, female gametophyte formation, and ovule integument differentiation (Offer et al. Critical Rev. in Plant Science 2023) support the (cycad, *Ginkgo*) sister relationship.

S.154.3 The Cuba Conundrum: Insights into Caribbean Zamia (Zamiaceae, Cycadales) evolution

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We used SSR and Single Copy Nuclear Gene molecular markers to explore patterns of genetic variation across 130 wild populations of Caribbean zamias sampled throughout the entirety of their geographic range. We report the results of several genetic analyses with an emphasis on populations occurring in Cuba, the country with the highest species richness (6 currently accepted spp.) and morphological diversity in this group. We present the following findings: 1) The strongest genetic separation is between zamias in Florida and those occurring in the rest of Caribbean, 2) Cuban populations appear closest to the ancestral Caribbean zamia population and other Caribbean Islands where colonized from Cuba, 3) Bahamian populations are closest genetically to Cuban populations and there is a close relationship between populations in Dominican Republic and Puerto Rico and between populations in Jamaica and the Cayman Islands, 4) Hispaniola was colonized from Puerto Rico rather than from Cuba, explaining the unusual distribution of the genus on the island, where it is restricted to Eastern Dominican Republic, 5) 80% of Florida populations have Heterozygote excess indicating a recent bottleneck event, likely due to the massive starch industry in Florida. 6) Zamia lucayana, a species endemic to Long Island in the Bahamas, is more closely related to Cuban Zamia populations than to other Bahamian populations, 7) Cuban populations are the most morphologically distinct in the Caribbean, but are incredibly genetically admixed, suggesting a high degree of genetic connectivity between them in the recent past. 5) there is a high morphological convergence between genetically distinct populations in the Caribbean, and this extreme conflict between morphological resemblance and genetic similarity makes them a challenging group for morphology-based traditional species delimitation.

S.154.4 Symbiotic microbial and metabolic diversity and age estimates of coralloid roots: deciphering cycad's resilience secrets

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Cycads are known to host symbiotic cyanobacteria, including Nostocales species, as well as other sympatric bacterial taxa within their specialized coralloid roots. Even if it is reasonable to expect that Nitrogen-fixing microbiomes contribute towards the remarkable adaptability of cycads, it remains to be elucidated if (i) these bacteria share a phylogenetic origin and/or common genomic functions that allow them to engage in facultative symbiosis; (ii) how the metabolic products of these microbiomes mediate and sustain 'symbiotic' interactions amongst conserved bacteria and with the cycad host; and (iii) what is the role of these communities, and of the whole coralloid root, on cycad's longevity, which remains to be determined. In this presentation, we provide an integrated view on the cycad's coralloid root, including its microbiome composition and related metabolic products, as well as the anatomy of the host itself, obtained after a broad range of analytical approaches. These include phylometagenomics and functional analysis of synthetic sub-communities, to evaluate evolutionary and functional relationships; metabolomics and imagining DESI mass spectrometry, to provide mechanistic insights underlying the symbiosis functions; and q-FISH to measure telomers lengths and laser ablation tomography to analyze internal anatomy of colonized and non-colonized coralloid roots. Results derived from our integrated approach support a role of coralloid roots on cycad's adaptive resilience, central to the notion of developing cycads as an evolutionary plant model and with a bearing on conservation strategies of this highly endangered plant group.

S.154.5 Enemy-free space in cycad-herbivore interactions: a case study of Zamia cycads and Eumaeus butterflies

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Cycads support fascinating insect herbivore faunas composed of mutualists like brood site pollinators, as well as parasitic herbivores such as folivorous caterpillars. While most research on cycad-insect interactions has focused on insect pollination, parasitic herbivores also significantly affect the fitness of many cycads, with sometimes dire consequences for cycad conservation and management. These herbivore associations are strongly influenced by cycads' defensive traits, particularly their unique chemical defenses, requiring significant adaptation on the part of the insects to be able tolerate, excrete, and/or detoxify cycads' phytotoxins. For this reason, the majority of parasitic cycad herbivores are obligate cycad specialists. For example, the neotropical butterfly genus, *Eumaeus*, is a wholly cycadivorous lineage that feeds primarily on *Zamia* cycads and provides an emerging model system for investigating cycad-herbivore interactions. Recent research in into *Zamia-Eumaeus* interactions includes genomic investigations of both the insects and plants, toxicity and survival assays, and chemical analyses. In this presentation, I synthesize recent research on *Zamia-Eumaeus* interactions (both published and in progress), including results from preference-performance assays conducted with cycad-specific toxins, and descriptive and experimental investigations into the importance of higher trophic levels driving cycad-insect interactions. I evaluate these results in the framework of enemy-free space, using a multi-trophic approach to understand the evolution and ecology of cycads' fascinating symbioses with insects.

S.154.6 Multi-modal pollination signaling in cycads, an ancient plant lineage

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Cycads are an ancient lineage of dioecious gymnosperm that overwhelmingly rely on insect mutualists for pollination services, providing an excellent opportunity for studies into the ecology and evolution of insect pollination, plant-insect signaling, and the maintenance of mutualisms. Specialized cycad-beetle pollination has existed since at least the early Jurassic, placing it before the ecological dominance of angiosperms and the accompanying diversification of major lineages of pollinators such as butterflies and bees (Cai et al 2018). Entire lineages of beetles exclusively live on and pollinate cycads in what has been suggested to be a classic case of co-evolution. Chemical communication (scent) has been shown to be important for the maintenance of these mutualisms (Salzman et al. 2021) and for plant reproduction through 'push-pull pollination' (Terry et al. 2007), the most ancient pollination mechanism yet documented (Salzman et al 2020), yet scent is not the only signal influencing pollinator behavior (Salzman et al. 2023). These entomophilous plants produce dense woody reproductive cones without the overt visual signals commonly employed by angiosperms and must rely on other signals and cues for communication with their insect partners. As such, they are thermogenic plants, producing internal heat within their reproductive structures that in turn alters the carbon dioxide, humidity, and scent of the cones. All of the plant produced primary and secondary metabolites that are perceived by pollinators are used in decision making. I discuss plant signaling and morphology in an ecological and evolutionary framework to understand extant and ancient pollination.

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S.155 KEY MORPHOLOGICAL INNOVATIONS IN FLOWER EVOLUTION

S.155.1 Development of sexually deceptive petal spots

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Gorteria diffusa, a South African daisy, has at least 15 distinct populations that differ in their floral morphology, specifically in the number, complexity, and position of petal spots. However, all morphs are pollinated by the same bee-fly, *Megapalpus capensis*. Floral morphs with simple spots lead to foraging and resting by the bee-fly, while those with complex petal spots mimic the female bee-fly, tricking the males into pseudo-copulation. Our research suggests multiple genetic pathways may have been co-opted and integrated to produce an effective bee-fly mimic. We are comparing these pathways across the populations of *G. diffusa* to identify processes underlying the evolution of this novel character.

S.155.2 Macroevolutionary patterns of floral diversification

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Since crown group angiosperms originated more than 140 Mya., flowers have diversified into a multitude of floral forms. Their diversification was shaped by the combination of extrinsic physical (e.g., climate) and biological (e.g., pollinators) factors as well as by their intrinsic structural and genetic constraints. The continuing progress in phylogenetic and phylogenomic analyses in angiosperms, together with results from comparative floral development and morphology, provide a unique opportunity to understand macroevolutionary patterns of floral diversification. In this study, we trace the evolution and diversification of various floral traits related to the three main organ categories (perianth, androecium, and gynoecium) and key aspects of floral structure (e.g., merism, phyllotaxis, and union of organs). We base our analyses on an extensive, referenced and continuously updated and curated dataset of floral morphology, which we compiled over the past decade in the collaborative database PROTEUS, as part of the eFLOWER initiative. The current dataset comprises 30 floral traits scored for 1201 species, representing all currently recognized angiosperm families. We apply ancestral state reconstructions using parsimony, maximum likelihood, and Bayesian inference, exploring different evolutionary models, to trace the evolution and diversification of pivotal floral traits. In addition, we reconstruct and re-evaluate ancestral flowers at the crown node and additional deep nodes in the angiosperm phylogeny. We find that floral diversification was shaped both by modification and innovation and that similar evolutionary trajectories were often explored repeatedly and independently in different parts of the angiosperm phylogenetic tree. Our study complements earlier and ongoing studies from the fields of paleobotany, comparative morphology, and evo-devo in their attempts to answer key questions on the early evolution and diversification of flowers in angiosperms.

S.155.3 Developmental patterning of head-like inflorescences in Asteraceae

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Asteraceae (sunflower family) represents one of the largest and most diverse families of plants. The inflorescences of Asteraceae mimic solitary flowers but are in fact compressed, head-like structures typically comprised of multiple florets with specialized functions. This unique architecture has been considered as a key innovation behind the evolutionary success of the family. Flower heads are also iconic examples of geometric regularity found in nature; the involucral bracts and florets are arranged in regular left- and right-curving spirals whose numbers follow the mathematical Fibonacci series. We have explored the growth dynamics and patterning of the enlarged inflorescence meristem in the model plant *Gerbera hybrida* and shown with DR5 auxin reporter lines how the high spiral numbers emerge. The molecular data was integrated into a computational model to explain phyllotactic patterning of Asteraceae heads. We have extended our studies to explore how head vasculature is associated with organ phyllotaxis. By applying synchrotron-based micro-CT imaging, we have explored the vascular networks in heads of diverse Asteraceae species. The observed diversity and irregularities of vasculature stand in contrast with the regularity of phyllotactic patterns, confirming that phyllotaxis in heads in not driven by the vasculature. We discuss how our recent discoveries on meristem patterning relate to distinct scenarios of the evolutionary origin of Asteraceae heads.

S.155.4 Gene Duplication Facilitates but does not Trigger Floral Color Pattern Diversification

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The genus *Clarkia* exhibits a tremendous diversity of floral color patterns. Patterns consist of a small number of pattern elements, including background petal color, spots, sprays, white patches. The presence/absence, positions and sizes of these elements frequently differ between very closely related species. In general, different pattern elements are controlled by different paralogs of R2R3Myb proteins that have arisen *via* duplication, and similar pattern elements (e.g. spots) are controlled by different paralogs in different species. The spatial locations of elements are determined by the expression domains of the genes coding for these proteins. While gene duplication clearly has facilitated the diversification of color patterns, this does not necessarily imply that duplication events actually triggered his diversification. By exploring the presence of different paralogs in *Clarkia* and related genera, we have found that the *R2R3Myb* duplications occurred long before diversification of color patterns, indicating a substantial lag time between duplication and the association of these genes with color pattern elements. Duplication events thus did not trigger pattern diversification. Instead, this lag suggests that pattern diversification did not occur until environmental conditions made it advantageous to have novel patterns.

S.155.5 A generalized polarity-based modeling system for plant lateral organ morphogenesis and evolution

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Shape and form are basic attributes of objects. Exploring how the various shapes of Organisms were made through development and evolution is the key to understanding biodiversity. Peltate organs, such as the prey-capturing traps of carnivorous plants and nectary-bearing petals of ranunculaceous species, are widespread in nature and have intrigued and perplexed scientists for centuries. Shifts in the expression domains of adaxial/abaxial genes have been shown to control leaf peltation in some carnivorous plants, yet the mechanisms underlying the generation of other peltate organs remain unclear. Here, we show that formation of various peltate ranunculaceous petals was also caused by shifts in the expression domains of adaxial/abaxial genes, followed by differentiated regional growth sculpting the margins and/or other parts of the organs. By inducing parameters to specify the time, position, and degree of the shifts and growth, we further propose a generalized modeling system, through which various unifacial, bifacial, and peltate organs can be simulated. These results demonstrate the existence of a hierarchical morphospace system and pave the way to understand the mechanisms underlying plant organ diversification. Based on this generalized organ modelling system, we are extending it into a more powerful framework available for multiple organs as well as complex biological structures.

S.155.6 Developmental genetics of corolla tube formation: a key morphological innovation during angiosperm evolution

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About one third of all angiosperm species produce flowers with petals fused into a corolla tube. Differences in the length, width, and curvature of the corolla tube have led to an endless variety of differently shaped flowers that attract specialized groups of pollinators (e.g., beeflies, hawkmoths, hummingbirds, nectar bats). As such, the corolla tube is considered a key morphological innovation that contributes to plant diversification and speciation; yet it remains one of the least understood plant organs from a developmental genetics perspective. In this talk, I present our work towards understanding this problem using monkeyflowers (*Mimulus*) as a model system. Through genetic analyses of several *Mimulus* mutants with split corolla tubes, characterization of corolla tube ontogenesis in the wild type and mutants, and a series of transgenic experiments, we have established a regulatory pathway and a new conceptual model for the developmental genetic control of corolla tube formation. At the heart of this model is auxin-induced synchronized growth between the bases of the petal primordia and the inter-primordial regions during early stages of flower development. Upstream of this core module is the tasiRNA-ARF3/4 pathway that regulates auxin homeostasis in the synchronized growth zone; downstream is an organ boundary gene (*MlNAC1*) that suppresses localized tissue growth if not repressed by auxin signaling. We expect that this conceptual model and the regulatory pathway (i.e., tasiRNA-ARF3/4-auxin-MlNAC1) will serve the foundation for many interesting studies on corolla tube development and evolution in the coming years.

S.156 RELICT PLANT VULNERABILITY TO CLIMATE CHANGE

S.156.1 Algerian relict trees under global and climat change: statuts, threats and conservation

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In the context of global and climatic changes which prevail today, many trees are threatened with disappearance. Algeria is a vast country which is located between two large geographical areas: Mediterranean (Northern Algeria) and desert (Southern Algeria). This situation has generated a remarkable diversity of habitats and ecosystems. Unfortunately, global and climatic changes have negatively affected this diversity (deforestation, grazing, desertification, forest dieback, etc.). Among the important elements of this biodiversity, relict trees occupy an important place in the landscapes. Having lived in different geological eras, these trees are witnesses to the environmental changes that have taken place over millions of years. They also constitute a natural heritage of great ecological, economic and cultural value which must be preserved for future generations. In this work, we present the state of knowledge on the relict trees of Algeria, their ecological and biogeographical status, the threats and the problems linked to their conservation under global and climatic changes.

S.156.2 Diversity of Taxaceae in Northeastern China during Middle-Late Jurassic

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Taxaceae (the yew family) are a small family of conifers comprising about 25 extant species in five genera, including *Taxus*, *Amentotaxus*, *Torreya*, *Pseudotaxus*, and *Austrotaxus*. Their axillary ovulate structures are characterized by bearing a single terminal seed with a fleshy aril, which makes the family very different from other extant conifers. Taxaceae have a long fossil history with the earliest occurrences from the earliest Jurassic (Hettangian, 201–197 Ma) of southern Sweden. Recently, we discovered well-preserved, diverse Taxaceae fossils from the Middle- Late Jurassic Daohugou Biota (~165-158 Ma) in eastern Inner Mongolia, northeastern China. These include a least four species that could be assigned to *Amentotaxus*, *Taxus*, *Torreya* and probably an extinct genus different from all extant genera of Taxaceae. Among the new fossils, *Amentotaxus ningchengensis* sp. nov. and *Taxus daohugouensis* sp. nov. are based on leafy shoots with attached seed-bearing structures, and they resemble those of extant *Amentotaxus* and *Taxus* respectively in vegetative as well as ovulate features. *Torreya daohugouensis* sp. nov. is based on leafy shoots with well-preserved cuticles. It is also comparable to extant *Torreya* in morphology of leaves as well as detailed cuticle structures. The new fossils from the Dahugou Biota show that the yew family had been diverse in Northeastern China since the Middle-Late Jurassic and this pattern of diversification is also seen in early Cretaceous floras of Mongolia. *Amentotaxus*, *Taxus* and probably *Torreya* appeared early in the evolutionary history of the family. The Asian fossils also indicate that *Amentotaxus* and *Taxus* may have undergone little morphological change since the Middle-Late Jurassic.

S.156.3 Meta-analysis of genomic vulnerability of relict plants under rapid climate change in East Asia

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Relict species form an essential component of contemporary biodiversity as representatives of a patrimony nested in the Tree of Life. Rarity and restricted distributions obviously place relict species in special demographic jeopardy of extinction, especially in the face of ongoing climatic changes and other ecological perturbations (Habel et al. 2010). East Asia harbors hundreds of relict species, as several long-term climatically stable refugia provided chances of species-level persistence (Tang et al. 2018). However, climatic-derived genetic diversity loss of relict species in the coming decades has few reported. In this study, we evaluated the population-level climatic vulnerability of 10 relict taxa by genetic-environment associated loci data, considering local adaptation by heterogenous habitats. We aimed to (1) identify the most fragile areas with highest genomic vulnerability, highlighting prior local populations for conservation; (2) assess effects of rescue via migration with or without distance limitation; (3) reveal the traits/genetic basis that enable populations overcome the adaptive challenges. Our work quantified the maladaptation and migration to understanding the extinct risks of relict plants, further help target future conservation actions.

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S.156.4 The origin, speciation, and adaptive divergence of the relict genus Pterocarya under the climate change

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The integration of past, present and future spatial-temporal patterns is crucial in all research areas of biogeography and conservation biology. Combined with the phylogenomics, biogeography, and adaptive genomic variation, we explored the origin, speciation, hybridization, and adaptive evolution of the small Cenozoic relict genus Pterocarya that live in riparian areas with six to eight species. Our results clearly confirm the division of the genus into two monophyletic sections: the Platyptera section and the Pterocarya section. The climate changes during the Early Miocene era coped with the divergence between the two sections. The climate cooling and formation of Gobi Desert in the Middle Miocene epoch caused a split in the continuous distribution of the genus and formation of the disjunction. Focus on East Asia, the phylogeographic break of Pterocarya hupehensis conformed to the boundary of the Sino-Himalayan and Sino-Japanese forests sub-kingdoms. However, in contrast to the nuclear gene, two chloroplast clades within the eastern lineage further diverged along the Yangtze River, and the extensive pollen flow may be the primary factors. Three genetic lineages within P. macroptera: the Qinling-Daba-Tianmu Mountains, Western Sichuan, and Northwest Yunnan lineages, which showed significant signals of isolation by distance (IBD) and isolation by environment (IBE). The identified GEA SNP-related genes were involved in chemical defence and gene regulation and may exhibit higher genetic variation to adapt to the environment. Gradient forest analysis revealed that the genetic variation was mainly shaped by temperature-related variables. A limited adaptive potential was suggested by the high levels of genetic vulnerability in marginal populations. Environmental gradient mainly shaped the population differentiation of P. macroptera. Marginal populations may be at high risk of extinction, and thus proactive management measures, such as assisted gene flow, are required to ensure the survival of these populations.

S.156.5 Local belief as a conservation driver of golden larch (Pseudolarix amabilis) in China

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Pseudolarix amabilis is a specific mono-species genus plant in China, and one of the most internationally influential ancient relict plants in China. *P. amabilis* is facing various threats such as habitat fragmentation, population isolation, and number dwindle. Fortunately, it has been pointed out that the village *fengshui* forest provides shelter for the natural population of *P. amabilis*. However, how can the village *fengshui* forest protect the natural population of *P. amabilis* remains to be explored in depth. Therefore, based on the methods of field investigation and community interview, this study conducted a comprehensive investigation of the recruitment status, conservation behavior, and disturbance degree for the natural population of *P. amabilis*. At the same time, we took the natural population of *P. amabilis* in Linjiatang as an example to reveal the protection and management paradigm of *P. amabilis fengshui* forest and explore its role in the effective protection of *P. amabilis*. The results showed that DBH structure of *P. amabilis* in *fengshui* forest was more continuous, and the seedling density was higher, compared with other habitat types. *Fengshui* and taboo culture carried by *shuikou* forest, cemetery forest, and *yangji* tree are the internal reasons why the *fengshui* forest can effectively protect the natural population of *P. amabilis*. The development of rural tourism has further promoted the protection of the *P. amabilis fengshui* forest. Our results can provide a basis for making an effective protection paradigm for the natural population of *P. amabilis*.

S.156.6 Deep phylogeographic divergence of beaked hickory calls for transboundary conservation in a biodiversity hotspot

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The conservation of endangered plants is a crucial step for the maintenance of biodiversity in a changing world. However, the lack of comprehensive phylogeographic information for most endangered species greatly impedes effective action, especially for species distributed across national borders. Beaked hickory (*Carya sinensis*), which is endemic to China and Vietnam, part of the Indo-Burma biodiversity hotspot, exemplifies these issues. Here, based on comprehensive field sampling, we used three genomic datasets (i.e., plastid, mitochondrial, and nrDNA) and ecological niche modeling to reveal its genetic diversity, phylogeographic structure, and population history, shedding insights into conservation. Three distinct clades were resolved, i.e., Clade A in Vietnam, Clade B in China, and Clade C covering both countries. Genetic diversity is low at species and within-clade levels, but multiple private haplotypes were observed in each clade. The three clades diverged between 6 and 8 Mya, making this a far older species than others within *Carya*, and each likely had a separate glacial refugium. Bottlenecks were detected in all three clades after the LGM, probably driven by the late Pleistocene glacial oscillations, but Clade C experienced a recent (~800 years ago) expansion which might have been anthropogenic. From this, we recommend treating the three clades as distinct conservation units for *C. sinensis* and propose a precise evidence-based *in* and *ex situ* conservation management strategy, as part of a practical transboundary conservation framework. This sets a model for transboundary conservation through joint efforts between nations, for other threatened species using a similar integrative approach.

S.157 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 7

S.157.1 Predicting the effects of climate change on seed germination: implications for woodland regeneration and tree seed sourcing

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Expanding and connecting woodlands to capture atmospheric carbon and enhance resilience to environmental change is garnering support as a climate change mitigation action. This requires an unprecedented increase in tree planting, which demands the efficient use of limited native seed resources. Thus, there is a need to develop improved practices to overcome hurdles posed by the variable quality, dormancy states, and germination requirements of native seeds. Moreover, as the climate changes, species germination requirements may no longer be fulfilled or be met at an unfavourable time for seedling establishment, impacting woodland regeneration and ecosystem diversity and services. We aimed to investigate intra-specific variation in seed germination traits of two native broad-leafed species of forestry importance in the UK: *Alnus glutinosa* and *Betula pubescens*. We tested seeds from six populations of each species collected in the wild and stored at the RBG Kew's Millennium Seed Bank, to represent the latitudinal gradient across the country. Germination tests were conducted on collections of each population at a range of constant temperatures, both with and without a cold stratification pre-treatment to alleviate dormancy. The collected data were then used in a modelling approach to estimate thermal thresholds for seed germination (base, optimum and ceiling temperatures; sub- and supra-optimal thermal time) and determine the requirement for cold stratification for all collections. In addition, we modelled germination parameters under different climate change scenarios to identify plant populations at the greatest risk. Finally, we explored the potential of morphological traits serving as predictors of germinative behaviour. This information helps evaluate the impact of climate change on woodland regeneration and allows for informed adaptive 'climate-smart' seed sourcing to enhance reforestation practices. The results also provide insights on how climate and provenance shape the functional diversity of tree seeds.

S.157.2 Revealing within tree sensitivity to drought in temperate forest species differing in shade tolerance

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Droughts are becoming a recurrent event worldwide, which reduce carbon uptake and increase tree mortality risk threatening several ecosystem functions and services. Global change is increasing the intensity, duration, and frequency of droughts due to a combined effect of scatter precipitations, atmosphere warming and soil erosion. However, droughts do not affect equally to all forest tree species due to species-specific differences in drought resilience and niche partition. Furthermore, leaf physiology, anatomy and morphology acclimate within the tree canopy to changes in light intensity and quality, evaporative demand and soil water availability. However, not many studies analyse within tree canopy inter-specific drought tolerance and plasticity, which in turn may constrain the adaptative strategies of the species shade tolerance. Here, we measured leaf gas exchange and hydraulics within the canopies of four forest tree species differing in shade and drought tolerance. Trees were in transects of increasing soil depth at the Natural World Heritage Site of "Hayedo de Montejo", a relict European forest growing under Mediterranean conditions, and measurements were done during very dry and wet years. We show that shaded leaves are more susceptible to water stress than sun-developed leaves, and that decreased photosynthesis is due to the combined effect of reduced stomatal and mesophyll conductances and to a lesser extent by biochemical constrains, while top canopy leaves are mainly limited by the stomatal closure. This results in earlier lower carbon balance of the more shaded leaves within the canopy, what explains the earlier leaf shedding of the more shaded leaves. More shade tolerant species were more affected by drought along the canopy, while more drought tolerant ones were able to maintain modest gas exchange rates but only in sun-exposed leaves. Climate change may promote open forests which may benefit the more drought albeit less shade tolerant species.

S.157.3 Strategies for enhancing urban air quality through vegetation

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Cities face diverse environmental challenges, making it crucial to identify the most significant ones for each city to design effective urban strategies. Implementing urban green infrastructure is a promising approach that can significantly improve public health by reducing air pollution. Vegetation controls pollutant flow and distribution, with some tree species being more effective at trapping pollutants than others. Key traits for improving air quality include canopy density, foliage longevity, water-use strategy, and high stomata conductance, which is essential for gaseous pollutants capture. However, trees can also emit volatile organic compounds (VOCs), which react to form ground-level ozone (O3). Therefore, avoiding tree species that emit high VOC levels is important, particularly in residential areas. Advanced models and tools can help estimate ecosystem services and support urban greenery management. These tools assist public institutions and citizens in selecting species that maximize air pollution reduction. The effectiveness of urban greenery varies with fragmentation, green cover, and plant species. In conclusion, while beneficial vegetation traits enhance pollutant capture, they do not guarantee suitability for all contexts. Selecting tree species with high pollution mitigation potential does not always yield desirable results. Plant species must be adapted to local conditions, and stress tolerance should be prioritized in urban environments, especially roadside areas facing multiple stressors.

S.158 TELLING PLANT SPECIES APART WITH DNA. SESSION 2

S.158.1 Comparative analysis of complete plastome sequences of Tulipa L. (Liliaceae Juss.) species from Kazakhstan

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The *Tulipa* L. genus belongs to the Liliaceae Juss. family, consisted around 100 species all over the world. *Tulipa* species are native to southern Europe, North Africa, the Middle East, and Central Asia. The mountainous regions of Central Asia (including Kazakhstan) are considered the primary center of *Tulipa* origin. According to Ivaschenko (2019) 42 wild *Tulipa* species are found in Kazakhstan, 18 of them listed in the Red Book of Kazakhstan. These plants have an important economic, floricultural, ecological significances, cultural value in many regions of the World. Wild species are important genetic resources for breeding and play a significant role in ecosystems, especially for pollinators and insects. Ten *Tulipa* species from Kazakhstan were studied based on complete plastome genome sequences using NovaSeq 6000 (Illumina) platform. All the sequenced *Tulipa* species from Kazakhstan were deposited to the National Center for Biotechnology Information GenBank and publicly available. *Tulipa* species plastomes contained 136 genes, including 90 protein-coding genes, 38 transfer RNA, and 8 ribosomal RNA genes (including duplicated genes). The forward, reverse, and palindromic repeat elements and mononucleotide, dinucleotide, trinucleotide, tetranucleotide, pentanucleotide and hexanucleotide repeats were detected in four *Tulipa* species from Kazakhstan. Furthermore, tandem repeats in each of the *Tulipa* plastome were identified. Comparative analysis of plastome genome sequences revealed the genes with high polymorphism, which can be used as candidate DNA barcode markers for further studies.

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S.158.2 Large scale DNA sequencing of plant biodiversity in global biodiversity hotspots – the China plant barcode of life

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Vascular plants dominate terrestrial ecosystems and provide food, drugs, timber, fibers, fuels and ornamentals for human beings. Our understanding of plant diversity remains a substantial challenge and identification becomes particularly difficult where material is juvenile, fragmented, or processed. The combination of plastid *rbcL+matK* sequences was proposed to be the standard barcode for land plants in 2009, followed by our proposal to incorporate the nuclear ribosomal ITS into barcoding practice. Because of the development of next-generation sequencing, it is possible to enhance the plant barcode, focusing on increasing discriminatory power via either gene capture of nuclear markers or genome skimming. Genome skimming has the advantage of using existing protocols, being backward compatible with first-generation barcode, and the depth of sequence coverage can be increased as sequencing costs fall. We made a practical trial of routine recovery of rDNA and plastome sequences from herbarium collections. We sequenced specimens up to 80 years old by using as little as 500 pg of degraded starting DNA, and it can be performed with limited sample destruction. We gathered genome-skimming data of 25,583 individuals representing 20,260 species of 431 genera in 473 families of vascular plants, mainly from biodiversity hotspots in China, to build up a large-scale reference database for the China plant barcode of life initiative. Analyses of recalcitrant genera (or subgenera, or species complex) showed that organelle-scale barcode, together with rDNA sequences increased the discriminatory power by 10-15%. However, using Skmer, a method for estimating genomic distances between the query and reference genome skimming sequences, after removing the rDNA and plastome sequences, the discriminatory power was further increased. Furthermore, using deep genome skimming, particularly where a reference genome is available for the genus, a large number of single-copy orthologs can be acquired, opening up a new avenue for nuclear DNA barcodes.

S.158.3 Plant Species Identification by Multispecies Coalescent (MSC) Method Using Single-Copy Orthologs (SCOs)

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Standard barcodes and ultra-barcodes face challenges in delimitation and discrimination of closely related species with deep coalescence, hybrid speciation, gene flow or low sequence-variation. Single copy orthologs (SCOs) have been recommended as standardized nuclear markers in metazoan DNA taxonomy. Here, we assessed the performance of SCOs in identifying recently diverged species in *Cymbidium* subgenus *Jensoa* which has been poorly settled by ultra-barcode. More than 90% of target 9094 reference SCOs inferred from three genomes of *Cymbidium* were successfully retrieved for all 11 representative species in subg. *Jensoa* by ALiBaSeq from as low as 5× depth whole genome shotgun sequences. Species tree reconstructed from multiple refined SCO matrices under multispecies coalescent model successfully discriminated all species and discerned wrongly identified or labeled species. Plentiful and refined SCOs matrices obtained by implementing our pipeline facilitate not only phylogenetic study, but also high-resolution species diagnosing. Biparentally inherited SCOs as multi-locus marker not only advances the force of DNA barcoding, but also facilitates an eventual transition to species-tree-based barcoding strategies. We also test the performance of SCOs in other taxa among embryophytes to screen sevel universal and capable SCOs as the new barcodes to advance the plant species identification under the multispecies coalescent.

S.158.4 DNA barcoding of Chinese and Japanese Morus alba (Moraceae) documented by genome resequencing

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In Pharmacopoeia of the People's Republic of China 2020th edition, Mori Folium, Mori Cortex, Mori Ramulus, Mori Fructus, however, botanical origin of all of these four medicines are limited to only one species, *M. alba*. The Japanese Pharmacopoeia Eighteenth Edition also limit the botanical origin of Mori Cortex to *M. alba*. Because of polyploidization and hybridization occured frequently in *Morus*,we found that not a few individuals and specimens of *Morus* plants are difficult to identify because of their intermediate morphological characteristics between species especially *M. alba* and other species. For the safety and standardization of medication, it is particularly necessary to answer that the mecinal plant *Morus alba* is really a “good” species or not? The previous phylogentic analysesof ITS and cpDNA have been reported most of the *Morus* speices collected in China were grouped into a clade lacking for phylogentic resoulition. Genome skimming has the potential for generating large data sets for DNA barcoding and wider biodiversity genomic studies, particularly via the assembly and annotation of full chloroplast (cpDNA), nuclear ribosomal DNA (nrDNA) sequences and single copy orthologs (SCOs). Based on phylogenetic analyses of plastome sequences and ITS sequences, most Morus species grouped into a large clade lacking for phylogenetic resolution. Except for M. notabilis, other 8 species all should be considered as the botanical origin od Mori Cortex. However, based on 272 SCOs, *Morus alba* could be a monophyletic species. Plant species identification is difficult because of the main reasons being incomplete lineage sorting, artificial cultivation, natural hybridization and chloroplast capture. It appears that nuclear genome data have a vital role in species identification and are expected to be used as next-generation nuclear barcodes.

S.158.5 Whether cryptics are the reason for adulteration in plant herbal products? – case studies from Indian subcontinent

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Authentic species of Parpataka (*Hypertelis* & *Oldenlandia*) and Gokshura (*Tribulus terrestris*) are well known due to their synergistic effect with other herbs for anti-pyretic activity and urinary disorders respectively. The vernacular conflicts and its co-existence with other morphologically similar species lead to unintentional adulteration in the trade. To validate both i.e., Parpadaka and Gokshura, the samples were purchased from herbal raw drug stores across India for Gokshura and within southern India for Parpataka. These samples were further validated using *rbcL* gene of chloroplast for Parpataka and ITS2 region of nuclear genome for Gokshura respectively. DNA from the market samples was extracted and amplified with the selected barcodes and validated using Bayesian phylogenetic framework in MrBayes 3.2. Trade analysis of “parpadaka” samples revealed five different species of Molluginaceae and a species of *Oldenlandia* in the trade. The tree showed nearly 72.5% of *Hypertelis umbellata*, found in Indian trade for the first time and thus were achieved as a new report to India from this study since there was no report on its natural occurrence in any regional flora. Out of the remaining 27.5%, four different species of *Mollugo s.l* resulted into 17.5%. In Gokshura, *Tribulus lanuginosus* had replaced the *T. terrestris* (an authentic species) with 40.7% and *T. subramanyamii*, an endemic species had replaced it with 18.5%. Our results show that, market samples of Parpataka sold in southern India contains few substitutes, though among them, *H. umbellata* showed the cryptic nature with its counterpart i.e., *H. cerviana*, was predominant and completely replaced the authentic substitute in the indigenous trade. Similarly, in case of Gokshura, *Tribulus* had showed high degree of cryptic nature along with its counterpart, i.e., *T. subramanyamii* that evident by means its prevalence in the trade.

S.159 ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS. SESSION 5

S.159.1 From chlorine to biodiversity: a project for the naturalization of urban ponds.

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"From chlorine to Biodiversity", a short phrase that titles the project that is being developed in the Royal Botanic Garden of Córdoba (Spain). The main objective of this initiative is the naturalization of urban ponds, removing chlorinated water and introducing autochthonous aquatic species and charophytes meadows in order to create a hot spot of biodiversity. In this way is not only possible to eliminate chemical compounds harmful to the environment and reduce water consuption but also ecological restoration points are created in cities and villages. One of the greatest strengths of this project is that the species used are autochthonous aquatic macrophytes and algae. After the five years that the project has been developed and having naturalized 22 spaces, it has been possible to establish a protocol that imitates the natural processes that occur in the ponds of the countryside, it is possible to establish a trophic chain that allows the self-regulation of the new ecosystems. More than 1500 people have participated in the programme and 44 students have completed their internships within the project. Furthermore, naturalized sources have been revealed as a novel and attractive instrument to explain the complex concept of Biodiversity. The educative programe offered by the Royal Botanical Garden of Córdoba conceives the ponds as ecosystems that allow the observation of associated flora and fauna, as well as the interactions that occur between them. The growing pollution of cities, the scarcity of water and climate change can be tackled through urban policies and management strategies that considers green structures as backbones of the design of cities and villages. Experience has shown us that citizen participation is essential. The creation of synergies with associations and collectives helps to drive the transformation of these urban green infrastructures.

S.159.2 Ethnobotanical significance of Zingiberaceae in southern Western Ghats of Kerala, India

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India has a rich diversity of Zingiberaceae and constitutes one of the ten largest families in the country. The family is considered one of the important families in monocotyledons because of their economic, medicinal and ornamental values. Ethnobotanical studies on Zingiberaceae of Kerala identified 26 taxa with ethnobotanical significance and were used by various tribal communities in Kerala, India. The study covered 34 tribal communities distributed over 14 districts of Kerala and informants were interviewed during house-to-house surveys. The information from tribal practitioners was compared with results obtained during earlier visits. Taxonomic studies were carried out and voucher specimens were deposited at CATH. The specimens are conserved in the Ginger House of Catholicate College Botanical Garden (CCBG). The collected data were analyzed using the informant consensus factor (Fic), fidelity level and use value (UV). The plants were utilized in traditional medicine, food, fodder, religious purposes, *etc*. The Fic values of various species were analyzed and calculated for 22 categories. The highest values of Fic for Zingiberaceae were calculated in the case of the ENT category (1.0) and the lowest value was estimated for gynaecological ailments (0.28). The highest use value was determined for *Curcuma longa* (0.056). The highest fidelity level was reported for *Curcuma longa* (92.4%) followed by *C. amada* (87.1%) and *Zingiber officinale* (86.3%). The documentation of traditional knowledge and conservation of the valuable plants are very important, and the information collected will serve as baseline data for future phytochemical and pharmacological research to develop new drugs and services.

S.159.3 Phytochemical studies and anti-diabetic activities of Plumbago zeylanica, Neolitsea cassia and Wrightia tinctoria at Palamalaihill

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Medicinal plants have been identified and used in traditional medicine all over the world since the dawn of civilization. Medicinal plants are a rich source of novel drugs, which are used in traditional medical systems (**Bauri** *et al*., **2015**). More than 50,000 plant species are reported to be used for medicinal purposes around the world. Diabetes mellitus (DM) is a metabolic disorder caused by an insufficient amount of insulin in the body, either during its production or action, or both (**Mukhtar** *et al*., **2019**). If DM is not treated properly, serious complications such as muscular tissue damage, retinopathy, neuropathy, nephropathy, heart complications, and ulceration problems can occur. Insulin and glucagon are pancreatic hormones that regulate blood glucose levels in a normal range based on the body's needs (**Arden and Ramsey, 2015**). Although synthetic drugs are primarily used to treat diabetes, they have significant and irreversible side effects, and their accessibility to the general public is also difficult due to their high cost (**Amin** *et al*., **2013**). Little research has been done on the anti-diabetic properties of ethanolic extract of leaves and stems *Plumbago zeylanica, Neolitsea cassia* and *Wrightia tinctoria*. Due to the rising prevalence of diabetes, antihyperglycemic drugs are in high demand. Because of the minimal side effects and medicinal importance of ethanolic extract of *Plumbago zeylanica, Neolitsea cassia* and *Wrightia tinctoria*, the current study is being conducted to conduct anti-diabetic studies. The results of the study suggest that the ethanol extract of the leaves and stems has antidiabetic properties. Oral hypoglycaemics such as acarbose, which belongs to the α-amylase inhibitor class, have been shown to inhibit alpha-amylase. As a result, in the assays, acarbose was used as a positive control.

S.159.4 Anti-inflammatory activity of Curcuma putii rhizome extracts in HaCaT cell via NF-κB nuclear translocation inhibition

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Curcuma is a genus in the Zingiberaceae family. Previous studies have demonstrated their diverse medicinal benefits, including antioxidant, anti-cancer, antimicrobial and anti-inflammation activities. The objective of this research is to investigate the anti-inflammatory activity of the rhizomes of *Curcuma putii*, a species discovered in Thailand in 2019. To determine the anti-inflammatory activity, the inhibition of nuclear translocation of a transcription factor is employed by disrupting the nuclear translocation of NF-κB from cytoplasm into nucleus. Dried rhizomes of *Curcuma putii* were extracted using six different solvents including ethanol, methanol, acetone, hexane, ethyl acetate and dichloromethane. Initially, cytotoxicity experiments through the MTT assay were performed and found that concentration of 50 µg/mL is the highest concentration in all solvents determined to be non-toxic to human immortalized keratinocyte HaCaT cells. In addition, the NF-κB nuclear translocation activity was performed and found that the extracts from all six solvents at 50 µg/mL non-significantly inhibited against HaCaT cells. This serves as a direction for future studies on the anti-inflammatory potency and other bioactivity of *Curcuma putii.*

S.159.5 Biogeography of Medicinal Plants registered in the State of Hidalgo, Mexico

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Mexico is the second country with the greatest diversity of medicinal plant species in the world, after China. In Central Mexico, the state of Hidalgo is in an area with high floristic diversity, that is in the Mexican Transition Zone, between the Neartic and Neotropical Regions, composed of six types of vegetation: cloud forest, semi-evergreen tropical forest, xeric scrub, coniferous and fir forest, pine-oak forest and induced grassland. The objective of this work was to develop a specialized database of medicinal plants registered in the state of Hidalgo, through taxonomic, phytochemical, biogeographic, and ecological parameters, to make thematic maps on geographic distribution patterns, analyze ecological relationships of secondary metabolites. with climatic variables from biogeographic and physiographic provinces, as well as evaluating floristic richness by documenting the composition between nine ecoregions. Likewise, a mini drone was used to carry out multistage *in situ* sampling of aerial photography, with which 21 areas were characterized in strata: 10 geocultural regions of Nahua, Otomi, and Tepehua ethnic groups, 9 ecoregions, 6 types of vegetation, 4 biogeographic provinces and 3 physiographic provinces. Also, based on the registration of 400 species of medicinal plants, belonging to 80 botanical families, and consulting international databases, species distribution models were designed. The results show thematic maps with geographical distribution patterns of species characteristic of each type of vegetation, organized by ecoregions, for plants for medicinal use to fine-scale. Also, with spatial analysis, it was found that altitudinal gradients influence the diversity of second phytochemicals at different spatial scales. Finally, the state of Hidalgo constitutes 1.1% of the Mexican territory, with a record of 400 species for therapeutic use and 4,000 similar plants that are distributed throughout the country, so 1% of the country is home to 10% of the medicinal plants' diversity.

S.160 POLYPLOIDY AND HOMOPLOID HYBRIDIZATION AS EVOLUTIONARY DRIVERS

S.160.1 Reticulate genetic set-up of endangered species and its consequences for conservation strategies.

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Gladiolus palustris (marsh Gladiolus) of wet grasslands is an extremely rare and highly endangered species in Central Europe. Ongoing loss of habitat, population fragmentation, drought, and higher mean annual temperatures caused by global warming have all contributed to a severe decline in its population over the past few decades. Additionally, hybridization with other species, such as *G. imbricatus* and *G. illyricus*, and genetic depletion may pose a significant threat to the species' survival. The focus here is set to characterize major gene pools of the species in southern and southwestern Germany and illustrate that past hybridization and introgression in Central Europe are more extensive than previously thought, posing a challenge to conservation strategies targeting taxonomically defined species. A parallel exploration into the water plant *Nuphar pumila*, a post-glacial relic in Central Europe, sheds light on the diverse signs of introgression from the widespread *Nuphar lutea*. These genetic imprints serve as historical markers, reflecting centuries-old processes and changes in the landscape. Contrary to expectations, hybrid gene pools did not invariably result in intermediate morphologies. Instead, introgression appears to have played a pivotal role in enabling these species to adapt to evolving environmental conditions, such as heightened nitrogen levels and water temperatures. Given the longstanding presence of these populations in the region and their vital contribution to the active gene pool, the evidence suggests a need to champion and safeguard these populations. In light of these findings, it is proposed that conservation efforts should also prioritize naturally occurring hybrids and introgressed populations. Recognizing their resilience and adaptive capabilities, these populations emerge as crucial custodians of biodiversity, embodying the intricate dance between genetic diversity and environmental change.

S.160.2 Investigating conserved floral scent profiles acting as a driver of hybridization in Heuchera

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Little is known about environmental drivers of hybridization, but its phylogenetic distribution across plants is heterogeneous, suggesting that plant traits play an important role. Because animal vectors are responsible for gene flow in most plants, conservatism of biotic niche could explain why some plants are more prone to hybridization, a hypothesis yet to be tested. The taxonomic tribe Heuchereae (Saxifragaceae) is a well-characterized system for pollinator interactions, with studies in *Asimitellaria* and *Lithophragma* suggesting the VOCs comprising floral scent are hypervariable at the population level and responsible for pollination selectivity, leading to divergent pollinator assemblages. High levels of pollinator attractant divergence may be responsible for the relatively low levels of hybridization observed in these groups. *Heuchera* flowers, by contrast, are thought to be pollination generalists and *Heuchera* species hybridize frequently. Measurement of floral volatiles, yet to be characterized for *Heuchera*, would offer insight into whether divergence of pollinator attractants can more broadly explain hybridization rate differences across taxa. Given that pollinator-mediated gene flow primarily hinges on VOCs in the relatives of *Heuchera*, we investigated whether high rates of hybridization observed in *Heuchera* are associated with low interspecific divergence of VOCs, using as a system the hybrid zone between *H. americana* and *H. richardsonii*. We optimized a GC-MS (gas chromatography-mass spectrometry) protocol to characterize VOCs. To identify floral visitation and effective pollinators, we conducted pollination observations at 47 different populations over two years. GC-MS data from ~110 *Heuchera* representing 21 populations, analyzed with a suite of statistical methods, suggests that VOC compound classes and individual compounds are largely shared within the hybrid complex, while other *Heuchera* that do not hybridize with these species have distinct species-specific compounds. Pollination observations confirmed shared effective pollinators in the hybrid zone and the overall importance of VOCs in shaping gene flow.

S.160.3 Genomics of hybridisation in British native flowering plants

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Hybridization can have various evolutionary outcomes, from homogenizing the differences between populations to generating phenotypic and genotypic novelty. However, the majority of these important phenomena are evaluated in isolated case studies of evolutionary model species chosen for their notable hybridization outcomes, and how well the current findings represent generalities of natural hybridization in a wider range of taxa remains unknown. As such, this project aims to explore the general patterns of natural hybridization in the British flora using genomic approaches. The British flora is very well-studied with extensive records of hybrids, rendering it the ideal system for understanding natural hybridization at a broad scale. Specifically, we evaluate the extent of introgression in native flowering plants, using model-based demographic inference on whole genome resequencing data. Six conspicuous hybridizing species pairs were selected, each pair from a distinct taxonomic family, including genera that are well known for their common natural hybrids, such as *Primula* and *Geum*. The results support models with asymmetrical gene flow in focal pairs. Additionally, using a demographically explicit genome scan approach, we were able to estimate heterogeneous gene flow across the studied genomes and identify candidate barrier regions to gene flow. By studying hybridization outcomes of species pairs from diverse taxonomic lineages, we hope to provide a comparative perspective to understand how introgression is affected by intrinsic factors, such as parental species divergence.

S.160.4 Genetic integration of species diagnostic characters and their evolutionary responses to selection within hybridizing oaks

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The European oak species complex *Quercus petraea/robur* represents the best studied system for temperate tree speciation and population dynamics. Due to their extensive historical introgression, genetic clustering follows a continuous transition between the species, with only few species-specific clusters rather than strong species differentiation. Investigation of GxE and species' integrity found that GxE decreases with increasing species integrity, and therefore GxE interactions across the studied species discriminant leaf traits were strongly driven by the level of introgression between species across tested forest stands. Using a marker-based relationship matrix, we estimated coefficients of genetic integration for each trait, with those leaf traits being the least integrated that showed the highest species discriminatory power. Historical introgression seemed highest within cooler and wetter environments, while organismal modularity allowed for the independent evolution in oak species' morphology relating to ecological adaptation. This was corroborated by networks of genetic correlations. Hence, low within-species genetic integration of traits allows for the highest difference in evolutionary response to selection between species. Thus, less integrated traits can effectively drive *Quercus* species divergence, and more specifically, the evolutionary response to selection for leaf veins' function could explain the difference in water use efficiency and gas exchange between the different oak species. Our study highlights the importance of knowledge about the genetic, epistatic, and plastic effects associated with species diagnostic traits when considering conservation units in oak.

S.160.5 Deciphering complex reticulate evolution of Asian Buddleja (Scrophulariaceae)

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Species of the genus *Buddleja* in Asia are mainly distributed in the Sino-Himalayan region and form a challenging taxonomic group, with extensive hybridization and polyploidization. A phylogenetic approach to unravelling the history of reticulation in this lineage will deepen our understanding of the speciation in biodiversity hotspots. For this study, we obtained 80 accessions representing all the species in the Asian *Buddleja* clade, and the ploidy level of each taxon was determined by flow cytometry analyses. Whole plastid genomes, nuclear ribosomal DNA, single nucleotide polymorphisms and a large number of low-copy nuclear genes assembled from genome skimming data were used to investigate the reticulate evolutionary history of Asian *Buddleja*. Complex cytonuclear conflicts were detected through a comparison of plastid and species trees. Gene tree incongruence was also analysed to detect any reticulate events in the history of this lineage. Six hybridization events were detected, which are able to explain the cytonuclear conflict in Asian *Buddleja*. Furthermore, PhyloNet analysis combining species ploidy data indicated several allopolyploid speciation events. A strongly supported species tree inferred from a large number of low-copy nuclear genes not only corrected some earlier misinterpretations, but also indicated that there are many Asian *Buddleja* species that have been lumped mistakenly. Divergent time estimation shows two periods of rapid diversification (8–10 and 0–3 Mya) in the Asian *Buddleja* clade, which might coincide with the final uplift of the Hengduan Mountains and Quaternary climate fluctuations, respectively. This study presents a well-supported phylogenetic backbone for the Asian *Buddleja* species, elucidates their complex and reticulate evolutionary history and suggests that tectonic activity, climate fluctuations, polyploidization and hybridization together promoted the diversification of this lineage.

S.160.6 Sub-Genome Influence on Tree Topology in the Tribe Brassiceae of the Mustard Family (Brassicaceae)

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The Brassiceae tribe of the Mustard Family has a complex evolutionary history of whole genome duplication and hybridization. These mechanisms contribute to phenotypic plasticity and adaptability of the tribe, while also confounding attempts to understand the relationships among the species of the tribe. To account for these complications, we utilize a genome-guided phylotranscriptomic method that leverages genomic synteny to inform phylogenomic inference. With this method, we infer a nuclear tree with a novel topology that places the *Crambe* clade as sister to both the *Nigra* and *Rapa/Oleracea* group species. Further investigation of single copy genes from the ancestral sub-genome of the tribal hexaploidy identified differences in topology among genes derived from different parental genomes. These findings help explain why we see various topologies based on the data type method of inference when attempting to reconstruct clade relationships.

S.161 PALEOBOTANY AND PALEOPALYNOLOGY: DIVERSITY, TAXONOMY, AND PALEOECOLOGY

S.161.1 Balkan Neanderthals: the Late Pleistocene palaeoecological sequence of Pešturina Cave (Niš, Serbia)

Juan Ochando[1,2], José S. Carrión[1,3], Donatella Magri[2], Ana B. Marín-Arroyo[4], Federico Di Rita[2], Manuel Munuera[5], Fabrizio Michelangeli[6], Gabriela Amorós[1], Stefan Milošević[7], Katarina Bogićević[8], Vesna Dimitrijević[7,9], Draženko Nenadić[8], Mirjana Roksandic[10,11], Dušan Mihailović[7]

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The Central Balkans are a key biogeographical region in Southern Europe, influenced by a central European-Mediterranean climate, which acted as a refugium for flora and fauna, and favoured the dispersion of Neanderthals and migration of modern human populations during Late Glacial Period. This study presents pollen analyses of sediment and hyaena coprolites from Pešturina Cave in Serbia to reconstruct the vegetation landscapes faced by Balkan Neanderthals and early Anatomically Modern Humans between MIS 5e-3. Between MIS 5e-5c (archaeological layers 4c and 4b) and MIS 5b-5a (layer 4a), semi-forested environments prevailed, characterized by *Pinus*, deciduous *Quercus*, *Tilia* and other angiosperm woody taxa, accompanied by heliophytes such as *Artemisia* and Poaceae. During MIS 4-3 (layers 3-2), the vegetation was dominated by *Artemisia*-Poaceae steppes with *Quercus* patches, conifers and legumes. Overall across the sequence, pollen assemblages are highly diverse and include a number of deciduous trees and sclerophylls. In addition, the occurrence of several herbaceous taxa reinforces the view that the Balkans were outstanding for endemicity. Neanderthals and early Upper Palaeolithic hominins lived in a highly diverse refugium, offering multiple opportunities for survival during the warm interstadials and, more critically, the cold stadials of the Pleistocene.

S.161.2 Paleohistories for Conservation Practice from Quaternary Paleoecology of the Iberian Peninsula

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The Quaternary flora and vegetation records of the Iberian Peninsula provide insights for biological conservation strategies in the context of large projects like Rewilding Europe and other initiatives aimed at restoring ecosystem dynamics and functionalities from pre-anthropogenic periods. It is crucial to integrate information derived from the identification and characterization of glacial plant refugia, considering their significance as biodiversity sinks and sources of geographic expansion during critical moments in the glacial history of the European continent. It is important to note that many of these refuges are more hydrorefuges than thermorefuges, as aridity conditions became the limiting factor in many stadial episodes across extensive territories of the southern Mediterranean peninsulas. Likewise, it is worth considering that refuge areas were located on emerged coastal platforms and intra-mountain valleys at medium altitudes. From a structural perspective, many pre-anthropogenic Quaternary forests were influenced by herbivory, a factor that has been overlooked for decades and is now emerging as a consideration in the renaturation of protected or pilot areas. During the Holocene, it is important to analyze cultural collapses resulting from state changes in the paleoecosystem caused by anthropogenic disturbances. An example of ecocide could be the Argaric collapse. Finally, the dynamics of Quaternary vegetation aid in understanding the explanatory patterns of the floristic and ecological configuration of current plant communities, while also allowing the establishment of plausible scenarios in the near future under the influence of climate change and environmental crisis.

S.161.3 Ecosystems of North-Western Iberian Peninsula in the Last Glacial Maximum based on paleoecological modelling

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Southern European peninsulas provided refugia for temperate and mediterranean ecosystems during the Last Glacial Maximum (LGM). Despite pollen data, fossils and distribution modelling have been all used to understand vegetation during the LGM, we still lack a spatially explicit approach to map ecosystem types from modern climatic analogues. Here, we develop a framework for mapping ecosystem diversity of North-Western Iberian Peninsula during the LGM. First, we classified the Iberian Peninsula in climatic regions based on LGM climatic models and k-means unsupervised classification. The selected regions were sampled to conduct distribution models that were extrapolated to modern climates of Europe to detect modern climatic analogues. The areas with the highest climatic similarity to each one of the Iberian LGM regions were characterized with recent vegetation data to estimate the relative dominance of functional ecosystem types under modern climate conditions. In addition, we performed distribution models for modern forest types occurring in the ecoregion as a second approach to understand changes in the forest distribution. Our results highlight the complexity of Iberian ecosystems during the LGM, including mixed distribution of temperate and mediterranean climates as detected by modern analogues. We also found a similar bioclimatic zonation of the Iberian Peninsula in both LGM and modern climates, with the northwestern regions experiencing a relative stronger Atlantic influence. Additionally, available pollinic records were used to validate the potential vegetation of the Iberian Peninsula during LGM. Our approach allowed us to establish new hypotheses about the LGM distribution of ecosystem types in southern Europe, to be used in historical and ecological biogeography.

S.161.4 Palynology of the Canaan Peak Formation in Utah (United States of America)

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The Canaan Peak Formation, overlying the Campanian Kaiparowits Formation, in southern Utah (United States of America) is mostly conglomeratic unit with mudstone intervals containing plant debris and vertebrate remains (Bowers, 1972). This author indicated a lower or middle Campanian age for this formation on the basis of palynological assemblage studied by R.H. Tschudy due to its similarity to other palynological zonation in Montana, however, taxa are not determinative for this age. New palynological sampling from this dark grey mudstone interval yielded well-preserved palynomorphs, mainly composed by pollen grains (genera *Alisporites*, *Carolinapollis*, *Fraxinoipollenites*, *Holkopollenites*, *Inaperturopollenites* and *Taxodiaceaepollenites*, *Discoidites parvistriatus*, *Rhoipites globosus*, *Tschudypollis retusus*, among more common taxa) and scarce spores (*Cyathidites minor*, *Laevigatosporites hardtii*). The presence of *Discoidites parvistriatus* whose first apparence is the late Maastrichtian and K-taxa *Tschudypollis retusus* suggests a late Maastrichtian age.

S.161.5 Early angiosperms: New insights from a pre-Aptian pollen flora of Portugal

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The timing of the origin of angiosperms is a long-standing topic of debate in plant evolution. Different disciplines and approaches provide highly variable age estimates. It is generally accepted, that early macro- and mesofossils showing unequivocal angiosperm features occur in lower Aptian deposits. Workers employing palynology, i.e., the extremely durable, abundant, and widespread pollen record, have suggested much earlier, but highly disputed ages. To date, it remains questionable how far back pollen with unequivocally angiospermous features can push back the age for the origin of (early) angiosperms. Here we present new 'early records' from pre-Aptian coastal marine strata from the Lusitanian Basin of Portugal that are known for their rich and unique fossil assemblages and excellent pollen preservation. Based on strontium isotope stratigraphy, we provide a refined high-resolution stratigraphic framework for existing and newly studied sections to better constrain the age assignment of our new palynological findings of subsequent palynological findings. Employing a new fluorescence-based screening method paired with the standard light-microscope approach, we try to find the needle in the haystack. We document challenges and solutions to finding the extremely rare angiosperm pollen and illustrate new finds of early angiosperms with super-resolution microscopy (Airy Scan). The rare but exciting finds of four triaperturate pollen grains from the Early Barremian (124.63–126.24 Ma, GTS2020) of Portugal indicate the presence of eudicot angiosperms in pre-Aptian strata and provide a new, well-dated calibration point for phylogenetic approaches.

S.162 IAPT EARLY CAREER INVESTIGATOR SYMPOSIUM: THE EDGE OF THE UNKNOWN IN PLANT, ALGAE, AND FUNGAL SYSTEMATICS. SESSION 2

S.162.1 Molecular and morphological diversification of the family Inocybaceae (Agaricales, Fungi) in tropical Africa

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Over the past decade, Africa has recorded the highest annual rate of forest loss with 3.9 million hectares destroyed. This forest destruction causes the extinction of many species and at this rate of destruction, many species can go extinct and perhaps without being known. Whereas, despite the scientific community's efforts to estimate and catalog fungal diversity, worldwide only a small fraction (ca. 3%) of fungal diversity has been named and described. In recent years, with the progress of science, mycology has undergone a rapid development. Thus, since 2017, we have been interested to the diversity of Inocybaceae in Tropical Africa through the description and documentation of new species with an update on known species. The results show that in Africa, the diversity of Inocybaceae is about 80 species against 1,100 species in the world and the members of Inocybaceae are one of the most dominant in the soil of the woodlands and gallery forests after Russulaceae Lotsy. Nine new species are described and published in three genera like *Inocybe* (*I. beninensis, I. flavipes, and I. fuscobrunnea* and *I. pallidiangulata*), *Inosperma (I. africanum, I. bulbomarginatum, I. flavobrunneum, and I. macrocarpa)* and *Mallocybe (Mallocybe africana).* We are convinced that there are still enough unknown Inocybaceae species and we must redouble our efforts in sampling and also the exploration of new habitats in Africa.

S.162.2 Reconstructing an allo-decaploid: identifying the ancestors of Fragaria cascadensis

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Allopolyploidy is widespread among plant lineages and is an important driver of speciation. Understanding how allopolyploid species have formed through reticulate evolution is a challenging task. How can we infer the ancestry of extant allopolyploids when many ancestral diploids and lower-level polyploid ancestors are extinct? Moreover, genomic signal is often eroded in the allopolyploid genome through homeologous exchange. Using a suite of genomic tools, we developed a pipeline for identifying the progenitor lineages of high-level allopolyploids (6x and above). We test our pipeline on *Fragaria cascadensis,* a recently described allo-decaploid which is narrowly endemic to a single mountain range in western North America. The species has acquired five subgenomes through sequential interspecific hybridization events likely taking place in Beringia in the last 1 million years. Using whole genome alignments between extant diploid and polyploid strawberry species, a phylogenetic hypothesis testing framework, and k-mer based inferences of transposon activity, we reconstruct the allopolyploid ancestors and identify putative diploid progenitors of the decaploid strawberry *F. cascadensis*. Our new genomic evidence suggests a revision of the current ancestry hypothesis. We characterize the extent of asymmetric subgenome evolution and compare the decaploid strawberry to closely related octoploid species. Finally, we consider the implications of a new allo-decaploid hypothesis on the biogeography, systematics, and evolution of mating systems in polyploid *Fragaria.* We anticipate that our pipeline for reconstructing the origin of polyploids will be informative in other lineages with complex allopolyploids.

S.162.3 New approaches in the study of the sexual reproduction of the green microalga Trebouxia: when free-living means more sex

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The aero-terrestrial green microalgae of the genus *Trebouxia* Puymaly are the most frequent photobionts of lichens, but our comprehension of their sexual life is very limited, because in the lichen symbiosis it is typically suppressed by the fungal partner. In this study, innovative techniques were applied to characterise the formation and destiny of zoospores in four axenically cultured *Trebouxia* species (*T. decolorans*, *T. vagua*, *T. gelatinosa*, and *T. angustilobata*), selected to represent three of the four primary phylogenetic clades(A, A, I, and S, respectively)recognized within the genus. Frequent zoosporogenesis was achieved by increasing the concentration of glucose and peptone in the growth solid medium. By light transmitted and scanning electron microscopy(SEM)on samples treated with theCO_2 critical point dryer, we identified two distinct zoospore morphotypes, conserved among the major clades of the genus: spherical to sub-spherical vs. broadly ellipsoidal to ovoid. By observing zoospores stained with OsO_4 at the SEM in backscattered electrons mode, we could easily identify lipid bodies, as confirmed by the detection of Os by energy dispersive X-ray spectrometry, whose presence varied among species. These lipid bodies, which serve as energy sources in motile gametes of other green algae, led us to hypothesise that the heteromorphic zoospores of *Trebouxia* could represent true gametes. Sexual reproduction was corroborated in *T. decolorans* by confocal observations, through the assessment of the DNA content at cell population level, thus providing the first insights into the ploidy of this organism. Finally, cells with four flagella, which might be interpreted as the first direct evidence of a kariogamic event, were documented by light and SEM microscopy in populations of zoospores isolated by cytofluorimetry. The role of heteromorphic zoospores in the life cycle of *Trebouxia* and the implications of sexual reproduction in the photobionts of lichens will be thoroughly discussed.

S.162.4 To the mountains and beyond: diversity and systematics of Agarista (Ericaceae) in the Americas

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Agarista is a little-known and understudied genus of subshrubs to trees in the blueberry family, comprising about 35 species. One species is distributed along the mountains of tropical Africa and the islands of the western Indian ocean, and the other 34 species are endemics from tropical mountains and temperate lowlands of the Americas. Despite previous monographic and cladistics studies providing an excellent framework of *Agarista* circumscription through a phyletic approach, sampling for phylogenetic assessment has been sparse. Only 6% of the *Agarista* species are represented in phylogenetic, biogeographic and evolutionary studies based on molecular data. Thus, this research provides a systematic study of *Agarista* focusing on the American species, especially in the Brazilian diversity center. The study comprises morphological data, taxonomic revision, molecular phylogenetic analysis, evolutionary character reconstruction, and biogeographic analysis. We are testing the monophyly of *Agarista* and reconstructing a phylogenetic hypothesis for its evolution. The American species are distributed among five main geographic areas previously defined and each of these areas comprises an endemic set of species. On this hand, we are also in search to understand how morphological characters evolved within the group and, based on biogeographic analysis, test hypotheses of past connections among these currently isolated set of species. Herbaria reviews included in person consults to 31 American herbaria, plus the herbaria revised online through their specific websites. Typifications were made for 17 names in *Agarista*. Four fieldwork expeditions allowed collecting 15 samples of distinct taxonomic entities. We confirm the occurrence of 34 species in the Neotropics, 24 of them Brazil, being 22 endemics to this country. Additionally, three new species were described. Molecular analysis is in progress with the Botanical Research Institute of Texas in view to clarify the evolutive and biogeographical history of the genus based on the Angiosperms-353 kit.

S.162.5 Phylogenomics of the tropical African genus Hymenocoleus Robbr. (Rubiaceae)

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Hymenocoleus is a small genus in the coffee family (Rubiaceae). It belongs to the pantropical tribe Palicoureeae of the subfamily Rubioideae, and the species of the genus are herbs or undershrubs restricted to rainforests in tropical Africa. Infrageneric relationships in *Hymenocoleus* have received limited attention since its description and phylogenetic relationships have never been investigated, but the genus has undergone a recent taxonomic revision, recognising 19 species. Several species are newly described, and some are rare and as far as known endemic to narrow geographic ranges. Here we present the first phylogeny of *Hymenocoleus*, inferred using a phylogenomics approach. We used the Angiosperms353 probe set to capture hundreds of low-copy nuclear genes and inferred a species tree using coalescent-based methods. The result is a fully resolved, highly supported species-level phylogeny of *Hymenocoleus.* Data produced using the Angiosperms353 probe set here showed capable of resolving relationships in the genus, including some infraspecific relationships. Moreover, the topology proved robust to different analytical approaches, and use of different data partitions and filtering schemes. *Hymenocoleus libericus* is sister to the remaining species, however, incomplete lineage sorting is affecting the deepest splits in the genus and it is possible that cytonuclear discordance will be detected in future studies, for this node as well as a few others. It is further interesting to note that there is morphological support for several clades in the species tree.

S.162.6 Evolution and megaspore morphology in Isoetes (Lycophyta)

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Isoetes L. (Isoetaceae, Isoetales) is a cosmopolitan genus of heterosporous lycopods with an ancient and diverse evolutionary history that presumably reached its zenith in the Paleozoic. The genus belongs to the order Isoetales, which appeared in the Late Devonian and had its greatest diversity and ecological dominance in the late Carboniferous when arborescent lepidodendrids were widespread in the coal swamps of Euramerica. But living alongside and outliving their tree-shaped relatives were also several genera of smaller and mostly unbranched isoetaleans that were common in the Triassic and continued to diversify throughout the Mesozoic and Cenozoic. The age of the living clade has however never been satisfactorily clarified and no fossils have been phylogenetically placed within the extant clade. With little morphological (and molecular) divergence among species, megaspore morphology may be one of the best hopes for resolution of relationships in the group as well as relationships among extant and extinct forms. We have studied the megaspore morphology, ornamentation and surface texture/structure, in 74 phylogenetically placed samples representing 59 species of *Isoetes* and discuss evolutionary implications of the results. The samples were studied with scanning electron microscopy, and ornamentation and surface structure/texture were mapped onto a phylogeny constructed based on molecular data from the same samples whenever possible. While there are general features common to all megaspores of the family (trilete with an outermost siliceous coating) there is in addition ample morphological variation, of which some appears clade-specific.

Symposia Session 10

S.163 GENOMICS OF LOCAL ADAPTATION. SESSION 2

S.163.1 Genome-wide differentiation along elevation corresponds to the Mediterranean and cold temperate climate niches in lichens

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Lichens are known to withstand extreme environmental heterogeneity such as seasonal and diurnal temperature differences, and regular hydration-desiccation cycles. Many species also have a wide distribution range across multiple climate zones. However, little is known about the mechanisms and genomic basis of environmental adaptation in lichen-forming fungi. In this talk, we present genomic work on *Umbilicaria* species, which are obligate lichen-forming fungi that grow on rocks. Using samples collected (1) from different mountainous gradients in Europe and USA; (2) from low-elevation Mediterranean zone to high-elevation cold temperate zones; and (3) with different reproductive modes (asexual or sexual), we compared patterns of genomic differentiation and signatures of adaptation to climate niches. Specifically, we ask: (1) How do population genomic features of different species vary along replicated elevational gradients? (2) Which genomic regions are associated with the climate niche transition from the Mediterranean to the cold temperate zone? (3) Which bioclimatic variables are important predictors of population genomic change at the boundary between the two climate zones? (4) Do species with contrasting reproductive modes show different genomic features? Some of our results include clear genomic differentiation between samples collected from the Mediterranean versus the cold temperate climate niche. Cline analyses showed one bioclimatic variable (winter temperature) as a strong selective pressure that led to allele fixation. Coupled with genomic scans for selective sweeps and subsequent gene ontology analyses, we present strong evidence that this bioclimatic variable is a major driver of genomic differentiation and hence adaptation. Overall, our results enrich our knowledge of fungal genomic functions related to climatic niche, population genomics, and the response of long-lived, sessile species to environmental heterogeneity.

S.163.2 Local adaptation-induced evolutionary trap in alpine plants under climate change

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Evolutionary traps occur when populations deviate from local adaptation and become maladapted under rapid climate change. Alpine plants, with genetically distinct ecotypes in sky islands, are susceptible to being trapped by rapid climate change. We employed landscape genomics to test a local adaptation-induced evolutionary trap in the alpine perennial plant *Roscoea tibetica* (Zingiberaceae) with three distinct ecotypes along altitudinal gradients in the Hengduan Mountains. Strong local adaptation to alpine environments was observed through isolation-by-environment and rapid decreases in effective population size following interglacial niche contraction. Genomic offset increased with climate warming and was positively correlated with the intensification of local adaptation. Instead of high-elevation ecotypes, an evolutionary trap was indicated in the low-elevation forest ecotype, which showed the strongest local adaptation and niche loss, requiring the greatest shift in allele frequencies to keep pace with future climate change, and will likely experience the largest population decline. Therefore, stronger local adaptation induces evolutionary traps more easily and aggravates the harm to alpine plants facing rapid climate warming. Our study provides the first empirical case of local adaptation-induced evolutionary traps for alpine plants and highlights that it is crucial for alpine biota conservation to consider and disarm evolutionary traps under climate change.

S.163.3 GWAS analysis reveals genetic basis of some phenological and morphological traits in Chouardia litardierei (Hyacinthaceae)

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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.

S.163.4 Perennial Grass Ecotype Ecological and Genetic Responses to “Home” and “Away” Microbial Inocula is Ecotype-Specific

Eli Hartung[1], Soumyadev Sarkar[2], Anna Kazarina[1], Kian Fogarty[1], Brad Olson[1], Matt Galliart[3], Jack Sytsma[1], Ari Jumpponen[1], Sonny Lee[1], Loretta Johnson[1]

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Andropogon gerardii (big bluestem) is a dominant grass of the US Great Plains and its broad distribution across a steep rainfall gradient has given rise to locally adapted wet and dry ecotypes. While abiotic factors that drive local adaptation have been well-studied, little is known about the role of soil microbiomes in local adaptation. We used reciprocal inoculation to investigate how home and away microbiomes affect local adaptation. We collected seed and A. gerardii rhizosphere soils from prairies in Kansas (dry ecotype, 580 mm rainfall year-1) and Illinois (wet ecotype, 1167 mm rainfall year-1). We cultured microbes from roots and native soils, and reciprocally inoculated wet and dry microbes weekly into wet and dry ecotypes growing in common garden soil for 12 weeks in greenhouse. We measured plant form and function weekly for a variety of ecological responses. We extracted mRNA from leaves to analyze transcriptome responses. Genetic background between ecotypes determined most of our results. In addition to ecotype, inoculation increased biomass, especially that of the dry ecotype by ~30%. Furthermore, ecotypes had higher chlorophyll absorbance when grown with local soil microbiomes suggesting biotic local adaptation. Gene expression differed between ecotypes with ~7000 genes differentially expressed between ecotypes. However, when ecotypes were inoculated with their local soil microbes, with whom they share evolutionary history, inoculum strongly affected diverse aspects of plant growth and development. We conclude that plant microbial interactions for ecological and genetic responses strongly depend on ecotype context.

S.163.5 Patterns and Consequences of Subgenomic Variation in Invasive Johnsongrass (Sorghum halepense)

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Johnsongrass (*Sorghum halepense* (L.) Pers.) is an invasive, polyploid grass found throughout disturbed and agriculture areas of temperature, subtropical, and tropical regions. This species is thought to be an allotetraploid formed through the hybridization of sorghum (*Sorghum bicolor* (L.) Moench) and *Sorghum propinquum* (Kunth) Hitchc. Since its introduction into the United States in the early 1800s and secondary introduction into Arizona, Johnsongrass has spread throughout much of the Southeast, lower Great Plains, portions of the Midwest, Southwest, and California. The movement of this invasive has been facilitated by the transport of agricultural products and the development of major railway and highway systems where Johnsongrass thrives in the disturbed areas surrounding fields, railroads, and highways. In this study, we assembled four genomes, resequenced 38 accessions at either 20X or 40X coverage, and low-coverage whole genome shotgun sequenced approximately 50 additional populations of Johnsongrass from diverse regions of the United States. Using these data, we assess patterns of overall genetic diversity between subgenomes within individuals, among accessions, and across populations to determine how subgenomic variation might drive adaptation to varying habitats. We also explore homoeolog retention and loss patterns, leveraging phylogenetic relationships to identify potential loci contributing to Johnsongrass’s success as an invasive species in the United States. Furthermore, we examine the abundance and dispersion of homoeologous exchange across the Johnsongrass genome and identify the extent to which different loci have either moved to homoeologous chromosomes or have been lost. Ultimately, this research sheds light on the impact of diploidization on the diversity of U.S. Johnsongrass germplasm, offering insights into how polyploidy influences patterns of invasion.

S.163.6 Repeated adaptation of Arabidopsis to challenging environments

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Repeated adaptation provides valuable insight into the predictability of evolutionary change through replicated natural experiments. We investigated the strength and genomic underpinnings of repeated local adaptation of two outcrossing *Arabidopsis* species (*A. arenosa, A. lyrata*) towards challenging environments. Based on structured sampling and genome sequencing of 50 ecologically divergent populations, transplant experiments and population genomics, we discovered rapid multi-parallel adaptation towards different environmental gradients (high elevations, toxic soils) and detected significant over-representation of shared adaptive candidate genes for each environment. Although vast majority of the parallel candidates sourced on shared allelic variation, we also discovered a small fraction of genes exhibiting convergent evolution from independent *de novo* mutations. In addition, a significant number of genes was identified repeatedly as candidates to two or more different environments (e.g. challenging soils and alpine), suggesting spatio-environmentally fluctuating selection may further contribute to the maintenance of diverse pools of adaptive standing variation. Then, we complemented our investigations with additional published gene lists and our genome scans from other Brassicaceae genera and found that the extent of genomic parallelism significantly decreased with increasing divergence between the compared lineages. This relationship was explained by decreasing probability of repeated selection on the same standing or introgressed alleles. We therefore conclude that genetic divergence between populations, species and genera, affecting the pool of shared variants, is an important factor in the predictability of genome evolution.

S.164 GRASSROOTS MULTIDISCIPLINARY AND INTEGRATIVE RESEARCH ON THE GLOBAL DIVERSITY OF THE GRASSES (POACEAE). SESSION 1

S.164.1 Grasses through space and time: An overview of the biogeographical and macroevolutionary history of Poaceae

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Grasses are widespread on every continent and occur in all terrestrial biomes. The dominance and spread of grasses and grassland ecosystems led to significant changes in Earth´s climate, geochemistry, and biodiversity. Abundant chloroplast DNA sequence data, and advances in placing grass fossils within the family allow for phylogenetic reappraisal of the family´s origins, timing, geographic spread, and factors promoting diversification. We constructed a time-calibrated grass phylogeny and inferred ancestral areas using chloroplast DNA sequences from nearly 90% of extant grass genera. With a few notable exceptions, the phylogeny is well resolved to the subtribal level and in agreement with our current classification. Using this phylogenetic, temporal, and spatial framework, we review the evolution and biogeography of the family and present biogeographical hypotheses concerning its origins, evolutionary tempo, and diversification. Extant lineages of the family began to diversify around the Late/Early-Cretaceous boundary (crown 98.54 Ma) in West Gondwana. All subfamily crowns (except Pharoideae) evolved between the Late-Cretaceous to Late-Eocene, with most tribe crowns between Mid-Eocene to Early-Oligocene, and stems of most genera between the Mid-Oligocene and Late-Miocene. The splitting of Gondwana appears responsible for the initial vicariance of Anomochlooideae from the rest of the family: It's genera lack true spikelets and are endemic to and the only subfamily (or tribe) with a crown (80 Ma) in South America. Africa was the center of origin for much of the early diversification of the family (Spikelet and Bistigmatic clades, Puelioideae, Core-Grass-clade, BOP and Oryzoideae, PACMAD and ACMAD clades, Panicoideae, Aristidoideae, Arundinoideae, and Chloridoideae). Bambusoideae and Micrairoideae exhibit Indomalayan origins. Pooideae and tribes exhibit Palearctic origins. Ehrhartoideae and Cyperochloeae are tribes of Australian origins. No tribes have North American origins. Key questions to answer are the roles of Antarctica, extinction, unequal-rates of sequence evolution (woody-bamboos, and annuals), and whether Aristidoideae or Panicoideae evolved first.

S.164.2 Nuclear phylogenomics of grasses (Poaceae) supports classification and reveals repeated reticulation

Grass Phylogeny Working Group III (Arthan W., Baker W.J., Barrett M.D., Barrett R.L., Bennetzen J., Besnard G., Bianconi M.E., Birch J.L., Catalán P., Christin P.-A., Clark L.G., Columbus J.T., Crayn D.M., Davidse G., Dunning L., Duvall M.R., Fisher A.E., Fjellheim S., Forest F., Gillespie L.J., Hackel J., Haevermans T., Hodkinson T.R., Huang C.-H., Huang W., Humphreys A., Jobson R.W., Kellogg E.A.E., Larridon I., Li D.-Z., Liu J.-X., Ma H., Macfarlane T.D., Maurin O., McKain M., McLay T.G.B., Moreno-Aguilar M.F., Murphy D.J., Peterson P., Saarela J.M., Simpson L., Snow N.W., Soreng R.J., Thompson E.J., Traiperm P., Verboom G.T., Vorontsova M.S., Walsh N.G., Washburn J.D., Watcharamongkol T., Waycott M., Welker C.A.D., Xanthos M., Zhang L., Zizka A., Zuntini A.R.)

Grasses (Poaceae) have over 11,800 species and are central for human livelihoods and terrestrial ecosystems. Knowing their relationships and evolutionary history is key to comparative research and crop breeding. We inferred a comprehensive nuclear species tree of grasses by combining new and published sequences, including paralogs, for 331 genes from genome, transcriptome, target enrichment and shotgun data. Our 1,153-tip tree covers 78% of grass genera and all but two small tribes. We compared it to a 910-tip plastome tree. The nuclear phylogeny matches that of the plastome at most deep nodes, with only a few instances of incongruence. Gene tree–species tree reconciliation suggests that reticulation events occurred repeatedly in the history of grasses. We provide a robust framework for completing the grass tree of life to support research on grass evolution, including modes of reticulation, and genetic diversity for sustainable agriculture.

S.164.3 How can grass taxonomy secure the future of Madagascar?

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Twenty million years before human arrival on Madagascar, the ancient ancestors of Fatakamanga or the Blue Bamboo, also known as *Lecomtella madagascariensis*, made their journey to the island. The only remaining population of this isolated lineage is restricted to the mountains of the Andringitra National Park. The list of Andringitra micro-endemics whose presence justifies protected area funding also includes the world's only grass that imitates Erica shrubs: *Panicum cupressifolium*. But savannas at lower elevations are not included in biodiversity protection campaigns and not believed to be worthy of protection. Landscape genomics of *Loudetia simplex* which dominates vast expanses of savanna are helping us reconstruct ecosystem history to help plan conservation. Traditional Malagasy livelihoods are based around herds of zebu dependent on the guilds of forage grasses forming grazing lawn assemblages, including the recently revised endemics *Panicum luridum* (*Panicum* sensu stricto), and *Panicum umbellatum* with *Brachiaria subrostrata* (which need to be given new generic names within the Melinidinae in the Panicoideae). Agriculture professionals are unaware of native forages, and we are working to promote their use. The most beautiful baskets are woven in the Fandriana region from harsh bunchgrasses called Haravola and Haravola namboa, which are threatened by expanding rice cultivation. One is a sorghum relative *Lasiorhachis viguieri*, and the other is a mystery likely affiliated with the South African *Phacelurus franksiae*. None of these natural history facts were known or connected to national policy before the start of the Madagascar grass project in 2011. Placing grasses at the centre, we are working to piece together useful stories combining herbarium taxonomy, ethnobotany, phylogenetics, and functional ecology interfacing with social science and biome modelling, livestock development, and conservation. This talk will present an overview of how Madagascar's grasses are being braided together to support the country's future.

S.164.4 Advances on a new classification for koelerioid grasses based on molecular studies and morphology (Poaceae: Pooideae: Aveninae)

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Analyses of molecular data accumulated over nearly two decades have revealed extensive polyphyly affecting many of the genera that make up the oats subtribe, Aveninae, a group of subfamily Pooideae grasses of global economic importance. Within Aveninae, Koeleriinae clades A and B (koelerioid grasses) contain most of the biodiversity in the subtribe, including mostly perennial lineages, such as *Trisetum* s.l. or *Koeleria* (both worldwide) and other American genera like *Sphenopholis* and *Graphephorum*, and a series of annuals like *Rostraria* and *Trisetaria* from the Mediterranean (except *Limnodea*). We present our latest results on the systematic relationships of the koelerioids resulting from the largest sampling of these grasses carried out to date. Our new phylogenetic trees have improved our understanding of the evolution of this diverse group and led to drastic revisions of their classification. Amendments have involved the publication of new genera and the expansion, reduction or resurrection of others. A notable case of reduction is *Trisetum*, before considered to host ca. 70 perennial species, and now restricted to only three species, one of them annual. In contrast, *Koeleria*, another large perennial genus from cold or temperate regions of all hemispheres, has grown from 25 to nearly 100 species after absorbing part of the diversity of *Trisetum*. *Aegialina*, *Acrospelion*, and *Cinnagrostis* were resurrected. The detection of past reticulation events forming *Graphephorum* and parts of *Rostraria* suggest the importance of the hybridization as driving force of evolution in these groups, a common feature with other lineages of supertribe Poodae.

S.164.5 Decoding hybridization events in temperate Loliinae grasses: a nuclear single-copy gene perspective

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Resolving the phylogeny of recently evolved groups that have experienced recurrent introgressions and polyploidizations throughout their history is challenging. Evolutionary reconstruction based on a large set of biparentally inherited single-copy nuclear genes is considered a suitable approach to recover relationships that might otherwise be obscured by nuclear ribosomal genes in concerted evolution or biased by maternally inherited plastomes. Here we present the first single-copy gene phylogeny of the ecologically and economically important grass subtribe Loliinae (*Festuca* and related genera) using 241 nuclear coding loci captured from the Angisoperm353 probe set and a large sample of 137 representative taxa of Loliinae, covering all of its 22 evolutionary lineages. We have further completed genome-skimming sampling of other nuclear (35S rDNA gene) and organellar (plastome) sequences to elucidate the reticulate history of the Loliinae from multiple and complementary genome sources. Concatenated maximum likelihood and multispecies coalescent trees of single-copy genes showed well-supported relationships that were generally consistent across analyses and with previous taxonomic and phylogenetic findings but also revealed high levels of gene discordance. Hybridization and topological incongruence tests between the nuclear and plastome-based trees confirmed the rampant introgression experienced by Loliinae at deep and shallow nodes, detecting hybridization in four broad-leaved (Subulatae-Hawaiian, Schenodorus, Tropical-South African, Mexico-Central-South American) and five highly-diversified fine-leaved (American II, Exaratae-Loretia, Aulaxyper, Afroalpine, American-Neozeylandic) Loliinae lineages. The levels of intragenomic discordance could have been magnified by the prevalence of allopolyploids in the Loliinae and methodological bias in the selection of orthologs; however, our nuclear and plastome trees have revealed key hybrid origins in these grasses.

S.164.6 Taxonomy of Digitaria (Panicoideae, Poaceae) grasses to support weed and forage management in Madagascar

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The Poaceae family is species-rich and functionally significant for Madagascar's ecosystems and agrisystems. As part of an interdisciplinary project on grass diversity and agricultural interactions, we revise the classification of the genus *Digitaria* in Madagascar. This complex group poses identification challenges due to strong similarities between species. Over 50% of the 14,000 Madagascar's Poaceae herbarium collections are housed in Paris, presenting a constraint for Malagasy botanists aiming to study grass microscopic features that are not discernible in digital images. Consequently, I undertook trips to both Paris and London to access the essential resources, supplementing fieldwork efforts. Through examination of herbarium materials and field collections, we identified 30 species in Madagascar, including seven endemics, and excluding five species previously believed to occur in the region. Noteworthy are a likely new species from central and northern Madagascar and a new record of *D. ternata*. Three names were placed in synonymy: endemics *D. psammophila* and *D. planiculmis* are synonyms of the non-endemic *D. didactyla*, while *D. madagascariensis* is a synonym of the endemic *D. fulva*. A key to the species is provided along with illustrations, descriptions, and distribution information. This revision updates the *Digitaria* data in the Weed Identification and Knowledge in the Tropical and Mediterranean Areas portal. Using the updated species concepts, ethnobotanical analyses revealed 11 *Digitaria* species considered to be weeds affecting agriculture and used as forages in the highlands. Weedy traits of *D. humbertii* include its entangling growth habit and the ability to infiltrate cropping systems. Phylogenetic analysis indicates independent evolution of weedy species in the paraphyletic *Digitaria* clade. In order to disseminate these findings, we created an illustrated field guide in English and Malagasy, developed collaboratively with national agricultural institutions and the Ministry of Agriculture to help farmers recognize native forages and identify weed control methods.

S.165 MORPHOLOGICAL, ANATOMICAL, AND EVOLUTIONARY BASIS OF HABIT TRANSITIONS IN PLANTS

S.165.1 Apocynaceae wood evolution matches key morphological innovations

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Apocynaceae are a wonderfully diverse group, widely studied for their variable evolutionary processes. The stem is one of the most functionally important plant parts, yet a wood anatomical overview of this family is missing. Here, we present a wood anatomical overview of the Apocynaceae, including reconstructions of wood evolution. To do so, we revised over 200 published wood anatomical descriptions and made original sections and light microscopic descriptions for another ~50 species. Changes in wood anatomical characters through time were visualized with ancestral state reconstructions on a selection of 26 informative traits for 147 woody species included in the family's most recent molecular phylogeny. We performed tests for correlated evolution on a combined dataset of anatomical and published morphological traits to identify potential synnovations and key traits associated with growth form adaptations. The most important finding was a shift towards a syndrome of derived wood anatomical traits within the paraphyletic apocynoid grade that include an increased presence of vessel multiples, vessel dimorphism, laticifers, cambial variants, and paratracheal axial parenchyma. These traits separate the grade into early- and later diverging tribes, and continue in the monophyletic Periplocoideae, Secamonoideae, and Asclepiadoideae. When we compared these trait reconstructions with morphology traits evolution, we found that key morphological innovations co-occur with wood characters on consecutive nodes in the family's phylogeny. In contrast to these abrupt trait changes, vessel elements and fibers gradually shorten along the phylogenetic backbone of the family. This correlates to a general plant size reduction, regardless of the many transitions towards (phylogenetically) derived woodiness and a scandent or erect growth form. In conclusion, there are clear evolutionary transitions in the wood anatomy of Apocynaceae –many associated with climbers – representing structural adaptations that are part of a cascade of morphological evolutionary changes across the family.

S.165.2 Ontogeny of inter- and intra-xylary phloem in eudicotyledons

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Migration of aquatic autophytes to terrestrial conditions compelled them to evolve a new strategy of specialised tissues for mechanical support and conduction, i.e., secondary xylem and phloem respectively. From them, the phloem is a relatively delicate tissue that plays a vital role in the translocation of photosynthates. In most of the eudicots, the phloem develops external to the vascular cambium and the xylem internal to it. Besides their position external to the cambium, in a small fraction of eudicots, it also occurs within (interxylary phloem that develops from the single ring of vascular cambium) and inside (intraxylary) the secondary xylem. Based on their unique ontogeny, interxylary phloem is classified variously (*Strychnos*, *Combretum*, *Azima* and *Calycopteris* types) by earlier researchers. The present study documents several additional examples that do not fit into any of the types mentioned above (i.e., it develops in a later stage by dedifferentiation of parenchyma and not from the cambium). Similarly, the intraxylary phloem located on the pith margin either initiates from procambial derivatives, ground meristem, from the adjacent pith cells or by developing intraxylary cambium. Little information is available on the formation of intraxylary cambium and its unifacial (deposition of the secondary xylem and phloem in the same direction) or bifacial (xylem externally and phloem internally) nature but

detailed information on its behaviour remains unexplored. Several such examples of intraxylary cambium with intermediate variants are also discussed herewith and their possible functions are attributed to defence against insect injury and herbivory based on pieces of experimental evidence available in the literature.

S.165.3 Just keep growing! Woodiness as a simple extension of herbaceous habit.

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Transitions between herbaceous and woody habits is a key to angiosperm ecological and evolutionary success. Some correlations between habits and climatic niches have been established, such as that the increase in herbaceous life forms since the Eocene was a strategy to evade seasonal frost, or that reversals to woodiness during the Miocene climate aridification enhanced resistance to drought-induced embolism. While these relationships are well-understood, intrinsic (organismal) traits governing angiosperm habit adaptability remain elusive. We take advantage of our extensive sampling to delve into the anatomical distinctions between woody and herbaceous plants. Do these differences extend beyond quantity of secondary xylem? Are there any qualitative traits universally distinguishing herbs from woody plants? What makes angiosperms so adaptable when their closest extant relatives (gymnosperms) are constrained to a narrow range of life forms? First, we observe that across diverse angiosperms, spanning magnoliids, asterids, and rosids, the rays of secondary woody may simply prolongate patterns from primary xylem, without qualitative changes. Then, we show that quantitative traits such as vessel area and vessel wall thickness develop at comparable rates in closely related herbaceous and secondarily woody species (i.e., shrubs derived from herbaceous ancestors). These underscore that woodiness may be a mere prolongation of patterns present in herbaceous ancestors. Finally, we propose a novel perspective: habit shifts are linked to changes in wood lignin content, influencing stem mechanical properties and, consequently, maximal height. We argue that this could foster morphological disparification contributing to angiosperms unparalleled diversity. In summary, our observations emphasize that angiosperm habit adaptability results from their ability to alter cambial activity and, possibly also, the amount of lignin produced and deposited in xylem. Simultaneously, while wood anatomical traits are crucial for adaptations to specific niches, they do not seem to be primarily related to life forms.

S.165.4 Developmental processes behind habit transitions from lianas to trees and shrubs in vascular plants

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The ancestral habit of woody plants is inferred as self-supporting i.e., either erect shrubs or trees. The vascular system in self-supporting woody plants fulfills the roles of water and photosynthate transport, mechanical support, storage, and longevity. Lianas, however, do not support themselves, therefore their stem anatomy, released from this role, undergo modifications towards other critical purposes. First, lianas have some of the most efficient hydraulic systems, with less fibers, wider and more abundant vessels per unit area. Second, liana stems undergo selection for flexibility, thus their stems have wider and taller rays, sometimes more abundant axial parenchyma, and the wholesale restructuring of the vascular architecture (vascular variants), which intermixes parenchymatous and lignified tissues. Interestingly, within several ancestrally lianescent lineages, self-supporting plants have re-evolved, when occupying semi-arid regions. In these unique cases, the vascular system, therefore, must provide support to keep the stem upright, which is reflected in the reversal to a secondary xylem with narrower vessels, smaller rays and more fibers, and sometimes with changes in the axial parenchyma abundance. Critically, when the self-supporting habit is regained, vascular variants in their stems may even be lost or greatly reduced. Conversely, if the emergent self-supporting habit is succulent, these plants co-opt the ancestral vascular variant for increased water storage, representing a case of exaptation. In this talk, we discuss the re-emergence of self-supporting plants from ancestrally lianescent lineages using case studies in Bignoniaceae, Convolulaceae, and Malpighiaceae.

S.165.5 Evolution of Development of Vascular Variants in a Large Lineage of Neotropical Woody Vines: Paullinieae (Sapindaceae)

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Climbing woody vines–– "lianas" –– are the snakes of the plant kingdom, capable of wrapping around host trees in search of light at the top of the forest canopy. Intriguingly, this lifeform has evolved independently multiple times, and in accordance, lianas have independently evolved significant modifications to their stem anatomy to meet the unique demand to twist without breaking. Unlike the stems of most trees and shrubs, comprised of a core of wood (xylem) sheathed by inner bark (phloem), lianas often have "vascular variants", expressed as aberrations in the typical distribution and abundance of xylem and phloem. In this study, we sought to elucidate the evolution of development of vascular variants in a large neotropical liana tribe, Paullinieae (Sapindaceae), comprised of 11 vascular variants across 495 species. We here leverage the newly developed molecular phylogeny of Paullinieae, comprised of 75% species of the tribe, together with robust developmental anatomy dataset to address the following questions: (1) How many times did each type of vascular variant evolve? (2) Do vascular variants have systematic value in defining clades? (3) How did changes in the mode and tempo (heterochrony), spatial reorganization (heterotopy), tissue identity transformations (homeosis), and the re-purposing of old tools (exaptation) contribute to the diversity of vascular architecture in lianas? This study represents the power of an integrative approach, bridging developmental anatomy, within a robust phylogenetic context, to elucidate the evolution of development of complex traits.

S.165.6 Cambial activity contrasts between trees and lianas in temperate and tropical regions

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The vascular cambium typically has a seasonal activity, both in trees and lianas, either in the tropics or in temperate regions. This seasonal activity is generally annual for both habits. Photoperiod is one of the main triggers of the resume of cambial activity after dormancy, but this is in concert to a rise in temperatures in the temperate regions and the end of the dry season in the tropics. Both the onset and offset of cambial activity occur within the favorable growing season, i.e., summer in the temperate region and rainy season in the tropics, indicating that cambial rhythm anticipates the seasons that come ahead. However, lianas typically have a much larger inter-specific variation than trees. Within a study under the same conditions, some lianas had only 2 months activity, others 5 month and others yet had the cambial activity throughout the year. We explore here the best methods to detect cambial activity, the most reliable initial and terminal growth rings markers, specificities in growth ring formation in lianas and how vascular variants of lianas may also greatly influence cambial activity.

S.166 PHYLOGENOMICS AND SYSTEMATICS OF LILIACEAE

S.166.1 Plastome structure, phylogenetics, and historical biogeography of Liliaceae subfamily Streptopoideae

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Liliaceae always have been a challenge to classify and the taxonomy of one subfamily, Streptopoideae, also has been plagued with controversy. As currently circumscribed Streptopoideae contain three genera: Prosartes, Scoliopus, and *Streptopus* with 17 species distributed across the Northern Hemisphere. A few of the species even exhibit inter-continental disjunctions. Although several higher-level molecular phylogenetic studies have included a handful of species from this subfamily as placeholders, the whole picture of finer scale phylogenetics among these plants has never been studied adequately. We resolved the phylogenetic relationships, estimated divergence times among clades, and reconstructed historical biogeography within Streptopoideae and several outgoup taxa using newly sequenced de novo assembled and annotated whole chloroplast genomes. We achieved a high level of sampling for the ingroup (15 of 17 species), and also considered a moderate level of intraspecific sampling for the two species, *S. amplexifolius* and *S. lanceolatus*, with the widest geographic distribution. We compared and contrasted the structure of Streptopoideae plastomes, demonstrating that they have relatively large genomes, but with same gene arrangement that characterizes other Liliaceae. A relatively well resolved and supported phylogenetic reconstruction supports the North American genera *Prosartes* and *Scoliopus* sharing a recent common ancestor, with *Streptopus* as sister to them. The subfamily diverged from its shared ancestor with *Tricyrtis* at least 57 Mya in the late Paleocene of either Western North America or East Asia. The species of *Streptopus* in North America appear to have migrated to the east from Asia more recently. Relationships within each genus are fully resolved, but mostly supported only by short branch lengths. One individual of *S. lanceolatus* from the Pacific Northwest showed evidence of chloroplast capture from sympatric *S.amplexfolius*. These results indicate that alternative molecular methods targeting the nuclear genome will be needed to further tease apart the evolutionary history of this group.

S.166.2 Phylogenomics, historical geography, adaptive radiation, and quantitative floral convergence in lilies (Lilium)

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Lilies – with ca. 125 species in *Lilium* and the former genus *Nomocharis* – are restricted to the Northern Hemisphere, with centers of diversity in East Asia, southern Europe, the Caucasus, and eastern and Western North America. Species vary widely in habitat and in floral form, orientation, color, and fragrance. To identify relationships within *Lilium* and reconstruct its adaptive radiation and geographic spread, we conducted the first phylogenomic analysis of relationships in the genus by sequencing, assembling, and analyzing more than 400 single-copy nuclear loci and whole plastomes of almost all extant species. The maximum-likelihood plastome phylogeny fails to resolve any of the traditional, morphology-based sections as monophyletic, with two origins for North American § *Pseudolirium*, two for Himalayan/Tibetan § *Nomocharis*, four for East Asian § *Sinomartagon*, two for Asian § *Leucolirion*, two for Asian

§ *Archelirion*, three for European and Central Asian § *Martagon*, two for East Asian § *Daurolirion*, and two for European § *Liriotypus*. The nuclear phylogeny, however, resolves most sections as monophyletic, except for polyphyletic § *Sinomartagon* and § *Leucolirion*. Reconstructions of historical biogeography point to an origin in East Asia or Himalayas/Tibetan Plateau, with subsequent dispersals into North America, the Himalayas/Tibetan Plateau, Europe, Formosa, Japan, and the Philippines. Within the North American clade § *Pseudolirium*, we found strong quantitative convergence in flower shape, orientation, and color associated with pollination by hummingbirds, sphingid moths, and bees, and apparent retention of ancestral characters in species pollinated by butterflies.

S.166.3 A monograph of Chinese lilies

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Lilies are amongst the most fabulous of cultivated flowers, being important subjects for both the amateur gardener and professional growers supplying the fresh cut flower trade across the globe. Compared to the great multitude of hybrid cultivars that have been developed the naturally occurring wild species are relatively few, just over a hundred of these being mainly concentrated in the northern temperate zone. Of the major distributional areas, Eastern Asia (mainly China) exhibits the greatest diversity of wild lily species, boasting over three-quarters of the taxa currently known to science. In addition to possessing the largest number of species, the Chinese lilies also display great diversity at the sub-generic level. At least 5 out of 7 of the sections that are commonly accepted are represented in the Chinese flora (though differences of opinion regarding classification within the genus do remain). Recent technological and scientific innovations, along with easier access to remote areas, mean that it is now possible to resolve many of the outstanding taxonomic puzzles relating to the lilies of China that remain from earlier times and also to incorporate the newly recognized species into a fully updated catalog of these wonderful plants. In this work, the make a substantial revision of all the *Lilium* species that are currently known to occur in China. By tracing the history of their discovery, verifying the relevant literature (i.e., the protologue and other related materials) and locating the type specimens; and combining these with the molecular evidence accumulated by the present, as well as the findings of over a decade of field investigation, this monograph aims to provide a fully updated catalog and enumeration of Chinese native lilies including each species' history, details of the type specimen, morphological description, distribution information, all accompanied by field images.

S.166.4 Phylogenomics of Liliaceae revisited

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The lily family (Liliaceae), which is distributed mainly across the temperate Northern Hemisphere, is of great horticultural, culinary, and medical importance. It is also a family with a long history of taxonomic uncertainty. Challenges in accurate species identification persist and phylogenetic relationships among genera within the family continue to be unresolved and/or weakly supported due to the use of limited molecular markers with insufficient variability. Here, plastome and transcriptome data were generated and combined with previously published data for this family, providing a total of 86 plastomes and 88 transcriptomes (plus one WGS data) covering all 15 currently recognized genera for analyses. Both plastid and nuclear phylogenomic analyses strongly confirm the recognition of four subfamilies: Tricyrtidoideae with four genera; Medeoloideae with two genera (*Clintonia* and *Medeola*); Lilioideae with eight genera; and a distinct subfamily, Calochortoideae, for *Calochortus*, which is sister to Medeoloideae and Lilioideae. Within Lilioideae, both plastid and nuclear phylogenomic analyses show that the Lilieae clade of (*Notholirion*, (*Cardiocrinum*, (*Fritillatia*, *Lilium*))) is sister to the Tulipeae clade of (*Gagea;* (*Tulipa*, (*Erythronium*, *Amana*))). However, plastid and nuclear trees show different topologies within Tricyrtidoideae, which is (*Tricyrtis*, (*Streptopus*, (*Prosartes*, *Scoliopus*))) in the plastid tree but (*Tricyrtis*, (*Prosartes*, (*Streptopus*, *Scoliopus*))) in the nuclear tree. This cytonuclear conflict is likely due to ancient hybridization. Our results provide a solid framework for future studies on the evolution of Liliaceae.

S.166.5 Updated molecular phylogenetic analysis, dating and biogeographical history of the lily family (Liliaceae: Liliales)

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Liliaceae *sensu* APG IV include *ca.* 600 species, and have been circumscribed into three subfamilies, Lilioideae, Calochortoideae and Streptopoideae. Molecular phylogenetic approaches to this family have produced dynamic changes in the generic circumscriptions. We conducted molecular phylogenetic analyses, time estimations and biogeographical analyses to confirm generic relationships, discuss their circumscription for classification and clarify the evolutionary history of the family. A phylogenetic analysis is presented as a combined data set of *ca.* 6.1 kb from four plastid coding gene sequences for 142 taxa representing all the genera of Liliaceae. Medeoloideae were newly defined as an independent subfamily from Lilioideae. *Tricyrtis* of Calochortoideae is embedded in Streptopoideae, despite its unique characteristics. The crown age of Liliaceae was calculated at *ca.* 85 Mya, and Liliaceae are considered to have originated in temperate Asia in the late Cretaceous and to have expanded their distribution via dispersal with the occurrence of repetitive vicariance events during their evolution.

S.166.6 Taxonomic revision of Tricyrtis (Liliaceae) and a new species Tricyrtis lingyunyanensis in Taiwan

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Tricyrtis Wall. (Liliaceae) is a perennial herb, including approximately 20 species, endemic to East Asia. *Tricyrtis* exhibit similar morphologies; thus, some species display infraspecific morphological variation and ambiguous boundaries within species. In this study, we examined the morphological characteristics, elevation, and physiology to revise this genus in Taiwan. As a result, we confirmed five species and one variety: i.e., *T. formosana* Baker., *T. lasiocarpa* Matsumura, *T. lasiocarpa* var. *ovatifolia* (S.S. Ying) Y.H. Chen & T.H. Huang, stat. nov., *T. lingyunyanensis* Y.H. Chen & T.H. Huang, sp. nov., *T. ravenii* C.I Peng & Tiang, and *T. suzukii* Masamune. *Tricyrtis lingyunyanensis* Y.H. Chen & T.H. Huang is a new species found only in the north of Wunfong Mountain, Chiayi Country, Taiwan, at an elevation of approximately 1100 m. The unique feature is that dried capsules fall off from the base of the capsule, and bulbils develop at the nodes of the aerial stem aboveground. Furthermore, we discovered bulb formation in this genus in Taiwan and described the growth patterns of its underground parts. This study seeks to provide a detailed assessment of the morphology of each species by offering descriptions and precise comparative photographs.

S.167 LEGUME SYSTEMATICS: FROM COLLABORATIVE NETWORKS TO GENOME SEQUENCING

S.167.1 Evolution of legumes: from introgression to whole genome duplication

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Introgression and duplication are two of the most dramatic phenomena that a genome may encounter, each with myriad outcomes, ranging from increased evolutionary potential through to a heightened likelihood of extinction. Both processes have greatly influenced the evolution of plant diversity, particularly within the legume family which holds more than 20,000 species. Among the most species-rich legume communities occur in tropical rainforests, which are emblematic for their diversity. Accordingly, here we explore the influence of introgression and genome duplication on legume tree genera found in tropical rainforests, spanning the tropics. *Sindora*, from the Detarioideae subfamily, comprises 20 species found in palaeotropical rainforests, and has experienced whole genome duplication in its history. As such, phylogenetic reconstruction is challenging within the group due to the high abundance of paralogues. *Sindora* is known to hybridise extensively, forming 'syngameons' of many interfertile species, and so here we investigate whether introgression has contributed to the present day ability of the genus to form interspecific hybrids using a bespoke phylogenetic pipeline that aims to account for paralogy. The extent of the syngameon and the nature of hybridisation are also studied using present day hybrids. *Inga*, from the Caesalpinioideae subfamily, comprises >300 species and typifies the rapid rainforest tree radiations that gave rise to most Neotropical tree diversity. Introgression can catalyse such events of rapid diversification, and so here we assess whether hybridisation catalysed rapid diversification in *Inga*. Firstly, we ascertain the extent of introgression across *Inga*, following which we test whether introgression of loci underlying chemical defences against herbivory facilitated rapid speciation, given the ecological advantage of novel defences in resisting the relentless insect herbivory experienced by rainforest trees. Overall, we aim to assess whether transfer of adaptive variation through introgression helped generate the unmatched diversity of rainforest trees.

S.167.2 The future of legume systematics: Embracing collaborative tools to enhance taxonomic, geographic and evolutionary knowledge

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The legume systematics community's long history of research and collaboration has greatly increased our understanding of the classification, biogeography and evolutionary history of the family. This is evident in the many activities and publications that have seen the light since 1978, when the first International Legume Conference was held at the Royal Botanic Gardens, Kew. In 2010, the Legume Phylogeny Working Group (LPWG) was founded, and has since published five papers under this name, including a new phylogeny-based subfamily classification and a revised higher-level classification for subfamily Caesalpinioideae. In 2020 the LPWG established five working groups to promote collaboration on specific aspects of legumes. The Taxonomy Working Group was created to work on a list of names that would feed into and support the underlay of the other four working groups. This has led to the publication of four versions of updated legume taxon names from which out of the 64 351 specific names ever published in the family we now accept 22 623 species and 797 genera. The Legume Taxonomy Working Group is now acknowledged as an active legume partner and contributor to the international World Flora Online project and Global Biodiversity Information Facility (GBIF) and serves as the authoritative source for legume names in both portals. A collaborative online platform, Rhakhis, was chosen for the community to continue updating names. Working with GBIF, the legume community developed a portal focused on the family, and this led to the launch of the first version of GBIF's phylogeny viewer based on a phylogenomic analysis of Caesalpinioideae. Other international collaborations to pursue phylogenomic analyses and data sharing, including morphological and geographical data, have been encouraged to facilitate monographic, phylogenetic, macro-evolutionary and biogeographical analyses of this ecologically important family.

S.167.3 Resolve tribal relationships of Fabaceae using nuclear, plastid and mitochondrial genomic data

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Tree of Life lies at the heart of almost all studies in evolutionary biology. However, it is challenging to resolve recalcitrant phylogenetic relationships caused by rapid evolutionary radiations, hybridizations, and whole genome duplications. Despite the ecological and economical importance of Fabaceae (Leguminosae), phylogenetic relationships among some subfamilial and tribal lineages remain poorly resolved. We reconstructed the backbone phylogeny of Fabaceae using plastomes, mitochondrial genes and transcriptome data of 909 species across 486 genera, representing all six subfamilies and almost all tribal lineages. Our results strongly supported the monophyly of the six subfamilies and 64 tribal clades, and clarified many long-controversial relationships. However, 14 sets of nodes remained unresolved due to conflicts among trees based on plastid and nuclear data, or different analysis methods. Through gene-tree quartet analyses evaluating alternative topologies and consistently strong support in ML and Astral tree both on the nuclear data sets, we resolved 18 of these recalcitrant nodes. Using relative quantification analyses, our study identified incomplete lineage sorting as the main source of conflict for deeper nodes (e.g., the root of Fabaceae), gene flow is the main source for shallower nodes (e.g., *Griffonia*, ADA clade, Wisterieae), both are involved conflicts for some nodes (e.g., core Papilionoideae, Erythrophleeae, Tachigalieae, Moldenhawereae). The study suggested when ILS and gene flow coexist to a considerable extent, resolving contentious relationships becomes exceedingly difficult. Our study provides a robust phylogenomic framework for exploring legume evolution and supplies a typical case to apply multiple types of molecular data and analysis methods to resolve recalcitrant phylogenetic relationships and explore the underlying conflict.

S.167.4 Phylogenomics understanding of the evolution and adaptation of RNS in Legumes

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Leguminosae is the third largest angiosperm family in species richness, spreading and adapting globally in a wide range of ecology. Many legumes are economically important food crops offering highly nutritious sources of protein and micronutrients for human beings and animals, which can partly attributed to its successful establishment of the nitrogen-fixing root-nodule symbiosis (RNS) with the mutualistic nitrogen-fixing bacteria. >95% of RNS are restricted in Legumes, however, how RNS in Leguminosae rised, stabilized, and widely adapted remains an unsolved mystery. With the development of genomic sequencing technologies and bioinformatics, the ability to "sequence everything" for an entire genus or even for an entire family, is becoming a reality. We thus initiated the "Legume Genome Sequencing Consortium" and started the Legume Nodulation and NFNC Phylogenomics v2.0 Project. 32 representative new legume species, carefully selected from all the six sub-families (Cercidoideae, Detarioideae, Duparquetioideae, Dialioideae, Caesalpinioideae, and Papilionoideae) as the diverse 'comparison pairs' of nodulating plants together with their closest non-nodulating relatives, are sequenced (PacBio + HiC), assembled and annotated into high-quality chromosome-level genome references. In addition, a matched phylo-pan-transcriptome from these species was constructed. This effort opens new ways to explore diversity of RNS in a broad comparative context (phylogenomics), to gain a deeper and more holistic view of the evolution in protein-coding genes, conserved non-coding elements, and differential gene expression for RNS, to utlinately reveal the molecular evolutionary mechanism of RNS either by divergence from a common ancestor over 100 Mya or by convergence following independent origins over that same time period. This study also provides great opportunity to understand the diversification and adaptation of Legumes.

S.167.5 Parallel domestication of New and Old World lupins: chromosome-level assemblies of Lupinus mutabilis and a crop wild relative

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The Andes are the domestication centre of many important and minor crops, but the list of Andean crops with available high-quality genome assemblies is biased towards crops with worldwide distribution, neglecting those cultivated locally that have significant agricultural and cultural value. *Lupinus mutabilis* (Fabaceae) is the only lupin crop domesticated in the New World, where it is cultivated for its high protein content and soil enrichment properties. There are high-quality genome assemblies and pan-genome data available for Old World lupin crops (i.e., *Lupinus albus* and *L. angustifolius*). However, there is no reference genome for *L. mutabilis*. We assembled the genomes of *L. mutabilis* and *L. piurensis*, its crop wild relative, using PacBio HiFi and chromosome conformation capture (Hi-C) reads into 828 Mb and 795 Mb assemblies, respectively. In each case we assembled 24 chromosomes (594 Mb and 591 Mb). In total we annotated 34,176 and 33,681 protein-coding genes in *L. mutabilis* and *L. piurensis*, respectively. BUSCO scores indicate 98% completeness for both annotations. Transposable element annotation reveals that 67% and 69% of the *L. mutabilis* and *L. piurensis* genomes are repetitive, with Copia the most abundant class. Synteny analysis between *L. mutabilis* and *L. albus* demonstrates that *L. mutabilis* chromosome 4, the largest super scaffold, represents a merger of *L. albus* chromosomes 4 and 24, resulting in a karyotype with one fewer chromosome total, which is characteristic of the western New World lupins. We are reconstructing the evolutionary history of the two Andean lupins in comparison to the predicted ancestral legume karyotype. We surveyed for genes under positive selection, and document gene-family evolution and the effects of parallel domestication in the New World and Old World lupin crops.

S.167.6 Why are some lineages more successful than others? Comparing distribution patterns across subfamilies in Leguminosae

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One of the central aims in evolutionary biology is explaining why some lineages are more evolutionarily successful than others, for example in terms of species richness, ecological versatility, and geographic distribution. Direct comparisons of lineages are complicated by the impacts of confounding factors such as differences in age and evolutionary relatedness. The six subfamilies of the legume family provide an ideal natural experiment to determine why some lineages are more successful than others. Since the origin of Leguminosae is a phylogenomic tangle which gave rise to all subfamilies within a very short time frame, the subfamilies are nearly identical in terms of age and relatedness. Notwithstanding these similar starting conditions, this natural experiment yielded vastly different results, ranging from subfamily Duparquetioideae, consisting of a single African species, to subfamilies Caesalpinioideae and Papilionoideae, which have respectively circa 4,700 and over 14,000 species across the globe. The other three subfamilies, Cercidoideae, Detarioideae, Dialioideae, are also widely distributed but harbour lower numbers of species. Here we assemble a legume-wide quality-controlled occurrence dataset to compare distribution patterns across the six subfamilies. We quantify differences between subfamilies in areas of species richness, ecological versatility, and geographic extents, to investigate links between richness and distribution. Furthermore, by combining this new geographic dataset with existing legume-wide and subfamily-specific phylogenies, we compare rates of long-distance dispersal and niche shifting through time to examine the roles of evolvability and phylogenetic conservatism in generating species richness. Our analyses reveal important differences between subfamilies in terms of their main centres of diversity, ecological versatility, and biogeographical evolvability through time. Notably, invasion of the temperate zone in Papilionoideae played a key role in generating its extreme species richness, whereas other subfamilies are largely constrained by tropical niche conservatism. These results shed new light on why some lineages are more successful than others.

S.168 SYSTEMATICS, BIOGEOGRAPHY, ADAPTATION AND UTILIZATION OF THE GRAPE FAMILY VITACEAE

S.168.1 The origin, diversification, and adaptation of the grape family Vitaceae

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Faced with environmental changes, plants may either "move" to track their ancestral habitats or "evolve" and adapt to new habitats. Vitaceae, the grape family, has evolved diverse adaptive traits facilitating a global expansion in wide-ranging habitats. This evolutionary history makes Vitaceae ideal for investigating for any preference between "move" or "evolve" strategies and their underlying mechanisms. We inferred patterns of biogeographic diversification and trait evolution in Vitaceae based on a robust phylogeny with dense sampling including 495 species (~52% of Vitaceae species). Vitaceae most likely originated from Asia, the diversity center of extant genera and the major source of dispersals. India and Australasia are recognized as the biggest sinks and dispersals to the two regions might be largely facilitated by land connection. At least four shifts in diversification rates have been detected respectively in *Ampelocissus*, *Cyphostemma*, *Tetrastigma*, and *Vitis*, which have either evolved key innovations or showed adaptation to specific habitats. In particular, we find that the Oligocene-Miocene boundary is a turning point in shifting strategies, before which Vitaceae lineages preferred to "move", and after which, to "evolve". The increase of niche opportunities mainly contributed to the frequent employment of the "evolve" strategy after the Oligocene-Miocene boundary, while putative key trait innovations also played a role.

S.168.2 Genomic adaptation to aridity in Cyphostemma (Vitaceae)

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Cyphostemma, the second largest genus (ca. 200 species) of the grape family, mainly distributes in continental Africa and Madagascar. Species of the genus have colonized various habitats including tropical rainforests, savanna, and deserts. The genus exhibits extraordinary diversity in morphological innovations, of which the development of succulent stem is the most striking. Previous studies revealed a disparity in genome size, which has been suggested to be related to the innovation of succulence. However, it remains unclear how the genome size diversity in *Cyphostemma* is generated, and how it contributes to the adaptation to various habitats. We investigate this problem from both the genomic and ecological aspects. We assembled genomes of two representative species of *Cyphostemma*, *C. dehongense* from the Asian rainforest and *C. currorii* from the African desert. We find that genomes of *Cyphostemma* are mainly inflated by the insertion of long terminal repeat retrotransposons (LTR-RT), especially the explosive insertions of several families in the Ale lineage. According to the dynamics of LTR-RT, these families show a preference for inserting into introns since the Oligocene-Miocene Boundary, when Vitaceae began to diversify rapidly. The intron-preferring LTR-RT families have a higher death rate, and the genes with longer introns are under more relaxed selection, suggesting the co-evolution of LTR-RTs and their host genome. To further investigate the relationships between LTR-RT amplification and environmental conditions, we collected genomic repeat profiles, genome size, and habitat climatic factors for more than 100 taxa in *Cyphostemma*. Analyses based on a linear model reveal that genome expansion is generally associated with adaptation to aridity but is limited by precipitation during the growing season. Moreover, we find that succulent species from arid regions of continental Africa and Madagascar exhibit different patterns of LTR-RT amplification, indicating different mechanisms for the origin of succulence.

S.168.3 Unraveling evolutionary diversification dynamics of North American grapes across different biomes

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Understanding the origin and distribution of species is a focal point of evolutionary biology. In North America, the current distribution and diversity of species have been substantially influenced by environmental changes during climatic oscillations, as well as historic and contemporary geographic barriers. Phylogeographic studies have revealed conflicting patterns among co-distributed taxa with distinct ecological requirements, suggesting dispersal ability and other life-history traits are crucial for shaping the diversity and distribution of the region's biota. However, a complete understanding of North America´s diversification dynamics is hampered by a limited number of comprehensive genome-scale phylogeographic studies that integrate phenotypic and environmental niche evidence. This is crucial for revealing intricate evolutionary mechanisms driving diversification, such as introgression/hybridization, ecological adaptation, and ecophenotypic plasticity, which might be overlooked through less integrative approaches. The grape genus *Vitis* L., especially subgen. *Vitis*, serves as an ideal model for studying North America´s biogeography and phylogeography. Recent progress in genomics, phenomics, and specimen digitization offers an unprecedented opportunity to explore the convoluted evolutionary history of two challenging species complexes: *Vitis aestivalis* and *Vitis cinerea*. These taxa have extensively overlapping distributions throughout several biomes in North- and Mesoamerica. In this study, we sampled both species complexes across their distributional range. We employed several phylogenomic inference approaches to identify relationships within these complexes and hybridization events. Complementary population structure analyses were used to assess genetic diversity within and among sampling locations. Environmental variables were used to evaluate ecological differentiation as a driver of diversification, and phenotypic differences in leaf and stem characters were quantified to determine the extent of the influence of ecophenotypic plasticity. Our results support the recognition of several species in both the *V. aestivalis* and the *V. cinerea* complexes. Geographic isolation was important for species differentiation, and key phenotypic differences were detected among different ecological zones.

S.168.4 Genomic insights into adaptative evolution and climate change vulnerability of the grape genus (Vitis L.)

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Wild grapes show a high level of species diversity and have been widely recognized as important germplasm resources of wine, table grapes, and resistance to biotic and abiotic stresses for the grape industry. However, the local adaptation and drivers of diversification of genus *Vitis* L. remain poorly understood. Hybridization and introgression events of *Vitis* are still lacking a comprehensive knowledge regarding their frequency, pattern, and adaptive landscape, particularly at the genome-wide scale. The reticulated evolutions, local adaptations and responses to future climate change of several widely distributed wild grape in East Asia are investigated based on population genomic data. Species network analyses identified several hybridization events within East Asian *Vitis*. These interspecific hybridization events may have caused the topological discordances and relatively low support detected in our analyses. Ecological niche modeling shows that most of the diversification of East Asian *Vitis* species is driven by temperature and precipitation environmental variables. Sympatric parallel diversifications of major clades also may have facilitated the rich diversity in East Asian *Vitis*. Our results emphasize the significance of comprehensive genomic data, including single-nucleotide polymorphisms (SNPs), insertion/deletions and structural variations (SVs), to predict environmental adaption of wild grapes in the context of rapid climate change.

S.168.5 Population genetics analyses reveal the genetic basis of important agronomic traits and facilitate grape breeding

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Grapevine is among the first domesticated crops. However, its breeding is impeded by the investigations of the genetic basis of important agronomic traits. Based on population genetics combining multiple new analytic methods, such as pan-genome and machine learning, we identified many important trait-related quantitative trait loci (QTLs), and revealed the importance of introgression in shaping the current texture of grapes. We constructed a variant map by interrogating resequencing data from grapevine cultivars based on pan-genome including 18 newly generated telomere-to-telomere gap-free haplotype-resolved assemblies and performed genome-wide association studies (GWAS) related to 29 traits. 148 significantly related QTLs were identified, and 8.1% QTLs of 12 traits were identified as significant contributions by structure variations (SVs). We also found some QTLs were located in regions of divergent selection between wine and table grapes. Given the previous studies showing genomic signals of introgression from wild to wine grapes in Europe, based on machine learning-based population genetic analyses, we predicted the time, mode, genomic pattern, and biological effects of these introgression events, and found that continuous gene flow between European wild grapes (EU) and cultivated grapes over the past ~2000 years, especially from EU to wine grapes, suggesting EU wild grapes were an important resource for improving the flavor of wine grapes. We further found that introgression may be a historically important process for improving clonal systems like domesticated grapes. Despite the potential benefits of introgression in grape improvement, the introgressed fragments introduced a higher deleterious burden, and most of these deleterious variants were in a heterozygous state in grapes. In general, our study facilitates the breeding of superior cultivars via genomic selection of multiple traits and the understanding of beneficial and harmful effects of introgression is critical for genomic breeding of grapevine to take advantage of wild resources.

S.168.6 Cenozoic seeds of Vitaceae reveal a deep history of extinction and dispersal in the Neotropics

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The remarkably diverse plant communities of the Neotropics are the result of diversification driven by multiple biotic (e.g., speciation, extinction, and dispersal) and abiotic (e.g., climatic fluctuations and tectonics) processes. However, in the absence of a well-preserved, thoroughly sampled, and critically assessed fossil record, the associated processes of dispersal and extinction are poorly understood. We report an exceptional case documenting patterns of extinction in the grape family (Vitaceae Juss.) based on fossil seeds discovered in four Neotropical paleofloras dated between 60 and 19 Mya. These include a new species that provides the earliest evidence of Vitaceae in the Western Hemisphere. Eight additional species reveal the former presence of major clades of the family currently absent from the Neotropics and previously unknown dispersal events. Our results indicate that regional extinction and dispersal have substantially impacted the evolutionary history of Vitaceae. They also suggest that while the Neotropics have been dynamic centers of diversification through the Cenozoic, extant Neotropical botanical diversity has also been shaped by extensive extinction over the last 66 million years.

S.169 HERBARIOMICS, AN INVALUABLE RESOURCE FOR PLANT RESEARCH

S.169.1 Herbariomics unveils endangered chemistry across the world's flora

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Plants are essential for human health. However, little is known about how much of their chemical diversity is threatened with extinction. Here, we characterised the phytochemical space of endangered plant species and quantify, for the first time, how much chemodiversity may vanish globally with the loss of threatened plants. We find that 29% of the 1,463 species with chemical studies contain unique compounds. For the other 23,689 chemically neglected species, we developed a metabolomics workflow to accelerate their chemical study. Essentially, we test to what degree the diversity of alkaloids, terpenoids and flavonoids in living plants can be detected on herbarium specimens of the same species covering diverse taxa. Overall, our herbariomics approach to study chemodiversity brings a new dimension to conservation planning (beyond the currently used metrics of biological, phylogenetic and functional diversity) by highlighting priority species for future research (e.g. discovery of natural products) and imminent conservation action (i.e., threatened species with unique chemistry).

S.169.2 Making the most of it: what can be done with poor data from bad specimens?

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Herbarium data can be of varying quality, some if surprisingly good, some is terrible. How do you decide if a sample is worth working with and what can you get from samples which will not yield up good sequence? We use examples from our own work to explore the limits of herbarium genetics and present an outline of approaches which can maximise useful information from samples which would never pass quality control in a commercial company.

S.169.3 Integrative species delimitation of Xanthium sect Acanthoxanthium based on herbarium specimens and type material

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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.

S.169.4 Systematics in the age of herbariomics: a tale of sweet potatoes

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Sweet potato (*Ipomoea batatas* (L.) Lam.) is a top ten food crop worldwide. Cultivated in all tropical and subtropical regions of the world, it is a hexaploid species with a complex evolutionary history. Dozens of studies have tried to untangle its origin since the 19th century, but they accumulated as much useful information as error. This was due to a poor understanding of the relationship between sweet potato and its wild relatives, poorly defined species boundaries, and lack of robust phylogenies. In summary, the lack of a good taxonomic knowledge has hindered progress in sweet potato research. Herbarium specimens are an extraordinary resource for molecular data. However, the optimal use of these data requires a decisive, parallel taxonomic effort. We have dedicated the last ten years to investigating the origin and evolution of sweet potato in the context of a taxonomic monograph of *Ipomoea*. During this time, we have studied ca. 30,000 herbarium specimens with molecular sequence data from ca. 3,000 specimens – Sanger sequencing, HybSeq and whole genome sequencing. This enabled important results pertaining to sweet potato, including species delimitation, the identification of sweet potato closest diploid and tetraploid wild relatives, or their differentiation from modern hybrids. In this talk, we discuss the role and importance of herbarium specimens and herbariomics in our work, as part of a taxonomic monograph and with a focus on sweet potato. We discuss our previous results and ongoing work on the origin, evolution and domestication of this important crop, and will highlight the importance of integrating genomics and taxonomy using herbarium specimens to accelerate tropical plant diversity studies.

S.169.5 Herbariomics for plant conservation: the study case of the presumed extinct Armeria arcuata

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Herbaria play fundamental roles in many fields, including plant taxonomy, systematics, and conservation biology. In this framework, Herbariomics offers invaluable -and sometimes unique- opportunities to obtain data that can inform species' conservation. While investigating extinct plant species in Europe, we found at the Utrecht Botanical Garden a living specimen labelled as *Armeria arcuata* Welw. ex Boiss. & Reut., a species endemic to Portugal assessed as extinct (EX). After many years in cultivation, the specimens' morphological characteristics changed making a correct identification difficult. To unequivocally identify the accession of "*A. arcuata*" from Utrecht, we compared its DNA with herbarium and fresh material from type material and other related *Armeria* species. We collected and analysed samples of *A. arcuata* from the living specimen at Utrecht and three ancient herbarium specimens (including type materials, ca. 1848; G, LISU herbaria), *A. neglecta*, also extinct, from the type specimen (1882; COI), *A. caespitosa* from recent herbarium specimens (2003-2009; JBAG, HSS), *A. pinifolia* (1970; GOET), *A. pungens* (1997; GOET), and *A. curvifolia* (living;

Teplice Botanic Garden). We applied DNA extraction techniques suitable for old herbarium material, along with adaptation of the normal double-stranded library preparation protocols. Genome skimming was performed on a lane of a NovaSeq sequencer, which allowed us to gather about four Gb of sequence information per sample. After quality trimming of the received reads, we performed reference-based assembly of plastomes and of the nrDNA region (about 12,000 bp long) and inferred phylogenetic tree and networks. Results from the phylogenetic analyses indicate that the plants cultivated in Utrecht are not actually *A. arcuata*. Moreover, network analyses suggest a hybrid origin of these cultivated plants.

S.169.6 Explainable AI powered by shape analysis to capture the phenotypic variation of plants in the field and in herbaria

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Plant leaves vary not only between species, but also within populations of the same species. A persistent challenge in botany is to accurately document this variation directly in a plant's natural environment. In this study, we investigate the phenotypic variation of buttercup leaves in natural plant populations using an easy-to-use smartphone app called Flora Capture, designed for citizen scientists. We exploit the strengths of machine learning and geometric morphometrics to address three key questions: (1) Can smartphone images effectively capture leaf variation comparable to traditional herbarium methods? (2) Do image differences detected by computer vision correspond to actual variation in leaf shape? (3) Can smartphone images of leaves achieve detailed resolution for identifying plants at high taxonomic levels? Our approach incorporates several deep learning techniques, including Grad-CAM for interpretable AI and EfficientNet for feature extraction from images. We analyze the same leaves using computer vision and quantitative morphology - by extracting their shapes using landmark geometric morphometrics. Through dimension reduction and covariation analysis, we discover common patterns in both the image features and the corresponding biological shapes. Using machine learning algorithms such as Random Forest and Support Vector Machine, we evaluate the suitability of leaf images for classifying plant populations at high taxonomic levels. The goal is to understand the decision-making processes of computer vision in biological shape classification. This work represents a step towards reliable and reproducible phenotyping of plants in their natural habitats.

S.170 FROM DEVELOPMENTAL SWITCHES TO BROAD EVOLUTIONARY TRAJECTORIES: UNDERSTANDING MECHANISMS OF SEX DETERMINATION

S.170.1 Evolutionary developmental biology of sex in the Salicaceae

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The Salicaceae, and especially *Salix* and *Populus*, are becoming a leading model for the "clade biology" of sex determination, as dioecious, monoecious and polygamous forms are common. In angiosperms,dicliny (the production of single sex flowers), evolves through one of two contrasting evolutionary developmental mechanisms: organ deletion or organ abortion. Organ deletion, under which sex organs never form, may involve MADS-box genes, as these genes are required to produce floral organs of a given identity. Organ abortion, under which sex organs form but during development become vestigial or non-functional, are less likely to involve MADS-box genes, and more likely to involve late-stage developmental modifiers of organ development. Phylogenetic studies strongly suggest that there are necessary pre-adaptations for plant lineages to adopt either the deletion or abortion pathway. *Populus* and *Salix* are both examples of the deletion pathway, in which no trace of stamens is ever seen in female flowers, and no trace of carpels in male flowers. In poplar we show that the B-class MADS-box genes *PISTILLATA* (*PI*) and *APETALA3* (*AP3*) are strongly down-regulated in early female flower development. This is expected as these genes are required for stamen development under the canonical ABC model. A powerful way of dissecting the role of the MADS-box developmental module in dioecious species is provided by CRISPR/Cas9 gene editing. Recent developments in efficient poplar transformation coupled with engineered hyper-precocious flowering have facilitated novel experiments in this area. Preliminary experiments on MADS-box genes in poplar show the potential for functional dissection of pathways to dioecy. The development of CRISPR/Cas9 technology in other systems could greatly accelerate understanding of the evolutionary developmental genetics of dioecy in diverse lineages.

S.170.1 The transition from dioecy to monoicy in liverworts is a case of convergent evolution

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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 9 th small chromosome (1/10th of the size of the large eight chromosomes). The eight large chromosomes are collinear with the eight autosomes of M. polymorphashowing many intra- but few inter-chromosomal rearrangements. By contrast, the small 9thchromosome 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 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.170.3 Sex and/or asex: insights from brown seaweeds

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In many eukaryotes, male and female sexes are determined during the (haploid) gametophyte stage of the life cycle, by the presence of a female (U) or male (V) sex chromosomes. The rise, evolution and demise of U/V systems have remained enigmatic to date. I present how we analyzing genomes spanning the entire brown algal phylogeny to decipher their sex- (and asex) determination evolutionary history.

S.170.4 Analysis of sex determination system in Cannabis sativa

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Cannabis sativa is mainly a dioecious plant, which means that female and male flowers develop on separate individuals. This crop presents high sexual dimorphism, as we can see biochemical, vegetative and reproductive differences between the two sexes. *C. sativa* has a XY sex determination system: female have two X chromosomes and male plants carry an X and a Y chromosome; but the sexual system of this crop is much more complex, as the sex is not only determined genetically, but also by environmental and hormonal factors. While the developmental processes of male and female *Cannabis sativa* flowers clearly involves the orchestrated activation of numerous genes, it is conceivable that one or two key genes act as molecular switches for sex determination. The aim of our research is to understand how genes, phytohormones and environmental conditions interrelate and contribute to sex determination in hemp. Utilising transcriptomics analysis, we have pinpointed potential candidate genes on the sex chromosomes apparently associated with both female and male functional development in *Cannabis sativa*. Among those candidates are transcription factors with homologs know to be involved in reproductive development and sex determination. We have also developed a PCR-based method to determine sex genotype and establish genotype-phenotype relationships. Our results indicate that sex determination is established very early during *Cannabis* development by a network of gene regulatory proteins, and that the genetic basis of sex determination is robust across different cultivars and chemotypes.

S.170.5 The dynamic evolution of heteromorphic sex chromosomes in Cannabaceae

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The Cannabaceae family has a deep history regarding their dioecious flowers and sex chromosomes. One century ago, the XY pair that controls the development of the sexes was identified in the hop *Humulus lupulus* var. *lupulus,* owing to the cytologically smaller Y chromosome relative to the X. Curiously, examinations across other species in *Humulus* and in the sister genera *Cannabis* uncovered varying cytological differences. In *Cannabis,* the Y chromosome is bigger than the X, while other varieties of *Humulus* remain homomorphic or have evolved a multiple sex chromosome system (e.g., XXYY). Despite these early discoveries, we know little about the Cannabaceae sex chromosomes at the molecular level. This is largely due to the complexities of assembling XY pairs in genome references. Here we use a combination of Illumina, PacBio HiFi, and Dovetail Omni-C data to assemble fully-phased genomes for XY males of *Cannabis* and *Humulus*. Using these assemblies, we first show that the XY pairs match the known cytology. We next use these assemblies to explore the dynamic patterns of gene gain and loss, as well as structural changes that have shaped the XY pairs. Ultimately these comparative analyses across Cannabaceae will uncover genes that control the development of the economically valuable females of hop and hemp.

S.170.6 Long read sequencing to explore the repeated evolution of sex chromosomes in plants

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Sex chromosomes have evolved hundreds, if not thousands, of independent times across flowering plants. However, only a small number of master sex determination genes have been identified, largely due to a lack of high quality genomic resources for complex plant genomes that contain sex chromosomes. We have built computational pipelines for 1) assessing if a species has XY or ZW sex chromosomes, 2) assembling highly contiguous and fully-phased sex chromosome assemblies in heterogametic sexes, 3) delimiting the non-recombining sex determination region on these sex chromosomes, and 4) exploring the evolution of these regions in diverse plant species to identify putative sex determination genes in non-model plants. We use these computational tools to explore the repeated evolution of sex chromosomes in flowering plants, which is uncovering a hidden world of sex chromosome variation within and among species.

S.171 PRESERVATION AND PROMOTION OF TRADITIONAL ECOLOGICAL KNOWLEDGE IN THE ERA OF OPEN SCIENCE: BENEFITS AND CHALLENGES

S.171.1 The legitimacy of empirical sciences under the oversight of an Ethical Committee? Defending a critical ethnobotany

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In my ethnobotanical research in 2018 and my recent sociology-of-science fieldwork in Jujuy (Argentina), I address ethical challenges and question the need for expert committees in empirical sciences. I analyze how certain institutional mechanisms force a choice between the privatization of knowledge or its anonymization in the name of scientific universality. In Argentina, despite the 2023 Open Science Law (Law 27738), field research remains trapped in neo-developmentalism and patrimonialistic dynamics, especially when accessing biocultural information in an indigenous context. This reflects a dominance relationship of Jujuy institutions over scientists and their civil informants. The mistrust between academic and indigenist institutions is manifested in police controls and specific protocols for working with *Pueblos Originarios* (PO). Instead of addressing social exclusion from a Human Rights perspective, a contractual practice is prescribed. Consent is seen as the legal solution to dialogue between "different cultures," leading to clientelistic practices among local authorities and researchers, namely by controlling field access. The patrimonialistic regime may promote these pre-research contracts to appropriate knowledge in favor to PO interests. Paradoxically, anti-colonial resistance is expressed through an anti-extractive discourse. In practice, then, control over science is transcended through underground dialogues, driven by a "community resistance" ethic that shapes the identity of both native populations and field scientists advocating empirical, inclusive, and critical methodologies within a "decolonial" framework. Critical ethnobotany is based on a "dialogue of knowledge" from a position of subalternity, promoting "interdisciplinarity" and "institutional coordination" to subvert the hierarchical and authoritarian structures of the neoliberal academic playground. However, this decolonial framework can perpetuate conservative dynamics if it does not overcome mistrust and secrecy in the transmission and production of knowledge. On a material level, effectively challenging the patrimonialistic regime requires expanding social justice policies by the State, ensuring academic autonomy in designing collaborative projects directly with the public.

S.171.2 The language of land and life: importing data

sovereignty lessons and tools from linguistics into ethnobiology

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Ecological knowledge and Indigenous languages are tightly interwoven and have been eroded in tandem in many parts of the world. To bolster or revitalize this cultural heritage, many Indigenous Peoples have worked with linguists and/or ethnobiologists, either from within or outside of their communities. Despite an increase in interdisciplinary projects at the intersection of these fields, there has been limited exchange of best practices, ideas, and resources related to ethical and effective work with communities. One area where linguists and ethnobiologists have innovated in parallel is *data sovereignty*. While linguists tend to deposit data in large centralized archives with different levels of access depending on community preferences, equivalent archives and graded-access capabilities for ethnobiology are much less common. At the same time, some scholars have been experimenting with Traditional Knowledge Labels and Biocultural Labels as a mechanism to ensure that community preferences for information use accompany the data. Linguistics and ethnobiology share significant overlaps not only related to the classification and encoding of biological knowledge, but also in the need for methodologies that foster ethical engagement with local communities. Cross-communication between the two disciplines on data sovereignty, community engagement, and other areas may lead to mutual benefit. Here we outline approaches taken to address these issues by both fields, examine opportunities for mutual enrichment, and share experiences from our project with Wixárika (Uto-Aztecan) communities in West-Central Mexico.

S.171.3 The centers of origin as spaces for dialogue of knowledge

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Capitalism and colonization systematically persecuted and destroyed the knowledge of indigenous peoples. Currently, numerous argue the need for a new paradigm based on the dialogue of knowledge, which reverses positivist reification, vindicates traditional knowledge, decolonizes knowledge and establishes epistemic justice. In this article we maintain that since Nikolai Vavílov postulated the theory of the centers of origin of cultivated plants, these have become an important space for dialogue of knowledge between various scientific disciplines and the traditional knowledge of numerous cultures on topics such as the conservation of wild and domesticated biodiversity. The beginning of this dialogue sparked a scientific revolution, transformed the organization of knowledge and contributed significantly to the birth of multiple ethnosciences. In this text we ask ourselves: what importance does it have for the history of science that the centers of origin have become a space for dialogue between scientific disciplines and traditional knowledge? And what benefits has this dialogue brought to the various scientific fields? What are the main threats to the continuity of the centers of origin? And finally, how could they protect themselves? To answer these questions we follow bibliographically in the footsteps of Nikolai Vavílov, we integrate a large corpus of rom very diverse disciplines who recognize contributions of traditional knowledge; the factors that threaten them and the proposals to protect them. In our conclusions we agree with Casas and Parra (2016) who point out that farmers in the centers of origin constitute an evolutionary force, since of the total of 7000 species and hundreds of thousands of varieties of current agricultural and horticultural systems: “it is the result of evolutionary processes shaped by domestication, faster and more dynamic than those that occur in nature” (Casas and Parra, 2016).

S.171.4 Historical documentation in the inventory of traditional knowledge associated with biodiversity: a tool for the recovery of neglec

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The author has participated in several initiatives in Spain and Latin America related to the inventory of knowledge associated with bio- and agro-diversity, always working with historical documentation, not only with that contained in textual sources but also from graphic and archaeobotanical sources. These include its participation in the IECTB and IECTBA (Spanish inventories of traditional knowledge associated with bio and agrodiversity), the FAFA (Agricultural and Forest Flora of al-Andalus), the CultIVA-CYTED network for the recovery of NUS (neglected and underutilized species) or various projects for the recovery and management of cultural landscapes in archaeological sites such as the Alhambra and Generalife or Medina Azahara in Andalusia (Spain) or the Jesuit reductions in the missionary-Guarani area. This experience demonstrates the interest of retrospective research in Historical Ethnobotany and its usefulness in recovering forgotten crops, phytotherapeutic knowledge, forms of agrofood consumption and forest uses that are once again of interest today in the fight against hunger, poverty and especially as elements of adaptation and even mitigation of climate change. They also make it possible to document the traditional value of many of these crops within a historical process of germplasm transfer between cultures, countries, and continents, turning apparent innovations subject to new codes of germplasm exchange and associated knowledge into archaeophytes, requiring a new analysis of the rights and sovereignty of peoples over part of their genetic and ethnobiological heritage. Some examples are examined such as the case of the argan tree [*Argania spinosa* (L.) Skeels] and its current potential cultivation in countries outside its natural range.

S.171.5 Useful Plants and Fungi of Colombia: traditional knowledge for conservation, and conservation of traditional knowledge

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Colombia is one of the world's most biodiverse and ethnically rich countries. As the nation continues resolving its socio-economic challenges, biodiversity, and the traditional ecological knowledge (TEK) associated with it are under increased threat by climate change, deforestation, habitat loss, acculturation, and other factors. The Useful Plants and Fungi of Colombia project aimed to develop pathways to enhance nature's contribution to people in Colombia by increasing, consolidating, and making accessible the knowledge of its useful plants and fungi for the benefit of society. The project produced catalogs of useful species, online portals, and a platform to facilitate sustainable value chain markets, alongside a wide range of publications, including books and scientific articles. A core research question was how the knowledge of useful plants could inform national conservation priorities and sustainable utilization. We applied the Important Plant Areas (IPA) approach to identify key sites for in-situ conservation, with 980 sites meeting IPA thresholds. We found 46 sites to be of high priority and highlighted 10 top-priority sites for further investigation and conservation actions. We also found that complementing scientific and traditional knowledge can better inform the conservation and support the sustainable use of plants in Colombia. We investigated whether citizen science could help mitigate the erosion of traditional ecological knowledge on useful plants through the use of digital surveys involving local citizen scientists. The trial in three pilot areas was successful, and we recommend building and strengthening the engagement of citizen scientists. Lastly, we carried out gap analyses at the spatial and taxonomic levels, to identify areas lacking floral inventories or ethnobotanical surveys, as well as underrepresented taxa. Overall, the project enhanced the baseline knowledge of useful plants and fungi, and the associated TEK, providing crucial information to support Colombia's transformation towards a greener, more sustainable economy whilst protecting its biodiversity.

S.171.6 IECTB and CONECTe: two copyleft Spanish initiatives to document and

protect traditional plant knowledge

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In the current global change framework, the erosion of traditional ecological knowledge is pronounced, remarkably in industrialized countries like Spain. Ethnobotanical studies conducted in the country reveal that this erosion varies across territories and knowledge domains, with health or food exhibiting a less profound decline. The overall erosion trend is attributed to factors such as the abandonment of traditional agricultural practices and shepherding, changes in land use, the diminished necessity of wild plants for subsistence, reduced time spent in the field, or negative associations with certain species deemed famine food. Conversely, there are multiple motivations that promote wild plants use. Some view gathering as a recreational and community-building activity, while others appreciate the unique flavors of wild plants that cannot be replicated by cultivated or commercial varieties. Additionally, the medicinal role of food, particularly in uses closely aligned with medicine such as beverages and condiments, remains highly valued. Recognizing the significance of traditional ecological knowledge, two initiatives in Spain are actively promoting its documentation, protection, and reintroduction to society. Firstly, the Spanish Inventory of Traditional Knowledge related to Biodiversity compiles and disseminates information on the traditional use and management of biodiversity. Six volumes have been published since 2014 and two more are being edited, including monographs about 837 plant species. Secondly, CONECT-e (www.conecte.es) is an online platform enabling citizens to document knowledge and uses of both wild and domesticated species, and includes 3772 monographs. By employing open data and copyleft licenses, these endevours contribute to the traditional knowledge preservation in the public domain, ensuring the unrestricted exchange and reproduction of this valuable knowledge.

S.172 NATURAL HYBRIDIZATION AND SPECIES CONSERVATION. SESSION 1

S.172.1 Hybridization in Mexican Pinus - implications for management and conservation

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Hybridization is common in plants. Its outcomes are wide and contrasting, from detrimental or causing merging of species, to increasing their evolutionary and ecological resilience and even resulting in hybrid speciation. In western and northern Mexico, hybridization frequency among *Pinus* species ranges from occasional (e.g., isolated individuals of *Pinus chihuahuana* × *P. lumholtzii*) to stable populations (e.g., of *P. arizonica* × *P. cooperi*). There is also a wide range of fitness outcomes, from hybrid swarms

composed by low fitness individuals (e.g., *P. arizonica × P. engelmannii*) to populations exhibiting hybrid vigor (e.g., *P. herrerae × P. luzmariae*). Some are recent (isolated F1s), and others are part of ancient introgressions (e.g., *P. cembroides × P. discolor*; *P. strobiformis × P. flexilis*); a syngameon encompassing pinyons has been recently recorded showing how sequential hybridization might have accelerated the speciation in this group. Gene flow among these species increases along ecological or geographical range edges and in disturbed communities. The high rate of hybridization in the zone may be owed to the facts that: a) Mexican pines are relatively recent (6 - 10.5 Ma), allowing for species to hybridize in absence of genetic incompatible systems, b) northwestern Mexico is a very rugged region offering multiple and diverse niches that favor diversification, and c) it is a boundary area for many species reaching there their northern or southern limits. Despite the evidence about their commonness, natural hybrids are not yet considered in forestry policies in Mexico. Combined names indicating hybridization or introgression are not allowed in inventories and monitoring reports nor in official paperwork. A shift of paradigm is needed to adjust forestry policies and management to the real situation in which genetically merged biological entities are common in forest ecosystems.

S.172.2 Multiple glacial refugia and impacts of environmental variables on hybridization between Betula species of differing ploidy levels

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Natural hybridization frequently occurs in nature and plays a crucial role in evolution of biodiversity. Here we use the genus *Betula* to address the following questions: (1) where are their glacial refugia? (2) does hybridization occur between *Betula* species of various ploidy levels, (3) which environmental variables explain the spatial patterns of genetic admixture? We collected samples representing *B. costata* (2x), *B. dahurica* (8x), *B. ermanii* (4x) and *B. platyphylla* (2x) in northeast China and *B. ashburneri* (2x) and *B. utilis* (4x) from north to southwest China. We integrated microsatellite data of 2,609 individuals, species distribution models and spatial autoregressive models to address these issues. Our results revealed multiple glacial refugia for *Betula* species. Microsatellite data analysis showed frequent bidirectional genetic admixture among *Betula* species, irrespective of the ploidy difference. The amount of genetic admixture from either *B. costata* or *B. ermanii* to *B. platyphylla* is partially explained by their overlapped range and from *B. dahurica* to *B. platyphylla* is partially explained by precipitation of the coldest quarter (PCQ) and changes in PCQ. The amount of genetic admixture from *B. ashburneri* to *B. utilis* is partially explained by the mean temperature of the wettest quarter (MTWQ). Our results show asymmetrical gene flow from high to low ploidy levels and indicate that envrionemtal factors play a role in shaping the patterns of genetic admixture between *Betula* species.

S.172.3 Optimal mating strategy in secondary sympatry may oppose reinforcement of premating isolation – A whole-genome study of mangroves

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Reinforcement, the process by which premating isolation is strengthened by selection against the investment in maladaptive hybrids, is a key prediction of the evolutionary theory. Exceptions may therefore shed light on this controversial topic. Two mangrove species (*Bruguiera gymnorhiza* and *B. sexangula*) on the Indo-Malayan coasts come into secondary contact on the Hainan island, China, but rarely elsewhere. Strikingly, hybrids account for 30% of the individuals in sympatry and exceed the number from the parental species, *B. gymnorhiza*. Furthermore, while the two species in allopatry have different flowering times, they both flower year-round in Hainan. Counter-reinforcement thus appears to be at work in *Bruguiera.* To analyze the unusual hybridization, we sequenced and *de novo* assembled the high-quality genomes of the two species, followed by the re-sequencing of 63 individuals from allopatric and sympatric populations. The genomic analysis identifies both F1s and multiple generations of backcrosses. The hybridization pattern suggests weak postmating isolation and, likely, ecological speciation. Based on these patterns, we develop a theoretical model whereby the allele that does not exercise mate choice can be advantageous. In this model, the mating allele of the weaker species may do better by mating with the stronger and more common species. The case of *Bruguiera* thus shows that the evolution of mating preference as well as reinforcement is a function of genic fitness, rather than the fitness of the species itself.

S.172.4 Genetic bases of the flower color variation in a natural hybrid zone

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The Angiosperm radiation can be characterized by its outstanding flower color diversity, spanning the entire color spectrum of human and pollinator vision. Moreover, flower color is an evolutionary labile trait which can differ between sister species, among populations or even among individuals at different life-stages. In *Pedicularis comosa*, two subspecies/morphs display distinct flower color, *Pedicularis comosa comosa* has yellow flowers while *Pedicularis comosa asparagoides* has pink flowers. In order to better understand this species taxonomy, to get an overview of the overall genetic diversity and differentiation, and to unravel the possible evolutionary origins and genetic bases behind both morphotypes, we applied a population genomic approach. The phylogenetic tree provided us keys to settle an old debate on *Pedicularis comosa*'s classification, supporting that the two "subspecies" are not reciprocally monophyletic, and that genetic structure is rather consistent with geography. Cline analyses and genetic structure results revealed the existence of a hybrid zone between the two morphotypes, suggesting a strong selection on certain parts of the genome, therefore maintaining differences between *P.c. asparagoides* and *P.c. comosa*. Finally, the investigation of potential outlier SNPs associated with genetic structure as well as phenotypic and environmental data allowed us to find genes involved in color differentiation but also in light and cold stresses adaptation. To uncover the subtle color differentiation from pink to yellow, we applied comparative transcriptomic and metabolomic approaches. All together, these results provided us key information to draw recommendations for the conservation of these species as a whole.

S.172.5 Can hybrids modify the adaptive trajectories of parental species in contact zones?

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The species hybridization is a phenomenon which consequences can go from the collapse and loss of diversity to the rise of this diversity. Global change, are promoting the secondary contact and hybridization between diverging taxa with incomplete reproductive barriers. These hybrid zones have the potential to shed light on evolutionary processes driving adaptation and are particularly powerful natural systems for studying the interaction between divergent genomes to explore how the rise of phenotypic novelties can modify the evolutionary trajectory. We have studied a total of 480 plants belonging to six populations and two transects of two *Erysimum* (Brassicaceae) species presenting a contact zone in the Serra da Estrela (Portugal). The plants were phenotyped using 25 traits and genotyped using more than 4000 SNPs across their whole genomes. Plants also were tagged during a complete session of reproduction and we used different component to quantify their fitness. We analyzed the patterns of hybridization using genomic approach, identifying two hybrid zones in different stages of hybridization. When we explore the patterns of natural selection acting on the parental and hybrid plants, we found different traits related to plant size and reproductive investment driving the population evolution for the parental plants. However, the natural selective pressures acting on hybrids were variable depending on the evolutionary stage of the hybrid zone. In the hybrid zone enriched with F1-hybrids we identified new adaptive trajectories acting on traits not selected in parental species. But the hybrid zone enriched by F2 and backcrosses, the adaptive trajectories were similar to those found at parental sites. Our results demonstrate that hybrids promote the rise of novelties in plant evolution but in absence of transgressive phenotypes the hybrid zone tends to become in parental secondary contact zones.

S.173 ASSESSING AND CLASSIFYING THE POSITIVE AND NEGATIVE IMPACTS OF ALIEN PLANTS

S.173.1 Employing the Environmental Impact Classification for Alien Taxa (EICAT) on coastal areas: the example of the Costa Brava (Spain)

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High human population density and habitat fragmentation, in a future climate change scenario, may lead to an accelerating trend of biological invasions, particularly in Mediterranean coastal areas. A paradigmatic example of this is represented by the Costa Brava, a coastal strip of ca. 250 km stretching from the French-Spanish border to Blanes (Girona Province, Spain). It harbours a great richness of native species, some of them endemisms, as well as diverse natural habitats. However, it is under enormous anthropogenic pressure due to nassive urbanization, mass tourism, and the presence of numerous invasive plant species, mostly escaped from gardens. In order to minimize new introductions of alien plants and improve the management of invasive species present in the Costa Brava, an European Union LIFE Program project (LIFE medCLIFFS https://lifemedcliffs.org/es/) is underway. The initial phase required the design of around a hundred transects of 0.5–1 km in length distributed throughout the coastline to monitor by trained volunteers the evolution of 33 invasive or potentially invasive plant species populations (i.e., using citizen science). Large amount of data was gathered as a result of our field trips derived from examining the areas for the transects, together with the first results provided by the volunteers [which included the area (m²) and the size (census) of the detected populations of alien species]. All this information let us to identify and categorize the main impacts of these 33 invasive (or potentially invasive) species on native communities according to the Environmental Impact Classification for Alien Taxa (EICAT) criteria of the IUCN (2020). To our knowledge this is the first time that this standard classification has been used in a LIFE project and, also, specifically for a coastal area. Future projects employing this assessment methodology will contribute to a more accurate understanding of these impacts.

S.173.2 Positive and negative invasive plant species ecological impacts in Europe

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Despite that many invasive species threaten biodiversity and ecosystems, their effects are highly idiosyncratic and context dependent. We compiled a comprehensive database of 287 publications on 4622 field studies on the ecological impacts of 114 invasive alien plants in 30 European countries to analyse their direction and frequency. Impacts were categorized across levels of ecological organization, taxa and feeding mode. Furthermore, if the information was available, the impacts were also classified based on the feeding mode of the impacted species or communities. Forty-four percent of the studies found significant impacts with more significant decreases (26.8%) than increases (16.6%) on the impact response variables. Negative impacts (i.e., statistically significant decreases) were more frequent on species and communities than on ecosystem properties. The impacts on ecosystem properties were highly variable. The frequency of negative impacts to species and communities was higher on plants than on animals, but the frequency of finding positive impacts (i.e., statistically significant increases) was similar between taxa. Finally, the frequency of negative impacts was higher on primary producers, herbivores and parasites than on decomposers, pollinators and predators, while the frequency of positive impacts was generally similar among feeding modes. Our database provides the first information system on field studies of the ecological impacts of invasive plant species at the continental scale. This information can be of interest for academic, management and policy purposes.

S.173.3 Not all impacts are negative: a bidirectional impact assessment of the alien tree Robinia pseudoacacia

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Alien species cause various environmental impacts worldwide. Negative impacts have received considerable attention, as impactful alien species, named invasive, are a major driver of biodiversity decline. The IUCN Environmental Impact Classification for Alien Taxa (EICAT) has been developed to assess negative impacts on native biodiversity. Alien species can also have positive impacts, e.g., through habitat/food provisioning or dispersal facilitation. However, these impacts have never been systematically examined, mostly due to the absence of a standardized protocol to assess their magnitude and diversity. We have filled this gap by developing EICAT+, a framework which structurally resembles IUCN EICAT, can be applied to all alien taxa at different spatial and organizational scales, and uses five semi-quantitative scenarios to describe the magnitude of observed positive impacts of alien taxa on native biodiversity. In EICAT+, the highest levels of impact magnitude are assigned to alien taxa increasing the area of occupancy of native species through local population re-establishment or preventing local extinction. EICAT+ also describes the underlying impact mechanisms by which alien taxa facilitate native biodiversity. To illustrate the functionality and utility of the framework, we have applied EICAT+ to studies reporting positive impacts of the alien tree black locust (*Robinia pseudoacacia*) and used IUCN EICAT to assess its negative impacts. About one third of all impacts were positive. Most impacts, both negative and positive, involved changes in population size of native species and were caused by alterations to abiotic conditions. Species that benefit from the introduction of the black locust show a preference for nutrient-rich soils and higher light intensity, in contrast to species negatively affected. Our results align with the existing literature on the black locust and demonstrate how the combined use of IUCN EICAT and EICAT+ enables to obtain a comprehensive understanding of alien species impacts on native biodiversity.

S.173.4 Assessing the Ecological Impacts of Invasive Alien Plants of France using adapted protocols of EICAT and EICAT+

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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.

S.174 PARADIGM SHIFTS IN FLOWER COLOR

S.174.1 New insights into the impact of non-pollinator agents of selection in flower color over the past ten years

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Besides the predominant role of pollinators in floral evolution, it has been suggested that the selective pressures exerted by abiotic agents may also contribute to variability in flower color. In the past ten years, we used the shore campion (*Silene littorea*) as a model species to develop studies aimed at gaining a better understanding of modifications of flower color driven by these selection agents, mainly focusing on the effect of solar, and more specifically in the UV light. We used different approaches to unveil color variation in this species, such as common garden experiments, transcriptomic and biochemical studies. Our results have highlighted that flower color in *S. littorea* is influenced to some extent by sunlight and UV radiation. However, the specific regulation of anthocyanin production in petals, the main pigments responsible for the flower color in this species, may reduce drastic changes on that trait, presumably due to its importance for pollinators. This is manifested in the lower plasticity observed in anthocyanin biosynthesis in petals compared to vegetative tissues. Additionally, transcriptomic and biochemical analyses have evidenced that petal pigmentation is tissue-specific regulated, resulting even in the occurrence of individuals with white flowers lacking anthocyanins without hindering anthocyanin accumulation in other tissues. Pollinator attraction seems to be at least partially favored by the presence of petal anthocyanins, although white-flowered plants can overcome this limitation by utilizing their mixed mating system and reproducing through autonomous selfing. Finally, the rarity of plants lacking anthocyanins in both vegetative and reproductive tissues suggest that anthocyanins in photosynthetic tissues are the targets of non-pollinator mediated selection. In conclusion, we suggest that environmental stressors may drive anthocyanin accumulation in the whole plant, although it may be limited in petals, at least in *S. littorea*. Future research will incorporate further transcriptomic and biochemical analyses.

S.174.2 Does allopolyploidy lead to transgressive red pigments in Silene?

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Determining how and why reproductive traits evolve between and within species is key to understanding patterns of speciation. In plants, both genome duplication as well as selection on floral traits, such as color, have been major drivers of angiosperm diversification. *Silene* (Caryophyllaceae) is a largely white- and pink-flowering diploid genus distributed throughout temperate regions. However, at least two independent polyploidization events occurred in the genus's expansion into North America, and most extant North American species are at least tetraploids. Two novel floral pigmentation strategies arose in the North American polyploids – red flower color and UV bullseyes. Insights into how these two floral color traits arose as well as the revised phylogeny of North American *Silene* polyploids are made from target capture of herbarium specimens, gene silencing, and character mapping of floral pigments to answer the following questions: What is the most likely driver of floral color evolution in *Silene* - pollinator shifts, habitat specialization, sympatric competition, abiotic factors, or polyploidy?

S.174.3 The impacts of global change on floral pigmentation

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Floral coloration is nortoriously important for mediating plant-pollinator interactions though support for abiotic selection on floral pigmentation has increased over that last few decades. Pigments produced in the anthocyanin biosynthetic pathway both give rise to floral color diversity and are critical compounds for abiotic stress responses. As such, rapid abiotic shifts associated with global change have the potential to drive temporal change in flower coloration. I discuss results from collections-based studies exploring whether flower color has changed over the last ~100 years across a diverse set of angiosperm taxa and whether such change is linked with abiotic factors such as temperature and ozone (a proxy for ultraviolet irradiance). I then present data testing whether abiotic-induced flower color plasticity has the potential to contribute to responses of flower color to global change. Results show that taxa that have experienced stronger temporal changes in ozone and temperature have experienced greater change in floral pigmentation. The response to abiotic change depended on whether anthers are exposed to external environmental conditions or concealed by petal tissue, which is in line with petal pigmentation's role in protecting pollen from abiotic stress. Plasticity studies revealed that UV exposure induced a pigmentaiton response in one focal species, but not in all populations. Thus, there is genetic variation for pigmentation plasticity. Temperature change induced a weaker pigmentation response that was not population-specific. Together, results show that floral pigmentation has responded to global change, and plasticity is one mechanism by which plants have elicited phenotypic responses. This change in pigmentaiton has the potential to impact plant-pollinator interactions, and plant reproductive output.

S.174.4 Flower colour communities across elevation - a case study on calcareous vs silicious bedrock from the European Alps

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Flower colour plays an important role in structuring plant communities and is under selection by pollinators. Recently, the significant discrepancy between flower colour vision by humans versus pollinators has been discussed, which must be taken into account when considering the role of flower colour in communication with pollinators. Since bedrock and soil conditions are known to affect plant community composition, and can also affect flower colour directly, studies on flower colour composition of a community should include bedrock as an environmental variable. Elevational gradients in high mountain ranges are particularly suitable to study patterns and drivers of plant community diversity, including plant functional trait distribution relevant for trophic interactions. We measured flower colour spectra within six highly diverse grasslands on both calcareous and silicious bedrock across an elevational gradient in the European Alps: Hohe Leite (500 m asl), Brunnenkopfalm (1500 m), Obergurgl (2500 m), Kaserstattalm Stubai (1850 m), Arnspitze (1700 m) and Furkapass (2400 m). We collected flowers or petals of 315 locally occurring, insect-pollinated plants and measured their light reflectance property using ocean optics spectrophotometer. We used the 'bumblebee color vision model' to translate spectral data into "bee-colours" because bumblebees are representative insect pollinators from low to high elevation in the European Alps. Our primary results suggest that for humans 'white' and yellow' flowers increase with higher elevation, whereas for bees 'blue' and 'green' flowers increase. Our data shows that calcareous grasslands have a higher color diversity than siliceous grasslands based on human vison, but higher number of blue and bluegreen flowers based on hymenopteran vision. Subalpine area shows a higher color diversity based on human vision, despite alpine regions harboring a higher number of plant species. Based on pollinator vision, more species with blue and bluegreen flowers occur in the alpine than in the subalpine region.

S.174.5 On colour to rule them all: the evolutionary rise of the betalains

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The evolution of betalains within the order Caryophyllales, was a singular evolutionary event, both in the evolution of a completely new biosynthetic pathway to make pigments, but also in its replacement of the anthocyanin pathway. It has had profound implications for the ecology and evolution of Caryophyllales, from the evolution of floral colour to the structural arrangment of the genomes. In talk I outline how our knowledge of the evolutionary fate of the betalain pathway and anthocyanin pathways in Caryophyllales has been transformed, through transcriptomic and genomic resources, coupled with synthetic biology approaches. I address the role of modulation of the interface between primary and secondary metabolism, the prevailing importance of gene duplications, and the evidence for convergent origins of betalain pigmentation and iterative loss of anthocyanins. I explore how flavonoid pathways have more generally changed in the context of a shift to betalain pigmentation, and discuss the impact of this on the variety of floral colour hues within Caryophyllales. Given the increasingly strong support for convergent evolution of betalains, I revisit hypotheses for the evolution of betalains and consider new and emerging evidence for their functions in the context of floral adaptation, and the unique adaptational advantages they offer with respect to flower-pollinator interactions.

S.174.6 Identification of TFs controlling pigment synthesis in the endoholoparasite Pilostyles boyacensis and its host Dalea cuatrecasasii

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Chlorophylls, carotenoids, flavonoids, and betalains generate colors in plants. Anthocyanins, a type of flavonoids, are the pigments responsible for red, pink, and purple hues in vegetative and reproductive tissues of plants. The synthesis of these pigments is primarily regulated at the transcriptional level by R2R3-MYB transcription factors assigned to subgroup 6. These genes have extensively studied in model plants such as *Arabidopsis thaliana, Antirrhinum majus, and Petunia hybrida*. In this study, we focused on a system composed by the endoholoparasite *Pilostyles boyacensis* and its exclusive host *Dalea cuatrecasasii*, both exhibiting purple perianth organs. Two R2R3-MYB homologs from subgroups 5 and 7 were identified in *P. boyacensis*, and four homologs from subgroup 6 were isolated from *Dalea cuatrecasasii*. We found that R2R3 MYB genes from subgroups 5 and 7 are actively expressed in the endophyte, flowers, and fruits of *P. boyacensis*. Meanwhile, R2R3 MYB subgroup 6 homologs are expressed in the in the *D. cuatrecasasii* inflorescences, as expected. Interestingly, R2R3 MYB S6 homologs were also found expressed in the *P. boyacensis* endophyte. These results suggest that anthocyanin synthesis in the flowers and fruits of the holoparasite *P. boyacensis* may be mediated by host-specific R2R3 MYB S6 genes, which are known to be mobile at least, from *Citrus* to *Cuscuta*. Alternatively, anthocyanins in *P. boyacensis* can be endogenously produced R2R3 MYB genes from subgroups 5 and 7. We discuss our results in the broader context of convergent floral pigments and the resulting color hues in parasites with significant reduction in their body plan and complete dependence upon their hosts.

S.175 PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE. SESSION 8

S.175.1 How will leaf nutrients in C2 vs C3 salad crops fare under climate change?

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Climate change is placing immense pressure on agricultural systems to ensure sufficient production for an ever-growing global population. Producers must not only increase yields to satisfy these demands, but also safeguard crop nutrition to prevent deficiency-induced diseases and consequent malnourishment. Some crop species experience nutritive decline under ambient atmospheric CO_2 concentrations in comparison to crops grown historically when atmospheric CO_2 levels were much lower. Of course, elevated CO_2 does not occur in isolation and the problem is further exasperated by other environmental factors such as high temperatures or drought. The extent of nutritional demise, however, may be determined by the mode of photosynthesis employed by the crop. Currently, the only commercial food crop to use the rare C_2 type of photosynthesis is wild rocket (*Diplotaxis tenuifolia*), a nutritionally dense salad crop with rich potential to provide both high nutrients and yield under climate change. Unlike C3 species, plants using C_2 photosynthesis divide the photorespiratory pathway across mesophyll and bundle sheath cells, which functions to effectively concentrate and reassimilate carbon released from photorespiration to ultimately improve photosynthetic efficiency under warm and dry conditions. However, how C_2 physiology influences leaf nutrients remains unknown. Here we present the first study of intraspecific diversity for C_2 photosynthesis across 15 cultivars of wild rocket. We investigate how mineral and phytonutrient profiles change across a range of growth temperatures and in response to elevated CO_2 concentration across these C_2 wild rocket cultivars as compared to closely related C_3 salad greens. Our results suggest that wild rocket will retain nutrients better than related C_3 salad crops under climate change. This work has significant commercial application for current and future agricultural systems.

S.175.2 The ultimate guide of mycorrhiza and abiotic stress polytolerance in woody plants

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Mycorrhizal symbiosis is an ancient association between plants and fungi, crucially important especially for woody plants, as they have to maintain aboveground structures. Our current understandings of how woody plants respond to abiotic stress and how mycorrhiza mitigates this stress is very limited and considers almost exclusively just a single stress factor at a time. Functional diversity of both woody plants and mycorrhizal fungi interacting with them, variability of the strength and composition of multiple stress conditions in different regions of the world – all this makes it difficult to predict the patterns of these interactions from both the adaptational and mitigational point of view. In this study we used top-down approach, where known interactions are partitioned into functional and biogeographical groups, and then the stress tolerances and interactions are mapped into overlapping heatmaps to provide us large-scale patterns of these associations. We compiled a concordant dataset of 621 woody species stress polytolerance (including shade, drought, waterlogging, cold stress) and their known species-specific mycorrhizal interactions. We tested how stress polytolerance correlates with different mycorrhiza functional types. Our results confirmed contrasting patterns between single vs. multiple type, arbuscular vs. ectomycorrhiza, and obligate vs. facultative mycorrhizal interaction. Functionally different symbionts form significantly polarizing abiotic stress mitigation patterns with woody species with different life forms, growth forms, and biogeographical origin. These results provide insight into both evolutionary and biogeographic patterns related to the development of plant-mycorrhiza interactions.

S.175.3 miRNA profiling in maritime pine (Pinus pinaster Ait.) subjected to water stress using grafting as an experimental system

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Growing body of evidence has stablished miRNAs as a key regulation component of multiple biological processes across diverse species. Yet, studies focusing on miRNAs in forest species, particularly in gymnosperms like conifers, remain scarce. This scarcity limits our comprehension of how forest trees sense and respond to environmental stimuli to manage stress. *Pinus pinaster* Ait., a native conifer to the western Mediterranean, has held significant ecological and socioeconomic value for decades, emerging as a European model species due to its remarkable genetic variability, which has made it possible for this species to thrive in a wide variety of habitats, ranging from Mediterranean areas to the Atlantic coast. All these features make *P. pinaster* exceptional for studying the response and adaptation of conifers to water stress. In this study, we explored miRNA profiles from sampled stems of four different graft constructs. These grafts combined four genotypes that showed contrasting response to drought in previous studies. We used Gal1056 (drought-sensitive) and Oria6 (drought-tolerant) as scions grafted onto either R1S (drought-sensitive) or R18T (drought-tolerant) rootstocks. The rootstock genotypes are F1 siblings derived from the controlled cross Gal1056 x Oria6, vegetatively propagated. Three biological replicates of each graft construct were grown under water deficit and control conditions. This study will likely reveal potential roles of some miRNA families regulating transcripts associated with the response and tolerance to water stress. We can envisage they might regulate the expression of genes involved in response to osmotic and oxidative stresses, signalling of growth regulators (abscisic acid or ethylene) and controlling compatible solute metabolism. Additionally, other miRNA families, including two novel families, are involved in regulation of defence response and signal transduction.

S.175.4 The effects of rising temperatures on the foliar and reproductive traits of the snowbed specialist Salix herbacea L.

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Snowbeds are those environments in temperate high mountains that remain covered by snow until mid-summer, and where only a set of specialised species are able to thrive. Climate change represents a major threat for these ecosystems and species. The rising temperatures cause an earlier snowmelt, and snowbeds become then favourable environments for the more competitive species growing in the surrounding alpine grasslands. The way snowbed specialists respond to changing environmental conditions through their vegetative and reproductive performance may be crucial to face not only new abiotic stresses but also the higher competition exerted by grassland species. In 2017, we set four pairs of control and OTC (Open Top Chamber) plots in four Pyrenean study sites with presence of the dioecious dwarf shrub snowbed specialist *Salix herbacea* L., with the aim to induce a moderate increase of temperatures on this species. In year 2021, we collected from 3 to 5 *Salix herbacea*'s female ramets with mature fruits per plot, and we analysed a set of foliar and reproductive traits, among which leaf area, LDMC, SLA, viable seeds/fruit, total seeds/fruit or proportion of viable seeds. Preliminary results showed a site dependent trend towards a higher leaf productivity inside OTC, where we usually observed larger leaves with higher SLA and lower LDMC. Moreover, we also observed an increase of soil N in many of the OTC plots. Concerning reproductive traits, we found a trend towards a lower reproductive performance of *Salix herbacea* inside the OTC, with lower seed production and seed viability. Overall, the results suggest that increased temperatures have a fertilising effect in snowbeds, that enhance leaf productivity of *Salix herbacea*. However, the lower reproductive performance inside the OTC suggests that *Salix herbacea* may be approaching to its thermal fertility limit, which may pose a threat to its colonizing ability.

S.175.5 Comparisons of genetic diversity between congeneric plants elucidates vulnerability of species in the face of environmental change

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Environmental change, accelerated by anthropogenic activities, threatens many species and can be particularly challenging for rare plants with potentially limited capacity for migration and adaptation relative to more common species. Plant species differ dramatically in their prevalence in natural landscapes with some species characterized as rare due to restricted geographic distribution, low local abundance or habitat specialization. Several questions arise from these observed patterns, including ecoevolutionary causes and consequences of rarity. Our metanalyses of population genetic diversity, fitness and functional traits in rare and common congeneric plant species compared 252 rare species and 267 common congeners. Patterns identified for rare species included reduced population genetic diversity and fertilization efficiency, inbreeding depression and depressed fitness among other traits. Our recent comparisons of phenotypic plasticity and genetic diversity between rare and common congeners collected from natural populations elucidate rarity and vulnerability of an endangered riparian plant, *Pityopsis ruthii*, compared to more common congener, *P. graminifolia*. *Pityopsis* ruthii (Asteraceae) is a narrowly endemic perennial herb that grows in rocky crevices within a short distance along the banks of two rivers in Tennessee, USA. *Pityopsis graminifolia* is widespread within wooded savannahs, open grasslands and roadsides across the southeastern USA. Genetic diversity across the range of both species was estimated at nine putatively neutral microsatellite loci. Results indicated that *P. ruthii* exhibited reduced genetic diversity relative to its more common congener. These results were compared with other population genetic studies of field collected congeneric pairs of rare and common perennial herbaceous species in the southeastern USA and evaluated along with other measures of fitness. Overall, rare species exhibited lower levels of genetic diversity and limited capacity to adapt or migrate in response to environmental change, highlighting potentially significant vulnerability to future change.

S.175.6 Regulation of metal micronutrient homeostasis and toxicity by glutathione and phytochelatins in Marchantia polymorpha

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As with all living organisms, photoautotrophs face challenges in regulating metal homeostasis. Plants have evolved mechanisms to control the uptake and accumulation of both essential and non-essential metals, including chelation and sequestration by ligands such as phytochelatins (PCn). These thiol-peptides are synthesized by the phytochelatin synthase enzyme (PCS). PCn production is a widespread strategy for detoxifying harmful metal(loid)s, such as cadmium (Cd), mercury (Hg), lead (Pb), and arsenic (As). However, recent studies suggest that PCn and PCS roles may extend beyond detoxification of harmful metal(loid) s, to include responses to homeostatic needs and toxicity of essential metals, including copper (Cu), zinc (Zn), and iron (Fe). Yet, PCS function in early plant lineages remains largely underexplored. This study focuses on the PCS of the model liverwort Marchantia polymorpha L., namely MpPCS. Using a recombinant MpPCS protein, we confirmed that the MpPCS gene encodes a 530 amino acids polypeptide with a molecular mass of ~57 kDa. In vitro activity assays with Zn, Cu, and Fe demonstrated that MpPCS catalyzes a transpeptidation reaction, with activation effectiveness in the order of Zn, Cu, and, to a lesser extent, Fe. Gene expression and in vivo function of PCS were investigated under conditions of starvation, metal excess and physiological concentrations of Fe, Cu, and Zn, with a range of different exposure times. Metal-induced impacts were monitored through photochemical efficiency analysis using a chlorophyll fluorometer, offering insights into light absorption, trapping, photochemistry, electron transport, and PSII structure. Our results reveal that MpPCS plays a crucial role in detoxifying metal excess and regulating the homeostatic control of metal micronutrients. Thus, thiol-peptides such as glutathione and PCn have proven their efficiency in managing metal needs and detoxifying their excess. It is worth noting that PCn production appears to be regulated by enzyme activity rather than gene expression levels. Furthermore, this study highlights a potential novel extracellular detoxifying role for PCn and glutathione in M. polymorpha.

S.176 SPEEDING UP CONSERVATION IN POORLY KNOWN ORGANISM GROUPS – NEW APPROACHES TO BRYOPHYTE CONSERVATION. SESSION 2

S.176.1 A systematic review of the success of translocation experiments for bryophyte species.

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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 academic papers were filtered to 144 relevant articles (WoS = 138, EthOs = 4, ProQuest = 1, and Scorpus = 1), in which the subject and focus were assessed. From the remaining literature the estimated 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 144 journal articles there was a total of 133 bryophyte species, of which 82.7% were moss species and only 17.3% were liverworts (4.7x more moss species compared to 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.

S.176.2 Global assessments of bryophyte extinction risk

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Bryophytes are fundamental ecological components of peatlands and tropical forests and provide important services such as carbon storge and nitrogen fixation. About 20% of species worldwide might be threatened with extinction (Brummitt et al. 2015), yet fewer than 3 % globally have been assessed under IUCN Red List criteria. Of those that have, two thirds are threatened with extinction (Vulnerable, Endangered or Critically Endangered) or Near Threatened, a further 10% classified as Data Deficient, but almost one third already need updating. These results reflect bias in the species selected for assessment; instead, we have randomly selected and assessed 1500 bryophyte species from around the world, and show that 215 are at risk of becoming extinct, 68 were classified as DD and 725 are Least Concern; the rest are poorly known and left as Not Evaluated. The greatest number is found in Africa, followed by the American continent, Asia, and Australasia. 70% of threatened bryophytes are found in tropical forests, and the major threat is habitat loss. We hope this is a significant step towards extinction risk evaluation of bryophytes, but acknowledge its flaws. It is time-consuming, taxonomic knowledge may be lacking, publication is complex, information can already be out of date when it is published, species classed as Not Evaluated or Data Deficient due to taxonomic issues and/or poor recording are not adequately dealt with. New artificial intelligence techniques using morphological traits are being developed to indicate which species are pre-disposed to becoming threatened, tackling uncertainties and narrowing down the species to prioritize for IUCN Red List assessment while also speeding the process. However, collaboration between taxonomic specialists, ecologists and conservationists is paramount to fully estimate and understand the true number of bryophytes at risk, which and where they are, what threatens their survival and how to halt their extinction.

S.176.3 Breaking the homogeneity of the eastern North American boreal forest: identifying bryophyte biodiversity hot spots for conservation

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Conservation of bryophytes across boreal North America is complicated by the large spatial scale of the landscapes, the difficulty of access of many areas, and the relatively few bryologists studying this landscape. Consequently, the detailed habitat niche of many species are not identified, and many species are described as simply "boreal forest", which does not permit meaningful evaluation of the amount of habitat available for a given species, or even estimations of population sizes. Combining results from several large-scale field studies including nearly 1000 systematically sampled plots, we are able to determine patterns at different spatial scales from sites to regions that illustrate the heterogeneity of bryophyte species distribution patterns, but also of community diversity. Individual species showed clear patterns of frequency among ecosystem types and across landscapes, linked to their species traits and their ability to find the right microhabitat conditions with different combinations of macrohabitat factors. While alpha diversity within an ecosystem type varies with microsite richness as previously described, beta and gamma diversity varied across landscapes within ecosystem types, in association with topographical elements and regional gradients. Consequently, describing site, landscape and regional patterns in bryophyte communities allows us to refine the existing concept that boreal bryophyte species are inherently not rare because of the size of their potential biogeographic niche. With these results we are able to identify areas of diversity and high interest for conservation.

S.176.4 About disturbed landscapes and the unseen diversity of a miniature plant

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Habitat loss is the primary driver of species diversity decline. One effect of habitat loss is changes in the occurrence of new land cover (composition) and the spatial pattern of different land cover (configuration) at different scales across the landscape. Although the effects of changes in landscape composition and configuration (LCC) on species richness are increasingly well understood, little is known about the response of genetic diversity to such changes, particularly in non-vascular plants such as mosses. In this study, we used a multiscale approach to assess the effects of changes in LCC on the population genetics of the dominant asexual reproduction moss *Dicranum flagellare*. We sampled and SNP-genotyped 191 stems of *D. flagellare* from 12 old-growth boreal forest fragments in eastern Quebec, Canada. Our results indicate that genetic diversity (e.g., nucleotide diversity and allelic frequency) of *D. flagellare* is primarily negatively influenced by old forest reduction at large landscape scales (8-9 km radii; landscape composition). In addition, patch density (landscape configuration) of young forest areas reduces the genetic diversity of *D. flagellare* from old forest at small scales (2 km radius). We also found evidence of spatial genetic structure between and within populations depending on the old forest percentages (<40 % and >40 %) in the landscape. Our study shows that habitat loss at large scales and aggregation of recent disturbance areas at small scales affect the genetic diversity and spatial structure of non-vascular plants. Because of habitat loss at large scales, our results are useful for establishing logging thresholds that promote species conservation in landscapes with logging plans.

S.176.5 Bryophyte communities in broad-leaved forests in relation to substrate and environment along forest age chronosequence

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Broad-leaved forests are rich in bryophytes and provide microhabitats for many rare bryophyte species. Forest transformation to agricultural lands in the past and intensive forestry has led to fragmentation of broad-leaved forests in Latvia. Previous studies in broad-leaved forests mostly focused on bryophyte communities in old-growth forest stands, but there is still a lack of bryophyte studies in young and middle-aged forest stands. We studied bryophyte communities in 30 forest stands dominated by European ash (*Fraxinus excelsior* L.) and linden (*Tilia cordata* Mill.) in Latvia. The aim of the study was to evaluate the changes in bryophyte communities along the forest age chronosequence from younger forest stands to middle aged and old-growth forest stands in relation to substrate and environmental variables that affect bryophyte communities in each forest age class. The results of the study can be applied to determine the best conservation practices to enhance bryophyte species diversity in broad-leaved forests of different ages.

S.176.6 Spore germinability and longevity of four Sphagnum species along the gradient of altitude in the Changbai Mountains

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Elevation can strongly influence the vitality and longevity of sexual propagules (seeds and spores) of mountain plants. Germination behavior of sexual propagules at a certain elevation can vary with microhabitats. To date, little is known about how elevation and microhabitat differences in peatland ecosystems affect the germination and longevity of *Sphagnum* (peat mosses) spores. Here, we selected five peatlands in the Changbai Mountains along an elevation gradient (562-1472 m.a.s.l.) and conducted a three-year burial experiment with spores of four *Sphagnum* species. Our aim was to explore the effects of elevation and microhabitat on the germinability, dormancy percentage, and longevity of *Sphagnum* spores. We found that intermediate elevations were favorable for the germination of *Sphagnum* spores but unfavorable for dormancy maintenance and spore bank formation. Overall, *Sphagnum* spores had greater longevity in hollow microhabitats at low elevations and in hummock microhabitats at high elevations. Correlation analysis showed that spore germination of hollow species was more sensitive to temperature change than that of hummock species, with *S. squarrosum* demonstrating the clearest response to both temperature and precipitation changes. Our study suggests that elevation and habitat may interactively affect spore germinability and persistence of spore banks in peatlands. This highlights the importance of considering the difference of both elevation and microhabitat in vegetation restoration by using spore banks in degraded peatlands in the future.

S.177 SYSTEMATICS, FLORISTICS, AND CONSERVATION: FACILITATING DATA INTEGRATION TO PROMOTE SOUND SCIENCE. SESSION 3

S.177.1 Conservation Challenges and Priorities for Rafflesia (Rafflesiaceae) in the Philippines

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We present a synthesis of the taxonomy, distribution, and conservation status of *Rafflesia* 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 action. 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 of designated protected areas, underscoring the necessity for targeted conservation effort. Even within protected areas, some *Rafflesia* species face habitat degradation and tree cover loss. To ensure their conservation, 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 will be vital for achieving positive conservation outcomes. Furthermore, we identify strengthening legal frameworks and enforcement, habitat restoration efforts, regular monitoring, and raising awareness as essential steps towards the recovery of *Rafflesia* in the Philippines.

S.177.2 Mulshi Watershade Catchment, NWG, India: Floristic Assessment, impact analysis and Biodiversity Conservation

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The Western Ghats (WG) are a UNESCO World Heritage site in India and one of the world's recognized biodiversity "hot spots." It is shrunken by 25% over the past decades, degrading unique & valuable ecosystem. The physiography and climate of the NWG sustain tropical semi-evergreen to moist deciduous forest vegetation, which has enormous worldwide relevance for biodiversity conservation. Research area is biogeographically located in the Sahyadri mountains and spans multiple ecological zones such as the crestline of the Western Ghats, hill ranges, and a gently sloping section abutting the Deccan plateau, supporting numerous plant communities. Due to high rainfall, processes of soil formation are relatively faster than low rainfall areas on plains, though happening at geological time scale. All of these distinct physical characteristics have resulted in the formation of distinct habitats. Study area is centrally located in NWG at 18 °25′N to 18 ° 41′ N and 73 °20′ E to 73 °25′ E. which covers 240 sq. km in Pune district, Maharashtra. Extensive surveys reported 1592 flowering species from 776 genera and 162 families. Number of flowering species from dicotyledones were 1185 and 337 from monocotyledones, of which 150 are endemic species and more than 50 IUCN categorized. Study also documented 74 sacred groves with rich flora. In 2013, state government designated Tamhini as a wildlife sanctuary from Mulshi. Important water catchments includes-Mulshi, Temghar, Varasgaon and adjoining Pawana dam. Besides a private planned cities like- Lavasa, Sahara and Amby valley lies in the study area. Further, more hill cities are proposed in various parts of Mulshi threatening the biodiversity. Iconic' Western Ghat is facing a threat due to forest loss, encroachment & conversion. With this backdrop the documentation of floristic diversity, impact analysis and conservation of diversity was carried out for future ecosystem management.

S.177.3 Plagiarism in Botany and Plant Classification: Unearthing Ethical Dilemmas in Scientific Research

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Plagiarism in botany manifests itself in various forms, ranging from word-for-word replication of a text without due recognition to the appropriation of experimental data and research discoveries; the latter materializes most of the time in new combinations of nomenclature that eliminate and also obscure any original hip. However, this secondary result could also be an asset to use in a court of law in a civil case for plagiarism or copyright infringement, or both. The consequences of such unethical practices extend beyond academic misconduct because they undermine the foundations of scientific progress and thwart the development of accurate plant classification systems. It is no secret that plant classification within botany has played and will continue to play a fundamental role in expanding our understanding of the diverse plant kingdom, encompassing taxonomy, ecology, and evolutionary biology. However, in our haste to use phylogenetic data to validate, change, or generate new hypotheses about the evolutionary relationships within said plant kingdom, we are once again nullifying all scientific integrity with renewed acts of plagiarism; acts that unfortunately will be overlooked and little criticized and their perpetrators will feel covered, as happened in the past, under the false cloak provided by the international code of botanical nomenclature. The presentation explores specific instances of plagiarism within the large fern family Thelypteridaceae over the past 60 years, and its implications for the reliability of some taxonomic and genomic databases, as well as for regional floras; all of this hinders true progress in our understanding of the diversity and evolution of Thelypteridaceae. It also emphasizes the need for collective efforts within the scientific community to combat plagiarism in botany.

S.177.4 Assessing curatorial practices and improving access to natural resource data

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Herbaria represent vast repositories of data that are integral for conservation work and have the potential to contribute to research across biological disciplines. The value of herbaria and the data of the specimens within depends largely on the accessibility of this information and the accuracy of specimen identification, which in turn depends on curatorial work. Here, we assessed the current practices in curation and identification in a global survey for herbarium curators. The results were compared by the size of the responding herbaria, which were identified as small, medium, or large institutions based on the number of specimens held. This assessment found that there is a vast need for more global standards in herbarium curation. Curators of herbaria are limited by the resources they have available and the training in curation they have received. Curation practices are often varied within herbaria themselves and differ by size and geographical region of the herbarium. Curators each have different approaches to continually changing taxonomic information, and these discrepancies cause further challenges for the researchers using herbarium specimens and data. Here, we present the survey results, an overview of current herbarium curation practices under different resource limitations and propose a recommended workflow for curators with varying resource restrictions. Three levels of curation standards were identified, and a checklist associated with each level was developed for use in future curatorial work.

S.177.5 Advances in the systematics of genus Ternstroemia Mutis ex L.f. (Pentaphylacaceae s.l.): Towards a taxonomic monograph

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Ternstroemia Mutis ex L.f. has been, until recently, a poorly known genus from tropics and subtropics of America, Africa, Australia, and Southern Asia, with one species reaching Korean peninsula and Japan. In the last years a wealth of contributions spanning from classic taxonomy and biogeography to phylogenetic systematics have shown the existence of two main clades. As a product of a revision of literature and a new combined analysis, including DNA, morphology, and anatomy, major transitions within the genus can be traced along with morphologic shifts in flowers, related with pollination syndrome, and for the most part following a geographic structure. As a consequence of the new, updated phylogeny, the Asian genus *Anneslea* Wall. is transferred to *Ternstroemia*, resulting in an expanded circumscription where tribe Ternstroemieae becomes monogeneric. Six monophyletic clades can be distinguished, with type species (*Ternstroemia meridionalis* Mutis ex L.f.) embedded within a pantropical super-clade, still to be solved. Pistil morphology, especially in the stigmas are correlated with corolla, stamen, calyx and bracteole morphology, and all of them to certain anatomic features in leaves. After the present revision *Ternstroemia* Mutis ex L.f. is a genus with ca. 141 species, 87–103 of which are present in the Neotropics, ca. 49 in Asia (or its adjacent islands, including Papuasia), and 4 in Africa. A taxonomic overview of the genus is presented, including major areas of distribution and endemism, number of species per country, and species complexes. Future venues for systematic research in the genus are suggested, and a provisional species list is offered.

S.178 MOUNTAIN BIODIVERSITY AND EVOLUTION. SESSION 2

S.178.1 Origin and assembly of the alpine flora in the Northern Hemisphere

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The alpine biota above the treeline of the high mountains harbors unique floristic characters adapted to stressful environments and provides critical ecosystem services to our society. Yet, the origin, assembly pattern, and biotic interchange across different mountain regions remain enigmatic. Here, we investigated the diversification and assembly history of alpine biotas in the Northern Hemisphere aligning with paleoenvironmental changes. Our findings reveal that the alpine biodiversity is disproportionally assembled by colonization and *in situ* diversification. Alpine lineages initially diversified in the Tibet-Hengduan-Himalaya (THH) region as early as the Oligocene, playing a pivotal role as the primary source of alpine flora until it was overtaken by the arctic-boreal region by the Pliocene. The diversity of alpine plants in other major mountains of the Northern Hemisphere began accumulating since the early to middle Miocene, but significantly diversified until climatically suitable habitats expanded towards the end of the Miocene. Our study highlights the significant role of the THH region as both the cradle and museum of cold-adapted plants, with a subsequent increase in the importance of the arctic-boreal region.

S.178.2 Evolution and species diversification of seed plants in the Hengduan Mountains

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The Hengduan Mountains, also named Mountains of Southwest China (MSC), is one of the global biodiversity hotspots with the most extensively elevated surface on Earth, harboring around 10840 seed plant species from 1542 genera and 194 families. The origin and evolutionary history of the Hengduan Mountains flora remains unclear. We analyzed a time-calibrated phylogenetic tree of over 21000 seed plant species with 206 fossil calibrations based on 80 plastid genomic genes to investigate the evolutionary history and species diversification covering over 70% seed plant species from the Hengduan Mountains (7663 species from 1435 genera and 194 families). Our results showed that extant lineages (genera) in the Hengduan Mountains mainly immigrated from other floras and emerged after the early Oligocene. The rapid species diversification and accelerated diversification took place after the middle Miocene (ca. 15 Mya), especially in Pliocene (5.3–2.6 Mya) and Pleistocene (2.6–0.1 Mya), and the regional endemic species had the similar diversification pattern, which was likely driven jointly by mountain building, intensification of the Asian monsoon, Neogene climate cooling, and Quaternary climate fluctuations. The results of the molecular dating, species diversification, and ancestral area reconstruction analyses on nine representative genera of seed plants showed that the early lineages mainly immigrated from other floristic regions, and accelerated from early Miocene (ca. 20 Mya), and peaked in ca. 5 Mya, mainly from the Saharo-Arabian realm. The *in situ* speciation with an increased rate of in situ speciation started from the later Miocene-early Pliocene to Pleistocene, likely triggered by Hengduan Mountains orogeny, the intensified Asian summer monsoon, and Quaternary climate fluctuations.

S.178.3 Reconstructing the ecological and evolutionary assembly of the Alpine Flora

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Biodiversity genomics is an emerging field that leverages advanced sequencing technologies to analyze the genetic makeup of entire species assemblages in order to gain insights into their evolutionary history, adaptation, and ecological roles. I present the PhyloAlps project, which has now been running for over 10 years, and consisted in sampling and sequencing all vascular plant species of the Alps, a biodiversity hotspot harboring 20% of the European flora. This initiative has now expanded onto the flora of the arctic realm and other mountain ranges through the work of companion projects, thus providing an ever-growing, unique genomic resource aiming toward a comprehensive genomic characterization of the arctic-alpine flora. I finally present some use of these data to study the phylodynamics of alpine plant clades, the delimitation of novel species and the metabarcoding of sediment-cores time-series.

S.178.4 Genetic diversity assessment of Juniperus seravschanica populations from Central Asia

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Juniperus seravschanica Kom. is a widespread and important tree species in Central Asia, and grows extensively in the mountain ranges of Oman to Uzbekistan, Kyrgyzstan, and Kazakhstan. It is crucial in forming shrub-forest massifs in mountainous regions, contributing to soil drainage and stabilization at medium to high altitudes. To gain a comprehensive understanding of the current status of *J. seravschanica* resources and develop effective conservation strategies, a thorough study of the species' genetic diversity and population structure was conducted. To assess genetic diversity and population structure leaf samples were collected from 15 *J. seravschanica* populations across Uzbekistan, Kyrgyzstan, and Kazakhstan. Utilizing 11 polymorphic simple sequence repeat (SSR) markers genetic diversity parameters such as the number of alleles, number of effective alleles, percentage of polymorphic loci, and Nei's genetic diversity index were evaluated. Nei's genetic diversity index for the *J. seravschanica* populations averaged 0.450, ranging from 0.407 to 0.566. The AMOVA indicated that 90.3% of the total genetic variation was distributed within populations, suggesting a high level of genetic diversity within each population. Gene flow calculated using alleles from all populations, was estimated at 4.654. Population structure analysis revealed weak clustering among the studied populations, confirming the AMOVA findings. The results of this study provide valuable insights into the genetic diversity and population structure of *J. seravschanica* in Central Asia. The high genetic diversity within populations suggests that the species has a strong capacity to adapt to environmental changes. These findings can be effectively utilized to develop conservation strategies for *J. seravschanica*, ensuring the long-term sustainability of this important tree species in Central Asia.

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S.178.5 The signature of mountain uplift on biogeography, trait evolution, and phylogenomic complexity of the Andean flora

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The Andean mountains of western South America are one of the World's most species-rich biodiversity hotspots and are home to almost 15% of all angiosperm species. Much of this diversity originated in concert with relatively recent mountain uplift and the resulting landscape changes, including high levels of habitat heterogeneity. In this talk, I discuss how Andean uplift has left its mark on the evolution of its flora using *Freziera* (Pentaphylaceaceae) as a primary example. *Freziera* is an Andean-centered clade of 75 species of trees and shrubs that diversified during the late stages of Northern Andean uplift in the last 12 million years. Subsequently, *Freziera* dispered into the Central Andes repeatedly. Across the cloud forest habitats that it can now be found, it displays an impressive diversity of leaf morphology, which we demonstrate is connected to local environmental conditions (especially precipitation and seasonality). Finally, *Freziera*'s high levels of phylogenomic complexity can be attributed, in part, to high diversification rates and short times between speciation and introgression— both scenarios whose impacts were heightened by Andean uplift. Throughout the talk, comparisons between *Freziera* and other Andean plant clades will highlight generalities—and idiosyncracies—of Andean plant evolution.

S.179 PHYLOGEOGRAPHY

S.179.1 The role of hybrid zones on the phylogeography of two willow species pairs (Salix L.) in the European Alps

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The geographic distribution of genetic lineages is highly impacted by climate fluctuations. Cold-adapted plant species have survived the last glaciations on nunataks within the glaciated area of the European Alps, unglaciated areas at the periphery of the ice sheet, in the marginal lowlands, or in other mountains of the European Alpine Systems that have been less glaciated. Following the last glacial period, cold-adapted species started to spread to newly available areas. The colonization is influenced by species-specific factors as well as evolutionary processes like hybridization and is still on-going. Two closely related but previously isolated species that merge their marginal ranges during recolonization create a secondary contact zone where hybridization can occur and potentially block the recolonization. Using Restriction-Site-Associated DNA sequencing, morphometrics, species distribution modelling and fine-grained environmental data, we aim to identify potential glacial refugia and recolonization routes of two willow (*Salix* L.) sister species pairs that show vicariant distributions and secondary contacts in the European Alps. We aim to characterize the hybrid zones genetically, morphologically, and ecologically to test the hypothesis that hybrid zones influence biogeographical patterns of parent species. Different potential glacial refugia were found in the southern European mountain systems or alpine periphery and suggest recolonization of the Alps from both eastern and western marginal areas. Hybrid zones show patterns of introgression rather than hybrid speciation and extend over several hundred kilometers. A discrepancy between phenotype and genotype could have resulted from backcrossing and segregation of later generation hybrids. Suitable environmental conditions were found for each species beyond their current distributions. Ecological relevees of secondary contact zones indicate high ecological niche similarity with parents but also niche expansion. No apparent reduction of fertility of hybrids was observed in the field. Altogether, our results support the hypothesis that hybrid zones can block the recolonization of parents.

S.179.2 Phylogeographic insights to delimitate Mediterranean protected endemic species L. cuspidatum evolving in sympatry with close taxa

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While the protection statute of threatened plants is designed at species level, delimitating plant species is a challenge for conservation biologists, especially for diversified taxa evolving in sympatry. Species delimitation exist at the interface of population genetic and phylogenetic analyses. Here, we aimed to delimitate species to question the species statue of a rare and protected taxa in the *Limonium confusum* group. *Limonium cuspidatum* (Delort) Erben has a restricted range geographical distribution from Narbonne to Marseille in south France. Morphological descriptors are not sufficient to clearly distinguish this taxon from three others taxa cited in the same environments in the south of France: Limonium confusum (Godr. & Gren.) Fourr. 1869; Limonium legrandii (Gaut. &Timb.-Lagr.) Erben, 1978; Limonium densissimum (Pignatti) Pignatti, 1971, all belonging to the *Limonium confusum* group. To understand the evolutionary history of these populations and taxa belonging to Mediterranean lineage of *Limonium* genus, we analysed a comprehensive sampling of populations of *L. confusum* (23 from France, 8 from Spain) and 29 Mediterranean *Limonium* species by combining population genetic and phylogenetic approaches. First, using population genetic analysis of 31 populations of *L. confusum* with 12 Simple Sequence Repeat loci, we clearly identified three genetic groups. A first group includes Iberian-Provençal population, from the salty mud of the Bouches-du-Rhône (France) to the Tarragona and Ebro Delta region (Spain). The second group includes populations of the salt marshes located in the Languedoc coast between Leucate and Vendres (France). The third group includes three disjunct populations which however share similar ecological conditions. Second, we selected samples based on genetic and geographic origin and added representative species of Mediterranean Lineage of *Limonium* genus for phylogenetic analysis using plastid DNA variation. We expect to give insights for delimitating species of *L. confusum* and to define populations, which have to be protected in the future.

S.179.3 Phylogeography of Magnolia Sect. Macrophylla in Mexico: insights into its origin, diversification and evolutionary history

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In Mexico there are approximately 40 species of the genus *Magnolia* (Magnoliaceae), five of them included in the Sect. *Macrophylla*: *M. alejandrae*, *M. dealbata*, *M. nuevoleonensis*, *M. rzedowskiana* and *M. vovidesii*. Although most of these are threatened and some have sociocultural importance, its evolutionary history and the biogeographical events underlying their diversification and distribution are still unknown. In the present study, we analyse sequence data from four cpDNA regions (trnH-psbA, ORF350, trnK-matK and trnL-rpl32) of

Magnolia species Sect. *Macrophylla* distributed in Mexico in order to: (1) infer their phylogenetic relationships, (2) assess its genetic diversity and population structure, (3) evaluate possible signatures of demographic expansion and (4) infer its temporal and geographical origin. Bayesian inference and maximum likelihood analyses corroborated the monophyly of Sect. Macrophylla. Interspecific relationships were not resolved and *M. alejandrae* and *M. nuevoleonensis* were recovered as a single monophyletic group. The highest genetic diversity was found in populations of *M. dealbata*, *M. alejandrae* and *M. nuevoleonensis*. Bayesian Skyline Plots and mismatch distribution analyses indicate that, overall, the studied populations are in a process of demographic expansion, particularly, the populations of *M. alejandrae* and *M. nuevoleonensis*. Analyses of genetic and phylogeographic structure indicate that geography has played a fundamental role in shaping the genetic structure of *Magnolia* Sect. *Macrophylla* in Mexico. Based on molecular clock analyses, initial diversification of Sect. *Macrophylla* is estimated to have occurred ca. 16.1 Ma, whose ancestral area probably included the Sierra Madre Oriental, Sierra Madre del Sur and Trans-Mexican Volcanic Belt. Given that the origin of the Section broadly coincides with the climatic changes of the middle Miocene and with the emergence of the Trans-Mexican Volcanic Belt, these events could have played a fundamental role in the diversification of *Magnolia* Sect. Macrophylla in Mexico.

S.179.4 Phylogeographical patterns in Peruvian coastal desert Oxalis reveal two independent lineages

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The genus *Oxalis* is a rather notable and constitutive plant group in Peruvian lomas formations, displaying conspicuous traits to cope with aridity. The flora of this seasonal ecosystem is highly endemic, much like its inhabiting *Oxalis* members, thus placing this genus as optimal for testing evolutionary and biogeographic hypotheses. While elucidating the diversity and distribution of *Oxalis* along the lomas extension (latitude from 6 ° to 18 ° S), a total of 11 species were identified, largely showing connections with western Andean slopes. Two main lineages were identified and further examined, corresponding to succulent herbs in section *Carnosae* (subg. *Oxalis*) and sub-shrubs in section *Thamnoxys* (subg. *Thamnoxys*). The phylogenetic reconstruction revealed differing evolutionary stories for each lineage, directly linked with alternative adaptive strategies and geographical colonizing patterns. This study also allowed filling information gaps related to understudied and endemic taxa, that, in addition to the non-monophyletic arrangement detected in some endemic species, exposes the need for a taxonomic update in the genus. Furthermore, a set of genomic resources, such as plastidial markers and nuclear SSRs, were generated for future phylogenetic and population genetic studies, mainly centered in the broadly distributed sect. *Carnosae*. Lastly, these results provide valuable insights in the understanding of the origin of plant diversity in Peruvian coastal lomas.

S.179.5 Insights into the evolutionary and biogeographic history of the Carduus-Cirsium group in the African Sky-Islands

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The Afromontane archipelago consists of isolated humid and temperate areas on the highest mountains in Tropical and South Africa. This biome hosts a unique flora characterized by a high proportion of endemic species. Despite its uniqueness, the Afromontane flora is understudied from an evolutionary and biogeographic point of view. Several afromontane endemics belonging to subtribe Carduinae (Asteraceae) have traditionally been ascribed to the *Carduus-Cirsium* group, based on superficially similar morphologies. To investigate their evolutionary origin, we applied the Hyb-Seq approach on >500 samples comprising all genera of subtribe Carduinae. We recovered sequences for >1000 conserved orthologous nuclear loci plus the complete plastome, and conducted phylogenetic inference using concatenated and coalescence-based approaches. The Afromontane species constituted three distinct evolutionary lineages, one of them not even belonging to the *Carduus-Cirsium* group. Given the evolutionary and morphological distinctiveness of these three lineages, we propose three new genera, all endemic to the Afromontane flora: *Afrocarduus*, *Afrocirsium* and *Nuriaea*. Building on our highly resolved phylogeny, we conducted ancestral range estimation analyses. Our results indicate that these three endemic genera originated after two independent long-distance dispersals from the Mediterranean region. The first occurred during the Middle Miocene and resulted in *Nuriaea*, and the second occurred in the Late Miocene and gave rise to *Afrocarduus* and *Afrocirsium*. The current diversity within the three genera mainly results from speciation during the Pliocene and Pleistocene. The increased orogeny in Tropical East Africa during these periods, combined with the dramatic Pleistocene climate oscillations, likely fueled the diversification.

S.180 MORPHOMETRICS

S.180.1 A machine learning approach to morphometry of Armeria (Plumbaginaceae) in peninsular Italy

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In the contemporary era of genome-wide phylogenomic analyses, the significance of morphology in Botany is crucial but often overlooked. Morphometry emerges as a method for scientifically and statistically handling morphological data, particularly in intricate groups like *Armeria* (Plumbaginaceae) in peninsular Italy, which has undergone multiple taxonomic revisions without yielding conclusive outcomes. In this study, we measured 27 features from 587 herbarium specimens across 34 populations spanning across the Apennines. The specimens encompass the *A. arenaria*, *A. denticulata*, *A. canescens*, and *A. macropoda* complexes for a total of 11 taxa, 10 of which putatively endemic to Italy. Since *A. gracilis* has been always traditionally related to the Balkan *A. canescens*, we also included the latter species for comparative purposes. To analyze the data, we employed two innovative machine learning approaches. Dimensionality reduction was achieved using a novel non-linear technique called UMAP (Uniform Manifold Approximation and Projection). Additionally, Gaussian mixture models (GMM) were used to test alternative grouping hypotheses. The 3D - UMAP analysis along the Italian peninsula reveals six main groups, i.e., from northern to southern Italy: *A. arenaria*subsp. *praecox*, *A. arenaria* subsp. *marginata*, *A. denticulata* complex (*A. denticulata* and *A. saviana*), two groups within the *A. canescens* complex (including also *A. gracilis*, *A. garganica*, and two populations referred as '*A. macropoda*'), andthe *A. macropoda* complex (*A. aspromontana*, *A. brutia*, *A. macropoda* s.str., and a population from the Pollino Massif referred as '*A. gracilis*'). Bayes factor calculations, fitting a supervised GMM, support the recognition of these six groups over other grouping hypotheses, constituting a comprehensive overview of our taxonomic exploration. Seed morphometric, karyological, and phylogenetic studies are ongoing and will be integrated into a conclusive taxonomic study.

S.180.2 Morphology 2.0 - discovery through 3D imaging and big data of cacao and its relatives (Malvaceae: Byttnerioideae)

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We are beginning to realize the potential for discovery using big data and biodiversity archives. As 3-dimensional (3D) imaging with micro-computed tomography (micro-CT) and photogrammetry becomes more common, workflows to streamline processes and develop novel studies using large-scale digital imaging are needed, especially for botanical specimens in a vertebrate-focused field. We present a case study on the 3D pollination biology of *Theobroma cacao* and its relatives (Malvaceae: Byttnerioideae) that highlights discoveries possible through combining cutting-edge imaging modalities and big data, which we call Morphology 2.0. Despite the importance of chocolate, little is known about its specialized pollination (likely by micro-dipterans and/or -hymenopterans) and even less about other Byttnerioideae. First, we used micro-CT, 3D geometric morphometrics (GMM), and scanning electron microscopy to precisely quantify plant-pollinator geometry, functional size limits for pollinators, and floral reward structures in cacao. Then, we extended our methods to *Ayenia euphrasiifolia*, an endemic of endangered Florida pine rocklands. To gain baseline data on putative pollinators, we used a GoPro camera trap (modified for subjects <1cm), 3D imaging with micro-CT and DSLR camera photogrammetry, then 3D GMM analysis. After refining methods for cacao and *Ayenia*, we applied them to other Byttnerioideae (*Guazuma*, *Herrania*, *Byttneria*, *Commersonia*). Processing and analysis pipelines are open source and available on GitHub, CT datasets on MorphoSource, and 3D models for outreach on Sketchfab. By combining lab and field-based imaging technologies, we developed a novel tool for studying pollination biology of an important crop. Our 3D imaging also enabled high resolution comparative study of one of the nine major Malvaceae subclades, characterized by unusual floral morphology not captured in 2D. Moreover, we produced a large annotated imaging dataset (N>200) that will be repurposed to train computer vision models that automate 3D shape prediction and digitization of botanical specimens.

S.180.3 Innovative multi-scale phenotyping approach on Amaranthus spp. leaves reveals contrasting differentiation traits at young stage

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Imaging analysis can aid in phenotyping plant morphological traits at different scale levels, with options ranging from microscopy images to remote sensing acquisitions. Through this approach, it is possible to gain a minimally invasive understanding of physiological and structural trait diversity, as well as the relationship between plants and the environment. Much attention has already been paid towards the high phenotypic plasticity of the *Amaranthus* genus, as it includes highly invasive weed species harmful to summer crops. The identification of morpho-anatomical traits in amaranth leaves at early stage could be beneficial in gaining a greater understanding of the relation between their structural characters and their performance in the agroecosystem. In this work, we applied an innovative multi-scale phenotyping approach on single leaf morphometric traits of four *Amaranthus* species (*A. hybridus*, *A. palmeri*, *A. retroflexus* and *A. tuberculatus*) by processing digital images of intact leaves and confocal reflection microscopy acquisitions on adaxial surface imprints. The analysed morphometric variables belonged to three groups: macroscopic leaf traits, evapotranspiration-related traits and microscopic traits related to the leaf surface. The results evidenced that different investigation levels contribute to revealing species-specific characters even at a juvenile stage, which is crucial for plant development and the establishment of competition. In detail, some variables concerning macroscopic and evapotranspiration-related traits were those that best discriminated *A. tuberculatus* from the other three species. The approach proved to be an effective, reliable, and low-impact procedure for describing the functional characteristics of phylogenetically related species and quantifying traits associated with taxonomy and biodiversity studies.

S.180.4 Morphometric analysis of freshwater estuary endemic Bidens (Asteraceae)

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The unusual ecological conditions provided by freshwater estuaries, namely, high rate of sedimentation of nutrient rich minerals, twice-daily tides, waves, and ice-scouring, have induced the evolution of a highly specialized flora containing several endemics. The origin of this flora appears to be recent, dating at most to the last deglaciation 10,000-12,000 years ago, which is probably the cause of relatively minor morphological differentiation of most of the endemic taxa. Unfortunately, freshwater estuaries also are heavily urbanized and industrialized, contributing to habitat degradation and loss. Endemic *Bidens* taxa are an important component of the freshwater estuaries of Northeastern America and offer a great insight into understanding the recent evolution of the North American estuarine flora. Many of these endemics are hypothesized to have originated from hybridization and polyploidization (allopolyploidy). Unfortunately, taxonomic uncertainties of many of the *Bidens* taxa of Northeastern America are hampering conservation action. For instance, unclear morphological limits between species frequently result in misidentifications, which can lead to over- or under-estimation of the frequency of threatened taxa. We conducted a morphometric analysis to test species delineation, explore the relevance of new traits for identification, and test hybridization hypotheses. Most of the dissimilarity between species is correlated to flower and fruit traits, while vegetative characters show great lability that is largely uncorrelated with taxonomic boundaries except for species with composed leaf. We have obtained clear delineation between *B. eatonii* and *B. infirma* and between *B. tripartita* and *B. comosa*, species for which taxonomic status until this day were still uncertain. Even though more sampling is needed to better assess the full range of phenotypic variation of each species, the recognition of *B. infirma*, an endemic of the St-Lawrence estuary, Canada, would have a great impact on conservation action.

S.181 SYNANTHEROLOGY RELOADED: RECENT ADVANCES AND THE FUTURE OF EVOLUTIONARY STUDIES IN COMPOSITAE. SESSION 1

S.181.1 Dancing with Thistles

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Our research in tribe Cardueae was a challenge from the beginning for several reasons. Field collections faced many challenges due to the geographical distribution of thistles in complicated places. When we started investigating the group, our Botanic Institute in Barcelona was a very small research center with limited resources for studying such a large tribe. Obtaining an accurate classification was particularly challenging due to the thistle-like architecture of many genera, which is shared by many unrelated genera of the tribe. Development of molecular methods, from single-region DNA sequencing in the nineties to high-throughput sequencing in recent times, provided the tools for unraveling the true phylogeny of the tribe and allowed us to define a new classification. The new subtribal scheme in twelve subtribes was anticipated by morphological evidence, and molecular data confirmed that the system is robust. This presentation summarizes thirty years of wrestling with this fascinating group of plants.

S.181.2 An updated subtribal classification of Compositae tribe Anthemideae based on extended phylogenetic reconstructions

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An updated subtribal classification of the *Compositae-Anthemideae* is presented based on gene- and species-tree reconstructions considering sequence variation from the plastid (cpDNA *ndhF, trnL-trnF*) and nuclear genome (nrDNA ITS1-5.8S-ITS2, ETS; nDNA dual specificity phosphatase *DSP*, plus-3 domain-containing protein of the vernalization independence 5 complex *VIP5*, major facilitator superfamily protein of the Nitrate Transporter1/Peptide Transporter *NPF3.1*) for 113 of the 115 hitherto accepted genera of the tribe. As a result, six subtribes were newly circumscribed [i.e., *Anthemidinae* (including also *Xylanthemum*), *Artemisiinae* (including also *Hulteniella, Lepidolopha, Opisthopappus,* and *Tridactylina*), *Glebionidinae* (including also *Otoglyphis, Endopappus,* and *Nivellea*), *Handeliinae* (including *Cancrinia, Polychrysum,* and excluding *Xylanthemum*), *Leucantheminae* (including also *Daveaua, Heteromera,* and *Otospermum*), *Leucanthemopsidinae* (including *Phalacrocarpum*)]. Additionally, five unigeneric subtribes (i.e., *Brocchiinae, Inulantherinae, Lepidophorinae, Lonadinae, Vogtiinae*) were described as new to science due to their phylogenetically isolated positions, resulting in 18 subtribes accepted presently for *Compositae-Anthemideae*. A focal subtribe of a more detailed phylogenetic analysis is based on the W Mediterranean genus *Vogtia* Oberpr. & Sonboli that comprises two species, i.e., *V. annua* (L.) Oberpr. & Sonboli and *V. microphylla* (DC.) Oberpr. & Sonboli. To infer the phylogenetic position of this subtribe the complete chloroplast genomes of the two species and seven other representatives of additional subtribes of the Anthemideae were sequenced using long-range PCR and Oxford Nanopore technology (MinION) and subjected to maximum-likelihood tree reconstructions. The phylogenetic analysis confirmed the placement of Vogtiinae as sister to subtribes Anthemidinae+Matricariinae. Results of additional analyses concerning the phylogenetic relationships and the subtribal status of the monogeneric orphan genera *Brocchia, Lepidophorum,* and *Lonas* will be also presented.

S.181.3 Exploring the future of Compositae: advances in genomics, transcriptomics, and functional genetics

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Asteraceae or Compositae comprise 10% of all angiosperm species and include numerous species of economic, medicinal, and industrial value. Despite this, relatively few large-scale genomic resources exist for the family, especially given its size/diversity, which limits our ability to understand the evolution of this fascinating family and to link genes to phenotypes. Moreover, studies of genomic and evolutionary mechanisms that have driven the success of Asteraceae have been hampered by the lack of a well-resolved phylogeny. We have used a phylogenomic framework to fully resolve the Asteraceae backbone. This work supported a late Cretaceous origin followed by explosive diversifications that resulted in the family's 30,000+ extant species. Recently, our group has been working toward enhancing available resources for the family with genomic and transcriptomic resources for diverse species, including several key outgroups. We are also addressing the outstanding need for genome editing tools by working toward developing novel approaches in Asteraceae. These resources will be made freely available to enable comparative and functional genomics, as well as crop improvement efforts in the broader community. This work provides an integrative framework for future studies aimed at understanding the role of the macroevolutionary patterns and processes that generated the enormous species diversity of Asteraceae.

S.181.4 Anatomy of Asteraceae: methodological advances for an old science

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Plant anatomy used to be considered an ancient science, or a simple tool for answering equally simple questions. Thanks to recent advances in the molecular era, the understanding of systematics of the large and complex family Asteraceae has greatly advanced. In this process, plant anatomy has re-emerged as an important ally, enabling the investigation of complex evolutionary questions, answering new and old taxonomic questions, and, jointly with plant molecules, providing a wide range of data for the arsenal of new, species-level information, in addition to helping detect sources of secondary metabolites, through the integration of histochemistry and phytochemistry. The present work aims to address the most recent plant anatomy techniques used in investigations in the Asteraceae, focusing on methodological advances in the following sectors: evolutionary studies of morphoanatomical diversity; morphoanatomy to answer complex taxonomic questions; integration of anatomy and phytochemistry through histochemistry and *in situ* hybridization; and new developments in investigations using Transmission Electron Microscopy. Thus, this proposal intends to show botanists that this ancient science persists and thrives, uniquely contributing to increasing our knowledge of plants.

S.181.5 The Compositae in the Plant and Fungal Tree of Life

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The Compositae (or Asteraceae) are one of the largest flowering plant families with ca. 1,630 genera and ca. 24,700 species. They are distributed worldwide and display an amazing morphological diversity. Despite the challenging size of the family, molecular phylogenies have recovered a fairly consistent tribe-level backbone, which resulted in the current classification with 16 subfamilies and 51 tribes. However, up to now, phylogenomic studies have included less than 16% of the generic diversity of the family. Here, we present a robust phylogeny including ca. 90% of the genera of Compositae and all subtribes but one, based on combined data from two different probe sets (Angiosperms353 and Compositae1061). The monophyly of the family is challenged by the position of Calyceraceae as sister group of Barnadesioideae in some of the inferences. The evolutionary relationships between the main lineages are mostly in agreement with previous phylogenomic studies, except for Hecastocleidoideae emerging as sister to the clade Gochnatieae + Wunderlichieae + *Cyclolepis* and Tarchonanthoideae as sister group of Carduoideae (not Dicomeae). A few tribes are polyphyletic under their current circumscription (Wunderlichieae, Neurolaeneae, Bahieae, Madieae). The evolution of Compositae is marked by at least ten whole genome duplication and numerous hybridisation events, which may explain the incongruences found between different datasets and methods of phylogenomic reconstruction (e.g., coalescent-based Astral vs. concatenated supermatrix). This phylogeny will allow new insights about morphological evolution, diversification, and biogeography of the Compositae.

S.181.6 The Global Compositae Database: challenges and opportunities

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Online taxonomic databases are fundamental resources for a post-2020 framework for the Global Strategy for Plant Conservation, particularly Target 1 of that effort – “an online flora for all known plants.” Launched in 2019 as a revitalization of the Global Compositae Checklist, the Global Compositae Database is a freely accessible, expert-curated, online taxonomic database of all names for the largest angiosperm family Compositae (Asteraceae) that is generously supported by the World Register of Marine Species (WoRMS) and maintained by taxonomic specialists from The International Compositae Alliance (TICA). The team behind the data curation includes researchers from different backgrounds, with taxonomic expertise across the many tribes currently recognized in the family. This is a formidable task, involving almost 170,000 names for ca. 33,000 accepted species, and so TICA is actively recruiting additional taxonomic specialists i. The development of this database highlights the importance of collaboration and is being coordinated, in part, through a larger collaboration with the World Flora Online, for which TICA serves as the Taxonomic Expert Network (TEN). The database is hosted on the WoRMS platform, accessible via the TICA website (www.compositae.org), has a friendly interface, and provides tremendous flexibility in terms of editing and adding taxonomic data. Current challenges include a lack of specific resources to curate the database, and a general shortage of expert taxonomists. Among the groups in Compositae with most up-to-date information are the basal grade of the family, and various elements of the subfamily Asteroideae. A broader geographic participation of TICA members and taxonomic specialists, together with a series of workshops aimed at facilitating the access and usage of the database, will help increase momentum in advancing this important resource.

S.182 PRIORITISE, PLAN, ACT AND MONITOR - PROMOTING AN INTEGRATED APPROACH TO THREATENED TREE CONSERVATION

S.182.1 Strengthening the population of threatened tree species in the Colombian Caribbean region

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The Colombian Caribbean region houses three of the most threatened ecosystems and areas in the country: the tropical dry forest, the mangrove forests, and the Sierra Nevada de Santa Marta. Among the main threats are non-sustainable cattle farming, unplanned urban development that causes deforestation, and climate change. Aiming to strengthen the population of Caribbean threatened species, *Pachira quinata (VU), Libidibia punctata (VU), Handroanthus coralibe (VU), Clavija sanctae-martae (VU), Aspidosperma polyneuron (EN), Pelliciera benthamii ex. Pelliciera rhizophorae (VU),* and *Pterocarpus acapulcensis (VU), studies in their distribution, propagation and phenology were made.* No actions to conserve and strengthen their populations have been reported in the last decade, and the non-scientific public usually does not know their conservation status and importance. Few places that host the native population are under conservation status (public or private). However, there are currently no actions focused on their conservation and propagation in nurseries at a large scale. The Cartagena Botanical Garden's science and horticulture teams have worked together to strengthen the population of the previous mention native threatened tree species. The Garden strives to conserve, restore, and enrich the ecosystems through long-lasting actions involving local communities. Several field trips to coastal and middle-elevation localities have allowed seed collection, phenological annotations and the recognition of potential planting areas. The Garden has successfully established a partnership with local nurseries, one in the northern Caribbean municipality of Colombia, La Guajira, and the other in Magdalena, where the vulnerable endemic to Colombia specie, *Clavija sanctae-martae*, is the priority. Suitable landowners and changes in land use for planting actions are presented as one of the most challenging aspects. The result includes more than 10,000 planted plants, established propagation protocols, distribution niche models and regional capacity building.

S.182.2 Natural drivers leading Conifers to extinction

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Currently, over 28% of species are at risk of extinction, which could rise to 50% by 2100 since the rate of extinction has been particularly dramatic for the last 50 years. Conifers stand out as a highly endangered group, with a percentage of threatened species of *ca.* 34%. Reversing the situation is crucial since coniferous species, which are mostly trees, constitute key pieces for more than 39% of the world's forests and for the provision of ecosystem services globally. Deforestation and other man-made hazards, including climate change, threaten conifers which, like other gymnosperms, are also doomed to extinction due to natural causes. In this context, we explore intrinsic or natural traits (both biological and ecological) leading conifers to extinction in order to support decision-making on biodiversity conservation. Furthermore, we delved into the largest conifer family, *Pinaceae*. For this, we downloaded from the IUCN Red List database all the 610 species from the *Pinopsida* Class, assigning the global Red List category. For each species we also compiled traits related to altitude, adult plant size, and seed size. Moreover, for the *Pinaceae* family (225 species), we collected traits about leaves, seed cones, pollen cones, and seed wing, among others. Then we assessed the relationship between extinction risk (with values ranging between 1 (LC) and 5 (CR)) and traits, finding that the most threatened conifers are smaller in size, have smaller seeds, and inhabit a narrow altitudinal range at mid-mountain. Pinaceae showed similar trends, but the most endangered species had heavier seeds and smaller leaves in this case. Our results could guide conservation efforts for these plants custodians of an ancient and long evolutionary history since species with certain identified traits could be more vulnerable to moving to a higher threat category if no action is taken.

S.182.3 Tools and approaches for identifying and filling gaps in knowledge for the conservation of exceptional tree species

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Exceptional species cannot be conserved in conventional seed banks and will require other approaches for long-term, ex situ conservation. Cryobiotechnologies can be harnessed to preserve exceptional species, but currently these methods are not being implemented on the needed scale. Our recent analysis of the literature has shown that there are significant gaps in knowledge of cryopreservation and the supporting in vitro technologies in their application to exceptional species, particularly with exceptional tree species. While a high proportion of exceptional species are trees, a much lower proportion of trees are represented in both the cryopreservation and in vitro literature, with a particular gap in tropical trees. Filling these gaps and scaling up application will require developments in both science and technology. Currently, developing cryopreservation and in vitro protocols is primarily an experimental process, and information and tools are needed to develop greater predictability and efficiency Deeper analyses and understanding of reported research are needed, and the creation and analysis of large datasets of information could facilitate this. The Comparative In Vitro Database and the Comparative Cryopreservation Database will be introduced as platforms for these data that will align them with taxonomic, morphological, and climatic data to evaluate patterns and move toward the goal of predictability in developing new protocols. The companion Media Comparison Tool has also been developed, which provides rapid visualization and comparison of the components of tissue culture media as a way of analyzing past research and selecting or developing new formulations for species new to in vitro culture. These tools should both help identify more specific information gaps and help prioritize research for more efficiently applying cryopreservation and in vitro technologies for the ex situ conservation of exceptional tree species.

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S.182.4 Unveiling the extinction risk of Brazilian trees

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Brazil is the epitome of plant diversity and champion the global ranking of tree species' richness. However, this astonishing diversity confronts a looming crisis as human-induced activities intensify. Rampant habitat conversion for agriculture and cattle ranching, coupled with extensive overexploitation, imperils Brazil's tree flora. With great responsibility to protect its irreplaceable natural heritage, Brazil has recognized that assessing species' extinction risk is a vital step in setting up effective conservation strategies. The Brazilian National Centre for Plant Conservation (CNCFlora), from Rio de Janeiro Botanic Garden Research Institute (JBRJ), is designated nationally and internationally as the Brazil's plants Red List Authority and adopts the standards and procedures recommended by IUCN for at-risk species detection. Driven by initiatives tailored to deliver conservation assessments of trees, such as the Global Tree Assessment (GTA) from Botanic Gardens Conservation International (BGCI), CNCFlora/JBRJ has conducted full IUCN conservation assessments of over 3,851 Brazilian trees between 2015-2023. Our results show that 37% (1,276) of the assessed tree species are Threatened (187 as CR, 794 as EN and 295 as VU). NT and LC categories were assigned to 1,943 species, while 633 species were deemed as DD. Brazil has thousands of threatened endemic trees, and while advances in detect at-risk plants increased in recent years, only two native tree species have species-specific national Conservation Action Plans in-place. Most threatened trees in Brazil are found within two global biodiversity hotspots (*Mata Atlântica* and *Cerrado*), and in the Amazon, where selective logging is pressing timber species towards extinction. A comprehensive evaluation of Brazil's entire tree diversity is imperative to strategically guide interventions and prevent irreversible losses, emphasizing the immediate need to extend conservation measures to safeguard endemic trees for the enduring preservation of Brazil's tree biodiversity.

S.182.5 A collaborative programme to protect, conserve and enhance the natural capital of the Mexican forests

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Mexico is a megadiverse country, hosting 23,314 species of vascular plants, 40% of which are endemic. Its ecosystems range from arid to wet and tropical to temperate. It is rich in cultural diversity and is home to one of the most important biocultural legacies of the world, resulting in more than 9,000 plants with known uses. The Royal Botanic Gardens, Kew (RBG Kew) has been collaborating in Mexico with the Facultad de Estudios Superiores, Iztacala of the National Autonomous University of Mexico (Fes-I UNAM) for over 20 years to conserve the rich flora of Mexico through seed banking, research, and training. Seeds are preserved at Fes-I UNAM, with duplicates stored at Kew's Millennium Seed Bank at Wakehurst, in the UK, under an Access and Benefit Sharing Agreement. Since 2015, RBG Kew and Fes-I UNAM have developed a programme to protect, conserve and enhance the natural capital of the Mexican forests, built around a detailed understanding of native tree seeds and their regeneration under future climatic change scenarios. We have published the first checklist of native trees of Mexico, with information on the distribution, uses and conservation status of 2,885 species. This information is used to prioritise taxa for seed collecting and conservation: seeds are either conserved *ex-situ* through conventional seed banking or propagated for *in situ* conservation. When propagated, trees are donated to local communities to support their livelihoods or used for reforestation in urban and peri-urban areas and degraded forests. This programme has been delivered through several projects funded by different sources and in collaboration with the NGO Pronatura Veracruz and the Instituto de Ecología A.C. Local communities are involved in the programme activities through a participatory approach and by applying gender equality and social inclusion principles.

S.182.6 Nutritional status of Pinus sylvestris and Quercus pyrenaica is improved in heterospecific neighbourhoods

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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.183 FERN AND LYCOPHYTE EVOLUTION: A PHYLOGENOMIC PERSPECTIVE. SESSION 1

S.183.1 Phylogenomic data reveal the complex evolutionary history of Neotropical Phlegmariurus (Lycopodiaceae)

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The clubmosses (Lycopodiaceae) are one of three extant families of lycophytes, which hold an important phylogenetic position as sister to the remaining vascular plant lineages. An ancient lineage, the Lycopodiaceae is comprised of an estimated 400 species distributed in 17 genera and presents a cosmopolitan distribution, though species richness is highest in the tropics. The most species-rich lineage of Lycopodiaceae by far is the genus *Phlegmariurus*, which includes at least 300 species that are distributed throughout tropical and subtropical regions of the world. A handful of studies have attempted to reconstruct the evolutionary history of this clade and revealed that it has been shaped by complex biogeographic scenarios and recent rapid diversification, but these studies relied on sequence data from a handful of chloroplast loci and thus were limited in the conclusions they could draw. In this talk, I present a new perspective on the evolution of *Phlegmariurus* in the American tropics, based on target-capture sequence data from hundreds of nuclear loci. These data reveal previously undetected biogeographic patterns, provide evidence for reticulate evolution, and illustrate the evolutionary success of *Phlegmariurus* in tropical America, from lowland rainforests to alpine grasslands.

S.183.2 The genomic landscape of ferns and lycophytes

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Cracking the giant genomes of pteridophytes had been seemed as a formidable challenge. However, thanks to the rapid drop of sequencing cost and the development of highly accurate long-read sequencing, we now have around a dozen pteridophyte genomes already published with many more in the pipeline. Here, I summarize the current state of pteridophyte genomics and synthesize the trends emerging from comparative analyses. I particularly highlight the genomic contrasts between homosporous and heterosporous lineages, and discuss the implications on the evolution of chromosome number and genome size. Lastly, I point out future directions and areas worth exploring further.

S.183.3 First genomic evidence of hybrid evolution in Phlegmariurus

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Phlegmariurus (Huperzioideae, Lycopodiaceae) is a worldwide genus of 200 to 300 species comprised of a Neotropical radiation predominantly associated with mountain chains, and a Palaeotropical radiation predominantly associated with the canopies of rainforests. Our understanding of evolutionary radiation and species diversity in the Palaeotropical clade has remained a frontier due to the unresolved nature of species-level phylogenies, extreme homoplasy, and morphological intermediates between distant species. We present the first species-resolved phylogeny for Palaeotropical *Phlegmariurus* based on a comprehensive Hyb-Seq dataset of 236 collections. We provide evidence that Palaeotropical *Phlegmariurus* comprises 13 major clades, each with morphological, ecological or geographic specialisation. Using the bioinformatics workflow HybPhaser, we present the first molecular evidence for hybrids in *Phlegmariurus*. *Phlegmariurus* of hybrid origin are common. We identify seventeen *Phlegmariurus* that are of hybrid origin, including five already described species and 12 that are newly identified, as well as evidence of hybrid species complexes. We postulate that, in addition to the long-distance dispersal, vicariance and habitat-driven diversification pathways previously identified, hybridisation has been an important species diversification pathway in *Phlegmariurus*.

S.183.4 Rampant hybridization in a tropical fern genus (Danaea, Marattiaceae)

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The amount of known hybrids has been observed to be lower in tropical than temperate ferns, but patterns of hybridization are poorly known in the tropics. We examined hybridization in the Neotropical eusporangiate fern genus *Danaea* (Marattiaceae) using a phylogenomic approach with single or low-copy nuclear and chloroplast loci. We found a relatively high rate of hybridization in *Danaea* and suggest that the apparent paucity of hybrids in tropical ferns is due to an observation bias. We also show evidence that hybridization can function as both a diversifying and a homogenizing evolutionary force within the same genus. We found further evidence for the previously proposed low reproductive barriers in ferns, enabling hybridization between lineages separated possibly as far back as the Cretaceous.

S.183.5 Population genomics of Woodwardia radicans (Blechnaceae) in northern Iberian Peninsula

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Climatic refugia, deemed as natural laboratories for investigating species' responses to historical climatic shifts, offer valuable perspectives into the evolutionary dynamics of floras. The Palaeotropical flora, originating in the northern hemisphere during pre-Quaternary times, is believed to have endured in microclimatic subtropical zones across Europe and the Macaronesian islands. This research focuses on *Woodwardia radicans* (Blechnaceae), a fern historically recognized as a Palaeotropical relict, thriving in the Macaronesian archipelagos and southern Europe, particularly the northern Iberian Peninsula. Employing the genotyping by sequencing (GBS) technique, we scrutinized the genetic and phylogeographic patterns of northern Iberian populations and estimated times of lineage divergence. Despite the species having diverged from its sister, *W. unigemmata*, around the Pliocene, European populations diverged in the Quaternary, challenging the presumed pre-Quaternary relict status of these continental populations. Population-level analyses of the northern Iberian Peninsula reveal low genetic diversity and noteworthy differentiation among populations. Our findings challenge the assumed pre-Quaternary relict status of continental populations, indicating a Quaternary recolonization from Macaronesia. The absence of a distinct phylogeographical pattern in the northern Iberian Peninsula is attributed to fragmentation and genetic drift, signaling a departure from a more widespread distribution range in the late Quaternary. Beyond illuminating the biogeographic history of this unique species, our results yield crucial insights for defining conservation strategies. The study underscores the imperative to reassess assumptions about the historical persistence of Palaeotropical species in subtropical environments and emphasizes the significance of considering late Quaternary dynamics in comprehending current genetic and phylogeographic patterns.

S.184 PLANT ECOLOGY - HOW AND WHY GENOME SIZE MATTERS

S.184.1 Ecological implications of the effects of genome size evolution on trait flexibility & diversification in a tropical plant family

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Survival of plants in their environment depends on their ability to adapt and diversify. Genome size, due to its biophysical effects, may influence evolution of functional traits, and hence adaptation and diversification. However, this has never been tested in a quantitative macroevolutionary framework. Here we hypothesize that genome size evolution plays a fundamental role in influencing 'trait flexibility' (i.e., evolvability of traits over macroevolutionary times), and hence diversification rates. We predict that larger genomes will lead to lower trait flexibility, while higher rates of genome size evolution will positively influence trait flexibility of plant lineages allowing for greater partitioning of ecological space, leading to speciation, and hence diversification. To address this hypothesis, we integrated genome size, functional trait, and phylogenetic data for palms (Arecaceae) - a pantropical plant family comprising ca. 2600 species that express wide functional diversity. Using macroevolutionary and structural equation models we show that diversification rates of palms increased ca. 20 Mya, concordant with increased rates of genome size and trait evolution. Furthermore, rate of genome size evolution was positively influenced by genome size itself, contrary to the idea that large genomes constrain evolution. Finally, we found that higher rate of genome size evolution was associated with greater trait flexibility (e.g., higher rates of fruit size, leaf size, and stem height evolution). Overall, our findings suggest that interactions between rates of genome size and trait flexibility have played a role leading to higher diversification rates in palms. Our results suggest that genome size evolution acts as a key driver of diversification in palms both directly, and indirectly via its influence on trait evolution. This may explain the complex interplay between genomic factors, traits and diversification leading to some of the most enigmatic evolutionary radiations across angiosperms and the ecological success of certain plant lineages.

S.184.2 Fine-tuning plants to the environment – a role for genome size

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Genome size has been postulated as being a key trait predictive of numerous anatomical, physiological, and ecological traits in plants. While genome size correlates with many organismal traits, the strongest relationship has been with minimum (or meristematic) cell size because a cell cannot be smaller than the volume of its nuclear envelope. Though mature cells are often orders of magnitude larger in volume than the minimum volume defined by the size of the genome, the maximum volume of stomatal guard cells–and possibly other cell types–is invariant across species. These patterns suggest that species with smaller genomes can produce not only smaller cells but also a greater range in mature cell size than species with larger genomes, i.e., smaller genomes may allow for greater plasticity to fine tune anatomy to the environment. Using intraspecific and interspecific data from various experiments and observations, we test the role of genome size in limiting trait plasticity. Our results highlight that while genome size may limit the range of cell sizes a plant can produce, there are multiple alternative ways of overcoming these limitations depending on the functional implications of these traits. Thus, partitioning the effects of genome size from higher-order architectural traits is important for understanding how abiotic conditions may select for leaf traits and, thus, on genome size and, similarly, the distributions of genome size across environmental gradients.

S.184.3 Ecological and evolutionary processes acting on plant species dependant on their genome sizes

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The amount of DNA in each cell of an organism, called the 'genome size', varies enormously between species. Indeed, amongst flowering plants there is a known ~2,500 fold range in genome size (from 60,000 -160,000,000 bp per 1C genome). However, most plant species have smaller genomes than would be expected given the incidence of polyploidy and (retro) transpostion in their ancestries, suggestive of evolutionary selection against large genome sizes. This talk first explores ecological selection acting on genome size, focussing in particular on nutrient limitation. We show from grassland nutrient experiments in UK, Germany, Inner Mongolia and from the Nutrient Network that species with large genomes are favoured in the presence of nitrogen and phosphate fertilizers, suggestive of ecological selection against large genomes when they are limiting (as in most soils of the world). But it is unknown if such ecological selection translates to evolutionary selection against large genomes, because available data suggests that there are only small rates of DNA loss per generation (4–70 Mb/million years, <500 bp/generation). This poses a problem as to how evolutionary selection might act, given that the size of even the smallest plant genome is three orders of magnitude larger than these DNA losses. We propose that a solution to this problem might be that genome downsizing is an emergent property of polyploidy, which after time has ecological advantages to plants growing in nutrient poor habitats.

S.184.4 How and why genome size constrains the global distribution of plants

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Angiosperms, spanning diverse habitats across continents, showcase substantial genome size variations, offering a prime platform to explore global genome size distribution hypotheses. Among these, the large-genome-constraint, mutational-hazard, polyploidy-mediated, and climate-mediated hypotheses stand central. We present the most extensive dataset to date, comprising 16,017 angiosperm species, representing over 5% of the known diversity. Leveraging this dataset alongside comprehensive geographic distribution data, we conducted an in-depth analysis of genome size distribution among angiosperms. Our findings reveal a correlation between small range sizes in angiosperms and larger genomes, supporting the large-genome-constraint hypothesis. Unlike the unimodal U-shape pattern in latitudinal distribution observed in polyploid proportions, we observed the S-shape with the increase in angiosperm genome sizes between the equator and 40-50°N/S and a decrease in genome sizes beyond 40–50°N northwards. Climate, especially temperature, emerges as a dominant factor shaping genome size distribution along this global latitudinal gradient. Conversely, the influence of polyploidy frequency and growth form types appears negligible. Our comprehensive analysis underscores the significant role of climatically mediated non-adaptive processes, including purifying selection, genetic drift, relaxed selection, and environmental filtering, in sculpting the global distribution of angiosperm genome sizes.

S.184.5 Genome size and cell size in mosses: the impact of DNA content on moss anatomy and physiology

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The DNA content in the nucleus, commonly measured as genome size (GS), is considered a strong predictor of minimum cell size in eukaryotic organisms. In tracheophytes, the scaling between GS and cell size determines leaf anatomy and, consequently, plant growth capacity. However, the few studies involving bryophytes, which only considered stomatal guard cells of the diploid phase, suggest that GS-cell size scaling does not apply to this group. We measured leaf area, cell dimensions and cell wall thickness from mid-lamina, largest and smallest cells in phyllidia of 160 moss species with known GS. From these, cell area and volume and different key anatomical traits determining photosynthesis were calculated. We contrasted cell sizes with GS data through Standardized Major Axis (SMA) analyses. GS weakly explained the variability of laminal and maximum cell sizes (width, area and volume), but explained more than half of the variability in minimum cell sizes. While GS positively correlated with moss phyllid area, it did not significantly explain cell wall thickness or other anatomical traits. Notably, SMA slopes for cell sizes were considerably steeper than those reported for tracheophytes. Furthermore, maximum to minimum volume ratios showed greater variability in species with smaller GS. Our findings suggest that GS is a determinant of the minimum cell size in mosses, resembling trends observed in tracheophytes. This similarity holds between tracheophyte sporophytes (diploid leaf and guard cells) and moss gametophytes (haploid leaf cells), but not in moss sporophytes (diploid guard cells), implying a differential impact of GS based on cell and phase function. The relatively steeper SMA slopes and maximum to minimum volume ratios support the hypothesis that smaller GS (as seen in mosses) allow a greater cell size variability. Although not directly determining their physiology, GS could indirectly influence moss productivity and growth capacity by affecting phyllid area.

S.184.6 Genome size is positively correlated with extinction risk in herbaceous angiosperms

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Angiosperms with large genomes experience nuclear-, cellular- and organism-level constraints that may limit their phenotypic plasticity and ecological niche. Therefore, we test the hypotheses that extinction risk is higher in large-genomed compared to small-genomed species, and that the effect of genome size on risk is mediated by life form, range size, and climatic zone. We combined an angiosperm-wide genome size dataset with the newly released World Checklist of Vascular Plants, the IUCN Red List of Threatened Species and a species-level angiosperm phylogeny to analyse the relationship between genome size and extinction risk across life forms, climates and range sizes using an evolutionary framework. We found that angiosperm genome size and extinction risk are linked directly, and indirectly via range size and climate. Across sampled angiosperms as a whole, genome size is positively correlated with extinction risk. Partitioned by life form, extinction risk increases with genome size in herbaceous species across climates, especially in single-country endemics. However, genome size and risk are not correlated in woody species. Genome size may serve as a proxy for difficult-to-measure parameters associated with resilience and vulnerability, especially in herbaceous angiosperms. Therefore, it merits further exploration as a useful genomic trait for understanding extinction risk and enhancing plant conservation efforts.

S.185 BEYOND BIOGEOGRAPHY: ADAPTATION AND DIVERSIFICATION ACROSS THE INDO-PACIFIC

S.185.1 From Refugium to Radiance: understanding Smilacaceae speciation in the Himalayas

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The Himalayan region, a biodiversity hotspot, has undergone significant geological and climatic changes over millions of years. Due to its unique ecological and evolutionary trajectory, the Smilacaceae family in the Himalayan refugium offers valuable insights into evolution and conservation priorities. The present study delves explicitly into how examining Himalayan Smilacaceae contributes to our comprehension of evolution, biogeography, and the impacts of climate change. The endemic nature of various *Smilax* taxa, such as *S. elegans* subsp. *osmastonii, S. microphylla, S. quadrata, S. sailenii, S. turbans* in the Himalayan refugium, along with their probable isolated evolutionary paths evident from the disjunctive distribution of *S. wightii*, unveils unique adaptations and genetic variations. Our findings shed light on fundamental evolutionary processes and the mechanisms underlying speciation. The investigation extends to analyzing inter/intraspecific morphological evolution among Himalayan *Smilax* species, aiming to decipher their phylogenetic relationships. Moreover, their plastome comparison enables the identification of molecular markers that contribute to the resolution of evolutionary relationships and the detection of genetic diversity within the Smilacaceae family. Past researchers underscored the pivotal role of the Himalayan *Smilax* in linking species across East Asia, Southeast Asia, and Africa. Therefore, examining the phytogeography of Himalayan *Smilax* becomes crucial in unravelling the temporal origins and biogeographic processes shaping the disjunctive distribution of these species. Smilacaceae in the Himalayan refugium not only aids in reconstructing historical biogeography but also provides insights into species movement, adaptation to changing environments, and the impact of historical events on plant evolution. Utilizing molecular data-derived phylogenetic insights facilitates evaluating evolutionary relationships among the *Smilax* species in the Himalayan region. This research also endeavours to resolve longstanding taxonomic discrepancies, synthesize synonyms, and establish a more comprehensive framework for identifying and classifying Smilacaceae in the region.

S.185.2 Taxonomic circumscription and biogeography: Dysoxylum s.l. (Meliaceae) across Indomalesia-Australasia and the Southwest Pacific

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Dysoxylum s.l. had long been speculated to be a polyphyletic taxon. Recently, six strongly supported clades within the group were exhibited based on phylogenetic analyses employing several DNA marker regions. To ensure monophyly, five previously recognized genera (*Didymocheton* Blume, *Epicharis* Blume, *Goniocheton* Blume, *Prasoxylon* M.Roem. and *Pseudocarapa* Hemsl.) were reinstated, and *Dysoxylum* s.s. Blume ex Raspail was re-defined. This taxonomic revision, based on the most extensively sampled molecular phylogenetic tree of this group established so far, and morphological characters, resulted in the re-assignment of 94 presently acknowledged *Dysoxylum* species, generating forty-five new combinations and complementary lectotypifications as required. This taxonomic groundwork set the stage for biogeographic exploration. Our sampling encompassed 75% of the *Dysoxylum* s.l. species diversity, covering the entire distribution range and all major lineages. Results showed that *Dysoxylum* s.l. originated and firstly diversified in the western part of its current distribution range (including Indochina) during the Miocene to Pliocene, followed by an overall eastern range expansion towards Malesia, Australia and the Southwest Pacific in the Pliocene. This southeastward expansion into Wallacea and Australia coincided temporally with the convergence of the Asian and Australian tectonic plates and followed the expected dispersal directionality bias. We were able to establish long-distance dispersal as the primary mechanism shaping the current distribution. Furthermore, we identified two dispersal pathways into the Southwest Pacific: one from New Guinea and the Solomon Islands to Fiji, and another one from New Zealand to Fiji. Remarkably, Fiji served as an important secondary source area for dispersal into the Southwest Pacific from both New Guinea through the Solomon Islands, as well as from New Zealand.

S.185.3 Using community-scale genetic data to understand adaptation and diversification in island systems

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Islands are classical 'natural laboratories', encompassing the majority of terrestrial endemic species, yet they are substantially vulnerable to numerous human impacts (agriculture, invasions, climate change, etc). The relative isolation of islands, so important for generating their striking patterns of endemicity, also make them tractable systems for modeling biodiversity processes. Many open questions remain as to how the biodiversity we observe in nature has accumulated. For example, how do the dynamics of adaptation, competition, speciation, and colonization result in the communities that we observe today? And, how have local environmental conditions and human mediated disturbance modulated or amplified these processes? Community-scale genetic sequence data (e.g. DNA metabarcoding) provides a record of past population dynamics that can unveil processes that have structured contemporary observed biodiversity. In this talk I describe the Massive Eco-evolutionary Synthesis Simulation (MESS) model, a multi-scale model of biodiversity which jointly accounts for processes operating on ecological, population genetic, and phylogenetic timescales. The goal of MESS is to integrate abundance and trait data with phylogenies and population genetic data into a single mechanistic framework, with the goal of estimating the contribution of colonization, local adaptation, and ecological interactions to the generation and maintenance of biodiversity in insular systems. MESS can also provide insight on "community genetic health" and all for development of indicator metrics which can reliably identify genetically healthy and unhealthy communities. MESS simulations coupled with machine learning inference methods facilitate the investigation of processes that lead to resilient and genetically healthy communities and reciprocally address questions of how community genetic health contributes to promoting invasion resistance and/or providing resilience to disturbance. As a case study, I demonstrate the application of MESS to understand the impact of forest fragmentation and land use on floral community structure using DNA metabarcoding data from rainforests on Sumatra.

S.185.4 Phylogenomic data informs biogeographic and diversification patterns of Serianthes (Fabaceae) in the Indo-Pacific region

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The Indo-Pacific region contains six of the 25 world's biodiversity hotspots harboring many endemics. *Serianthes* consists of 17 island endemics and one littoral species, *S. dilmyi*. The endemics occur in the Pacific Islands, while *S. dilmyi* occurs in Malaysia, Indonesia, and the Philippines. Twelve of the 18 *Serianthes* species are listed on the Red List of Threatened Species. Although the circumscription of the genus has not been questioned, the phylogenetic relationships and diversification through time and space remain unclear. To study diversification we collected 81 samples across *Serianthes'* Indo-Pacific distributional range and employed a targeted sequence capture approach and produced a time tree. We present the first robust, genus-wide, time-calibrated phylogeny and biogeographic hypothesis of *Serianthes* based on phylogenomics and densely sampling all species. We identified two well-supported clades representing two subgenera: One clade, subgenus *Serianthes*, comprising all taxa from Malesia, Papuasia and southern Micronesia, and the other clade, subgenus *Hayunia*, is uniting all taxa from Polynesia and northern Micronesia. Both Micronesian species, *Serianthes nelsonii* and *S. kanehirae* have disjunct populations with unique genotypes within their archipelagoes. Testing geographic range evolution under the DEC+j model, we inferred the most common ancestor originated in either Papuasia or New Caledonia during the Miocene. Most founder events in *Serianthes* happened during the Quaternary, aligning with the ages of the islands and supporting the progression rule of oceanic islands. *Serianthes dilmyi* crossed the Wallace Line and established populations in the Philippines and Indonesia. We may attribute this to its ability to thrive in mangrove habitats during the Quaternary era when sea levels were lower. Our study highlights the role of LDD during the diversification of *Serianthes* in the Indo-Pacific corroborating the important role of LDD using a Austro-Melanesia dispersal route similar to other tropical lineages such as *Hernandia* and *Pandanus*.

S.185.5 Exploring the Diversification of Araucariaceae with Targeted Capture Data

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The gymnosperm family Araucariaceae consists of 27 extant species organized in three genera: *Araucaria*, *Agathis*, and the monospecific *Wollemia*. The extant Araucariaceae are confined to the southern hemisphere, although there is evidence of their presence in the northern hemisphere during the Mesozoic. The rich fossil record of this family, combined with the distribution patterns of its extant species makes the Araucariaceae an ideal system to explore evolutionary hypotheses about the diversification and biogeography of the Indo-Pacific region. We generated a large nuclear dataset from 126 Araucariaceae samples using targeted enrichment with the GoFlag 408 flagellate land plant probe set. These data help elucidate species boundaries and resolve phylogenetic relationships among taxa. We dated the tree and described the geographic patterns of diversification, focusing on the putative radiation in New Caledonia.

S.186 BENEFICIAL PLANT-MICROBE INTERACTIONS. SESSION 1

S.186.1 Comparative altitudinal analysis of microbial diversity in cultivated soils in Ecuadorian Andes

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The Ecuadorian Andes are a unique and highly exploited ecosystem both ecologically and economically. Several species of agricultural interest are produced only in these areas and are therefore known as "Andean crops", that is, they are produced above 2000 meters above sea level and under climatic, hydrological and geological conditions typical of the Andes. The type of soil in these ecosystems directly influences the growth of these plant production systems.

Taking into account that existing microorganisms are key actors in soil formation, we carried out an analysis of the diversity of native bacterial communities in cultivated soils of the Ecuadorian Andes. These communities could influence carbon and nitrogen fixation, promoting soil fertility and promoting innovations in sustainable high mountain agriculture. Genetic material was extracted from soil samples from potato crops (Solanum tuberosum) located in two altitudinal levels at 3400 and 3800 m. The 16s rRNA V4 region was amplified using the Illumina technique to perform a diversity analysis of the microbial community. These sequences were subsequently refined in silico using the Mothur software. As a result, a central community or "core" with 437 identified genera was obtained for each altitudinal level, of which 19 are representative members at 3400 msnm and 16 for 3800 msnm. The predominant genera regardless of the altitudinal level were: Raoutella, Stenotrophomonas, and Lysobacter. Rhodanobacter was representative for the community at 3800 m and the Gemmatimonas for 3400 m. We establish then that the richness of the bacterial communities found in the two altitudinal levels and their metabolic functionality balances the agricultural system and contributes to its health and fertility, which promotes the development and productivity of cultivated species and soil conservation.

S.186.2 Plant-soil feedback as a key of competitors' coexistence

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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 were 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 suggests that PSF play a key role in regulating population dynamics of competing species, challenging the conventional understanding dominated by direct competition.

S.186.3 Effect of AMF and PGPB inoculation on the growth and volatilome of Artemisia annua plants

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Artemisia annua is a ruderal plant belonging to the Asteraceae family. Besides the production of artemisinin, a bioactive compound used against malaria *Plasmodium,* the glandular trichomes of this plant release many VOCs (Volatile Organic Compounds). Since arbuscular mycorrhizal fungi (AMF) and plant growth promoting bacteria (PGPB) can strongly affect plant growth and physiology, the aim of this work was to test (in controlled conditions) different AMF and PGPB strains (alone or in combination) on two artemisia clones (CL7 and CL26) to assess their effects on plant growth parameters and secondary metabolite production. Plants were grown in growth chamber for two months and irrigated three times a week with Long Ashton solution. At harvest, AMF colonization in root, plant biomass (fresh and dry), leaf pigment and artemisinin concentrations (HPLC analysis) were detected.

Moreover, the composition of leaf volatilome was analyzed in CL26 clone by GC-MS. The results highlighted that the two clones differently responded to the different tested inocula and, conversely, different microorganisms affected the same clone in a different way, especially for plant growth parameters. The GC-MS analyses of the leaf volatile profile resulted in the identification of 120 molecules (a higher number than that reported in previous works). All these compounds (some of which detected for the first time in this plant species) were grouped in the most representative chemical classes (alkenes, alcohols, aldehydes, acids, ketones, ethers, esters, and "other compounds"), whose percentage changed depending on the used inoculum. The fact that some molecules were only present in a certain treatment and that others were present in different percentages meant that plants of each treatment had its own specific particular odor, mainly due to the bioactive molecules present in the complex mixture of plant essential oil, whose production was modulated by the interaction between plant and soil beneficial microorganisms.

S.186.4 Root Rhythms: revealing the biota's dynamic dance in response to the climatic symphony in Rhododendron anthopogon

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Lately studies on root microbe interactions have gained prominence as plant roots in their natural environment are in constant interaction with diverse microorganisms. Plant roots assemble two distinct microbial compartments rhizosphere and endosphere. Root biota influences plant growth and performance by modulating the effects of biotic and abiotic stressors. However, climate change is causing changes in the composition of root biota that affects host plant functions. While plant's primary response to changes in climate is adjustment of their physiology, root biota which has shorter generation times, responds by rapid changes in community composition. Changes in climatic factors occur in combination of precipitation, temperature and their fluctuations. Understanding the separate and interactive effects of different climatic drivers is important. Vegetation composition and soil chemistry also strongly affect root biota. Identification of the direct effect of climate on root biota is difficult as both soil chemistry and vegetation composition are changing along climatic gradients. Hence, there is a need to deepen our understanding of how root microbial diversity and functional composition will shift in root biota of specific plant species as climatic and edaphic conditions are changing most strongly in montane ecosystems. In this study root associated fungal communities were studied along a climatic gradient in a dominant alpine Himalayan shrub species. Site and elevation significantly affected both rhizosphere and root fungal communities. Variation in rhizosphere and root fungal communities was related to soil moisture, soil chemistry and plant community composition. Highest number of OTUs were found in rhizosphere as compared to endosphere fungal communities. This study contributes to our knowledge of below ground biotic mechanisms that affect the functioning and adaptation of natural plant populations under stressful conditions in vulnerable ecosystems. It will enable in the formulation of evidence-based conservation and management strategies especially for species under threat of climate change.

S.186.5 The genera Gymnostoma and Ceuthostoma (Casuarinaceae) can establish symbioses with cluster 1 and with cluster 3 Frankia.

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The family Casuarinaceae comprises four genera (from more basal to more recent): *Gymnostoma*, *Ceuthostoma*, *Casuarina* and *Allocasuarina*. Casuarinaceae have actinorhizal symbioses with *Frankia* N-fixing actinobacteria. This symbiosis is an intriguing model of evolution of plant-microbe interactions, as *Gymnostoma* established a nonspecific symbiotic association with easy-to-isolate, more saprophytic *Frankia* strains which belong to cluster 3 frankiae, whereas the genera *Casuarina* and *Allocasuarina* are in symbiosis with hard-to-isolate strains from the cluster 1c frankiae. To date, there is no information about the symbiont associated to the genus *Ceuthostoma*, whose origin is intermediate between *Gymnostoma* and *Casuarina* + *Allocasuarina*. To advance our knowledge on the *Frankia*-Casuarinaceae symbioses and to obtain first evidences on the strains associated to *Ceuthostoma*, a genus with a narrow geographical range, we collected actinorhizal nodules from the species *C. terminale*, *Gymnostoma nobile* and *G. sumatranum* from different sites in Sabah (Malaysia). After surface sterilisation and peeling, we extracted DNA from the nodules and amplified and sequenced a fragment of the bacterial *pgk* gene, which has been used previously for the identification of *Frankia* strains. After aligning our sequences with published sequences of standard *Frankia* strains covering all the diversity in the bacterial genus, we constructed a maximum-likelihood tree. We found that all the *G. nobile* and the majority of *G. sumatranum* and *C. terminale* trees had symbioses with cluster 3 frankiae, whereas 10% and 18% of the *C. terminale* and *G. sumatranum* trees had symbioses with *Frankia* strains in cluster 1. Interestingly, those strains were not grouped with the strains from *Casuarina* and *Allocasuarina*. Instead, they were in a different group, closer to *Frankia* species that enter symbiosis with *Alnus* and *Morella*. Overall, this study points to a complex scenario of evolution of actinorhizal symbiosis in this group.

S.186.6 Microbial communities and seeds: Home-field advantage effects in holm oak germination

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Germination onset is the first choice in the phenological plant cycle, influenced by abiotic and biotic factors. Both soil and seed microbiota are key drivers of germination, influencing seed storage, dormancy release, and germination rates. Interactions between plants and soil microbes contribute to plant adaptation to their environment. Therefore, plants could benefit more from interacting with soil microbes from the local ('home') environment rather than with those from different origins. As crucial germination drivers, plants may select for specific microbial taxa that provide them with a *home-field advantage*, despite having less microbial richness and diversity. Here, we look at the role of seed-associated microbes on holm oak (*Quercus ilex*) germination, whether the soil or the seed microbes have a greater impact on this process, and how the interaction between the seed microbiome and soil microbiota influence holm oak germination. We found that microbes on *Q. ilex* seeds have a significant effect on germination, with non-sterilised seeds having higher germination rates than sterilised ones. Moreover, when co-occurring, soil microorganisms enhance the effect of seed-associated microbes on holm oak germination. Overall, our results evidence a *home-field advantage* where local soil communities, along with seed-associated microorganisms, enhance *Q. ilex* germination over that of different soil or species-linked communities.

S.187 EVOLUTION AND DIVERSITY OF CARBON CONCENTRATING MECHANISMS (CCM) IN LAND PLANTS. SESSION 1

S.187.1 C2 photosynthesis across scales

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Plants have evolved extraordinary diversity in the carbon fixation pathways of photosynthesis that allow species to survive and thrive across a broad array of ecological niches. While most plants use only C_3 photosynthesis, this physiology is heavily affected by high rates of photorespiration under warm and arid environments. In response, some plant lineages have evolved carbon concentrating mechanisms (CCMs) to improve net carbon assimilation in these high photorespiration environments. C_2 photosynthesis is one such CCM that can increase net CO_2 assimilation by capturing, concentrating, and re-assimilating CO_2 released from photorespiration. This talk will discuss C_2 photosynthesis across scales, from the evolutionary history and biogeography of C_2 plants, to their unique whole-plant growth patterns, and to specifics of their mesophyll structure, vascular patterning, and ultrastructure. In all cases, C_2 plants will be compared to their close C_3 and C_4 relatives for context. The talk will conclude with a discussion on the potential for C_2 photosynthesis engineering programs to improve the efficiency of C_3 crops.

S.187.2 Evolution of facultative and constitutive gene regulation in plants with CAM photosynthesis

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The evolution of stress response mechanisms and their regulation have broad implications from the origins of evolutionary novelties to climate change adaptability across the tree of life. Crassulacean acid metabolism (CAM) is an adaptation to water and CO_2 limitation that has evolved convergently in many dozens of plant lineages through the co-option of core carbon metabolic pathways. Despite the near-universal set of gene families exapted in each CAM origin, a diverse landscape of CAM phenotypes has evolved that vary along multiple axes, including the extent of nocturnal stomatal conductance, the amount of CO_2 sequestered as malic acid, and the degree to which CAM is facultative or constitutive. The mounting genomic resources for CAM species across the vast number of convergent CAM origins makes CAM an ideal system for understanding the evolution of stress response gene regulation, and how such facultative responses can become constitutive. Here, we compare the regulatory elements of CAM gene networks from multiple independent origins of facultative and constitutive CAM plants to identify convergent patterns of regulatory evolution.

S.187.3 Comparative analysis of distribution and climatic preferences of C4 lineages

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Photosynthetic pathways play a pivotal role in shaping the ecological and structural diversity of plant species. The C_4 photosynthetic pathway has independently evolved over 61 times in multiple angiosperm lineages and consists of a series of anatomical and biochemical modifications to the ancestral C_3 pathway increasing plant productivity under warm and light-rich conditions. C_4 eudicots entail an enormous structural and ecological diversity, whereas the C_4 syndrome in grasses is more uniform and phylogenetically constrained. Using GBIF (Global Biodiversity Information Facility) database we compiled an occurrence data matrix for 1514 C_4 taxa, covering more than 80% of currently known C_4 grasses and eudicots. The highest C_4 species diversity is in Mexico/Southern United States and Australia. Furthermore, C_4 grasses predominantly thrive in more humid regions compared to their eudicot counterparts, and among the latter, various biochemical subtypes exhibit specific climate preferences, with C_4 eudicots often adapting to drier conditions through features like succulence and salt tolerance. Our study illustrates that GBIF is a valuable resource for meta world-wide biogeographical studies.

S.187.4 CAM evolution is associated with gene family expansion in an explosive bromeliad radiation

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The subgenus Tillandsia (Bromeliaceae) belongs to one of the fastest radiating clades in the plant kingdom and is characterised by the repeated evolution of the water-conserving Crassulacean Acid Metabolism (CAM), which is regarded as a key innovation trait and driver of ecological diversification in Bromeliaceae. By obtaining physiological and transcriptomic data under control and drought conditions of a Tillandsia species pair representing the phenotypic extremes of photosynthetic metabolism found in the clade, we were able to characterise the range of CAM phenotypes in Tillandsia with unprecedented detail. We found that species previously identified as C3 are CAM intermediates which activate a latent CAM cycle under drought conditions. However, the CAM-specific response to drought in this facultative species has little overlap with the constitutive CAM cycle of the strong CAM species. By producing high quality genome assemblies of a facultative and a constitutive CAM Tillandsia, and combining genome-wide investigations of synteny, TE dynamics, sequence evolution, gene family evolution and temporal differential expression, we were able to pinpoint the genomic drivers of CAM evolution in Tillandsia. Our analyses show that rewiring of photosynthetic metabolism towards constitutive CAM is mainly obtained through regulatory evolution rather than coding sequence evolution, as CAM-related genes are differentially expressed across a 24-hour cycle between the two species, but are no candidates of positive selection. Gene orthology analyses reveal that CAM-related gene families manifesting differential expression underwent accelerated gene family expansion in the constitutive CAM species, further supporting the view of gene family evolution as a driver of CAM evolution.

S.187.5 Diversity and evolution of CAM and CAM-related traits in the most species-rich Macaronesian plant radiation

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CAM photosynthesis involves the nocturnal assimilation and storage of carbon in the form of malic acid in the vacuole. It is mostly but not exclusively associated with succulence which may optimize the vacuolar storage capacity of malic acid. Plants that express CAM rely on diurnal closure of stomata while internal CO_2 concentrations are high, limiting transpiration to its cuticular rather than stomatal component during parts of the day. Cuticular transpiration barrier properties may thereby represent an understudied trait related to CAM. To investigate the interrelation and evolution of cuticular transpiration barrier properties, succulence and CAM expression, we set up a climate chamber experiment sampling most species of *Aeonium* and *Aichryson* (Crassulaceae), the iconic houseleeks that largely diversified on the Canary Islands. Under varied treatments of heat and drought, over-night acidification of leaves was quantified as a means to study CAM expression patterns. Transpiration barrier properties of the cuticle as well as the degree of succulence were quantified through leaf drying curves and measurement of minimum conductance (g_{min}). Our results reveal a negative correlation of CAM activity and g_{min} such that species with strong or constitutive CAM were more likely to have an efficient cuticular transpiration barrier. However, leaf succulence was not correlated with CAM activity which is in contrast to the remarkable role of succulence in the function of CAM photosynthesis. In conclusion, we present first evidence for the need of reduced cuticular transpiration in CAM plants which is to be expected under selection for high water-use efficiency.

S.187.6 Leveraging facultative CAM for engineering synthetic CAM into C3 photosynthesis plants

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The global climate crisis is rapidly increasing major crop losses around the world due to increased intensity and duration of drought events. Therefore, novel strategies are needed to create more climate-resilient crops. Remarkable progress has been made in advancing our understanding of the functional genomics of crassulacean acid metabolism (CAM) in the last decade. Dozens of CAM plant genomes have now been sequenced including obligate CAM species such as *Kalanchoë fedtschenkoi*, facultative CAM species such as *Mesembryanthemum crystallinum*, and important crops such as *Agave*, *Ananas*, *Hylocereus*, and *Opuntia*. Well-annotated genomes along with extensive transcriptomic, proteomic, and metabolomic datasets and associated co-expression and transcriptional regulatory networks provide a strong foundation for understanding the biochemical and regulatory frameworks that underpin the diel and circadian operation of CAM. Detailed time-resolved transcriptome profiling analysis in the facultative CAM plant *M. crystallinum* has revealed hundreds of genes with putative CAM-associated functions that provide the building blocks for creating synthetic versions of CAM in the C_3 photosynthesis model *Arabidopsis thaliana*. We have built different gene circuits to recreate synthetic versions of the carboxylation, decarboxylation, and core diel carboxylation + decarboxylation modules of CAM. The carboxylation module increased CO_2 assimilation, nocturnal malate accumulation, and plant biomass whereas the decarboxylation module improved water-use efficiency. Combining the carboxylation and decarboxylation modules resulted in increased CO_2 assimilation, nocturnal malate accumulation, plant biomass, and improved water-use efficiency. Design and implementation of new iterations of the SynCAM design cycle (SynCAM 2.0) also target soybean, a major crop that suffers large economic losses due to damage from drought events. CAM functions optimally within succulent leaves so the benefits of tissue succulence engineering will also be discussed.

S.188 ADVANCES IN MICROCLIMATE RESEARCH FOR CRYPTOGAM ECOLOGY. SESSION 1

S.188.1 BryoMicroClim: collecting bryophyte-relevant microclimate data to assess the gap between macro- and microclimate

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Significant mismatches between macro- and microclimates challenge our ability to accurately estimate the climatic conditions experienced by organisms and thus to predict responses to climate change. This study aims to evaluate the relationship between macro- and microclimate for small-scale plants such as bryophytes, which are highly dependent on local environmental conditions. To achieve this, we established a Europe-wide collaborative network of bryologists (the BryoMicroClim project), to measure the microclimate experienced by a bryophyte species. The moss *Hedwigia striata*, evaluated as near-threatened in Europe (Hodgetts *et al.*, 2019), was selected as the target species. This species grows mainly in forests or rocky areas. We selected 15 sampling sites across Europe, spanning a wide range of climate conditions (Portugal, Spain, France, Belgium, Wales, Scotland, and Sweden). In each site, mostly continuous forested areas, we measured air temperature and humidity using three dataloggers (Envloggers, Environmental loggers) installed near H. striata populations. In the Iberian Peninsula, we also installed other dataloggers (BtMs, Bryolichen Temperature Moisture), specifically designed to measure ambient temperature, humidity, and water content of nonvascular cryptogams. We used the slope and equilibrium approach (Grill *et al.*, 2022) to infer if the microclimate temperature and relative humidity variability (as measured by the in-situ dataloggers) is buffered or amplified in relation to the macroclimate variability (from ERA5-Land and ERA5 data). We observed that microclimate temperatures were buffered or amplified depending on site conditions. As hypothesized, microclimate temperatures had a buffered variability in dense forest sites. Our results suggest that collecting bryophyte-relevant microclimate data at fine spatial resolutions and long time scales will be critical to better understand the potential vulnerability of bryophytes to climate change.

S.188.2 Microclimate and intraspecific variation mediate the effects of biotic interactions on lichen performance

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Climate and biotic factors, and their complex interactions, drive species performance and distributions. Climate at the local scale (i.e., microclimate) drives population dynamics, ultimately determining local species abundance and fine-scale distribution. If populations are locally adapted to their environment, we would expect different responses to environmental change among populations across the species' range. Understanding how microclimate affects biotic interactions and accounting for intraspecific variation in responses can improve our predictions of species performance and distribution. We examined the direct and indirect effects of microclimate and mollusc grazing on five distant populations of the ground-dwelling forest lichen *Peltigera aphthosa*. We transplanted individuals from each population to 56 boreal forest sites covering a wide microclimate gradient in central Sweden and recorded their growth for one year. We quantified the direct and indirect effects of microclimate, grazing and populations origin on lichen growth using confirmatory path analyses approaches (piecewise Structural Equation Models). We found indirect effects of microclimate and populations origin mediated by grazing: 1) lichen growth decreased with increasing grazing pressure, which was enhanced by increasing temperature and air humidity during the growing season; and 2) populations differed in their susceptibility to grazing, as one population experienced higher damage. Our study adds evidence on the importance of climate-mediated antagonistic biotic interactions. When predicting future species distributions in the face of climate change, in addition to microclimatic drivers, both the presence of natural enemies together with local population differentiation needs to be considered.

S.188.3 The most important microclimatic variables for temperate forest bryophytes and lichens

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The in situ measured microclimate is increasingly acknowledged as a pivotal determinant influencing species diversity and distribution. The affordability and widespread utilization of microclimate loggers in ecological research globally have yielded an extensive dataset from biotopes traditionally devoid of climate data due to the absence of meteorological stations. Forest interiors represent a paradigmatic case, exhibiting microclimates substantially divergent from meteorological observations typically obtained from open land. The influx of this massive volume of microclimatic data has facilitated innovative approaches and insights while concurrently introducing new challenges in the processing, analysis, and meta-analysis of microclimate data. In response to these challenges, we present the development of the myClim R package, specifically designed for seamless microclimate data processing and analysis, including the computation of standard, ecologically relevant microclimate variables. Leveraging myClim in conjunction with our expansive national forest microclimate monitoring network, "CzeMiN," and the national database gathering the occurrence of lichens and bryophytes "DaLiBor," we discerned the principal microclimatic variables steering the diversity and distribution of forest bryophytes and lichens. Moreover, through a comprehensive assessment, we partitioned the variance among microclimate, macroclimate, forest structure, and topography. Our findings indicate that the variation in temperate forest bryophyte and lichen diversity elucidated by in-situ measured microclimate cannot be accurately estimated through alternative proxy variables. This underscores the indispensable nature of microclimate data for comprehending the distribution of bryophytes and lichens and underscores its potential utility in their protection and conservation efforts. Specifically, our investigation identified growing degree days, maximum air temperature, and soil volumetric water content as the foremost variables influencing these ecological communities.

S.188.4 Variation of epiphytic bryophyte communities through the lens of a spatially-explicit microclimatic model in SE Asian sky trees

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At the interface between atmosphere and vegetation, epiphytes are exposed to dramatic variations of light exposure and microclimatic conditions along a tree, from the buffered conditions at the base to the amplified conditions in the outer canopy. They appear therefore as an ideal model to assess the impact of the spatial variation in microclimatic conditions at fine scales and its change under ongoing climate warming. A canopy crane giving access to 1.1 ha of tropical rainforest in Yunnan (China) was used to record hourly light, temperature and relative humidity from 54 sensors during 3 years and 408 plots of epiphytic bryophyte communities. To quantify how microclimates are buffered or amplified relative to macroclimates, we implemented, at each sensor, linear regressions between the hourly variation in microclimate and macroclimate. The slope of this regression represents an integrative parameter describing the buffering (slope < 1) or amplification (slope > 1) capacity of the canopy. We then employed a series of spatially-explicit predictors of canopy structure derived from a terrestrial LiDAR scan to predict the slope of the macro-microclimate relationship. This resulted in a spatially-explicit model of microclimatic variation in 3D, allowing for predicting the microclimatic conditions that prevail at any point in the canopy under present and future macroclimatic conditions. Microclimatic variation accounted for 33% and 18% of the variation in vertical turnover in mosses and liverworts, respectively, highlighting the crucial role of microclimates in determining the composition of epiphytic communities. Ensemble of small models were finally implemented to predict the distribution of the dominant species under present climatic conditions and evaluate the shift of their distribution under ongoing climate change.

S.188.5 Exploring environmental drivers of the non-vascular community with a process-based model

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Environmental filtering is a fundamental process that shapes plant community assembly. Understanding the impact of this process on composition of non-vascular vegetation, such as mosses and lichens, is important since the organisms provide essential ecosystem functions in many regions around the world. Responses of individual non-vascular vegetation to different environmental factors have been explored in a range of field and laboratory experiments. These observational data, however, have rarely been assembled into a comprehensive, consistent framework that allows quantitative exploration of the roles of multiple environmental factors for the performance of non-vascular vegetation, in particular across climatic regions. Here, we applied a data-driven mechanistic model that is driven by microclimate (air temperature, relative humidity, short- and longwave radiation etc.) at six study sites along a climate gradient from dryland, temperate to alpine regions to simulate the annual carbon (C) balance of lichen- and moss-dominated biocrusts, a key measure of their growth and survival. Furthermore, we performed several sensitivity analyses to investigate the relative importance of the driving factors. We found substantial effects of air temperature and CO_2 concentration on biocrust C balance, which differed, however, in their patterns across regions: ambient CO_2 concentration was the most important factor for biocrusts from drylands, while air temperature had the strongest impact at alpine and temperate sites. Further, we estimated a small annual carbon gain of biocrusts in drylands (e.g., 1.9 gm^{-2} yr^{-1} by moss-dominated biocrust), while the biocrusts lost substantial carbon at some temperate sites (e.g. -92.1 gm^{-2} yr^{-1} for lichen-dominated biocrust), which contradicts the observed survival of the organisms at the sites. We thus conclude that the uncertainties in air temperature, CO_2 concentration may be a relevant source of error and should be taken into account in future approaches that estimate the long-term C balance.

S.188.6 Urban lichens and bryophytes: diversity, distribution and response to the urban heat islands

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With the increasing urbanization and likelihood of extremely hot summers due to climate change, there is a need for investigating the impacts of the urban environment on the species communities living therein. Two ubiquitous, but often overlooked species groups are lichens and bryophytes, which have a historic background as bio-indicators. Here, we explore for the first time whether the urban heat island influences the diversity and distribution of lichens and bryophytes living epiphytically on urban trees. Additionally, we investigate the possibility of using these two groups as bio-indicators for the urban heat island. Furthermore, we investigate the patterns of temperature and humidity in different urban settings on a smaller scale using sensor data and link this with the prevalent lichen and bryophyte diversity. We conducted vegetation surveys on Tilia trees in three cities in the Netherlands (Amsterdam, Leiden and Rotterdam) and analysed species diversity and distribution patterns. Based on an indicator species analysis, we defined groups indicative for different levels of heat stress. For example, acrocarpous mosses are indicative for urban regions with much heat stress, whilst crustose lichens with photobionts belonging to the genus *Trentepohlia* Martius, 1817 are more indicative for the outer semi-rural regions. These results will be further analysed in relation to urban microclimate (temperature and humidity using sensor data) and are also being implemented in a citizen science project.

S.189 ORCHID PHYLOGENOMICS: DIVERSIFICATION, TRAIT EVOLUTION AND BIOGEOGRAPHY. SESSION 1

S.189.1 Assembling the orchid tree of life – origin and evolution of one of the largest plant families on earth

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Orchids represent one of the most striking examples of flowering plant diversification, thriving in nearly all terrestrial environments and often standing out as one of the most species-rich plant groups in tropical floras. However, their origin, spread across the globe, and hotspots of speciation remain uncertain due to the lack of an updated, densely sampled, robust phylogenomic framework. We present the most densely sampled phylogeny of the Orchidaceae utilizing combined high-throughput and Sanger sequencing datasets. Our analysis covers all five subfamilies, and included representative sampling for 17 out of 22 tribes, 40 out of 49 subtribes, 285 out of 736 genera, and ~7% (1,921) of the 29,524 accepted species. By integrating curated geographical distribution records, we infer geographic range evolution, diversity, and speciation patterns. We found that the orchids' most recent common ancestor probably lived in the Late Cretaceous Laurasia. Despite their ancient origin, modern orchid species' diversity mainly originated over the last 5 million years, with highest speciation rates in montane forests of Panama and Costa Rica. These results alter our understanding of the geographic origin of orchids, previously proposed as Australian, and pinpoint Central America as a region of recent and explosive speciation.

S.189.2 Scaphosepalum phylogenomics

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Scaphosepalum is a comparatively small orchid lineage (ca. 53 spp.) within the diverse Neotropical orchid subtribe Pleurothallidinae. Species within the genus are primarily restricted to microhabitats in Central America's and the northern Andes' premontane and montane forests. We use targeted enrichment data generated with the GoFlag 408 angiosperm probe set to infer the phylogeny of *Scaphosepalum* to test the monophyly of the genus and elucidate relationships within *Scaphosepalum* previously unresolved by Sanger sequencing. These data produced a strongly supported tree that illuminates our understanding of species circumscriptions, especially for groups (i.e., *Scaphosepalum antenniferum, S. breve, S. swertiifolium*) where a mosaic distribution of phenotypic characters has been confounding and has resulted in species over description. This well-resolved phylogenetic tree represents a fundamental tool towards a better understanding of the evolutionary and ecological drivers that led to the diversification of this orchid group. We also discuss insights from the first *Scaphosepalum* genome and metagenomic sampling of microbial communities within the flowers of *Scaphosepalum*.

S.189.3 Phylogenomics provides insights into the diversification and range evolution of the mega genus Bulbophyllum (Orchidaceae)

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The hyperdiverse orchid genus *Bulbophyllum* constitutes the second largest genus of flowering plants with more than 2,100 species and exhibits exceptional morphological and ecological diversity. The genus, comprising predominantly epiphytic species, exhibits a pantropical distribution with the highest species diversity in tropical Asia (over 1560 species), particularly in the floristic regions of Malesia and Papuasia. The high species richness and complex patterns of morphological diversity within this genus have presented significant challenges to constructing a stable and informative infrageneric classification, and to understanding patterns of evolutionary relationships and trait evolution (including ancestral range evolution). Poor resolution on phylogenetic trees from previous molecular studies based on few DNA loci has greatly hampered our understanding of the diversification of its evolutionary lineages in time and space. Here we present results from a broad-scale plastid phylogenomic study including over 450 samples, representing 398 species and 61 (of 97) sections of *Bulbophyllum,* with taxonomic focus on the highly diverse Asian clade. Maximum likelihood analyses based on 65 plastid markers yielded well-resolved and well supported phylogenetic reconstructions, clarified infrageneric relationships, and identified several non-monophyletic sections within *Bulbophyllum*, such as *Beccariana*, *Brachyantha*, *Cirrhopetalum*, *Minutissima*, *Polymeres* and *Sestochilus*. Divergence-time analyses based on secondary calibration points within a broader outgroup sampling in Orchidaceae using BEAST placed the origin of the genus in the early Oligocene and the onset of crown diversification in the late Oligocene. Species distributions were extracted from World Flora Online and biogeographic areas coded based on botanical continents and for a more-fine scaled coding within tropical Asia and Australasia, based on floristic regions following Brummit (2001). Ancestral range analyses were carried out in BIOGEOBEARS testing six biogeographic models. The findings of this study provide important insights into the phylogenomic relationships and spatiotemporal dynamics of the taxonomically complex genus Bulbophyllum.

S.189.4 Phylotranscriptomis to tease apart introgression from incomplete lineage sorting in the diversification of the Ophrys genus

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The orchid genus *Ophrys* is an outstanding example of an important and recent plant adaptive radiation. However, both this rapid diversification and the large size of its genome make its systematics and evolution difficult to study, and most of the phylogenetic hypotheses published so far are either poorly resolved and prone to display gene trees incongruences. In this context, we decided to use phylotranscriptomics as a genome complexity reduction technique to work at the genomic scale and be able to simultaneously obtain and compare thousands of gene trees to improve resolution and tease apart the relative contribution of introgression and Incomplete Lineage Sorting in *Ophrys* diversification. We *de novo* assembled more than 150 *Ophrys* floral transcriptomes to obtain an important pool of orthologous genes that we used to reconstruct a phylogeny of the *Ophrys* genus with an unprecedented resolution. This phylogeny largely confirms the relationships between the main *Ophrys* lineages obtained by other methods but also provides new insights within each of these lineages. We show that the incongruence between gene trees is not only due to Incomplete Lineage Sorting. Although introgression has been hypothesised to play an important role *in Ophrys* evolution we provide for the first time quantitative characterisation of this reticulate evolution at the genus scale. We implemented several introgression tests with different levels of complexity, from D-statistics to phylogenetic network inference, and were able to highlight several complex introgression events between the *Ophrys* lineages. This introgression analysis provides us a set of introgressed genes which will be further analysed to find their impact on phenotypic variation, in order to explore a putative adaptive role of introgression in *Ophrys* diversification.

S.189.5 Vanillomics: towards a phylogenomic monograph of neotropical vanillas

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The biodiversity of the Neotropics presents an excellent opportunity to study different evolutionary phenomena. Early divergent lineages, such as the genus Vanilla, show promise as a system to test these processes. Despite their unique characteristics, including a wide floral diversity and specialization in complex ecological interactions, many aspects of the evolution, taxonomy, and ecology of the genus remain poorly studied. This project aims to generate a comprehensive and detailed phylogeny of Neotropical vanillas through an unprecedented international collaborative effort that includes extensive taxonomic sampling and the use of high-throughput sequencing techniques, specifically the Angiosperm353 probe set. We use the species tree generated as a framework to examine the evolutionary relationships of the group, the diversification rate of major clades, their biogeography, and the evolution of certain characters. At the same time, we propose a modern monograph of the group by integrating the molecular data we generate with field studies and an extensive review of herbarium collections. Among the preliminary results are: a tissue bank of over 400 samples, covering ~85% of the total Neotropical species, with 70% resulting from the ' fieldwork; and a matrix of over 2500 specimens (including herbarium samples and flowers in alcohol) from 43 examined herbaria. This project demonstrates how regional collaborative work and the exchange of capabilities at different levels can contribute to the study of our Neotropical flora, the most diverse on the planet.

S.189.6 Assessing genomic diversity and taxonomic delimitation in the threatened Cooktown orchid species complex using target capture

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Conservation of wild species is a major responsibility given the global extinction crisis. Wild orchids face threats from illegal harvesting and trade, driven by demand for horticultural, ornamental, cosmetic, and medicinal use. For effective conservation management, it is crucial to accurately assess the genomic diversity of natural populations and determine their taxonomic boundaries. However, delimitation of species complexes in orchids remains a considerable challenge due to shallow genetic differentiation and conflicting morphological and genetic signals resulting from hybridization. The Cooktown orchid complex (*Dendrobium bigibbum* s.l.) comprises epiphytes and lithophytes with striking purple-pink flowers, rendering it a popular group for horticulture. Spanning over 140,000 km², the complex primarily occurs in the subtropical Cape York Peninsula of Queensland (Australia) and represents the state's floral emblem. Its popularity has caused overcollection in easily accessible areas, resulting in local extinctions and taxa of this complex being classified as endangered or vulnerable under national legislation. Despite being of high public interest, the taxonomic delimitation remains unclear. Since its original description, multiple species, subspecies and varieties have been proposed. This study uses next-generation sequencing to disentangle the evolutionary relationships within the Cooktown orchid complex. Over 200 individuals across its geographic distribution and morphological diversity were sampled, including associated taxa as well as intermediate forms. We compared the performance of three target capture bait kits regarding informativeness and capture efficiency: a universal bait set for all flowering plants (Angiosperms353), a custom bait set for Orchidaceae (Orchidaceae963), and a lineage-specific custom bait set for *Bulbophyllum*/*Dendrobium*. Based on our assessment, we selected the best-performing kit to generate target capture data. Our results shed light on the evolutionary patterns and genetic diversity within this threatened orchid species complex, allowing for a reassessment of taxonomic delimitation and informing conservation management to protect Queensland's botanical treasure.

S.190 NATURAL HYBRIDIZATION AND SPECIES CONSERVATION. SESSION 2

S.190.1 You may say I'm a hybrid, but I'm not the only one: assuming the dilemma of species admixture in conservation

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Speciation through hybridisation is a complex and long evolutionary process occurring in nature, where several intermediate stages might oc-

cur, all with divergent evolutionary outcomes and therefore, difficult to deal with in terms of conservation policies. The main existing tools to define conservation priorities are based on the delimitation of geographic areas and the elaboration of categorized lists of species usually prioritizing "pure species". Generally, these approximations are subsequently transposed into legislation (local, national or international) defining the uses and restrictions on the territories or taxa. The whole process has proven effective in most cases and has been adapted and updated throughout history. Yet, these conservation policies overlook any potential benefits in promoting the protection of hybrids. Despite potential advantages that many hybrids might have in facing environmental changes, they are often tagged with negative connotations: hybrids are not to be conserved as hybridization itself is a threat to the persistence of species. But even if we consider hybrids as a threat, there is an overall gap of knowledge limiting the success of any action or the creation of accurate guidelines to deal with hybrids. In this talk, we addressed the question of hybridization being considered a threat to species survival using 120,369 global species assessments available on the IUCN Red List Data. Altogether, the results showed that hybridization has been involved in species extinctions less often than thought, leaving the question: in what circumstances should hybrids be considered a threat? Should we only conserve natural hybrids? Considering the large evidence supporting the presence of hybrids, the debate dealing with the conservation of hybrids should be re-opened.

S.190.2 Identifying climatic drivers of hybridization with a new ancestral niche reconstruction method

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Applications of molecular phylogenetic approaches have uncovered evidence of hybridization across numerous clades of life, yet the environmental factors responsible for driving opportunities for hybridization remain obscure. Verbal models implicating geographic range shifts that brought species together during the Pleistocene have often been invoked, but quantitative tests using paleoclimatic data are needed to validate these models. Here, we produce a phylogeny for Heuchereae, a clade of 15 genera and 83 species in Saxifragaceae, with complete sampling of recognized species, using 277 nuclear loci and nearly complete chloroplast genomes. We then employ an improved framework with a coalescent simulation approach to test and confirm previous hybridization hypotheses and identify one new intergeneric hybridization event. Focusing on the North American distribution of Heuchereae, we introduce and implement a newly developed approach to reconstruct potential past distributions for ancestral lineages across all species in the clade and across a paleoclimatic record extending from the late Pliocene. Time calibration based on both nuclear and chloroplast trees recovers a mid- to late-Pleistocene date for most inferred hybridization events, a timeframe concomitant with repeated geographic range restriction into overlapping refugia. Our results indicate an important role for past episodes of climate change, and the contrasting responses of species with differing ecological strategies, in generating novel patterns of range contact among plant communities and therefore new opportunities for hybridization. The new ancestral niche method flexibly models the shape of niche while incorporating diverse sources of uncertainty and will be an important addition to the current comparative methods toolkit.

S.190.3 Recurrent natural hybridisation in Mediterranean Cyclamen: towards a conservation strategy for sites of ongoing evolution

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Homoploid hybridisation gives rise to new lineages having the same chromosome numbers as parental species. Therefore the reproductive isolation of hybrid individuals from parental ones is complex and slow. Moreover, homoploid hybrids act as a bridge between the two parental species, favoring introgression events among them. These often combined processes form hybrid zones where homoploid hybrid populations and introgressed parental populations coexist. This is the case for the western Mediterranean *Cyclamen* subgenus *Psilanthum*, composed of two closely related allopatric taxa (*Cyclamen repandum* and *C. balearicum*). *Cyclamen repandum* is a geographically widespread taxon (central Mediterranean Basin), whereas the second is endemic to the Balearic Islands and the south of France west of the Rhône valley. In 2002, three small populations of *C. balearicum*, *C. repandum* and bicoloured flowers were discovered in northern Corsica. These populations grow on limestone outcrops in a disjunct, until then unknown, peripheral part of the distribution of the endemic species and in an ecologically marginal area for the widespread species. Further, based on floral traits and genetic variability, it was highlighted that bicoloured floral types in these populations were of homoploid hybrid origin. Later a wide hybrid zone was discovered in north-western Sardinia, where bicoloured floral types dominate in hybrid populations, revealing a more advanced hybridisation process compared to Corsican populations. Recent findings showed that the cpDNA of all floral types in Sardinian populations is of *C. balearicum* rather than *C. repandum*, highlighting a bi-directional asymmetric introgression. These findings emphasise the need for precise comprehension of ongoing hybridisation processes to plan appropriate conservation strategies. These should include both small areas with incipient hybridisation events (like in Corsica) and wide hybrid zones where reticulate introgression among parental and hybrid lineages is the prevailing process on wide spatial scales (like in Sardinia).

S.190.4 Species delimitation in intensively hybridising genera based on herbarium specimens – the CARRARA approach

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In contrast to polyploid species formation, the high frequency of homoploid hybridisation among flowering plant species poses an even harder problem for an objective discovery and naming of phytodiversity. The formation of so-called syngameons and of introgressive hybrid swarms are incompatible with the biological species concept (BSC) and urge for additional criteria to delimit species in plant taxonomy. Even greater problems for species delimitation in hybridising plant groups arise when the biological situation is not studied and evaluated in the field, but a taxonomic judgement has to be based on herbarium specimens due to the deliberate or unavoidable abstinence from additional field work and/or the wilful usage of the rich treasure of plant specimens in museum collections. The different criteria stressed in the opposed species concepts varies among separate speciation events and are best considered being just mere indicators for independently evolving metapopulation lineages (the 'unified species concept' of De Queiroz). The Carrara approach to species delimitation in intensively hybridising plant groups follows the idea of classifying metapopulation systems as infraspecific entities (subspecies) vs. species by discriminating between primary and secondary hybrid zones. By implementing high-throughput molecular techniques based on herbarium material (AFLPseq) in combination with the automated extraction of morphological characters and ecological niche-modelling based on museum material, we aim at the fast discov-

ery and delimitation of evolutionary significant units (species) without the necessity of additional field work. Our approach will be exemplified in two plant groups of the sunflower family (Compositae, Asteraceae) known for their critical taxonomy caused by extensive hybridisation: the *Senecio nemorensis* syngameon (8 species) in Europe and the genus *Baccharis* L. in Chile (14 species, 26 hybrid combinations).

S.190.5 The Iberian Peninsula as a major hotspot for white oak conservation and analysis of species syngameons

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The Iberian Peninsula is a wide known hotspot and refugia for the Eurasian white oak species. In classic literature, this group of oaks are traditionally assumed to form common hybrid swarms, and their resulting nothotaxa have suffered of nomenclatural uncertainty. This comes from natural history artifacts and the unknown validation of putative parent species, as valid taxa that have been suffering of distinct rankings, with no consensus by the broad that treated the Iberian oaks. Here, we aimed to re-assess the phylogeographic relationships among species and investigate the occurrence of hybrid swarms in marcescent oak species (Subsection *Macrantherae*) across the Iberian Peninsula, disentangling putative hybridization and ancestral relationships. Towards this end, we used restriction-site associated DNA sequencing (RADSeq) to identify single nucleotide polymorphisms across the genomes of 275 samples representing eight widespread Iberian oak species, including infraspecific taxa and nothotaxa. Our results show that the marcescent oak species addressed in this study hold high levels of hybridization, validating several nothotaxa (*Q.×coutinhoi, Q. ×cerrioides, Q. ×subpyrenaica, Q. ×tlemcenensis*) known to form hybrid swarms in particular biogeographic areas of the Iberian Peninsula, where sometimes they exclude at least one of the parental species. We discuss these results in the framework of the Iberian oak forests conservation, and the implications it brings to understanding the western Mediterranean biogeography. Finally, we conclude that binding taxonomic and biogeographic awareness, rooted in strong historical collections and literature review is of extreme relevance for solving difficult groups of plants displaying reticulate evolution.

S.190.6 Supporting practitioners in the management of hybridization for the conservation and sustainable use of (genetic) biodiversity

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In the context of the ongoing biodiversity and climate crises, the conservation genetics community has a strong mission to support practitioners in suggesting the most useful and applicable management actions for the conservation of biodiversity, especially genetic diversity, and its sustainable use. Practitioners may have specific and variable knowledge on the effects of hybridization on biodiversity and a variety of views on its relevance in conservation strategies. To effectively support practitioners, we took advantage of the cooperation network of COST Action G-BIKE - Genomic Biodiversity Knowledge for Resilient Ecosystems - to consult practitioners, e.g., policy makers, natural areas managers, and coordinators of species action plans, from European countries about their experience, knowledge and perceptions with regard to hybridization in conservation and its management. We identified key actors in each country and presented them with a questionnaire to fill out either autonomously or through a guided interview. We interpret the results of the questionnaire in the context of the legal framework pertaining to hybridization in nature management in Europe. Furthermore, we derive recommendations combining common practices and current research findings for the management of hybridization in the most common situations or species where it occurs, in support of the conservation of genetic diversity and biodiversity more generally.

S.191 CLIMATE CHANGE EFFECTS ON ALPINE PLANT SPECIES AND COMMUNITIES: INSIGHTS FROM THE GLORIA NETWORK. SESSION 1

S.191.1 Emerging insights from global mountain research initiatives - MIREN & GLORIA meeting up at treeline

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We summarize and synthesize emerging insights from MIREN and GLORIA, including additional analyses on species reshuffling around the treeline ecotone. MIREN: Climate change threatens plant diversity in mountains worldwide. Evidence suggests that plant species respond by changing their elevational ranges. The Mountain Invasion Research Network (MIREN) systematically quantifies global patterns of native and non-native species distributions along elevation gradients and shifts arising from interactive effects of climate change and human disturbance. GLORIA: Global evidence suggests that species from lower elevations are colonizing habitats on mountain summits at an accelerating pace, with five times faster rates than half a century ago. Repeated in situ surveys in permanent plots showed a widespread transformation of alpine plant community assemblages toward more warmth-demanding and/or less cold-adapted species. Concurrently to widespread increases in overall species richness, high elevation plant species have declined in abundance and frequency. Strongly cold-adapted plant species may directly suffer from warmer and longer growing seasons. We suggest the treeline ecotone to be the critical observational zone for species reshuffling in mountain environments. Although MIREN and GLORIA permanent plots do not match in location, they jointly provide clues on changing alpine plant community dynamics.

S.191.2 Compositional shifts of alpine plant communities across the high Andes

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Climate change is transforming mountain summit plant communities worldwide, but we know little about such changes in the High Andes. Understanding large-scale patterns of vegetation changes across the Andes and the factors driving these changes is fundamental to predicting the effects of global warming. We assessed trends in vegetation cover, species richness (SR) and community-level thermal niches (CTN) and tested whether they are explained by summits' climatic conditions and soil temperature trends. Between 2012 and 2017/2019, using permanent vegetation plots placed on 45 mountain summits and soil temperature loggers situated along a ~6800 km N-S gradient, we measured species and their relative percentage cover and estimated CTN in two surveys (intervals between 5 and 8 years). We then estimated the annual rate of changes for the three variables and used generalized linear models to assess their relationship with annual precipitation, the minimum air temperatures of each summit and rates of change in the locally recorded soil temperatures. Over time, there was an average loss of vegetation cover (mean = -0.26%/yr), and a gain in SR across summits (mean = 0.38 species m2/yr), but most summits had significant increases in SR and vegetation cover. Changes in SR were positively related to minimum air temperature and soil temperature rate of change. Most plant communities experienced shifts in their composition by including greater abundances of species with broader thermal niches and higher optima. However, the measured changes in soil temperature did not explain the observed changes in CTN. High Andean vegetation is changing in cover and SR and is shifting towards species with wider thermal niche breadths. The weak relationship with soil temperature trends could have resulted from the short study period that only marginally captures changes in vegetation through time.

S.191.3 Using multi-scale tools to detect how climate change affects alpine vegetation dynamics in subtropical moist region

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Climate change is notably affecting natural vegetation, especially in mountainous regions. Alpine plants, adapted to harsh conditions such as cold, low nutrients, and high radiation, are particularly vulnerable to climatic shifts. Changes including uneven precipitation, increased droughts, and fewer rainy days significantly impact these plants. To assess the long-term effects on Taiwan's alpine vegetation, we established dynamic plots on 15 high mountain summits, aiming to study these impacts and develop conservation strategies. Our study used three methodological scales. On a landscape level, we employed the Standardized Precipitation Evapotranspiration Index (SPEI), Temperature Anomaly Index (TA), and Enhanced Vegetation Index (EVI) to link moisture balance with vegetation changes. Community-scale analysis involved examining alpine plant communities using moist-philic and thermophilic indices, diversity indices, and principal component analysis. At the species level, we assessed changes through climatic ecological niches to understand species richness variations. Our third survey revealed negative SPEI and extreme TA values, suggesting drought and high-temperature impacts. These conditions led to reduced plant growth, a decrease in EVI, fewer species, reduced diversity, and shifts towards species suited to warmer, drier environments. This suggests significant effects on Taiwan's alpine vegetation, decreasing its resilience to environmental disturbances. Considering ongoing climate change and its expected reduction in Taiwan's precipitation, our findings underscore the urgent threat of drought to alpine ecosystems, even in typically moist areas like Taiwan. Given the high sensitivity of alpine vegetation to these changes, proactive and robust conservation measures are critical to protect these vital ecosystems.

S.191.4 Climate-driven loss of plant diversity in African mountains

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Mountains host some of the most diverse and vulnerable communities of plants in Africa. With the 1.5 to 5 °C increase in temperature projected for the upcoming decades, it is hypothesised that plants will shift their distribution to track their environmental constraints along elevation and latitudinal gradients depending on their dispersal capacity. Responses like upslope and poleward shifts may result in accelerated rates of species turnover and amplified habitat loss in high elevations. Little is known about how such processes will transform the floristic composition of African mountains. Here, we apply a community-scale modelling approach to quantify and map how different climate change scenarios may affect species ranges and community richness of vascular plants in African mountains. Using niche models and dispersal buffers, we project the distributions of 416 species to three climate and land use change scenarios for the late century. Our comparisons between predicted ranges indicate that, without dispersal, species will lose an average of 22–52% of their suitable areas, depending on the SSP. We also observed a pattern of upslope elevational shifts and higher suitability losses for species occurring in higher elevations. Higher proportional losses are projected for ferns, herbs, and shrubs than for trees, with the highest losses projected for Southern Africa and Madagascar. Our results provide novel evidence for the disproportional impact of climate change on mountains and highlight target regions and species requiring more intensive conservation efforts and reforestation strategies, which need to improve the coverage of other life forms than trees. Furthermore, our findings emphasise that the current rate of change may be too rapid for some species to track based solely on their natural dispersal capacity, and alternatives like assisted migration must be carefully considered.

S.191.5 Plant ecology of Mediterranean high-mountains and GLORIA: two decades of research synergies

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Since the establishment of the GLORIA monitoring area in central Spain in 2005, a series of plant ecology research projects have been carried out, which have allowed us to gain a deeper understanding of the ecology of this type of ecosystem. In these environments, in addition to the stress factors of temperate high mountain communities (short growing season, low temperatures, snowfall, limited soil development, etc.), the existence of a summer drought period is an additional determining factor. Presented here are the most important findings from the past twenty years about the ecology of these Mediterranean communities in the heart of the Iberian Peninsula, and their global and continental contexts are also briefly discussed. Topics covered include the environmental influences on these communities composition, as well as their spatial and functional structure. Also discussed is the role of facilitative interactions in the structure of these communities. Additionally, C recycling research and the susceptibility of these ecosystems to changes to these cycles brought about by climate change have been addressed. Recent research has revealed that several species of the mountainous Mediterranean have developed unique physiological, metabolic, and morphological responses to water stress and photoprotection. Our understanding of the ecology of high mountain habitats in the Mediterranean has been enhanced by these contributions. Going forward, we are optimistic that the GLORIA monitoring data can provide additional insight on the ecosystems' vulnerability to the effects of climate change.

S.191.6 Shift in vascular plant diversity across alpine ecosystems: insights from the Italian Gloria Network

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Since 2001, the vegetation of 28 mountains has been monitored in the Italian Alps and Apennines across seven different GLORIA Target Regions (TR). The Italian Gloria Network aims to provide insights into how Italian alpine vegetation is responding to global warming. Here we present our preliminary findings regarding changes in species richness, species abundance and diversity. Species richness increased significantly in all TRs, with an average of +4.3 species per Summit Area Sections (SASs) recorded since the first survey. The highest numbers of new species were recorded in the Alps sites, with an average of +21.5 species (+13% of the total species richness), in contrast to what has been observed for Apennine TRs (on average +7 specie; +7.4%). Local species loss was also observed but was not as pronounced and did not show clear patterns, ranging from 7 species lost in the Dolomites (S-Alps) to none in the Mont Avic (W-Alps). Species' abundance changed significantly, with "winning" and "losing" species becoming more dominant or rarer, respectively, highlighting an ongoing process of community change. The disproportionate increment of "winning species" led to an overall decrease in species evenness, especially in the Apennines, which communities are becoming more dominated by fewer species. These findings highlight an alarming biodiversity loss associated with a warmer climate. Overall, although local site diversity (alpha-diversity) increased in most TRs due to new colonizing species, diversity among sites (beta-diversity) decreased consistently across sites, due to site-specific species loss and turnover, revealing a trend of floristic homogenization in Italian mountains. Finally, we observed a generalized increment of species belonging to similar growth forms (e.g., graminoids). However, further multidisciplinary studies (e.g., SENTINEL project, started in 2023) are needed to fully disentangle the role of functional traits in driving vegetation dynamics.

S.192 AN UPDATE ON THE PHYLOGENY OF SEED PLANTS. SESSION 1

S.192.1 Fossil Mesozoic Seed Plants and their Utility

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Paleontology provides a unique window on the history of life. Fossils reveal biological diversity that is now extinct and will remain unknown unless fossilized remains of these organisms are discovered, described, and interpreted. Knowledge of extinct diversity is essential to understanding the full diversity and evolutionary history of plants or animals. Paleontological data can also illuminate the history of climate or biogeography or morphological diversity through time. However, consumers of paleontological data must be aware that the identifications of fossils have the potential to be wrong, just as the identifications of herbarium specimens can be wrong and must be verified by the investigator who is using the specimens. Similarly, the stated ages of fossils can be incorrect or lack precision. If the fossils are being used as calibration points for molecular dating analyses, for example, these sources of potential error must be taken seriously. These cautions notwithstanding, this is an exciting time in plant paleontology and the fields that draw on paleobotanical data. Mesozoic age fossil seed plants have been the subject of much research in recent decades. A diversity of early fossil angiosperms have been described from a wide variety of fossil sites, and research is being conducted in geographic areas that were previously neglected. Documenting the morphology and timing of appearance of the earliest flowers continues to be of broad evolutionary and ecological interest. In addition, numerous fossil gymnospermous seed plants have also been described from many geographic areas and have included some very interesting newly discovered taxa. Understanding the origin of angiosperms and their phylogenetic relationships is important, but it cannot be accomplished without a detailed understanding of the diversity, morphology and relationships of gymnospermous seed plants. While much progress has been made there are still many discoveries to be made in the fossil record of gymnosperms.

S.192.2 Current challenges and perspectives on seed plant phylogeny

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Seed plants diversified profusely during the Paleozoic, giving rise to most of their major lineages, and a vast morphological and functional diversity. Reconstructing seed plant relationships has been a major challenge due to a deep conflict between morphological and molecular phylogenies. Here, we review some major challenges, summarize what has been learned, and propose potential ways forward. Representative sampling is a major obstacle because the number of extinct lineages vastly surpasses the five extant branches, and includes those derived from the earliest radiation of the group; extinct crown group lineages; and stem members of extant branches, which may hold clues to understanding relationships. The nature of plants typically results in fragmentary preservation and missing data. Recognition of the need to strive for whole plant reconstructions and to include species as terminals are important advances. Molecular phylogenetic estimation is complicated because extant species represent recent branches within lineages that diverged in the deep past. Molecular data has been shown to be systematically biased, and genomic datasets have not improved resolution. Paleobotanical discoveries and revised interpretations of fossil characters can critically improve phylogenetic estimation. Inconsistent taxon representation among different data sets precludes direct comparison of estimated relationships. Furthermore, different interpretations of primary homology, of structural attributes of particular fossils, and scoring philosophy result in phylogenetic lability. Analyses combining morphological and molecular data under model-based phylogenetic methods have been insufficiently exploited in the estimation of seed plant relationships, and implementation of novel approaches to model morphological character substitution hold promise. The Fossilized Birth-Death model, which integrates fossils and extant species into a single diversification process, may represent a potential alternative. Nevertheless, placement of fossils ultimately relies on morphological data, hence rigorous character assessment based on meticulous observations and thoughtful postulations of primary homology is inescapable.

S.192.3 A synthesis of new phylogenetic insights from phylogenetic studies of living and fossil seed plants

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Analyses of morphological data sets are especially important when attempting to reconstruct phylogenies for clades whose diversity has been significantly reduced during historic periods of high extinction rates. Two such clades are seed plants, and one of its included clades, the cycads. These clades have evolutionary histories that increase the difficulty of accurate phylogenetic inference from molecular data: They are deeply diverged and extant members represent a fraction of their former diversity. In the case of cycads, of the forty described genera, just ten are extant. In seed plants, approximately 70% of its major lineages are extinct. Morphology thus provides a critical line of evidence in efforts to infer accurate phylogenies for these groups. In this study, we seek to address some of the challenges inherent in phylogenetic analyses of morphological data using recently assembled morphological data sets. First, different character sets within a matrix of living and fossil taxa may vary considerably in information content and may have discordant phylogenetic signals. We therefore are using a Bayesian approach to explore information content, and using Bayes Factors to explore discordance among characters and character sets that might lead to erroneous results and/or reduced resolution. Second, development of models of evolution for use in phylogenetic analyses of morphological data sets has lagged far behind that of models of nucleotide evolution. Recent advances have, however, enabled analyses to be conducted under more realistic assumptions about the evolution of morphological characters. We thus are inferring trees using Bayesian methods that allow different relaxed models of character evolution to be tested. We discuss results from these analyses and from analyses that integrate morphological and slowly evolving molecular characters, which aim to obtain a synthetic understanding of seed plant evolution.

S.192.4 Dating the diversification of extant conifers

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Conifers are the most species-rich extant gymnosperms and have the longest and best-documented fossil history of any seed plant group, making them an excellent study system for investigating plant macroevolution. An accurate time-calibrated phylogeny is important for understanding their evolutionary history, and a number of studies have developed dated molecular trees for major conifer clades or the group as a whole. Except for the possible placement of Gnetales within conifers, backbone relationships among and within conifer families are generally stable across these studies, but inferred divergence ages vary widely depending on the dating method and calibration fossils used. Our previous work in this area used a Bayesian node dating approach and generated conifer divergence age estimates that appeared both too old for many deep nodes and too young for many shallow nodes, given paleobotanical intuition as well as more recent discoveries from Southern Hemisphere fossil assemblages. Angiosperm studies have shown that rate heterogeneity among clades can bias even sophisticated molecular dating analyses, particularly for deep nodes, and this phenomenon may be important in conifers given their long branch lengths and deep divergence ages. Here we develop an updated time-calibrated molecular phylogeny of conifers (as well as other gymnosperms) using a new node-dating approach that incorporates a hidden Markov model (HMM) in estimating divergence ages. This method allows different evolutionary rate classes to be assigned to different clades, which has been shown in simulation studies to improve divergence age estimates, particularly for deep nodes. We also suggest that node dating continues to be important for fossil plants, where important characters are often found in fragmentary remains like pollen grains that do not lend themselves to total evidence analyses.

S.192.5 The rise and fall of Peltaspermales

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Peltasperms are extinct seed plants with simple, forked, or variably dissected fern-like leaves having thick cuticle and sunken actinocytic stomata. Triangular ovules were borne on the underside of ovate or peltate appendages attached to a slender stalk. Clustered pollen sacs were arranged at the tips of loosely branched stalks. The attachment of reproductive and vegetative organs remains unresolved, but is critical to resolving their phylogenetic placement. The pollen is monosulcate or taeniate to non-taeniate bisaccate. Their wood and growth habit is unknown but they are commonly assumed to have been shrubs to trees of open habitats. Phylogenetic analyses have focused on only a few representatives of this palaeoecologically heterogeneous group. Past analyses have resolved a close relationship between Peltaspermales and Umkomasiales, but inferred affinities of these groups to other seed-plants vary widely. Peltaspermales were one of the few Paleozoic 'seed fern' clades to persist into the early Mesozoic. This order originated in the Late Carboniferous and diversified primarily within northern low- to middle-palaeolatitudes in the Permian. Several distinct groups have been recognized, generally occupying discrete regions during the Permian: supaioids (southwestern United States), callipteroids (euramerican province), tatarinoids (Volga-Uralian region), and possibly comioids (palaeotropical belt). Peltaspermales sparsely penetrated Gondwana and Cathaysia in the mid-Permian. However, following the hyperthermal end-Permian extinction event, the family abruptly spread globally and Early Triassic *Lepidopteris*/*Germaropteris* species developed thick cuticles, strongly protected stomata and small leaflets adapted to hot and seasonally dry conditions. The family rediversified through the Triassic, encompassing forms with complex reticulate venation. *Lepidopteris ottonis* markedly increased in abundance near the end-Triassic extinction event and produced aberrant pollen suggesting major disruption to reproductive strategies. Peltaspermales disappeared during the end-Triassic Extinction Event apart from two relictual Jurassic occurrences.

S.192.6 Mesozoic seed plants with recurved cupules and the stem relatives of angiosperms

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The "Mesozoic seed ferns", a loose group of extinct seed plants with cupulate ovulate reproductive organs, have long been considered to be key for understanding the origin of angiosperms. Traditionally this group has included *Caytonia*, *Petriellaea*, corystosperms, peltasperms and several other closely related groups of plants. However, most of these plants are known based on compression or impression fossils, hindering a detailed understanding of the structure and homology of their reproductive organs, and resulting in several distinct interpretations regarding the relationships of "Mesozoic seed ferns" with other extant and extinct seed plants. Recent discoveries and careful documentation of similar cupulate ovulate structures from the Early Cretaceous of Canada, Mongolia and China based on three-dimensionally preserved, lignified specimens, and anatomically preserved, permineralized material, have significantly enriched our knowledge of the anatomy, structure and homology of these cupules. Careful comparisons suggest that the recurved cupules of *Caytonia*, *Doylea*, *Jarudia*, *Geminispermum*, *Kannaskoppia*, *Ktalenia*, *Petriellaea*, *Reymanownaea*, *Umkomasia* are all fundamentally the same. Differences among these Mesozoic seed plants in the number of cupules per lateral unit, the number of seeds per cupule and the degree of seed enclosure probably reflect differences in their pollination ecology and/or seed dispersal strategies. These recurved cupules are fundamentally comparable with the second integument of an anatropous angiosperm ovule. Phylogenetic analyses suggest that the likely stem relatives of angiosperms are among these Mesozoic plants, which has important implications for continuing efforts to understand the phylogeny of seed plants and the origin of angiosperms.

S.193 THE ORIGIN AND EVOLUTION OF MODERN PLANT DIVERSITY: INSIGHTS FROM MULTIPLE DISCIPLINES. SESSION 1

S.193.1 Approaching the 'odd-man-out' of tropical rain forest diversity with a global perspective of Annonaceae evolution and biogeography

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The longitudinal distribution of tropical rain forest plant diversity presents a distinct 'odd-man-out' pattern: Neotropical and South East Asian forests are more biodiverse than their African counterparts. Understanding the contributing present and historical patterns and processes has remained challenging for decades. However, it promises to give important insights into the evolution, ecology and conservation of some of the simultaneously richest and most threatened floras of our planet. Focusing on the ubiquitous pantropical family Annonaceae with about 2450 species, we leverage a novel pipeline to curate, clean and merge herbarium specimen records from natural history collection databases, taxonomic revisions and publicly available biodiversity datasets. With these family-wide occurrences we produce species range estimates on a global scale allowing the generation of species richness maps across its distribution. We infer global and regional correlates of diversity and combine spatial data with a new species-level phylogeny of Annonaceae and modern methods of biogeographical inference to test environmental dependent diversification models using newly generated spatialized paleoclimatic simulations. Within this framework, we investigate longstanding questions on the evolutionary history and assembly of tropical rain forest floras and get one step closer to understanding the processes leading to the 'odd-man-out' pattern.

S.193.2 The evolution of phylogenetic community structure of the northern temperate flora

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Understanding the causes and evolution of the phylogenetic community structure (PCS) in the geological past is critical to explaining present-day biodiversity patterns and modelling biotic responses to climate change. The paleontological record provides a unique window into the causes and evolution of community dynamics. In this study, we compiled a large fossil community data during the Cenozoic for the North temperate zone. We quantified PCS for different geological times. We then reconstructed paleoclimate for the fossil assemblages and fit it to PCS. We finally estimated diversification rates for woody and herbaceous plants to discuss the driving factors of the evolution of PCS. Our results showed that most fossil communities were dominated by woody taxa and there was no significant latitudinal gradient during the warm early Paleogene due to the homogeneity of the environment and similar rates for woody and herbaceous plants. The establishment of the PCS latitudinal gradient coincided with global cooling and increased seasonality and the flourishing of herbs at high latitudes. The PCS latitudinal gradient after the Middle Miocene was less steep than that of the Oligocene and closer to modern times. Our comprehensive analyses shed critical insights into the evolution of the PCS latitudinal gradients and its climatic and evolutionary driving forces.

S.193.3 Late Cretaceous–Paleogene monsoon and vegetation evolution in South Asia

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The voyage of the Indian plate from the southern to the northern hemisphere took ~150 million years and experienced varied types of climate due to changing insolation at different palaeolatitudes. This makes the biota of the Indian plate unique and a perfect natural laboratory that offers a peculiar opportunity to understand the vegetation-climate relationship during the late Cretaceous–Paleogene. During this journey, India acted as a biotic ferry and facilitated the migration of biota from Africa to Asia. Besides this, India also acted as a homeland for several biota such as *Ipomoea* of Convolvulaceae from the late Paleocene, *Olea* of Oleaceae, *Eucalyptus* of Myrtaceae, and Burseraceae from the Maastrichtian–Danian sediments of Deccan Intertrappean beds. The plant fossil data compelled to believe that orders such as Sapindales, Myrtales, Solanales, and Lamiales have roots in east Gondwanaland. Moreover, the climatic reconstruction based on leaf physiognomy and nearest living relative methodologies suggests a warm and humid climate with seasonal rainfall during the entire journey of the Indian plate. The leaf morphological traits of fossils and modern forests also inferred an Indonesian-Australian type of monsoon during the Late Cretaceous–Paleogene.

S.193.4 Exploring an enigma - the geographic and temporal origins of the Western Ghats flora

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The Western Ghats are an ancient mountain range with an origin dating back to the Late Jurassic, and an extraordinarily diverse and endemic flora. The biodiversity of these sky islands has been influenced by the separation of India from Gondwana during the Late Jurassic period, and its ultimate collision with the Eurasian plate in the Late Cretaceous. As a consequence, the flora of the Western Ghats has the potential to have accreted from several regions, including Africa, the Himalayas, Continental Asia, and the Sunda Shelf. There is an emerging paradigm of tropical floras being geologically young and driven by high rates of species turnover. However, the unique journey of the Indian subcontinent alludes to the presence of an entirely unique floristic diversity in the Western Ghats. The aim of this project was to understand the temporal and geographic origins of the Western Ghats flora. A herbarium genomics approach was employed (Whole Genome Sequencing) to assemble DNA regions of species native or endemic to the Ghats and incorporate them into existing phylogenetic datasets of plant families with wider tropical distributions. Time-calibrated phylogenies and ancestral range evolution models were used to provide a synthetic view of the flora's origins using the families *Annonaceae*, *Begoniaceae*, *Chloranthaceae*, *Dipterocarpaceae*, *Ebenaceae*, *Lauraceae*, *Sapotaceae*, and *Zingiberaceae* as representatives. The ancestral area reconstructions show that the Western Ghats flora originated predominantly from the regions of Continental Asia and the Sunda Shelf during the Miocene-Pliocene period, showing a flora strongly influenced by geologically recent dispersal rather than ancient vicariance.

S.193.5 Angiosperms preserved in Mexican amber: towards the integration of Neotropical Flora

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The Neotropics stands out as a region that harbors remarkable biological diversity, especially within the group of angiosperms or flowering plants. A comprehensive understanding of the origin of this biodiversity involves the integration of the fossil record, which, unfortunately, is scarce in this area. Bioinclusions of angiosperms preserved in Mexican amber emerge as a unique source of information. Their relatively recent antiquity, corresponding to the Miocene (approximately 23-15 Mya), provides valuable insights into the recent history of vegetation in the region. The Miocene period appears to have played a crucial role in the "modernization" of vegetation, as the angiosperms identified in Mexican amber are strikingly like contemporary plants. This phenomenon suggests a process of evolution and adaptation over time. This study focuses on reports of angiosperms in Mexican amber, identified as extinct members of the Staphyleaceae, Celastraceae, and Leguminosae families. These findings reveal a closer biogeographical connection with floristic elements of the Paleotropics, supporting the notion of a link between tropical regions through intercontinental dispersal routes during the Cenozoic, known as the Boreotropical Flora. To validate this hypothesis, it is essential to continue documenting the diversity of flowering plants in Mexican amber deposits. Analyzing current lineages with disjunct distribution patterns will allow the development of a more robust biogeographical hypothesis. This comprehensive approach will significantly contribute to our understanding of the evolution of biodiversity in the Neotropics and interconnections over geological time.

S.193.6 Ecuadorian páramos: towards a checklist of the vascular Flora

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The Ecuadorian páramos constitute a complex and heterogeneous biome, integrated by several ecosystems, whose plant composition vary according to climate, altitude, geology, biogeographic history, and disturbance degree. The uplift of the Andes and the Pleistocene glacial and interglacial events, in addition to anthropogenic activities, helped to consolidate the Andean plant communities. The present work is based on bibliographic data, field work, and the revision of herbaria collections, particularly QCA and MO. In our work, we have recorded 1897 vascular plant species, which is the highest number of species cited for this biome in Ecuador, (1682 Angiosperms, 210 Pteridophytes and five Gymnosperms), of which 1161 are native, 699 are endemic to Ecuador and 37 are introduced. We found that the 10 most diverse families in this biome were: Asteraceae, Orchidaceae, Poaceae, Melastomataceae, Campanulaceae, Cyperaceae, Rosaceae, Ericaceae, Polypodiaceae, and Lycopodiaceae; whereas the 10 richest genera were: *Epidendrum*, *Elaphoglossum*, *Phlegmariurus*, *Calceolaria*, *Senecio*, *Gentianella*, *Valeriana*, *Miconia*, *Gynoxys*, and *Carex*. 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.

S.194 ECOLOGY, EVOLUTION AND GENETICS OF STYLAR POLYMORPHISMS: LINKING FORM & FUNCTION

S.194.1 Deep homology or convergence? Comparative genomics elucidates the origins of the heterostyly supergene

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The rapid accumulation of high-quality reference genomes now enables us to re-examine long-standing questions on evolutionary convergence: Does convergence at the phenotypic level correspond to shallow convergence or deep homology at the genotypic level? Do the same genes and genetic architectures underlie convergent traits or can different genes be recruited to achieve the same phenotypic outcome? Heterostyly in Primulaceae represents an ideal system to investigate these questions. Found in 28 families of flowering plants, heterostyly refers to the co-occurrence in a population of different plants characterized by self-incompatible floral morphs with reciprocally placed male and female sexual organs, a combination promoting outcrossing while restricting selfing. Originally investigated by Darwin in *Primula*, heterostyly in this genus is now known to be controlled by the S-locus, a hemizygous supergene comprising a minimum of four genes with paralogues elsewhere in the genome. Published phylogenetic analyses of trait evolution showed that heterostyly evolved independently three times in Primulaceae, namely in the ancestor of *Primula*, in *Hottonia palustris*, and in *Androsace vitaliana*. However, it remains unknown whether the genes determining heterostyly also evolved multiple times concomitantly with heterostyly or were already present in the common ancestor of the three heterostylous lineages but were subsequently lost in non-heterostylous relatives. To test the alternative predictions stemming from these two hypotheses, we generated highly contiguous, chromosome-scale, haplotype-phased assemblies of heterostylous and non-heterostylous genomes of Primulaceae and performed comparative genomic analyses across Ericales, the order that includes Primulaceae. Preliminary results suggest that the three independent origins of heterostyly inferred via phylogenetic analyses of trait evolution might stem from both deep homology of duplicated S-locus genes and genetic reinvention. Primulaceae thus represent an ideal system to clarify the connections and disconnections of evolutionary convergence from the genotypic to the phenotypic level and back.

S.194.2 What we do and don't know about stylar polymorphisms in flowering plants

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Among the most remarkable floral strategies in flowering plants are those involving stylar polymorphisms. Unlike the majority of angiosperms with continuous phenotypic variation in style and stamen deployment, species with stylar polymorphism have discrete patterns of sex-organ variation and populations with morphologically identifiable, genetically controlled floral morphs. The most well-known stylar polymorphisms are distyly and tristyly. Since Darwin's classic book on heterostyly – "Forms of Flowers" – ecologists and evolutionary biologists have been fascinated by the origins and adaptive significance of these polymorphisms. We now know that at least some of these polymorphisms are controlled by linkage groups composed of major genes, and that they are maintained in populations by negative frequency-dependent selection resulting from disassortative mating between morphs. Work on unrelated distylous and tristylous species has revealed much about the variation in expression and the functions of the various components of the heterostylous syndrome. However, our understanding of the other four classes of stylar polymorphism – stigma-height dimorphism, enantiostyly, flexistyly and inversostyly – is far less complete. Here, I summarize what we currently know about the six stylar polymorphisms in an effort to synthesize similarities and differences between the polymorphisms and general principles that may apply to all of them. I focus on recent work on three main topics: 1) the genetic architecture of distyly and tristyly supergenes and patterns of molecular convergence among unrelated lineages; 2) efforts to understand the molecular underpinnings of enantiostyly and flexistyly; 3) the ecology and evolution of breakdown in the maintenance of stylar polymorphisms and the genomic consequences of the resulting transitions in the mating biology of populations. I conclude by highlighting unresolved questions in the study of stylar polymorphisms and why these polymorphisms remain attractive systems for the study of adaptation and evolution.

S.194.3 Telling left from right - the genetic and molecular basis of enantiostyly in Wachendorfia and Barberetta

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Telling left from right is a difficult task for organisms, as the two sides can only defined by reference to two other axes. While genetically encoded left-right asymmetry is found in many animals, it is very rare in plants. One example is the mirror-image flowers of *Wachendorfia* and *Barberetta*. Species of these two closely related genera show enantiostyly, i.e., they form flowers with the style deflected to the left of the midline and one of the three stamens to the right, or with the opposite arrangement. All flowers on one individual have the same handedness, indicating genetic control. Functionally, the reciprocal placement of the stigma and the opposing anther promotes pollen placement on segregated sites of the pollinators' bodies and efficient transfer to stigmas of the opposite morph. We are investigating the genetic, molecular and developmental basis of mirror-image style and stamen deflection in *Wachendorfia* and *Barberetta*. Genome assemblies and pooled sequencing of left- and right-morph individuals from natural populations have identified a hemizygous region whose presence causes right-styled flowers, whereas plants lacking this region form left-styled flowers. This region contains two conserved genes throughout all the species tested, one of which is expressed in the developing stamen, the other in the style around the time when the organs begin to deflect from the midline. Efforts to assign functions to these genes are ongoing. Identification of the hemizygous region opens up the possibility of assaying realized mating patterns in natural populations and testing the efficiency of enantiostyly in promoting disassortative mating. Thus, our results pave the way for a mechanistic understanding of left-right asymmetry in plants and its impact on plant reproduction.

S.194.4 Breakdown of distyly in tropical Rubiaceae: breeding system and morphometric changes

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The Rubiaceae is a widely distributed, megadiverse angiosperm family. Distyly is the prevalent floral system in many Rubiaceae, especially in the Brazilian

Cerrado and other tropical environments. Besides two floral morphs with reciprocal stigma and stamens heights, distyly is associated with a heteromorphic incompatibility system and other ancillary morphological traits. Since the majority of Rubiaceae depends on precise biotic pollination services for their reproductive success, distyly is vital for their persistence. Nevertheless, morphological changes followed by the loss of floral polymorphism are common, leading to anomalous species or populations displaying homostyly, monomorphism or even dioecy. These reproductive transitions have occurred repeatedly in the Psychotrieae alliance, which includes the most speciose distylous genera, *Palicourea* and *Psychotria*. Anomalous distyly cases do not show any clear phylogenetic clustering, but seem to be associated with anthropized/disturbed or island environments, and inefficient pollination. As in other distylous groups, these changes have been explained by sudden mutation events within a supergene model, which include both morphological and self-incompatibility alleles. However, community-wide approaches have shown that distylous Rubiaceae lack precise reciprocity in the height of their sexual organs, often displaying higher inaccuracies either in low or higher organs. These changes seem to be linked to reduced floral integration, possibly under pressure from the loss of precise pollination, which seems to be required for efficient distyly functioning. The losses of ancillary features and reciprocity are often associated with less strict self-incompatibility. We suggest here that the reduction of floral integration and reciprocity, besides other ancillary features associated with distyly, may be intermediate transition stages. In more advanced stages, these changes may lead to a complete breakdown of the system. Such trends can be used as indicators of environmental pressures on distyly functioning.

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S.194.5 Shift in pollinator effectiveness results in chronic pollen limitation in an enantiostylous, buzz-pollinated species

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Diverse floral mechanisms have evolved in angiosperms to promote cross-pollination and outcrossed mating. One such innovation is the sexual polymorphism enantiostyly ('mirror-image flowers') where styles are deflected either left (L), or right (R) of the flower's midline. This asymmetry is usually associated with heteranthery, the structural specialization of anthers for feeding and pollinating functions. Pollinating anthers are reciprocally positioned to the style promoting bee-mediated cross-pollination between flowers of opposite 'handedness' by 'buzz-pollinating' bees. *Cyanella* has nine species mostly endemic to the Western Cape, South Africa; six are straight-styled and two possess enantiostyly. Here, we present current research on *C. alba* using multiple populations in the Biedouw valley and Bokkeveld plateau, all of which contained three sex phenotypes – left- and right-handed plants and those with a mixture of both flower types (L, R, M, respectively). Surveys of handedness revealed average frequencies of L=0.47, R=0.43, M=0.10 among 15 populations with an average daily display size of 1.6 flowers. Censuses of marked plants throughout two seasons in three populations revealed an increase in M frequency concomitant with decreases in L or R plants. Controlled crosses demonstrated moderate self-incompatibility, with plants incapable of autonomous self-pollination. Comparisons of open- versus controlled cross-pollinations revealed chronic pollen limitation of seed set. Despite 74 hours of observation, we observed only two short visits by buzz-pollinating bees and most flower visits were by beetles. Observations of stamen dimorphism at the northern range edge suggest that heteranthery may be breaking down in some populations enabling generalist pollination, perhaps in response to the absence of visits by bees capable of buzz pollination. *Cyanella alba* plants display few flowers daily and this could enable enantiostyly to function effectively without genetic determinism of floral polymorphism. Breakdown of heteranthery in some populations has probably resulted from a lack of buzz pollination.

S.194.6 Pollinator composition explains the symmetry of pollen transfer between floral morphs of a distylous species.

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Populations of distylous species are composed of individuals of two floral morphs that exhibit contrasting but reciprocal spacial arrangement of sexual organs: in the short-styled morph (S-morph), stigmas are located below the anthers, while in the long-styled morph (L-morph) this arrangement is reversed. This feature predicts cross-pollination between morphs, promoted by the morphological fit of pollinators to flowers and sexual organs. However, it has been reported that the pollination process can occur more efficiently in one direction (from L- to S-morph flowers or vice versa), suggesting a sub-optimal efficiency of the pollinator assemblage. This study analyses the relationship between pollinator composition and pollination efficiency in 16 populations of a distylous species. Pollination efficiency at each population and direction was assessed by quantifying pollen deposition and pollen tube growth through epifluorescence microscopy. The data shows inter-population variation in the efficiency of pollen flow, which was explained by the composition of the pollinator assemblage. In particular, in populations with a lower proportion of visits from a beefly genus, pollen flow from L- to S-morph flowers occurred less efficiently. This result points to suboptimal pollination as a driver of asymmetrical pollen flow in distylous species and highlight the importance of pollinators in the proper functioning and probably evolutionary maintenance of distyly.

S.195 BEYOND PLANT BLINDNESS: BRINGING PLANTS INTO THE FOREGROUND

S.195.1 Children's perception and plant identification knowledge: Using drawing to tackle emic perspective.

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In small-scale societies, people learn to identify plant species during childhood. Plant recognition is an important baseline knowledge, immediately useful to avoid intoxication risk due to wrong identification. Plant recognition is at the basis of other ethnobotanical knowledge. However, despite many studies on folk classification, we still have a narrow understanding of the criteria locally used for species identification; the gap being even larger regarding children's plant identification criteria. Here, we study the criteria used by Betsileo children and adolescents to identify wild edible plant (WEP) species using a child-adapted method including drawings and follow-up interviews. We worked with 80 teenagers (from 12 to 17 years old; 51 girls, and 29 boys). Our results suggest that teenagers use a large spectrum of visual criteria to identify plants and that these criteria match with botanical and ecological knowledge documented in the literature and herbarium vouchers. We found that 35% of the identification criteria used were non-morphological (e.g., phenology, biotic interactions), suggesting deep ecological knowledge. On average, teenagers use more than nine distinct criteria per plant, which allows them to identify most plant species with a very high level of precision. The precision level of plant representation increases with age for boys, but remains constant for girls, suggesting different dynamics in plant identification knowledge acquisition. We also found that boys and girls use different identification criteria: girls focus on morphological criteria while boys also incorporate ecological criteria, such as landscape features and biotic interactions, in their spectrum of identification keys. Our results highlight the complexity of teenagers' plant knowledge and the importance of the ecological context for plant identification. Finally, our finding suggests that gender plays an important role in plant identification's knowledge acquisition, probably because gender differentiates daily interactions with plants.

S.195.2 Ethnobotany fosters the interest on plants. Different ways of returning knowledge to society in the Catalan linguistic area

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Plant blindness -or, at least a certain degree of plant myopia- does exist, as plants are often either neglected by people as objects of interest or much less considered than animals, the latter probably reflecting phylogenetic proximity and empathy. This concerns people in many aspects of their lives, and even students at different levels in academic subject preferences. Nevertheless, it is also true that there is an extended interest of people in nature, natural products useful for many purposes, and biodiversity. Ethnobotanical research can undoubtedly contribute to attracting general people's attention to plants, for different reasons. First of all, for its multidisciplinarity, for its situation in the interface between social and natural sciences, for highlighting biocultural aspects of plants. Secondly, for its important component of citizen science, in which academic and popular knowledge converge. Finally, for the ethical commitment that an ethnobotanist has to return to society (and not only to the scientific community, as is logical in any research) the knowledge that comes from it. In this communication, we delve into the ways our research team employed on ethnobotany of the Catalan linguistic area. Our objective is to disseminate the traditional knowledge on plant biodiversity and to try to increase people's interest in plants, their names and uses and their management. Different kinds of outreach publications, an open-access webpage, educational issues, conferences, practical workshops are powerful instruments to capture people's attention for plants and their biocultural aspects, and, therefore, to diminish the extent of plant blindness.

S.195.3 Unveiling plant blindness through mental models

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This study addresses the widespread problem of 'plant blindness', a phenomenon characterised by the neglect of plants in both everyday perception and educational settings. Focusing on 162 students aged 6-18, the research uses drawings as a tool to uncover their mental models (internal representations of concepts and ideas), providing insights into the depth of their understanding and attention to plants, trees, flowers, and grass. Through the analysis of drawings, the study examines the mental models associated with these botanical terms, shedding light on the prevalence of plant blindness and the simplification of ideas related to plants. The results show that the term 'tree' serves as a reliable indicator of how complex plants are perceived in nature and depicted in drawings. In particular, the study reveals consistency in mental models across age groups, highlighting common features in plant representations. Statistical analyses reveal age-related anomalies and changes in certain features of mental models. Notable findings include an increased occurrence of leaf veins from around 8–9 years of age. These findings contribute to a nuanced understanding of how students' perceptions of plants develop over the course of their schooling. Comparisons with previous research show consistency with existing findings. However, this study introduces new insights, such as the age-related emergence of specific features in mental models. These findings provide opportunities to optimise teaching strategies, address knowledge gaps and potentially reduce plant blindness. In addition, the study establishes a link between the term 'tree' and the detailed perception of plants in the environment, suggesting that drawings can be a valuable tool for assessing students' knowledge of plant structure and anatomy. Standardised methods of investigation using drawings may facilitate the identification of plant blindness within groups of students, providing a practical means of improving botanical education.

S.195.4 Beyond plant awareness disparity: intangible relationships with plants among ethnobotanical experts in the Catalan Pyrenees

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Although plants contribute to human well-being, their importance is vastly underestimated. This socio-psychological phenomenon, widely known as Plant Awareness Disparity (PAD), has been studied by looking at people's knowledge of plants, their interest on them, the level of attention they pay to them, and their general attitudes towards their conservation. Yet, the emotional dimensions, encapsulated through our intangible relations with plants, have been largely undervalued in the study of PAD. Moreover, while PAD has been documented among mostly urban and industrialized settings, traditional plant-related wisdom of rural communities is virtually absent from this discussion. This study explores the intangible relations between local ethnobotanical knowledge holders and plants at three levels – communal, familial, and individual – by exploring diverse aspects of expressive culture such as stories, songs, and personal recollections anchored in lived experiences. We propose a methodological approach to document and characterize these intangible connections with plants and recognize them in the study of PAD. In-depth interviews were conducted among 22 recognized ethnobotanical knowledge keepers in the Camprodon Valley (Catalan Pyrenees, Spain). Exhibiting notably low PAD levels, our informants reported a myriad of cultural, familial, and individual expressions of their bonds with the shared botanical heritage of the valley, including 36 distinct sayings, 53 anecdotes, 27 traditions, and 31 family customs. Our findings shed light on the intricate relations between humans and plants in rural communities, largely underpinned by emotional connections and a sense of cultural identity. These findings hold large implications for studies aimed at gauging plant awareness and quantifying PAD levels, while underscoring the breadth and depth of humans' many intangible relationships with the plant worlds around them.

S.195.5 Can plant blindness be detected on the vocabulary level: poor descriptions of personally important plants, in Tartu, Estonia

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In modern society, knowledge about plants can originate from the family, from official sources or many hybrid forms in between (coming from media). The history of the scholarly botanical terminology in Estonia dates back to 1881, when the first botany schoolbook in Estonian was published. The next botany book, intended for a wide readership, was published in 1922 and contained greatly different content and terminology. Changing technical terms over time is only part of the problem. Looking at the present day botanical literature in Estonian, we see that the vocabulary used in current botanical literature has become increasingly specialized, understandable just to the specialists in the field. For ordinary citizens, such terms often remain distant and ambiguous. We conducted a qualitative survey on the Google Forms platform, answered by 149 people living in Tartu. We asked to free list up to 10 trees/shrubs, herbaceous plants and cultivated plants that they consider important. As additional qualitative questions, we asked why these plants are important to them and how the respondents would describe these plants. Only a few plants were described. Moreover, comparing the description of the most popular tree (birch) with the official key book gave a noticeable difference. We can clearly see that as the terminology of botanical literature diverges greatly from the local plant-related terminology, people may have less interest in those books. Neither do they need to describe different plants to each other in their everyday life, which leads to a loss of local botanical vocabulary in Estonian. We propose to name this phenomenon linguistic plant blindness and invite colleagues to discuss whether plant key books should consider using local plant-related vocabulary in parallel with the scientific one and include local plant uses to promote the interest in plants and through that reduce linguistic plant blindness.

S.196 GRASSROOTS MULTIDISCIPLINARY AND INTEGRATIVE RESEARCH ON THE GLOBAL DIVERSITY OF THE GRASSES (POACEAE). SESSION 2

S.196.1 Floral trait syndromes in tropical grasses and their environmental associations

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Grass floral structures vary greatly but we have very little understanding of their functional significance. Due to the varied dispersal mechanisms shown by grasses, certain syndromes of floral traits would likely be associated with particular strategies for dispersal, and consequently, different environments. In particular, effective seed maturation and dispersal in fire-prone tall grasslands would require different floral trait syndromes than in short, frequently grazed ecosystems. Here we quantify floral traits of nearly 200 Poaceae species from savanna and grassland ecosystems in southern Africa and explore how their floral structures co-vary and correlate with other functional characteristics such as grass height. Using field information on the dominance disturbance regime of 163 of these grass species it was tested whether certain floral traits are more associated with fire vs grazing and mean rainfall arranged from 323–1256 mm.yr^{-1} in the study areas. Non-metric multi-dimensional scaling (NMDS) was used to illustrate how floral traits co-varied among grass species, and to group them into syndromes based on these traits. Analysis of variance (ANOVA) was used to test whether certain floral trait syndromes were more associated with fire vs grazing. We identified four clear floral trait syndromes separated largely by awn length and the presence of hooks/prickles or bristles. Long-awned species were more likely to be found in frequently burned environments and were also usually taller than species without awns. Grazer-dominated systems appear to select for two different floral trait syndromes which are no lemma awns, blunt or no callus sharpness. The study has improved our ecological and taxonomic understanding of how floral traits differ among the range of tribes in one family across African countries. It can help in understanding dispersal limitations in grasses and predicting which species are likely to flourish in particular grassland habitats.

S.196.2 Poaceae as a model clade for understanding cold tolerance evolution and adaptation to temperate biomes

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Grasses (Poaceae) are thought to have originated in the moist tropics in the Late Cretaceous. Their long evolutionary history has seen multiple independent transitions to open, dry habitats as well as cold and freezing ones. The >11,000 species extant today are globally distributed, occurring on all continents including Antarctica and dominating biomes ranging from topical savannahs to alpine grasslands and boreal tundra. Grasses already constitute a model clade for understanding C4 evolution and biome formation (grasslands). This research benefits from 1) a large, active community of grass taxonomists, systematists and palaeobotanists, 2) rich genetic and genomics resources, centred on economically important species such as the cereals and the model organism *Brachypodium distachyon* and 3) the fact that many species grow fast and have short lifecycles, making them easy to cultivate and manipulate experimentally. Despite this, and although grasses are both diverse and abundant across the coldest places on Earth, we have a relatively poor understanding of the details surrounding evolution of cold tolerance in the clade, whether repeated topical-temperate-transitions were facilitated by precursor traits, what traits characterise the species that occupy the coldest habitats and the order of events leading to the suite of adaptations that have made grasses so successful in temperate biomes today. In this talk, we showcase grasses as a model for understanding tropical-to-temperate transitions and present ongoing multidisciplinary work across grasses as a whole, as well as in smaller clades. Comparative, experimental, ecophysiological, ecological and genetic work is providing new perspectives on cold tolerance evolution and adaptation to temperate biomes, with implications for other angiosperms as well.

S.196.3 Adapting to high stress environments: Grasses from geothermally heated areas of Iceland

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Geothermal areas are formed where Earth's inner heat is transported to the surface. This results in peculiar formations including fumaroles, geysers and heated soils. Geothermal areas are high stress, low diversity environments, with the main factor limiting the presence of most life there being heat. The diversity of land plants occurring on geothermally heated soils is relatively well characterised, with mosses and grasses (Poaceae) being particularly common at the hottest sites. However, the geographical origin of geothermal organisms is largely unknown, as are the effects of adapting to geothermal heat, e.g. phenological shifts or performance under cooler conditions. Here we present ongoing work on geothermal grasses from Iceland, a subarctic island where scorching geothermal areas and bitterly cold non-thermal areas occur side by side. We show for the genus *Agrostis*, which occurs on soils <70°C, that *A. stolonifera* has colonised Iceland at least twice, leading to one lineage exclusive to geothermal areas and another exclusive to non-thermal areas. In contrast, *A. vinealis* has colonised Iceland just once, leading to a single widespread lineage occupying geothermal and non-thermal areas alike. We further show phenotypic differences, increased heat tolerance, reduced performance under cooler conditions and a shift in flowering phenology for geothermal compared to non-thermal *A. stolonifera*, suggesting that geothermal *A. stolonifera* represents a specialised, thermophilic lineage. Finally, we study *Festuca rubra*, which is found on moderately warmed soils (<30°C). This species showed no difference in thermal tolerance, winter survival ability or phenology in response to geothermal warming, suggesting it is adjusting plastically to the geothermal conditions. Our results highlight that responses to geothermal warming can be idiosyncratic, even among close relatives, and pave the way for further studies of both adaptations to extreme environments and responses to moderate warming, using the natural laboratory afforded by geothermal areas.

S.196.4 Grass diversity in Brazil and the Flora of Brazil project

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Brazil is a megadiverse country and houses a larger number of plant species than any other country in the world. The study of its flora has a long history, including many foreign naturalists collecting in Brazil throughout the 18th and 19th centuries and sending these plants to European herbaria. Until recently, the most comprehensive treatment of the Brazilian flora was the "Flora Brasiliensis", edited by Carl Friedrich von Martius (1840-1906). Over the past 15 years, a huge number of taxonomists have joined efforts in the Flora of Brazil project, motivated to meet Target 1 of the Global Strategy for Plant Conservation (GSPC). The Flora of Brazil project currently recognizes more than 52 thousand species of algae, fungi, and plants that occur in the country. Identification keys, morphological descriptions, illustrations, and data on their habitat and geographic distribution are available online for most taxa, including grasses. Poaceae is the fourth richest angiosperm family in Brazil, with around 230 genera and 1.560 species. These numbers correspond to almost a third of the genera and about 13% of the grass species in the world. Of these, 24 genera and about 520 species are endemic to Brazil. Representatives of all subfamilies, except Puelioideae, occur in Brazil, including Anomochlooideae, the first lineage that diverged within Poaceae. This subfamily predominates in Brazilian forests, as do Pharoideae and Bambusoideae, while Panicoideae (the richest subfamily in Brazil) dominates tropical and subtropical grasslands. On the other hand, Pooideae and Danthonioideae have a predominantly extratropical distribution in Brazil, decreasing in species richness and density from south to north. Phylogenetic studies including Brazilian grasses have increased greatly in the last decade, as well as the number of new taxonomists in this family, improving our knowledge about genera and species and resulting in several nomenclatural changes in taxa from Brazil.

S.196.5 Taxonomic studies on the tribe Jansenelleae Voronts. (Poaceae: Panicoideae: Andropogonodae) in India

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Jansenelleae Voronts., a rare C_3 Asian grass lineage, was recently elevated as a tribe and comprises two genera, *Jansenella* Bor and *Chandrasekharania* V.J.Nair, V.S.Ramach. & Sreek. The former genus contains two species *Jansenella griffithiana* (Müll.Hal.) Bor and *Jansenella neglecta* S.R.Yadav, Chivalkar & Gosavi and the latter is monotypic with *Chandrasekharania keralensis* V.J.Nair, V.S.Ramach. & Sreek. Among the three species within the tribe *Jansenella griffithiana* is the only widespread species, and is reported from India, Sri Lanka, Myanmar and Thailand. The other two species are endemic to the Western Ghats. The restricted distribution and sporadic nature of this group is evident from the limited volume of literature regarding this group. Apart from the type, *Chandrasekharania* is represented by a few collections only. *Jansenella griffithiana* is the only species in the tribe in which few investigations are undertaken; and *Chandrasekharania keralensis* and *Jansenella neglecta* are not studied thoroughly. This paper discusses the taxonomy and nomenclature of the tribe Jansenelleae in detail.

S.196.6 The mitochondrial genome of the diploid oat Avena longiglumis

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Avena longiglumis Durieu ($2n=2x=14$) is a wild relative of cultivated oat (*Avena sativa*, $2n=6x=42$) with good agronomic and nutritional traits. The plant mitochondrial genome has a complex organization and carries genetic traits of value in exploiting genetic resources, not least male sterility alleles used to generate F_1 hybrid seed. Therefore, we aimed to complement the chromosomal-level nuclear and chloroplast genome assemblies of *A. longiglumis* with the complete assembly of the mitochondrial genome (mitogenome) based on Illumina and ONT long reads, comparing its structure with Poaceae species. The complete mitochondrial genome of *A. longiglumis* can be represented by one master circular genome being 548,445 bp long with a GC content of 44.05%. It can be represented in four circular DNA molecules (isoforms or contigs), with multiple alternative configurations mediated by long (4,100–31,235 bp) and medium (144–792 bp) size repeats. Thirty-five unique protein-coding genes, three unique rRNA genes, and 11 unique tRNA genes were identified. The mitogenome was rich in duplications (up to 233 kb long) and multiple tandem or simple sequence repeats, together accounting for more than 42.5% of the length. We identified homologous sequences between the mitochondrial, plastid and nuclear genomes, including exchange of eight plastid-derived tRNA genes, and nuclear-derived retroelement fragments. At least 85% of the mitogenome is duplicating in the *A. longiglumis* nuclear genome. We identified 269 RNA editing sites in mitochondrial protein-coding genes including stop codons truncating *ccmFC* transcripts. Comparative analysis with Poaceae species revealed the dynamic and ongoing evolutionary changes in mitochondrial genome structure and gene content. The complete mitochondrial genome of *A. longiglumis*, completes the last link of the oat reference genome and lays the foundation for oat breeding and exploiting the biodiversity in the genus.

S.197 GENOMICS OF LOCAL ADAPTATION. SESSION 3

S.197.1 Subgenomic stability of progenitor genomes during repeated allotetraploid origins of the same grass Brachypodium hybridum

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Both homeologous exchanges (HEs) and homeologous expression bias (HEB) are generally found in most allopolyploid species. Whether HEs and HEBs differ between repeated allopolyploid speciation events from the same progenitor species remains unknown. Here we detected a third independent and recent allotetraploid origin for the model grass *Brachypodium hybridum*, discarding alternative scenarios of potential introgressions of early allotetraploids with diploid progenitor species. Our HE with replacement analyses indicated the absence of significant homeologous exchanges in any of the three types of wild allotetraploids, supporting the integrity of their progenitor subgenomes and the immediate creation of the amphidiploids. The absence of HE is probably due to the distinct structure of the "homeologous" progenitor chromosomes. Specifically, the five *B. distachyon* chromosomes resulted from four centromeric nested chromosome fusions of the ten *B. stacei* chromosomes, making homeologous crossovers highly improbable in the *B. hybridum* nucleus. Further HEB tests did not uncover significant subgenomic dominance in different tissues and conditions of the allotetraploids. This suggests a balanced expression of homeologs under similar or dissimilar ecological conditions in their natural habitats. We observed that the density of transposons around genes was not associated with the initial establishment of subgenome dominance; rather, this feature is inherited from the progenitor genome. We found that drought response genes were highly induced in the two subgenomes, likely contributing to the local adaptation of this species to arid habitats in the third allotetraploid event. These findings provide evidence for the consistency of subgenomic stability of parental genomes across multiple allopolyploidization events that led to the same species at different periods. Our study emphasizes the importance of selecting closely related progenitor species genomes to accurately assess HE with replacement in allopolyploids, thereby avoiding the detection of false HEs when using less related progenitor species genomes.

S.197.2 Genomic and phenotypic responses to climate in European grasslands

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In recent decades, there has been an increasing number of studies on the genetic basis of adaptation in a variety of species of agricultural importance. These studies are based on the idea that we can predict the optimal genetic component to cope with climate change by identifying the current allelic frequencies of adaptive genes in particular climates or geographical regions. This approach assumes that, in the absence of temporal data (future climate), these can be replaced by geographic data.

Here we present results on geographic genetic variability in perennial ryegrass (*Lolium perenne* L.) but also temporal genetic variability in meadow fescue (*Festuca pratensis* Huds.). We identified the temporal genetic change in meadow fescue using populations sampled long enough to empirically analyze allele frequency changes over evolutionary time. We sampled three meadow fescue populations from Switzerland that have evolved without artificial reseeding. We performed whole genome sequencing of pooled samples (pool-Seq) on individuals derived from seed samples of these populations, which were sampled in the late 1970s and resampled in 2021, and analyzed allele frequency differences across the genome. We also grew these individuals in a common garden and measured agronomic traits associated with adaptation to climate. Analysis of allele frequency and phenotypic changes in these populations will provide information on the candidate genomic and physiological mechanisms of adaptation to climate change in grassland species.

S.197.3 Adaptation in unstable environments via global gene losses - Small but steady by the May-Wigner theory

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Although gene loss is common in evolution, it remains unclear whether it is an adaptive process. In a survey of six major mangrove clades that are woody plants in the intertidal zones of daily environmental perturbations, we noticed that they generally evolved reduced gene numbers. We then focused on the largest clade of Rhizophoreae and observed the continual gene set reduction in each of the eight species. A great majority of gene losses are concentrated on environmental interaction processes, presumably to cope with the constant fluctuations in the tidal environments. Genes of the general processes for woody plants are largely retained. In particular, fewer gene losses are found in physiological traits such as viviparous seeds, high salinity and high tannin content. Given the broad and continual genome reductions, we propose the May-Wigner theory (MWT) of system stability as the underlying mechanism. In MWT, the most effective solution for buffering continual perturbations is to reduce the size of the system (or to weaken the total genic interactions). Extending MWT to gene regulatory networks (GRNs), computer simulations and transcriptome analyses support the stabilizing effects of smaller gene sets in mangroves vis-a-vis inland plants. In summary, we show the adaptive significance of gene losses in mangrove plants, including the specific role of promoting phenotype innovation and a general role in stabilizing GRNs in unstable environments as predicted by MWT.

S.197.4 Genomic suitability of wild Robusta coffee to local climate in Vietnam

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Crops are generally cultivated outside of their native range. Optimal climatic suitability for crop production is raising more concerns, especially in the context of climate change. Robusta coffee (Coffea canephora) is indigenous to west and central Africa, but is also widely grown on other continents. Vietnam has been the world's largest Robusta producer since the 2000s, but is currently facing the risk of yield loss due to climate change. Assessing the suitability of wild genetic material to local climate conditions in Vietnam is essential for sustainable improvement of Vietnamese Robusta coffee. We first compared climatic conditions between native environments in Africa and that in Vietnam, using bioclimatic variables. The wild populations were highly differentiated into five main genetic groups, but only one of these (group ER from DRC) was mainly found in cultivated elite varieties in Vietnam, with a minor proportion of group AG from Gabon and Angola. A negative relationship between climate distance to the native range of group ER and coffee yields at the planted areas was found, and used to predict future coffee yields. The climate distance suggested higher suitability of the minor group (AG) in Vietnam. Using a reference-free approach, more than 18M of k-mers (substrings of sequence reads at 31-bp length) were detected in association with bioclimatic variables. Functional annotation of these candidate k-mers identified putative proteins related to gene regulation. They were used to predict the genetic changes that the wild individuals would require to fit the local environment (genetic offset) in the present and future Genetic offsets revealed variation between the different groups, and also suggested that the most suited genotypes came from the group AG. The results would be useful for planning strategies to improve adaptability of Vietnamese Robusta coffee.

S.197.5 Conservation genomics of the narrow endemic Zoysi's harebell (Favratia zoysii Feer)

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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.

S.197.6 Determinate root growth in Cactaceae and exploring its genetic regulation

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To thrive in deserts, Cactaceae plants possess numerous developmental adaptations. Determinate root growth, i.e., the root apical meristem (RAM) consumption, or exhaustion, and subsequent differentiation of all root-apex cells soon after germination, is one of these adaptations (Dubrovsky, 1997). Determinate growth of primary and lateral roots of seedlings of many Cactaceae species from the Cactoideae subfamily (Shishkova *et al.,* 2013) leads to the formation of a compact root system that might provide seedlings with an advantage for survival in arid and semiarid environments. We analyzed the primary-root growth pattern, determinate or indeterminate, for ca. 150 Cactoideae species and most species exhibited determinate growth. Notably, a few species that exhibit indeterminate primary root growth belong to the sole epiphytic tribe, Hylocereeae. In contrast, both *Maihuenia* species and few analysed *Pereskia* (and *Leuenbergeria*) species exhibit indeterminate primary root growth, while this character could be variable between and within Opuntioideae species. To explore the genetic regulation of the RAM exhaustion in Cactaceae, we performed RNA-seq of the primary-root apex of *Pachycereus pringlei* (Rodriguez-Alonso *et al.*, 2018) and *Carnegiea gigantea* (this work) on the developmental stages with active and exhausted RAM; and inferred a genetic regulatory network that operate in the root apex. The putative orthologs of the most important regulators of the RAM maintenance reported for *Arabidopsis thaliana* were also expressed in the root apex of the mentioned cacti species. These transcriptomes, as well as the improved *C. gigantea* genome (Copetti *et al.*, 2023) and highly fragmented draft genomes of five more Cactoideae species (Copetti *et al.*, 2017, Zhen et al., 2021) allowed us to start the exploration in Cactaceae of the PLT and WOX5 pathways of RAM maintenance described in *Arabidopsis thaliana*. *Acknowledgements*: This work was partially funded by PAPIIT-UNAM IN210221, IN208824 and CONACyT-CF304301.

S.198 MOUNTAIN BIODIVERSITY AND EVOLUTION. SESSION 3

S.198.1 Contrasting origins of two seemingly related mountain endemics: Saxifraga wahlenbergii (W Carpathians) and S. styriaca (E Alps)

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The Carpathians and the Alps are the largest mountain ranges of the European Alpine System and important centers of endemism. Among the distinctive endemic species of this area is *Saxifraga wahlenbergii*, a Western Carpathians member of the speciose genus *Saxifraga*. It was frequently suggested a taxonomically isolated Tertiary paleopolyploid and paleoendemic. A recently described narrow endemic of the Eastern Alps, *S. styriaca*, was hypothesized to be closely related to *S. wahlenbergii* due to the presence of pelicular glandular hairs. Clarifying the origin and phylogenetic relationships of both species could provide valuable insights into evolutionary and biogeographical history of the Carpathian and Alpine floras. To this end, their nuclear and plastid DNA were analyzed using Sanger and NGS (MiSeq) in a broad taxonomic context. Different evolutionary courses were found: *S. wahlenbergii* has a complicated hybrid origin. The maternal parent is a part of a West Eurasian lineage consisting of high mountain taxa within subsect. *Androsaceae* and could be widespread *S. androsacea* itself. The paternal lineage belongs to the distantly related subsect. *Tridactylites*, which also includes *S. adscendens*, the presumed second parent of *S. wahlenbergii*. The NGS screening revealed presence of sequences from both lineages. The second species *S. styriaca* was clearly assigned to subsect. *Androsaceae* and is not the sister of the first species. The similarity of the glandular hairs of both taxa is thus based on parallelism, and both species are not an example of a close evolutionary connection between the Western Carpathian and the Eastern Alpine floras. Since the origin of the paternal *S. adscendens*-like ITS DNA is estimated to be ca. 3.0 Ma, *S. wahlenbergii* cannot be relict of the mid-Tertiary climate optimum. Its hybrid origin is much younger and most likely took place in the Pleistocene.

S.198.2 Phylogeny, species boundaries, and morphological evolution in a Himalayan-Hengduan clade of honeysuckles (Isoxylosteum, Lonicera)

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The Himalayan-Tibetan-Hengduan region is one of the most important biodiversity hotspots for high-altitude plants. However, owing to the trans-boundary nature of this region and its remote peaks and valleys, many taxonomic problems remain unresolved. In turn, this has impeded our understanding of its evolutionary history. Here we resolve the phylogeny and delimit species in an endemic lineage of honeysuckles – the *Isoxylosteum* clade of *Lonicera* – using restriction-site associated DNA sequencing (RADSeq) combined with morphological and ecological data. These plants occupy almost the entire length and breadth of the Himalayan-Hengduan system, as well as the Tien Shan and Pamiro-Alai mountains to the north of the Tibetan Plateau. They also span an altitudinal range from ~2000-5000 m and occupy several major biomes, from wet and dry temperate forests to cold deserts and alpine areas. Phylogenetic and population structure analyses support the recognition of five species. One of the previously recognized varieties – *L. rupicola* var. *minuta* – was found to form a clade that is sister to *L. spinosa*. This is surprising because the geographic range of *L. minuta* is contiguous with the other varieties of *L. rupicola* in the northern Hengduan region and it is widely separated from *L. spinosa* whose range is confined mainly to the west of the Tibetan plateau. However, on close examination, several morphological and ecological traits also favour a closer relation of *L. minuta* to *L. spinosa* than to *L. rupicola*. This finding raises the possibility of ring speciation around the Tibetan Plateau. Our analyses demonstrate contrasting patterns of diversification between the predominantly lower-elevation *L. angustifolia*-*L. tomentella* clade and the higher-elevation *L. spinosa*-*L. minuta*-*L. rupicola* clade. We also found repeated parallel evolution into alpine habitats in *L. angustifolia*.

S.198.3 Structure, diversity and regeneration of vulnerable Pseudotsuga forests in southwestern China

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Our study sought to comprehensively understand *Pseudotsuga forestii* and *Pseudotsuga sinensis* forests, exploring forest structure, species diversity, and regeneration characteristics. The analysis of various indices, including species richness, Simpson diversity, Pielou evenness, Shannon-Wiener diversity, and phylogenetic diversity, consistently revealed comparable values across different forest types, indicating consistent biodiversity patterns. Forests are multilayered, reaching a maximum height of 42 m and a maximum diameter at breast height (DBH) of 143 m, with an age of 570 years. The age frequency distribution exhibited a multimodal pattern, with a distinct absence of individuals in the 0-20 years age range. Seedlings and saplings were predominantly found in unstable micro-habitats. Forests undergoing moderate disturbance displayed a higher number of *P. sinensis* individuals younger than 30 years compared to areas with no, slight, or severe disturbance. Our findings highlight the significance of moderate disturbance in the regeneration of both *P. forrestii* and *P. sinensis*. This information provides valuable insights into the conservation strategies needed for these vulnerable coniferous species, emphasizing the importance of managing and preserving habitats with a focus on maintaining moderate disturbance levels to support their sustainable regeneration and long-term survival.

S.198.4 Flower form and function in a speciose tropical mountain ecosystem

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Climate change is altering the costs and benefits of plant investments in reproduction. Knowing the costs of flowers and the mechanistic linkages between floral traits and floral performance is crucial to predicting how plants will respond to these changes in the future. Yet, the physiological costs of flowers and the traits influencing these costs of floral production and maintenance remain poorly studied. A few studies have addressed how water and carbon costs relate to flower longevity, but these have been restricted to only a few genera and mostly to cultivated plants that were not growing under natural conditions. To address this fundamental knowledge gap, we investigated how flower longevity and size – two traits associated with the likelihood of pollination – are related to traits influencing the water and carbon costs of flowers in naturally occurring montane plant communities. We sampled 19 species belonging to 15 families in the endangered Brazilian *campos rupestres*, a montane ecosystem known for its high diversity and endemism. We found that variation in traits related to carbon construction costs (petal mass per area and petal thickness) was explained by the longevity of individual flowers, while traits related to water maintenance costs (residual conductance and water residence time) were associated with flower size. Our results showcase how the physiological costs of flowers are related to pollinator attraction and thus play an important role in plant reproduction. Furthermore, our results highlight that shifts in the relative strengths of pollinator and non-pollinator selection may alter floral traits depending on the physiological costs of the flower. Therefore, our results can provide insight into how flower production and function may be affected by different components of climate change.

S.198.5 Molecular phylogenetics in Andean Caryophyllaceae

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The family Caryophyllaceae has a Worldwide distribution. In the Andes, this family is represented by approximate 250 species. In the framework of this work, several tribes are treated at the phylogenetic level including morphology and their correspondent distribution. Results indicate that high radiations occurred in the Andes and speciation events derived in numerous unknown species that yet remain undescribed. Our conclusions corroborate the high diversity of species concentrated in the Central Andes (Peru, Bolivia).

S.198.6 Mistletoes as key component of high-mountain temperate rainforests of southern South America

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Mistletoes are a key component of most forest habitats, as they offer valuable fruit resources for animals during scarcity times. Despite their parasitic habits, mistletoes exert many positive effects in forest communities via indirect interactions. While our knowledge about plant-animal interactions in which mistletoes are involved is reasonably good, our knowledge about the plant-plant interactions that take place with their hosts remains limited. The temperate rainforests of southern South America are considered a biodiversity hotspot due to its highly-endemic relic flora. There are two common mistletoe species at those forests: *Tristerix corymbosus*, a highly-abundant generalist mistletoe in the evergreen forests, and *Desmaria mutabilis*, a deciduous mistletoe that parasitizes only *Nothofagus* trees. Those mistletoes are almost exclusively dispersed by the relict arboreal marsupial *Dromiciops gliroides*. While both mistletoes are sympatric at mid-elevations, where we found *T. corymbosus* in *Nothofagus* spp. trees by parasitizing *D. mutabilis* (hyperparasitism), as *D. gliroides* feeds simultaneously on both species during the austral summer. However, above 1250 m of elevation only *D. mutabilis* is found as forest vegetation change from evergreen to deciduous. From 1250 m until the forest treeline (~1600 m) the deciduous tree *Nothofagus pumilio* becomes dominant, concentrating most of *D. mutabilis* plants. The presence of *D. mutabilis* represents a major food source for *D. gliroides* at those forests, where other fleshy-fruited plants are nearly absent. We recorded many *D. gliroides* visits to those mistletoes using camera traps, even at temperatures as low as -6°C, as mistletoes generate amenable microclimatic conditions. Besides *D. gliroides*, we recorded many other animal species associated with *D. mutabilis* (e.g., parrots). Whereas both mistletoes play a key role in southern South America temperate rainforests, *D. mutabilis* is particularly relevant in high-mountain forests where food is limiting, and environmental variations are broader than in the evergreen forests.

Symposia Session 12

S.199 SYSTEMATICS, EVOLUTION AND DIVERSIFICATION OF MAGNOLIALES (ANNONACEAE, EUPOMATIACEAE, MAGNOLIACEAE, MYRISTICACEAE)

S.199.1 Integrative species delimitation, biogeography, and conservation of Cuban magnolias (Magnoliaceae)

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An accurate taxa delimitation, based on a complete understanding of evolutionary processes involved in taxon differentiation, can be gained from a combination of ecological, morphological, and molecular approaches. The taxonomy of Cuban magnolias has long been debated and exclusively based on a traditional morphological study of a limited number of individuals. Our goals are to delimit the Cuban species of Magnolia and to understand their biogeographic history in order to update their conservation status. Samples for the ecological, morphological, genetic, and phylogenetic analyses were collected throughout the entire distribution range. The variability of each group was analyzed through ecological niche models, multivariate and geometric morphometrics, genetic markers, and a fully sequenced plastome. The conservation status of each species was given based on the IUCN guidelines. Seven species of Magnolia are reported for Cuba, six of the endemics. Almost all the species showed a restricted distribution and evident differences in the ecological niche used. The observed leaf morphological variability was different between groups and from that described by previous studies. The population genetic and phylogenetic results showed good limits for all the species except for *Magnolia minor* and *Magnolia oblongifolia*, in which a recent or still ongoing hybridization event was reported. The phylogeny showed three different colonization events in Cuban magnolias: from North America, Central America, and the Caribbean Islands. All the Cuban magnolia are included in one category of threatened, due mainly to mining, deforestation, and invasive species.

S.199.2 Mutualistic interactions with seed-dispersing vertebrates determine global and regional variation plant dispersal trait syndromes

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Tropical rainforests are the most diverse ecosystems in the world, but the underlying drivers of this diversity remain debated. Mutualistic interactions between fruits and frugivores (i.e., fruit-eating and seed-dispersing animals) are prominent in tropical rainforests, and may influence diversification and diversity. These interactions are facilitated by the evolution of functional trait matching between plants and frugivores, leading to the evolution of 'fruit dispersal syndromes'. Here, we hypothesize that co-diversification and selection on co-evolving traits has shaped plant-frugivore interactions and co-occurrence across broad-scale assemblages. We integrated global occurrence and novel frugivory-related trait data for >2000 species of a pantropical plant lineage (Annonaceae) with data for all 5,159 frugivorous birds and mammals. We applied functional diversity metrics, structural equation models, and fourth corner analyses to evaluate whether there is a match in the global distribution of plant and frugivore taxonomic richness and dispersal syndromes. We show that global variation in Annonaceae species and functional diversity was strongly influenced by the diversity and trait matching of co-occurring frugivorous mammals, whereas frugivorous birds affected Annonaceae diversity within particular regions: the Asia-Pacific and Afrotropics. Additional direct and indirect effects of climate, elevation, and net primary productivity on plant and animal diversity were found. This suggests that high diversity of fleshy-fruited plants across tropical forests is at least partly shaped by diversification-dependent co-evolutionary dynamics and selection on co-evolving frugivory-related traits – such as fruit length and growth form with beak volume, hand wing index, body mass, and colour vision. Our results also suggest that biogeography and scale-dependence modulate how mutualistic interactions promote diversity, with mammals shaping intercontinental and birds primarily shaping intracontinental patterns. Our work builds on studies of particular animal groups or regions by providing a global view of how frugivores have shaped pantropical variation in plant species richness and traits.

S.199.3 Phylogenomic evidence sheds light on phylogenetic relationships and infrageneric classification of Neotropical magnolias

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The genus *Magnolia* includes around 390 species inhabiting the Nearctic (~10 spp.), Neotropical (~170 spp.) and Oriental and Palaearctic (~210 spp.) biogeographic regions. Although several studies have been carried out to elucidate their phylogenetic relationships, the Neotropical taxa have been underrepresented, whereas the number of Neotropical species described has doubled in recent decades. Hence, this research focused on determining the phylogenetic relationships of Neotropical *Magnolia* using phylogenomic procedures to understand the infrageneric classification of Neotropical clades. The study included 137 samples from 90 taxa: 75 Neotropical and 15 Nearctic and Asian, covering one-third of all Neotropical species and including related clades to maintain phylogenetic representativeness. A list of 25 macromorphological characters for *Magnolia*, emphasizing Neotropical species was provided to delimit lineages. Two primary clades were identified: the first grouped the Neotropical sections *Talauma* and *Splendentes*, as well as *Gwillimia* from Asia, while the second was composed of the Neotropical sections *Macrophylla* and *Magnolia* and the four remaining Asian and Nearctic groups. These two main clades corresponded to those found in previous studies based on plastome data. The section *Talauma* was divided into two geographically patterned clades: one included species from Mexico and Central America, and the other comprised species from South America and the Caribbean. The *Splendentes* section was also subdivided into two subclades corresponding to the former sections *Cubenses* and *Dugandiodendron*. The phylogenomic evidence showed a species complex in the *Macrophylla* section, where taxa intersected among lineages. Relationships within the *Magnolia* section were unclear due to inconsistent topologies. All recognized Neotropical clades can be diagnosed by a combination of macromorphological traits, and they were confirmed as monophyletic, while certain Nearctic or Asian groups were not. The infrageneric classification of Neotropical clades was updated based based on the phylogenomic evidence and a taxonomic key is provided.

S.199.4 A Taxonomic update of Brazilian magnolias

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The genus *Magnolia* (Magnoliaceae) has a wide and disjunct geographic distribution ranging from Eastern and South Asia to Malaysia, extending across the Neartics (Canada and USA) and reaching into the Neotropics, which is one of its two diversity hotspots. Regarding its infrageneric classification, the genus is divided into three subgenera: *Yulania*, *Gynopodium* and *Magnolia*, the latter including the section *Talauma* in which the native Brazilian taxa are classified. The species of *Magnolia* sect. *Talauma* can be recognized by two parallel longitudinal scars on the petiole formed by the shedding of the stipules, in addition to a woody syncarp that breaks into irregular plates at dehiscence. Currently, in Brazil, species delimitation within *Magnolia* is not clear on national platforms that are of great importance to the Brazilian botanical community (e.g., Flora do Brasil), with only two species of native *Magnolia* being recognized: *M. amazonica* and *M. ovata*. The lack of knowledge about the species and their distinguishing morphological characteristics has resulted in many identification errors in the main Brazilian herbaria, leading to the lack of knowledge about their current conservation status. We conducted a complete taxonomic revision based on extensive fieldwork, herbarium survey, and literature. In addition to the abovementioned species, we recognize three previously described species, which increases the number of recognized native Magnolias occurring in Brazil to five, namely: *M. amazonica*, *M. brasiliensis*, *M. irwiniana*, *M. ovata* and *M. sellowiana*. The results of our work are highly relevant for future studies that aim to unravel the evolution of the genus in Brazil, such as those on population and landscape genetics, as well as its inclusion in a phylogenomic study in a Neotropical framework.

S.199.5 Global map of taxonomical and functional diversity of Annonaceae and implications for tropical rain forest conservation

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Protecting tropical rain forests (TRFs), home to half of the world's plant diversity, is essential for mitigating the global biodiversity crisis. TRFs not only exhibit an impressive taxonomical diversity (TD) but are also renowned for their diverse morphological traits, indicating high functional diversity (FD). However, our knowledge of the spatial patterns of their TD and FD remains incomplete, severely impeding our ability to implement effective conservation measures. In particular it remains unclear is both these dimensions of diversity overlap or not across global scales. To address this issue, we assembled the most comprehensive distribution and morphological traits datasets within Annonaceae, a diverse and ecologically important pantropical family. We examine spatial correlations between TD and FD, and overlap the hotspots of both to identify the hottest hotspots. We further assess the current protection and threat status of these hotspots by overlaying them with protected areas, global tree cover loss and regional land use datasets. The hotspots exhibiting high levels of both TD and FD, lack of protected areas, and high coverage of disturbed areas should be given utmost priority in tropical rain forest conservation efforts.

S.199.6 Genomics sheds light on the diversification of the amazonian tree genus Duguetia (Annonaceae)

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The genus *Duguetia* (Annonaceae) is composed of 97 species of trees found mostly in tropical America with the Amazon basin representing the main centre of diversity for the genus. Some species occur in the Atlantic coastal forest, Central America and South American savannahs. Although the Amazon basin is the world largest tropical forest hosting an estimated tree flora between 9 and 16 thousand species, drivers and dynamics of tree species diversification are not yet fully understood. Previous studies have showed that *Duguetia* started diversifying during the Eocene, probably within the Amazon basin. Additionally, *Duguetia* species are present in virtually all vegetation types found in the Amazon. These characteristics make *Duguetia* an outstanding example to study the diversification and biogeography of Amazonian trees. We produced a genomic dataset with near-full taxon sampling, based on low copy nuclear genes, to infer species relationships. Consequently, we were able to infer a fully resolved and strongly supported species-level phylogenetic tree which we used in conjunction with a selection of morphological and biogeographical characters to reconstruct the historical biogeography and investigate possible drivers of diversification in *Duguetia*. Our results show that the genus *Duguetia* likely originated in Africa and diversified in the Amazon basin with a few independent range expansions into the Atlantic forest and Central America. We hypothesize that a combination of characters within a particular vegetation type, rather than single characters, has led to accelerated diversification rates. Our results contribute to an improved understanding of the origin and diversification dynamics of the Amazonian tree flora.

S.200 TAXONOMY AND EVOLUTION OF BAMBOOS IN THE PHYLOGENOMIC ERA

S.200.1 Phylogenomics of bamboos using reference genomes and deep genome skimming data

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Bambusoideae is a typical legacy of complex reticulation. It has diverse ploidy levels (herbaceous bamboos, temperate and neotropical woody bamboos, and paleotropical woody bamboos being diploid, allotetraploid, and allohexaploid, respectively) and cytonuclear discordance is manifest, making it a difficult plant group in which phylogenetic relationships and taxonomy of some tribes, subtribes, genera and species remain controversial to varying degrees. Ancient hybridization, polyploidization, and complex reticulate evolution history have led to extensive cytonuclear discordance and difficulties in accurately identifying orthologous genes applicable to phylogenetic studies of allopolyploid plants. Also, great challenges have been encountered in elucidating the complex history of deep reticulation.

In order to recover the phylogenetic framework of bamboo and explore its evolutionary history, we sampled 43 representative species across the 19 bamboo subtribes with reference to traditional taxonomy and previous molecular phylogenies based on plastomes and ddRAD data whenever available. Of the sampled 43 ingroups, there are 12 reference-level genomes and 31 assemblies generated from deep genome skimming data. We compared four different analysis strategies (i.e., single-copy gene, perfect-copy syntenic gene, RT ortholog group, and syntelog group) for identifying orthologs, and finally selected a large number of syntelog groups to carry out phylogenomic analyses and to resolve relationships at deep nodes for reconstructing the subtribal-level phylogeny of bamboos. Moreover, the evolutionary history was deciphered by integrating published bamboo transcriptome data and multiple lines of evidence such as the detection of potential hybridizations and introgressions, divergence time estimation, etc. Ultimately, this study offers a robust phylogenomic framework for further taxonomic studies of subtribal delimitations from a molecular biology point of view and provides an example for tracing the origin and evolutionary history of deep reticulation in polyploid plants.

S.200.2 Into the unknown: long-lost knowledge of bamboo diversity in Thailand

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Biased documentations of bamboo diversity are observed in species-rich Indochina region towards a few countries. Thailand is situated at the center of the region and shares floristic regions with neighboring countries China, Myanmar, and Malaysia and cover varieties of habitats favoring different bamboo species. However, robust and up-to-date references of bamboos from Thailand are absent. Approximately 100 bamboo species are enumerated by global databases. However, the number still reflects the underestimation of Thai bamboo species since discovery of new species and genera and species records points out unrecognized wild bamboos and long-utilized species by the locals. More than two decades of extensive fieldwork and specimen examinations proved unexpected high diversity of Thai bamboos, which not only encompass morphological diversity but also delivers biogeographic and evolutionary meanings. The majority of tropical woody genera belong to the evolutionary complex clade of *Bambusa, Dendrocalamus, and Gigantochloa* (BDG clade) in which multiple cases and observations of natural hybridization, such as a hybrid species x*Thyrsocalamus liang* and suspected *Dendrocalamus* hybrid contribute to the overall diversity. *Schizostachyum* exemplifies gaps in diversity knowledge that the recorded number of its species is underrepresented. Minor and other endemic genera such as temperate genus *Chimonocalamus* and tropical genera *Holttumochloa*, *Maclurochloa*, *Phuphanochloa*, and *Temochloa* are accounted for diversity and new unknown genera represent rare morphological characters distinct from other genera and require further data to delimit the genus. For the first time, we represent a compilation of bamboo diversity in Thailand in taxonomic and diversity perspectives. Morphological comparison and relationships of bamboos are discussed. We proposed future directions in studying evolution and ecology of bamboos in Thailand as foundation knowledge and how biodiversity knowledge of Thai bamboos can drive national Bio-Circular-Green economic model and Sustainable Development Goals (SDGs) in the global context.

S.200.3 Macroecology of world bamboos

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Occurring all over the world (being introduced or native), bamboos represent one of the most familiar group of plants worldwide. Serving as sources of shelter, sustenance, and economic livelihood for a substantial segment of the global population, these versatile plants also play a pivotal ecological role in their native biomes. Their influence extends to the structuring of ecosystems by offering cover and habitats for a diverse array of animal taxa, spanning from invertebrates to mammals, in addition to fostering symbiotic relationships with countless microorganisms. Despite their ecological significance, the systematic study of bamboos poses considerable challenges, leading to periodic reassessments of their classification. The factors underpinning the overarching patterns of diversity and distribution on a global scale remain inadequately understood. This knowledge gap encompasses environmental parameters, historical contexts, dispersion events, and anthropic influences that can shape the distribution of the various bamboo clades. Understanding the correlation between these factors and the observed diversity and distribution patterns is crucial to decipher how environmental have shaped the diversity and distribution of bamboos as observed today. Especially focusing on extremes, like drought or freeze known to limit the ranges of several other plants groups. Such knowledge not only enriches our understanding of the ecological and evolutionary processes at play but also holds intrinsic value in addressing societal needs and exploring nature-based solutions. Our project with its particular emphasis on bamboo-centric approaches, will provide useful primary data that can be generalized to allow understanding the effects of global climate crisis and its consequences for other groups of plants.

S.200.4 Evolution and diversity of Chusquea (Poaceae: Bambusoideae: Bambuseae)

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Although bamboos (Bambusoideae) are typically associated with the Eastern Hemisphere, especially China, India and Japan, >600 bamboo species (of over 1700) are native to the Americas. Of these, 203 (one-third) belong to *Chusquea*, the most diverse genus of bamboo, and the description of new species in this genus continues unabated. *Chusquea* is the most widespread bamboo genus in the Americas, extending from 25°40'N in Mexico to 47°S in Chile and Argentina. Species of *Chusquea* grow primarily in montane forests and high elevation grasslands in Mesoamerica, the Greater Antilles, the Andes and eastern Brazil, and are often dominant elements in these habitats. *Chusquea* has the broadest elevational range of any bamboo genus, from sea level to over 4300 m, although few of its species occur below 1000 m. Morphologically, *Chusquea* has a uniform spikelet structure of four glumes and one fertile floret with no rachilla extension, but exhibits extreme vegetative diversity, from aerially unbranched culms bearing leaves to 4 m long and 30 cm wide to highly branched culms with 2-200 subsidiary branches per node, bearing leaves 1-40 cm long and 0.06-8.5 cm wide. Understanding of the complex evolutionary history of the woody bamboos, which involves ancient hybridization and polyploidy, has been enhanced by recent genomic-level analyses, but no WGS resources for *Chusquea* are available. Elucidation of species-level diversification has been hampered by lack of resolution in plastid sequence data but also likely rapid and recent radiation in the Euchusquea clade and homoploid hybridization. We are exploring the utility of nuclear target capture data (Angiosperms353) to study the evolution of this diverse and ecologically important genus. Questions include revisiting the apparent paraphyly of *Neurolepis* relative to *Chusquea*, testing the monophyly and relationships of morphologically defined groups within *Chusquea*, and unraveling the biogeographic history of the genus.

S.200.5 Advances in the knowledge on systematics and evolution of Neotropical herbaceous bamboos (Poaceae, Bambusoideae, Olyreae)

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The tribe Olyreae includes weakly lignified plants bearing unisexual dimorphic spikelets which inhabit the understory of tropical forests, almost exclusively in the Americas. Its monophyletic status is well supported, as are the relationships of its subtribes (Buergersiochloinae sister to the Olyrinae + Parianinae clade). However, in the past five years new information about this tribe has been gathered using integrative approaches. Molecular phylogenies based on plastid and nuclear sequences, as well as morphological and micromorphological data, were used to reveal novel relationships and identities within the group. Three genera (*Piresiella*, *Miniochloa* and *Ekmanochloa*) were recently transferred from Olyrinae to Buergersiochloinae, enlarging the circumscription of the group to four genera and five species. In Parianinae, another new genus is being described, also increasing its generic number to four. Most novelties, however, come from the Olyrinae, the largest subtribe, which has undergone in-depth investigations. One important result is the confirmation of the paraphyly of *Olyra*, which will be resolved by transferring some of its species to *Arberella* and recognizing five new genera. Thus, the subtribe now encompasses 20 genera, increasing to 30 the total number of genera of Olyreae. Most richness of this tribe is found in Brazil (25 genera, six of them recently described) from where several species are endemic and threatened. In this sense, our efforts have focused on the recognition of taxa the diversity of which was and continues to be underestimated due to their complexity and rarity. We are also developing genomic studies to better explore the evolutionary history and biogeography of this interesting bamboo group.

S.200.6 How can we use the macro and micro morphology for the bamboo taxonomy in the era of phylogenomics?

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The bamboos are notorious for the difficulty in taxonomy. Morphological characteristics are the cornerstones for classification. As in other plants, the macro morphology including both reproductive and vegetative features is used in traditional bamboo taxonomy, particularly that of inflorescences and spikelets. Woody bamboos usually flower after decades of vegetative growth, therefore, taxonomists rely much on their vegetative characters, such as rhizome, culms, culm leaf, branch complement, and foliage for classification. However, vegetative characters are more plastic and variable in different environment, which brings confusions for bamboo taxonomy. On the other hand, some micromorphology, such as foliage leaf blade anatomy, epidermis characters, and phytolith (silica body) are exploited as supplementary evidence for bamboo taxonomy. With the development of molecular phylogenetics and phylogenomics, the relationships within Bambusoideae have been changed incredibly, which also render researchers to reassess the evolutionary significance of macro and micro morphology of bamboos. Homoplasy or convergence of some morphological features, including inflorescence has been detected at different taxonomic levels. In addition, inconsistency in terminology for some characters (e.g., inflorescence vs. synflorescence, sheath scar vs. nodal line) exists in current floristic and/or morphological accounts. Those terms should be unified for taxonomic constancy and meaningful evolutionary studies under the Bamboo Phylogeny Group II, a joint international effort. We also propose to establish an image database with an array of morphological characters onto the BambooBase.

S.201 INTEGRATING FLORISTIC, BIOGEOGRAPHIC AND ETHNOBOTANICAL STUDIES FOR CONSERVATION

S.201.1 Local perceptions of the benefits versus negative impacts of weedy grasses in Central Madagascar, focused on the genus Digitaria

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Plants and agricultural practices are an integral part of human food systems and well-being. In Madagascar, agricultural products are both self-consumed but also constitute the local economy basis. Beside climate change, weeds are one of the main problems that hinder production, and most of them are grasses belonging to the Poaceae family. Conversely, some Poaceae considered bad for crops are used for food, medicine, and ornamentation purposes. *Digitaria* species, commonly known as finger grasses, are typically found in Malagasy crop fields, interacting with cultivation. This work aims to identify the best-known Poaceae weeds and understand their roles in agricultural systems. To increase our understanding of the relationship between these plants and farming activities, information on their recognition and the farmers' perception of the Poaceae weed status in cropping systems was analysed. Our approach was based on field surveys and farmer interviews with plant voucher specimens and photographs in three areas of Madagascar central highlands. Additionally, we present detailed data on *Digitaria* species. 51 Poaceae, including 11 *Digitaria* species were mentioned. Farmers classify Poaceae weeds in three ways: their impacts on agricultural activities, use category, and vegetative growth patterns, the latter especially significant for *Digitaria*. Locally common grasses are perceived as weeds when they are abundant and cause yield loss. Overall, 67% of the species mentioned are judged useful. More than 40% of the farmers use Poaceae weeds in composting, more than 20% as fodder, and more than 8% as medicine. The diversity of useful species and the associated indigenous knowledge is important to the local communities, but weeds are still perceived as overall negative. The Poaceae are overall neglected in Malagasy ethnobotany. The data obtained will be useful for weed control as well as the conservation of agrobiodiversity, especially endemic species that are not widely known.

S.201.2 Fern and palm species biogeographic patterns in Amazonia

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Species occurrences are strongly affected by environmental properties. To understand the interplay between historical, environmental, and anthropogenic effects in shaping the current distribution of used and non-used plants in Amazonia, we developed species distribution using species records, top-notch remote sensing products, deforestation masks, soils and climatic variables. Applying several modelling approaches, we reveal the main drivers of human use, species distributions and biogeographic patterns of selected Amazonian plants. In nutrient-richer soils, palm species richness is lower, but, a higher proportion of the species are used and each species is more diversely used by humans. For ferns, the opposite was found: richer soils harbor a richer fern flora than poor soils. For both ferns and palms composition patterns, the primary floristic gradient was strongly related to soil nutrient concentration, and the secondary gradient, to climatic variables. Traditionally, the relative importance of soils as opposed to climate as drivers of species distribution has been considered a matter of scale. However, we conclude that the effects of soils are often underestimated and vary according to species characteristics.

S.201.3 Tropical Important Plant Areas (TIPAs) in Bolivia: identification, documentation, and impact on the protection of plant ecosystems

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The concept "Important Plant Areas" (IPAs) was developed by PlantLife International in the early 2000th and initially implemented in Europe and the Mediterranean, identifying IPAs in 27 countries. Given the impact of the IPAs program, the "Tropical Important Plant Areas" (TIPAs) program was launched in 2015, with Bolivia as the first country in South America for its application. The three main objectives of TIPAs are to: 1) identify the most important areas and habitats for rare, threatened, endemic and useful plants or habitats; 2) designate priority TIPA sites for their conservation; and 3) promote the sustainable management and protection of TIPAs through the participation of government decision makers, local communities and conservation institutions. To date, the Bolivia TIPA program has identified 37 sites in two ecoregions of the country: the Chiquitano Dry Forest and the Inter-Andean Dry Valleys. In total, 319 species and eight habitats met the TIPA criteria for inclusion. In the process, we have also: a) identified six centres of richness of useful plants; b) evaluated the risk of habitat collapse following IUCN criteria in the highly threatened Chiquitano Dry Forest ecoregion; c) discovered 12 species new to science; and trained 28 Bolivian professionals and 65 undergraduate students in IUCN and TIPA methodology. The TIPA network of sites has been adopted by the subnational government of Santa Cruz along with the RAMSAR and IBA sites, and has informed 1) the revision of the Master Plan of protected areas in the Department of Santa Cruz, 2) the delimitation of two areas protected areas, 3) the Comprehensive Natural Resources Plan of the Department of Santa Cruz, and 4) the recent review of the Key Biodiversity Areas (KBAs) in Bolivia.

S.201.4 Promoting the integration of different plant disciplines for biocultural conservation in tropical regions

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Plant biodiversity studies in tropical regions are mainly based on field inventories. Despite the large networks of plots and plant data banks, there is still a need for further fieldwork to document the enormous richness existing in these areas at local and regional scales. In addition, tropical regions are populated by different human groups that have extensive traditional knowledge on the use and management of plant species and communities. Studies of our research group are shown with the idea of promoting a greater integration of different data sets and disciplines: (1) Forest types and plant uses. The inventories show clear floristic differences between different habitats, although often the forests with the highest species richness are not necessarily those with the highest use value for human groups. (2) Elevation and uses. It is widely known that above 1500 m, the floristic richness in tropical areas decreases progressively, although this is not directly related to plant utilization patterns, since they vary according to the needs of local human populations. (3) Latitude and uses. Understanding the variation in plant communities along the latitudinal gradient is essential for comparing the use patterns across different human groups or different communities of the same ethnic group. (4) Traits and uses. There is a clear relationship between functional traits and the use of plants by different communities. Various traits can promote similar uses, however there are some use categories more dependent on a particular trait. (5) Dominance and uses. Plant species with higher abundances and frequencies are potentially more widely used than rare species and generally have uses in a greater number of ethnobotanical categories. (6) In studies with local communities, it is necessary to integrate gender studies, differences between generations and to understand the influence of socioeconomic variables on traditional knowledge.

S.201.5 Understanding Cerrado plant biodiversity to boost conservation actions in a UNESCO World Heritage site

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The Cerrado, a biodiversity hotspot, with only 1% of the total area legally protected, has its diverse flora at risk due to land conversion and facing local species extinctions. The Chapada dos Veadeiros National Park (CVNT), a UNESCO World Heritage site, appears as an iconic protected area, presenting a rich, heterogeneous and representative Cerrado flora. Hence, filling research gaps regarding patterns of diversity within the park, such as species composition on small-scales, beta diversity patterns and degree of threat. Here, the study goal was to evaluate and categorize flora composition across different vegetation types, considering vegetation coverage, species distribution and vulnerability. The study was conducted by analyzing open databases and literature reviews. Considering CVNP legal perimeter and surrounding vegetation patches, it was found a coverage of open environments of 65% (52% savannas), harboring 33% of unique species considering the total species pool already cataloged in the park. In contrast only 13% consists of forest vegetation, but exhibiting similar species richness, and about 32,5% of unique species. However, the bias of collection for woody and forest species is well known, even in savanna ecosystems, which might result in this similar percentage of species. Over 20% of the area is human altered, underscoring the urgent need for conservation and restoration actions. Threats such as biological invasion, tree planting, and unnatural fire regimes endanger both open and forested landscapes. The park flora represents almost a third of the total Cerrado species. Over 90% of the park species cataloged lack vulnerability data, and those with data are classified to some degree of threat. Our results pointed out the need to increase the taxonomic studies in critical biodiversity hotspots and urge to better catalog non-woody vegetation. This information is the basis for conservation actions in areas with global importance such as Chapada dos Veadeiros.

S.201.6 The Madidi Project: Monitoring tree diversity to understand environmental change and inform plant conservation

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The Madidi Project stands as a testament to the power of collaborative botanical research, particularly in tropical regions, where biodiversity remains largely undocumented despite centuries of study. Spearheaded by the Missouri Botanical Garden and the Herbario Nacional de Bolivia, along with a consortium of researchers and institutions, the Madidi Project represents a multifaceted approach to botanical exploration. Key elements of the project include floristic surveys, the establishment of an extensive network of forest plots, the collection of functional trait data, the gathering of information for population genetics and phylogenetics, and ethnobotanical research with several local communities. The data obtained from this project have been instrumental in studies aimed at understanding the dynamics of biodiversity. Notably, the project has shed light on the evolution of species in response to large-scale environmental changes in the geological past, as well as shifts in species distributions and the composition of forest communities in response to recent climate change. Increasingly, a significant application of the data from the Madidi Project lies in its contribution to conservation. It provides critical information that aids in identifying priority areas for conservation and informs the decision-making processes of policymakers in the regions affected by the project. Importantly, the project has served as a platform to train a large number of students, particularly in Bolivia, by addressing a major gap in local capacity for research and conservation. The Madidi Project, therefore, not only enhances our understanding of tropical biodiversity but also plays a significant role in guiding conservation strategies in Bolivia. Major conservation challenges remain in Bolivia – as in Latin America and the Tropics. The Madidi Project – as well as other major scientific initiatives – should simultaneously contribute to efforts to understand and preserve natural places for the benefit of biodiversity and people.

S.202 BENEFICIAL PLANT-MICROBE INTERACTIONS. SESSION 2

S.202.1 How plant-microorganisms interactions can help reveal insights about coevolutionary processes?

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As early as the 19th century, Darwin and Wallace considered the importance of plant-biotic interactions in promoting diversity and the intensity of selection. The extent to which coevolution may drive natural selection and shape angiosperm diversity is still debated, particularly because no unequivocal evidence has been provided regarding reciprocal evolutionary changes. For instance, the use of phylogenetic trees for the study of coevolutionary processes turns out to be inconclusive because phylogenetic patterns of coevolution exclusively reflect codivergence phenomena. The concept of coevolution is still subject to multiple debates and, apart from semantic questions, reflects the need to develop experimental approaches which take into account the complexity of biotic interactions. Experimental approaches under controlled conditions have been able to highlight selection pressures exerted by organisms connected in food networks generating changes in allelic frequencies. However, when species are integrated into complex and diverse interaction networks under natural conditions, reciprocal selection pressures can vary in time and space and depend on the ecosystem under study. Despite the known benefits of plant microbiota on growth and nutrition, the mechanisms of association and their degree of heritability remain largely unknown whereas they do constitute the basis and requirements for coevolution to occur. Here, I highlight the suitability of studying plant-microorganisms' interactions to disentangle the mechanisms and dynamics of biotic associations in light of coevolutionary processes. Studying genetic variability, gene expressions and functional responses of plant-microorganisms associations would provide exceptional insights on the mechanistic processes of coevolution.

S.202.2 Induction of stress tolerance genes and plant protection by endophytic bacteria

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The microorganisms which survive within healthy tissues of plants without causing any overt negative effect to the host are defined as endophytic microbes. These microbes develop a mutualistic relationship with their host and promote plant growth under different biotic and abiotic stresses. The endophytic bacteria were isolated and molecularly identified from different maize varieties including ancestral Teosinte and *Chloris* grass. Plant protection and stress tolerance was observed by treating endophytic bacteria to non-host plant. The over expression of stress tolerance genes of plants was analysed by qPCR (quantitative PCR). The plant salt stress tolerance was observed by up-regulation of the aquaporin gene family in maize plant treated with endophytic bacterium *Pantoea agglomerans*. The plasma membrane integral protein type 2 (*PIP2-1*) gene in tropical corn seedlings was highly up-regulated by *P. agglomerans* treatment under salt stress conditions. The species of endophytic *Bacillus* showed up-regulation of several defense genes of maize plant against biotic stress also. The induction of expression of pathogenesis-related genes, including PR-1, PR-4 and PR-10 was observed against fungal pathogen in maize seedlings treated with endophytic *Bacillus*. Plant protection was also observed in maize seedlings and *Arabidopsis thaliana* treated with endophytic *Bacillus* against fungal pathogen *Fusarium moniliforme*. The study suggests that endophytic bacteria may be further formulated and applied for the plant stress tolerance and disease protection.

S.202.3 Microbial effects on holm oak (Quercus ilex L.) germination

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Seed germination is a critical step in plant establishment and is influenced by both abiotic and biotic factors. Humidity, radiation, and temperature generally determine germination onset, which is also influenced by the microbiota. Germination rate depends therefore on the interaction between microbes hosted by the seed, soil microbes and environmental clues. Over time, plants selected specific sets of microbes and evolved together in response to local conditions. We looked at the role of soil microorganisms on holm oak (*Quercus ilex* L.) germination, and specifically whether soil microbes from its own habitat enhanced germination more than soil microbes from other habitats, testing whether the *home-field advantage* hypothesis (HFA) reported for litter decomposition applies to seed germination. We used *Q. ilex* seeds from different provenances sowed with a factorial design on sterilised soil from different habitats, and added soil extracts with the microbiome from the same soils. The objective was to tell apart effects from soil and microorganisms. We recorded seed germination daily for about 2 months. Overall, germination rate of *Q. ilex* seeds from Somiedo (N Spain) was higher than seeds from Ronda (S Spain). Soil extracts from Somiedo enhanced seed germination more than other extracts, pointing to the soil microbial community as the factor controlling seed germination. There was a significant difference in HFA between the two localities, being positive in Ronda and negative in Somiedo, suggesting stronger coevolution between plants and soil microbes under harsh than under mild environmental conditions. Our results evidence that soil community structure and diversity critically contribute to *Q. ilex* germination, all else being equal.

S.202.4 Molecular mechanisms involved in rhizobacteria-plant interaction in Solanum lycopersicum

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Plants cohabit and interact with diverse soil microorganisms, that are archaea, bacteria, fungi, and protists, which form the root microbiota. These communities play a pivotal role in enhancing plant growth through improved nutrient uptake, immunity, and stress tolerance. Here, we examine the role of bacterial species of a commercial compost on *Solanum lycopersicum* (tomato) growth and health. Firstly, we identified six main bacterial species from the culturable microbiota of the compost, belonging to *Bacillus*, *Kocuria*, *Glutamicibacter* and *Microbacterium* genera. Tests for their plant growth-promoting traits revealed their capacity to solubilize phosphorus, produce siderophores and synthesise auxin. To investigate the plant responses to the colonization, the tomato seedlings were grown in soil enriched with the inoculum of the single bacterial species. RTqPCR highlighted a specificity in the expression profile of genes representing pathways involved in plant-microbe interplays, such as flavonoid biosynthesis and ethylene production, in response to the different bacterial strains. RNAseq analysis of the host transcriptome will provide a wider overview of the plant response to the rhizobacteria, hence pointing out other pathways influenced by the interaction. Moreover, some of the isolated bacterial strains were transformed to express fluorescent-tag proteins. This will enable the tracking of rhizobacteria accommodation on the tomato root and the description of their spatial distribution from different plant root surfaces to inner tissues by confocal microscopy. This study aims to contribute to the decipherment of the molecular signalling behind the interactions between plants and bacteria in the context of the promotion of sustainable agriculture practices proposed by the European Union within the EU Sustainable Goals 2030.

S.202.5 Nitrogen-fixing bacteria boost floral attractiveness in a tropical legume species

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Legumes establish mutualistic relationships with nitrogen-fixing bacteria and pollinators critical for plant reproduction and ecosystem services. However, we know little about how nitrogen-fixing bacteria and soil nutrient availability affect the plant's attractiveness to pollinators. We conducted a two-factorial greenhouse experiment to investigate the impact of nitrogen-fixing bacteria (rhizobia) and soil types on flower traits in *Chamaecrista latistipula* (Fabaceae): rhizobia-inoculated (R+) and non-inoculated (R-) plants in organic-rich matter (OM) and sandy soils. We monitored bud and flower production and analyzed leaf, petal, and anther reflectance curves with a spectrophotometer. Using the bee hexagon model, we estimated chromatic contrasts, a crucial visual descriptor for attracting bees up close and from a distance. We partially corroborate our hypotheses, in which only plants R+ and under sandy soils had a high floral display and color contrasts. On the other hand, the absence of nitrogen-fixing bacteria in the root system or plants growing under OM soil severely reduced flower display and color contrasts, decreasing flower attractiveness to bee pollinators. Our findings indicate that rhizobia positively impacts pollination, particularly in nutrient-limited conditions. This study provides insights into the dynamics of plant-pollinator interactions and underscores the significant role of rhizobia bacteria in influencing key floral traits within tropical ecosystems. These results contribute to understanding the mechanisms governing mutualistic relationships and their consequences for plant fitness and ecological dynamics.

S.202.6 Holobionts comprised of grass Festuca species and their fungal Epichloë endophytes exhibit diverse coevolutionary mechanisms

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Epichloë endophytes (Clavicipitaceae, Ascomycota) are known to colonize the aerial part of temperate pooid grasses and the nature of their antagonistic or synergistic interactions with their host depends on the ability of the endophyte to reproduce sexually or asexually. Most of these endophytes can only be transmitted vertically and asexually through plant seeds, establishing mutualistic symbiotic interactions with their hosts. We are investigating the potential co-evolution of holobionts comprised of *Epichloë* taxa and species complexes of the worldwide distributed grass genus *Festuca* (Loliinae, Poaceae). This genus encompasses ~500 accepted species, most of which had never been surveyed for their interactions with these endophytes before. To assess this matter, we are conducting a worldwide scale research collecting information about all the reported symbioses between these two genera and studying material from ~200 *Festuca* species through both genome sequencing and bioinformatic pipelines. So far, we can affirm that at least 14% of the *Festuca* species interact with *Epichloë* endophytes. Additionally, we unraveled the existence of natural symbioses between 15 *Festuca* species and 13 *Epichloë* taxa and we were able to detect 20 lineage-specific relationships for temperate and tropical mountain fescues and their endophytes, a fifth of which presumably correspond to new *Epichloë* endophytes. We have applied a multidisciplinary approach that included morphoanatomical, histological, cytogenetic and phylogenomic studies to analyze holobionts formed by the *Festuca* rothmaleri polyploid complex and their endophytes. This study suggests a hybridogenic adaptive co-evolutionary scenario where the increasing ploidy-level of the grass host (tetra, hexa and octoploid individuals) might be correlated with the ploidy-levels of their respective symbionts. This scenario offers an opportunity to better understand the co-evolutionary mechanisms involved in the establishment of these relationships.

S.203 FILLING THE GAPS IN THE CATALOGUING OF ALIEN FLORAS IN THE MEDITERRANEAN BASIN

S.203.1 The alien flora of Greece: taxonomy, chorology, life traits and habitats preferences

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Biological invasions represent one of the most important threats to biodiversity, with invasive alien species (IAS) having severe negative consequences for the invaded environment. This contribution reports on the alien flora of Greece as well as on the worst invasive alien plant taxa in it. A compilation of the alien plants occurring in Greece has been performed resulting in 448 taxa (including 58 archaeophytes). For this task, various literature sources have been screened. Of those 448 taxa 270 are established, 171 are casual and 7 are of unknown establishment status. The richest families in number of taxa are Poaceae, Asteraceae, Fabaceae, Solanaceae and Amaranthaceae. Chorology of the established taxa indicates that 47,8% are of American origin followed by those of Asian (16,7%) and African origin (10,4%). Regarding their life form, therophytes prevail with 47% followed by hemicryptophytes and phanerophytes with 20% and 15% respectively. Artificial (man-made) habitats are the most invaded with 69% of the plant taxa found there followed by freshwater habitats and rocky habitats both with 12%. Taxa consisting the total alien flora of Greece as well as others that were added after a horizon scanning process were screened for their degree or potential of invasion. In total, 32 were considered as the most invasive ones and they were proposed to be included in the National Catalogue of Alien Invasive Species. The majority of these taxa have their native geographical distribution in the Americas. The most common introduction pathway is their use as ornamental and in horticulture. Risk assessments have been performed for all 32 plant species, to detect those presenting the highest risk to the local biodiversity and ecosystem services. Fifteen plants were found to have major impacts, with 80% of them being recorded in the wild, while 40% of them are already established in Greece.

S.203.2 Towards a complete and updated knowledge of exotic flora in Sardinia: diversity, ecology and activities for their control

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Since the appearance of *Homo sapiens*, humans have increasingly become a global force capable of altering the functioning of the entire planetary ecosystem. Among human-induced pressures, plant invasions are considered one of the most impactful processes on biodiversity, due to, among others, their negative influence on food webs, vegetation structure and ecosystem services. This is particularly true in the Mediterranean Basin, which has long been a crossroads for human populations, and especially on islands, where human pressures can be more impactful due to their inherent small size and wider fragmentation. Here we present a largely replicable regional approach from Sardinia (Italy), which starts from the presence and distribution of invasive plants and improves knowledge by investigating the ecology of the species of greatest interest. A dynamic checklist of exotic vascular plants was continuously updated by monitoring and reporting new introductions and changes in status, focusing in particular on those environments that are particularly sensitive, such as most coastal habitats highly threatened by humans' impacts. In parallel, the investigation of the ecophysiology of seed germination of some invasive species has made it possible to predict their potential invasion trend and future risk, providing further insights into their control. This information was put into practice by controlling the invasion of some introduced species in different contexts, such as small islands, wetlands and coastal sand dunes. These activities were evaluated not only on the basis of control success, but also on economic costs and feasibility. These experiences highlighted the importance of constantly monitoring the changing local status of exotic species and of sharing and recording all research and practical activities. From a bottom-up perspective, such local experiences provide crucial information to improve the effectiveness of efforts to halt the increasing environmental depletion of native resources.

S.203.3 Alien plants in Sardinian wetlands, their effects to the native biodiversity and ecosystems

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Biodiversity is declining globally and invasion by alien plants is regarded as one of the most significant threats to ecosystems worldwide. Despite their great value in biodiversity conservation, wetlands are one of the most vulnerable environments to Invasive Alien Species (IAS). This is attributed to the anthropogenic pressure, especially eutrophication, which favours new invaders and variations of flooding pulses. IAS plants can cause radical changes in aquatic ecosystems with severe consequences, either through competition for resources with the native plants or by physically altering the habitat.

Here are presented analyses on invasion by alien plants and how these affect the native flora. We monitored 500 wetlands around Sardinia (Italy), including different types. The field information was gathered following a rapid assessment protocol to provide a general overview of a maximum number of sites. Most of the wetlands investigated are threatened by biological invasion, a total of 128 alien plant species were found (ca. 1300 records), accounting for 8,5% of the total plant species.

Furthermore, invasive plants were found in the 50.41% of the wetlands, while the naturalized in 30.89% and the casual ones in 18.70% sites. Asteraceae species had the highest frequency, followed by Poaceae, and Fabaceae. Among invasive hydrophytes, we recorded *Lemna minuta*, *Hydrocotyle ranunculoides*, *Pontederia crassipes* and *Azolla filiculoides*. Higher concentration of IAS was detected in coastal wetlands than in inland or human-made wetlands. These wetland types include lagoons, estuaries and salt marshes of different surface and catchment size, human population and touristic pressure. We detected that multiple activities around coastal wetlands and their catchments directly and indirectly promote IAS proliferation, especially in the most easily accessible areas. These results lead us to enhance multidisciplinary research on the ecology and functioning of wetlands, to plan more effective conservation actions based on plant communities' knowledge.

S.203.4 Neophytes and archaeophytes in the segetal flora of artichoke fields in the Mediterranean island of Sardinia

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Segetal flora refers to the set of spontaneous plant species, almost exclusively annual, that grow in agroecosystems, within crops, and whose composition and biomass depend on habitat conditions and management adopted. Plant communities in conventional intensive cropping systems often include a limited number of species, with dense covering, which may represent a limiting factor as their presence affects crop yield. On the contrary, a more diverse segetal flora considerably increases the whole biodiversity of agroecosystems, supporting pollinators and other beneficial insects. The study was carried out in Sardinia (Italy) during 2019-2021 to assess the dynamics of species richness of the segetal flora in globe artichoke (*Cynara cardunculus* L. s.l.) cropping system. The data was collected in Sardinian fields of globe artichoke through random located georeferenced plots (1×1 m). Two different cropping systems were analyzed: conventional and organic. Based on floristic surveys, it was possible to make an inventory of 115 plant species classified as native or non-native (neophytes and archaeophytes). The most frequent and often also the most abundant species were three natives (*Calendula arvensis* (Vaill.) L., *Convolvulus arvensis* L., *Lolium rigidum* Gaudin), one archaeophyte (*Avena fatua* L. s.l.), and three neophytes (*Glebionis coronaria* (L.) Spach, *Oxalis pes-caprae* L., *Veronica persica* Poir). Our results showed that organic farming often has positive effects on species richness, improving the diversity of plant communities, reconciling the sustainability of agricultural systems and the provision of ecosystem services. However, a higher coverage of plant species was observed in the conventional systems compared to the organic. In the conventional systems the composition of the segetal flora is shaped by high nutrient availability, herbicide resistance and biogeographic origin. Such traits are often linked to species that are highly competitive and difficult to control.

S.203.5 Biological invasions in Marine Protected Areas (MPAs): trends in non-indigenous macrophytes in Italian MPAs

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Non-indigenous species (NIS), widely recognized as one of the main drivers of global change, may in time become invasive, determining significant environmental impacts, such as biodiversity loss and ecosystem services degradation. The impact of NIS on marine habitats within Marine Protected Areas (MPAs), whose major aim is biodiversity conservation, can be significant even highly detrimental. Therefore, monitoring NIS distribution is crucial in these areas for planning effective conservation strategies. Currently, in Italy have been established 29 MPAs that protect about 700 kilometres of coastline and are mainly concentrated in the two great islands, Sicily (7) and Sardinia (6). Of them, 11 are Specially Protected Areas of Mediterranean Importance (SPAMI). In Italy, 73 alien macrophytes (10 Chlorophyta, 16 Ochrophyta, 46 Rhodophyta, 1 Tracheophyta) is currently reported. Our research revealed differences among the MPAs with respect to the number of marine alien macrophytes, which could be linked to different reasons such as differences in the number of conducted studies or differences in geographical position. For instance, 12 marine alien macrophytes have been reported for the MPA Egadi Islands, 6 for the MPA Capo Carbonara, 2 for the MPA Miramare and 8 for the MPA Portofino. The research has also shown that data on fauna and terrestrial flora are more numerous than those on marine flora and that the last ones are not often updated. Despite their fundamental role in the conservation of marine biodiversity, MPAs are not immune to biological invasions, evidencing that protection does not hinder the introduction and spreading of NIS. Management actions within MPAs should include the planning of regular monitoring activities which will allow early detections and to follow the spread of species already present. This work represents an important starting point for the creation of a regularly updated list of alien macrophytes within the Italian MPAs.

S.203.6 Towards an updated catalog of the alien vascular flora of Spain

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Invasive alien species poses one of the main threats to biodiversity conservation, ranking as the second leading cause of native species extinction worldwide. The Mediterranean Basin, particularly Spain, has emerged as one of the most impacted regions by biological invasions. Several factors contribute to this vulnerability, including: (1) the profound human-mediated modification of natural habitats (habitat loss and fragmentation, contamination); (2) complex and varied topographic, lithological, and climatic gradients; (3) its key role as a global commercial and transportation hub; (4) its condition as one of the world's main touristic destinations; and (5) its recurrent identification as one of the biodiversity hotspots more susceptible to climate change. Biological invasions have profound impacts on the Spanish flora, since Spain is very rich in plant diversity, with plenty of narrow-range endemics; the latter being inherently vulnerable to human activities due to low effective population size but exhibiting taxa of high genetic distinctiveness. Knowledge on the status of alien species in a given area is essential for effective management and prevention of their further spread. Within this context, the Introduced Plant Working Group of the Spanish Botanical Society (SEBOT) is currently developing a comprehensive list of alien vascular plants found in Spain, aiming at: (objective 1) updating and completing the existing catalog of introduced plants in Spain, which was last published over two decades ago and excluded casual plants; and (objective 2) identifying alien taxa that are not currently included in the Spanish Catalog of Invasive Exotic Species, which legally regulates the possession, transport, movement, and trade of alien species. In this communication, we provide a summary of the progress achieved in this ongoing initiative that already agglutinates an important network of researchers working on invasive biology in Spain.

S.204 ADVANCES IN MICROCLIMATE RESEARCH FOR CRYPTOGAM ECOLOGY. SESSION 2

S.204.1 A new autonomous and low-cost electronic system based on Arduino for measuring the microclimatic conditions of lichens and their hydration

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The influence of climate on lichen physiology is directly shaped by its poikilohydric nature. While lichens exhibit high tolerance to extreme environmental conditions when dry, their sensitivity significantly increases when hydrated. Consequently, the primary impacts of climate on lichen physiology are confined to periods when the thallus is wet and actively metabolizing. Numerous ecophysiological studies on lichens have tackled the challenge of distinguishing microclimatic conditions during periods of thallus activity or inactivity, often employing measurements of thallus electrical conductivity. In response to this challenge, we have developed an autonomous and low-cost electronic system designed to measure the microclimatic conditions of lichen habitats and those of the thallus itself. Additionally, the device utilizes electrical resistance measurements to estimate the thallus' hydration level. Built on the open-source Arduino platform and complemented by readily available and affordable hardware components, the system is powered by lithium-ion batteries, which are recharged with solar energy, ensuring indefinite operation. Data is stored on an SD card and concurrently transmitted to a cloud server through the GSM network. The devices were tested with thalli of *Ramalina farinacea* growing in a mixed oak forest (Guadalajara, Spain). Over the course of a year, continuous data collection revealed that irradiance and temperature levels were lower when the lichens were in a hydrated state than when they were dry. Notably, the environmental conditions during the active phases of the thalli fell within the tolerance limits previously established for *R. farinacea* photobionts. In summary, this system enables the extended measurement of environmental conditions for both physiologically active and inactive lichens. This data is crucial for comprehending the dynamics of lichen communities.

S.204.2 Beach or mountain? Ecophysiological and microclimatic comparative study of the lichen Usnea aurantiaco-atra in maritime Antarctica

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Understanding the environmental responses of the polar cryptogamic flora and determining its ecological boundaries is a useful tool to evaluate the impact of ongoing global change on Antarctic regions. In maritime Antarctica, ice-free rocks on coastal areas and on nunataks within mountain systems offer suitable niches for cryptogams, particularly for lichens able to survive in severe environmental conditions. Due to their poikylohydric nature, these photosynthetic lithobionts are strongly tied to the local climatic conditions. The present study focuses on the fruticulose lichen *Usnea aurantiaco-atra* (Jacq.) Bory, an Antarctic endemism vastly spread throughout maritime Antarctica. The aim of the research is to assess the ecophysiological optimums and ranges of tolerance of *U. aurantiaco-atra* to environmental change. Two sites were chosen across an altitudinal gradient within the South Bay on Livingston Island (South Shetland Islands) with intent to cover an environmental-pressure range of the subject species: Punta Polaca (50 m a.s.l.) and El Castillo Nunatak (449 m a.s.l.). The photosynthetic and respiratory rates of thalli collected from each site were measured in relation to key drivers such as water content, temperature, and light under controlled laboratory conditions. Metabolic performance was analysed *in situ* for both locations through continuous chlorophyll *a* fluorescence monitoring paired with simultaneous recording of microclimatic conditions. To further understand potential acclimation or adaptation mechanisms adopted by the photobionts of *U. aurantiaco-atra*, induction-recovery curves were conducted. Additionally, an extensive network of temperature and relative humidity microsensors was deployed throughout multiple lithic niches at both sites and kept recording for over a year. Preliminary results suggest that the coastal population achieves significantly greater photosynthetic activity at higher temperatures. No dissimilarities have been found in the performance of coastal and mountainous individuals at lower temperatures. There seems to be strong environmental filtering in the nunatak, which points to greater ambient stress.

S.204.3 Ecophysiological response between populations of epiphytic macrolichens of Araucaria araucana (Mol.) K. Koch in Chile

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The *Araucaria araucana* forest is one ecosystem highly affected by climate change, global warming and fire. This conifer specie is endemic to southern South America at the Chilean and Argentinian mountain ranges, distributed from ~37°24´ to ~40°03´ S. The epiphytic lichens inhabiting this forest shows a close relationship with his phorophyte and are an important biological group increasing the biodiversity of the habitat. Some lichen functional traits like thickness of the thallus layer or state of the photosystems can vary in response to changes in light, humidity and temperature that can occur in the environment. However, it is unclear how in the scenario of global climate change (GCC) with a decrease in precipitation and an increase in temperature will affects the epiphytic lichens of *A. araucana* forest. Lichens are especially vulnerable to environmental conditions since they need availability of water to maintain their active metabolism. In this work we aimed to understand how lichens are adapted to the expected GCC we are studying the tolerance to desiccation of epiphytic lichens. Macrolichens collected on *A. araucana* bark from two different populations where compared, one located at Conguillío National Park (Andes Mountains) and the other at Nahuelbuta National Park (Coastal Mountains). We measured the photosynthetic performance of lichens after maintaining in dry atmosphere for a time period of 72 days. We found significant differences in the response of the maximum efficiency of PSII (Fv/Fm) to desiccation over time and in the anatomy of the thallus between species. The physiological response of the species compared to the anatomical responses and macroclimatic and microclimatic records are discussed.

S.204.4 The Immensity of Minutiae: Utilizing Bryophytes to Detect an Ice Age Refugium in the Northern Cascade Mountains

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Ice age refugia were ecologically stable areas that remained ice-free during the Pleistocene glaciations. As a result, they offered a level of suitable conditions to host arctic species associated with the climate of that time. About 16,400 years ago, the climate began to warm, the ice sheets in western North America began to recede, and these vestiges of the late Pleistocene became surrounded by the temperate ecosystems of today leaving disjunct and isolated species of a previous climate. A unique balance of microclimatic and topographical factors has allowed for these remnant species to exist today. Throughout the Pleistocene, ice age refugia were drivers of speciation, and currently are retainers of relictual species. Therefore, these places are biodiversity hotspots providing key insights into evolutionary histories of northern taxa. However, complete biological inventories of these places are lacking and many ice age refugia remain undetected. Tragically, due to climate change, these ecologically novel places are at risk due to the projected changes in moisture and temperature regimes for western North America. This study takes a comparative bryophyte floristics approach to detect an ice age refugium in an area of the northern Cascade Mountains of Washington state – Barlow pass. The results of two years of field work yields numerous disjunct northern taxa such as *Cyrtomnium hymenophylloides, Psilopilum laevigatum* and *Macrodiplophyllum* imbricatum found within a microclimatically significant area of Barlow Pass while absent from similar areas in the glaciated North Cascades. The maximum extent of the Cordilleran ice sheet is paired with reconstructions of the local paleo-alpine glaciers, suggesting that these species are relicts of an ice-free corridor during the last glacial maximum. Finally, the bryoflora of Barlow Pass is compared with floras of putative ice age refugia and is placed in the context of North American ice age refugia.

S.204.5 What role have changes in climatic conditions and atmospheric pollution played in the spatio-temporal variation of epiphytic bryop

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Because of their ecophysiological characteristics and their position at the interface between the atmosphere and vegetation, epiphytic bryophytes have long been used as indicators of air quality. The spectacular recolonization of these organisms over the last twenty years has paralleled the drastic reduction in SO2 concentrations. However, the concomitant variation in the concentration of other major pollutants (NOx, NHx, O3, fine particles) as well as climatic conditions complicates the interpretation of the factors responsible for the observed floristic changes. We carried out a diachronic analysis since 1980 to separate the impact of climatic conditions and concentrations of major atmospheric pollutants on the historical variation in floristic composition. This analysis was complemented by an assessment of the contribution of major pollutants and pesticides on the spatial variation of flora observed today. The results show that temporal changes in floristic composition within the same community are more than twice as great as spatial changes in composition between communities at present. This temporal variation in flora is largely explained by the decrease in SO2 and NO2 concentrations, but not by variations in climatic conditions. The absence of a relationship between historical concentrations of major pollutants and contemporary variation in flora at regional scale suggests that epiphytes have sufficient dispersal capacity to recolonize the areas that are favorable to them within a few decades. Our analyses have shown that the drastic reduction in major atmospheric pollutants has enabled the emergence of a contemporary segregation of floras based on regional variation in climatic conditions, even though other pollutants, particularly fine particles, are playing an increasing role.

S.204.6 Long-term effect of elevated CO_2 on desiccation-rehydration cycles of bryophytes

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The concentration of atmospheric CO_2 has been constantly increasing since the industrial revolution and it is projected to rise even further, surpassing 1000 ppm at the end of this century in the worst-case scenario. In vascular plants, influences of rising CO_2 have been studied extensively, but there are much fewer studies for bryophytes. This is a significant omission as these organisms are major contributors to biodiversity in high latitudes and play key roles in ecosystem functioning. We conducted a long-term in vitro CO_2 elevation experiment with four bryophyte species to assess the effect of elevated CO_2 (1000 ppm) on bryophyte desiccation tolerance and desiccation-rehydration cycles. Real-time kinetics of gas-exchange and chlorophyll fluorescence were monitored throughout a year, with measurements taken every four months. The results show a reduction of photosynthetic activity under elevated CO_2 in the four species studied. Long-term exposure to elevated CO_2 negatively affected the photosynthetic recovery and carbon balance after desiccation-rehydration, however interspecific differences were observed in the responses to elevated CO_2. These results highlight the importance of studying species-specific responses to climatic disturbances that might affect their photosynthetic characteristics in distinct ways. This study provides insight into the variable responses of bryophytes to environmental change that can potentially affect their fitness and role in the ecosystems under the current global change.

S.205 ORCHID PHYLOGENOMICS: DIVERSIFICATION, TRAIT EVOLUTION AND BIOGEOGRAPHY. SESSION 2

S.205.1 Australasian orchid diversification: phylogenomic insights from tribe Diurideae (Orchidoideae)

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Australia harbours a rich and highly endemic orchid flora with over 1,600 species of which over 90 % occur nowhere else. The terrestrial orchid tribe Diurideae is a morphologically diverse and characteristic element of the Australasian orchid flora and comprises nine subgenera and over 1,000 species. The tribe exhibits greatest diversity in Australia where it encompasses ca. 60% of native orchid species, extending into New Zealand, New Caledonia, New Guinea, tropical Asia and the Pacific. Previous phylogenetic studies provided only limited insights into the origins and spatio-temporal evolution of Diurideae lineages due to limited resolution and/or sampling. Here we present a thoroughly sampled phylogenomic study of Diurideae, encompassing all nine subtribes, all recognised genera and the vast majority of species of the tribe. Genome skimming data for over 1,350 Diurideae samples as well as for a broad outgroup sampling across Orchidaceae was generated and assembled either de novo or via reference-guided assemblies. Maximum likelihood analyses were carried out based on concatenated alignments of 62 plastid coding genes and divergence time estimations conducted based on secondary calibrations using BEAST. Biogeographic areas were delineated based on botanical continents and regions following Brummit (2001) and within Australia based on the terrestrial phytoregionalisation sensu Ebach et al. (2015). Range evolutionary scenarios were reconstructed using model-based inference methods as implemented in BioGeoBEARS. This study provides new insights into the diversification and range evolution of tribe Diurideae during the Cenozoic with its profound climatic and vegetational changes and constitutes an unprecedented phylogenomic framework for macroevolutionary studies in Australasian Orchidaceae.

S.205.2 Phylogenomics and the evolution of floral traits in the species-rich Pleurothallidinae subtribe

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Pleurothallidinae, with over 5500 species, stands as the most species-rich subtribe within the Orchidaceae, providing an ideal model for studying Neotropical diversity and its evolution. Recent estimates suggest that most groups within the subtribe have recently originated due to rapid diversification. This remarkable diversity is associated with significant morphological variation and pronounced homoplasy, posing a challenge in establishing robust phylogenetic frameworks. Previous studies relying on limited markers, such as nrITS and matK, have proven insufficient in resolving relationships within specific clades. To deepen our understanding of the relationships among Pleurothallidinae groups and the role played by critical morphological traits in their evolution, we present a comprehensive phylogenomic framework sourced from the Angiosperm353 kit. This dataset comprises 127 samples from 33 genera, representing 73% of the subtribe's genera. Our study includes an expanded analysis encompassing 1765 nrITS samples, 900 matK samples, and plastomes from 44 selected species. Utilizing these extensive phylogenetic datasets, we have explored the evolution of floral traits, such as anther position and pollinarium structures, employing cutting-edge phylogenetic comparative methods. Our findings establish a well-resolved backbone for most Pleurothallidinae clades, enabling the exploration of critical floral trait evolution. We have identified potential correlations between apical anthers and pollinaria featuring sticky viscidia in groups associated with high diversification rates, such as Lepanthes, Pleurothallis, and Stelis. By incorporating phylogenomic data derived from the Angiosperm353 kit, we have significantly advanced the understanding of the relationships among Pleurothallidinae groups, and their evolutionary patterns related to critical floral traits. However, a compelling need remains to increase species sampling to ensure more comprehensive conclusions and include a broader range of morphological characteristics. As phylogenomic and species sampling efforts continue to expand, our objective is to trace the origins and dispersal routes of Pleurothallidinae and elucidate the connections between assessed morphological traits and intriguing pollination mechanisms.

S.205.3 Phylogeny and diversification of Aeridinae (Orchidaceae: Epidendroideae), with a focus on Vanda s.l.

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The subtribe Aeridinae, consisting of approximately 90 genera and 1550 species, is recognised as one of the most diverse and taxonomically challenging groups within Orchidaceae. In this study, we reconstructed the most data-rich intergeneric phylogeny of Aeridinae by sequencing around 400 species from 60 genera with samples obtained from herbarium specimens and living collections that span its geographic ranges, from tropical Asia to the Pacific region. Our comprehensive analyses integrated data from Angiosperms353 target-captured and off-target nuclear sequences, complemented by plastid genome sequences retrieved from genome skimming. The preliminary results showed that increasing the size of data sets enhanced the congruence between analysis methods but did not alleviate gene tree conflicts. To address incongruence observed between nuclear and plastid phylogenies, we conducted further analyses to explore potential factors contributing to this disparity. Hypothesised historical hybridization events, conceivably linked to regional speciation and diversification were tested and discussed. A specific focus was directed towards the genus *Vanda s.l.*, aiming to resolve its ambiguous phylogenetic relationship with allied genera, namely *Aerides*, *Ascocentrum*, *Holcoglossum*, *Neofinetia*, *Seidenfadenia*, and *Rhynchostylis*. We further employed BAMM, GeoSSE, and niche analyses to infer patterns of species richness and diversification of *Vanda s.l.*, providing valuable insights into the evolutionary dynamics within these linages. This study, with its comprehensive exploration of Aeridinae and the detailed investigation of the genus *Vanda s.l.*, is poised to serve as a reference for future endeavors in the taxonomic, systematic and integrative phylogenetic studies within these groups.

S.205.4 First Phylogenomic exploration of Angraecinae with target capture: evolutionary history of Angraecum

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Recent attempts to classify *Angraecum*, the largest genus of Angraecinae (Epidendroideae, Vandae), have fallen short due to a lack of molecular sampling and of molecular characters as well as the paucity of available voucher material. Without a robust natural classification, however, the reconstruction of the evolutionary history of *Angraecum* is impaired. Using a new multi-locus dataset collected with the Angiosperm353 bait set, augmented by a comprehensive sampling now available through the orchid shade house network of the Missouri Botanical Garden in Madagascar, in parallel to extensive field work conducted on the Mascarene islands and East Africa, we aimed to revise the genus *Angraecum*, improving its classification and testing phylogenetic hypotheses. Using resulting data from Hyb-Seq, our analyses consistently retrieved a strongly supported clade grouping most *Angraecum* species from Madagascar and the Western Indian Ocean, but interestingly including species from three other Malagasy genera, *Lemurorchis*, *Oeoniella* and *Sobennikoffia*. Moreover, the resulting phylogenies allowed us to re-circumscribe sections and better understand intersectional relationships. Finally, a group of fifteen species were found to be polyphyletic and were described as a new genus, *Vavavoloina*.

S.205.5 Holocene climate change promoted allopatric divergence and disjunct geographic distribution in the bee orchid species Ophyrs aveyronensis

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Species with disjunct geographic distributions provide natural opportunities to investigate recent or incipient allopatric divergence. Although not rare, many of the cases observed result from successful colonization from a historical to a new range through dispersal or human-induced introduction which make the underlying eco-evolutionary processes sometimes difficult to decipher. The bee orchid species *Ophrys aveyronensis* presents a disjunct geographic distribution with two ranges currently separated by 600 km on both sides of the Pyrenees Mountains. To uncover the causes of such intriguing biogeographic pattern, we combined population genomics and Ecological Niche Modelling approaches. Population genomic data show that all the populations studied display similar patterns of genetic diversity and dramatic decrease in effective size. We found significant genetic differentiation between the two ranges of *O. aveyronensis*. Our results support a very recent divergence (*i.e.*, ca. 1500 generations ago). Ecological Niche Modelling results further indicate that the disjunct geographic distribution of the *O. aveyronensis* species complex is consistent with a range split of a broad ancestral range, contraction and shifts in opposite directions in response to climate warming during the Holocene. The congruence of both the results of population genomics and ENM approaches demonstrates that continental allopatric divergence is involved in the *Ophrys* adaptive radiation. *O. aveyronensis* is a promising candidate to study the onset of reproductive isolation immediately following an initial stage of geographic separation.

S.205.6 Geitonogamy blurs the distinction between autogamy and allogamy: a case study in Epipactis (Orchidaceae)

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The North Temperate orchid clade *Epipactis* has become a model system for the study of speciation through transitions supposedly passing from allogamy through facultative to obligate autogamy. Structural modifications said to encourage this transition include: (1) reduction in the size and/or hydration of the adhesive viscidial disc responsible for attaching the pollinaria to pollinating wasps and bees, such that pollinaria are less likely to be removed; (2) ontogenetic extension of the anther such that the gynostemium apex curves downward, bringing the pollinaria into closer proximity with the stigma; (3) decreased cohesion of the viscid threads that link the permanent tetrads of pollen within the pollinaria, allowing the formerly cohesive mass of tens of thousands of pollen grains to dissociate for abiotic dispersal, and; (4) reduction in the size and prominence of the rostellum that separates the pollinaria from the stigma, thus permitting pollinium fragments to reach the subjacent stigma through the effects of wind, rain-splash or gravity. Sramkó etal. (2019) used RADseq data to reconstruct the phylogenetic relationships of 108 plants representing 27 named ingroup taxa recognised by traditional taxonomy, which consequently were recircumscribed to 11 species that collectively spanned the full range of supposed reproductive categories. However, all species yielded *F* statistics consistent with dominant (but not obligate) autogamy; only the widespread, ecologically tolerant *E. helleborine* s.s. had a somewhat lower mean *F* value than the more ecologically specialised species, the majority of which evolved relatively recently from within the consequently paraphyletic *E. helleborine*. This consistently high level of self-fertilisation is attributed to extensive geitonogamy, facilitated by the upward movement of nectar-seeking pollinators within the many-flowered inflorescence combined with the absence of reorientation mechanisms in pollinaria once attached to the insect. Thus, reproductive strategies traditionally presented as alternatives driving speciation have proven considerably less distinct than previously believed.

S.206 LET PEOPLE COME TO BOTANY: NEW METHODS TO ENGAGE PEOPLE WITH PLANT DIVERSITY. SESSION 1

S.206.1 Lichens want you! Communication, dissemination and engagement strategies in lichenology

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Traditionally, scientific knowledge reached the public through passive mediums like television programs and museums. In the last decades, we've witnessed a paradigm shift, where museums and botanic gardens have transformed into interactive platforms, offering immersive experiences through multidisciplinary approaches. Technology is democratizing access to information, widening age range and user typology, and fueling collaborative efforts among people with common interests thanks to various online arenas for source searching, content sharing, and discussion. In the dynamic landscape of knowledge dissemination, the shift to virtual events, driven by health-security concerns during the COVID-19 pandemic, has proven to be a game-changer. Similarly, citizen science activities have emerged as a powerful tool in science, extending educational outreach beyond traditional boundaries. This paper analyses the strategies adopted in the last years by two scientific entities - the International Association for Lichenology (IAL) and the Italian Lichen Society (SLI) – for their communication, dissemination, and public engagement, showing the global reach and inclusivity achievable through online platforms. In the field of lichenology, virtual experiences and citizen science activities enhance scientific literacy and training, contributing to environmental conservation by fostering familiarity and appreciation for lichens.

S.206.2 Experiences of using citizen participation as a teaching tool for botany

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In a society increasingly affected by plant blindness, the need for botanical literacy is undeniable and urgent. In this context, we explore the transformative potential of citizen participation as a dynamic teaching tool in botany courses. The latest advancements in citizen science platforms provide now the opportunity to integrate classical botanical guides and taxonomic keys with the judicious use of cutting-edge technologies —notably artificial intelligence. These tools can be used to strengthen innate heuristic processes, such as the recognition of the General Impression of shape and size (GISS), sharpening participants' analytical observational skills. Simultaneously, these platforms foster a culture of collaborative learning, stimulating active engagement, promoting greater student participation, and facilitating the exchange of knowledge. In this way, this approach not only serves as an invaluable tool for biodiversity study but also immerses participants in a dynamic learning experience, enabling continuous growth and reinforcing the learning process. To illustrate the use of citizen participation as an educational instrument, several examples will be showcased, ranging from local projects in a university campus, spanning an entire botany course, to a national-scale flora bioblitz. Through the implementation of this educational method, people will develop a stronger interest in botany and students may even consider careers in the field due to their deeper connection and appreciation of plant diversity. Ultimately, this method accelerates the learning curve, propelling botanical education into a new era of plant knowledge accessibility and enthusiasm, that will contribute to the acceleration of taxonomy and the prevention of biodiversity loss.

S.206.3 Blossoming awareness: empowering communities through citizen science platforms to combat plant blindness

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Citizen science is increasingly becoming a methodology used in biodiversity monitoring due to the massive amount of data it allows to collect, greatly benefiting scientific work. In this way, it gains a vast array of allies, the citizen scientists, spread across the entire territory, enabling unprecedented sampling. Indeed, this is not the only advantage. The increase in environmental literacy and the shift of these citizens from a passive role to being considered key elements in the scientific process give them an importance they did not have before. Is crucial to understand how to achieve a wide diversity of citizens, making citizen science not only democratic, as it already is, but also inclusive. How can we ensure that everyone feels they can contribute? What strategies can be employed to reach social groups less engaged with these topics? Should we strive to reach everyone? How can citizen scientists be encouraged to explore taxonomic groups that may seem less appealing? How do we tackle "plant blindness" that affects so many? Can citizen science help citizens become less disconnected from nature? These questions will set the tone for this symposium, aiming for it to be dynamic and participatory.

S.206.4 The Flora-On portal: leveraging the potential of biodiversity data to provide new insights into species natural histories

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The Flora-On.pt platform was conceived with the mission of sharing botanical knowledge to the widest audience possible, on the distribution, ecology, threats, phenology, morphology, biotic interactions and bioclimatic niches of the plants of a given territory. It is built upon curated crowd-sourced and scientific data of different types and sources, including distribution data from project collaborators and iNaturalist. The primary focus is to deliver intuitive tools for exploring and relating the data in useful or unexpected ways, allowing users to quickly find the answers to their specific needs, or just satisfy their curiosity. This is achieved by offering a rich set of query possibilities: textual queries with partial matching (taxonomy, common name and ecologies); morphological queries (e.g. flower color, shape, leaf characters, etc.); phenological queries (search by exact flowering date or period, based on continuous dates); geographical queries (proximity to point coordinates and occurrence within boundaries or regions - UTM grid squares, municipalities, protected areas, etc.); bioclimatic queries (search by multivariate bioclimatic envelopes); rarity queries (search by area of occurrence); ecological similarity to other species (search using bioclimatic envelope similarity); biotic interactions (e.g. search species that parasite, or are parasitized by, other species). One of the innovative features is that the queries based on continuous numerical data (flowering dates, location, bioclimatic data) work in a probabilistic workflow, delivering results tuned and sorted according to probability, thanks to internal numerical processing algorithms. To empower these possibilities, query results can be displayed in a variety of views, for example point clouds in bioclimatic spaces, aggregated abundance distributions in a GIS viewer, multiway identificatoin key, in addition to the usual photo album. The software is on its way to be publicly accessible in an open source repository, therefore enabling anyone to implement the Flora-On system in other countries, or to other biological groups.

S.206.5 The Taylor Swift's Method: music videos as advance organizers for meaningful learning in Botany

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The COVID-19 pandemic changed the structure of classes in Brazil, teachers had the task of creating new strategies to make remote learning fluid. In Botany, this challenge was intensified, because, even though plants are essential for life, their study is considered unnecessary and uninteresting. Students' complaints are related to the nomenclatural complexity, traditional classes, lack of attractive teaching resources, also, teachers with a lack of enthusiasm, and they see no connection with plants in their lives. This negative image of Botany that society, students, and a few teachers of sciences carry, is called "Plant awareness disparity": the general public largely does not notice plants in nature and is not able to recognize how important they are to the biosphere and society. Therefore, the aim of this study was to use four music videos of the singer Taylor Swift, one per week, as advance organizers to introduce four different lessons to a second-year class (high school) in Natal, Brazil: 1. Plant awareness disparity and its consequences (week one: Blank Space – 1989); 2. Bryophytes and pteridophytes (week two: Cardigan - Folklore); 3. Gymnosperms (week three: Out of The Woods – 1989); 4. Angiosperms (week four: Willow – Evermore). One week before each remote lesson, they received the YouTube link to the video in their school system and watched it. In the first 20 minutes of the remote lesson, we discussed what kind of botanical elements they saw in Taylor Swift's music videos, this dynamic led them to identify vegetables, plants, moss, fruits, flowers, trees, roots, and even ecological traits, increasing their optical perception of plants. Our results showed that art can be an ally for meaningful learning in botany: classes were fun, students spoke botanical terms naturally, and, consequently, began to pay more attention to plants in the environment.

S.206.6 An Illustrated Flora of the Caribbean: from early botanical illustrations to a modern electronic flora

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The Caribbean region boasts a rich botanical diversity, encompassing a myriad of plant species with unique ecological and cultural significance. This conference presentation explores the evolutionary journey of Caribbean botanical documentation, tracing the transition from early botanical illustrations to the development of a contemporary electronic flora. The Caribbean has been a focal point for botanical exploration since the Age of Discovery, with early naturalists and artists meticulously capturing the region's flora through intricate illustrations. This presentation begins by delving into the historical context of these early botanical artworks, shedding light on the scientific and cultural contributions made by early explorers. From the vivid depictions of exotic plant life to the discovery of new species, these illustrations serve as invaluable snapshots of the Caribbean's botanical heritage. As technology advanced, so did the methods of botanical documentation. The transition from traditional illustrations to modern electronic formats marks a significant milestone in the representation and accessibility of Caribbean flora. This presentation explores the challenges and innovations associated with digitizing botanical information, emphasizing the advantages of electronic floras in promoting conservation, education, and research. The electronic flora under discussion is a comprehensive and interactive resource that integrates traditional taxonomic knowledge with modern technology. This platform aims to provide users with a dynamic and user-friendly interface for exploring the diverse plant life of the Caribbean. Features include detailed species profiles, distribution maps, and multimedia content, enhancing the overall accessibility and educational value of the flora. The presentation concludes by highlighting the collaborative efforts involved in creating this electronic flora, emphasizing the importance of interdisciplinary partnerships between botanists, illustrators, and technologists. By bridging the past and present, this project not only preserves the botanical legacy of the Caribbean but also facilitates ongoing research, conservation, and public engagement with the region's unique and threatened plant species.

S.207 ECOPHYSIOLOGICAL CHALLENGES IN THE ANTHROPOCENE. SESSION 1.

S.207.1 CLEANFOREST COST Action: helping forests to face the Anthropocene

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Forests are at the forefront of our efforts to mitigate climate change and achieve the UN's Sustainable Development Goals, to ensure a sustainable life on Earth. However, forest ecosystems are particularly threatened by global change components, such as increasing frequency and severity of climate extreme events, increasing atmospheric carbon dioxide and pollutants concentrations. Different global change drivers could play a synergistic, antagonistic or predisposing role in affecting forest ecosystem functioning and health. All these drivers, however, are generally considered in isolation, and their effects on key processes (at tree, soil and ecosystem levels) are investigated separately in natural, periurban and urban forests, thus leading to uneven, un-coordinated and scattered information among different research communities. CLEANFOREST is establishing an inclusive and multidisciplinary pan-European network, which capitalizes on existing expertise and infrastructures (monitoring networks, manipulation experiments) to i) coordinate research efforts (e.g. data collection), ii) compare approaches and define common protocols to standardize measurements and methods used in global change studies, and iii) foster collaboration among different research groups to exchange and synthesize data, thus contributing to advancing scientific knowledge, identifying research gaps and providing suggestions for the next generation manipulation experiments and monitoring networks. This includes summarizing main results on the effects of treatments applied (experiments) or observed deposition level (monitoring) on eco-physiological parameters, health, growth and diversity of forests, assessing the effects of atmospheric deposition and climate extremes on trees' nitrogen storage and cycling, and evaluating the role of aboveground biodiversity (tree diversity and identity) response to N depositions and climate extremes, as potential mitigation measures.

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S.207.2 Temperature shifts dynamically influenced reproductive development and fruit yield of apple (Malus x domestica Borkh.)

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Temperature plays a pivotal role in climate change, significantly impacting both natural and agroecosystems. While extensive research has elucidated temperature influence on bud dormancy and flowering in deciduous species, a notable gap exists in understanding its effects on fruit tree yield, particularly apples. Hence, this research aimed to explore the relationship between temperature, reproductive development, and fruit yield in 'Red Windsor' apple trees under controlled environments during the 2020 and 2021 seasons. Specifically, apple trees were subjected to ambient temperatures and fixed deviations (-4°C, +2°C, or +4°C) from these levels for eight months, spanning from budbreak to fruit maturation, with the treatments following the daily and seasonal temperature fluctuations. Results revealed that phenological shifts induced by temperature treatments altered the growth patterns of reproductive structures, subsequently impacting the developmental overlap between reproductive and vegetative organs. While flowering duration remained unaffected, fruit setting, trunk/branch wood volumes, thermal time requirements, and bud development displayed a magnitude change ranging from 11% to 31% per 1°C shift in temperature. Interestingly, manipulating temperatures by ±4°C from ambient levels did not significantly influence final fruit yield due to source limitations. Significant treatment effects were evident on fruit yield components, with the warmer temperatures prompting an earlier harvest with fewer but larger fruits. Sub-ambient temperatures remarkably enhanced fruit set but resulted in a considerable fruit drop incidence due to low assimilation rates. Moreover, warmer temperatures supported early fruit development by increasing photosynthetic pigment levels and assimilation rates but subsequent stimulation of vegetative growth intensified sink competition at the expense of fruit development. This research provides crucial insights into the complex physiological dynamics of temperature and their profound implications on apple fruit productivity. Further exploration of these relationships can contribute to the development of practical, resilient, and sustainable strategies to maximise apple yield under shifting climatic conditions.

S.207.3 From sea to farm: Rhizodesigning crop rhizospheres with marine bacteria synthetic communities to enhance plant tolerance to stress

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The world population is expected to reach 9.1 billion by 2050, thus raising the need for increasing global food production by 70% to match the growing demand. Alongside, the impacts of global climate change tend to reduce land fertility at a rate higher than the adaptation capacity of agricultural practices, imposing new challenges to agriculture, increasing physiological constrain factors (high atmospheric CO_2, drought, salinization, thermal stress). Thus, the need to search for alternative cash crops and nature-based solutions and practices towards sustainable and regenerative cultivation schemes arises. Recently several bacterial isolates have been identified from marine ecosystems with plant growth-promoting abilities displaying highly promising results upon application in crop cultivation, allowing plants to fight back physiological constraints. Plant rhizosphere bioaugmentation with marine plant growth-promoting bacteria (PGPB) appears as a reliable, low-cost nature-based solution to improve agriculture production under disadvantageous conditions. Among the available PGPB hosts, halophyte plants with recognized nutritional and agroecological value but also a high degree of tolerance to several physiological constraints such as soil salinization, drought, CO_2 rising, and disadvantageous thermal conditions. Nevertheless, despite this high tolerance degree to adverse environments, in common garden experiments, these species still suffer some biomass production decrease under extreme conditions. Thus, these species' thriving ability in natural ecosystems indicates that this is not only boosted by their intrinsic tolerance but also by the presence of key microorganisms that improve these tolerance and resistance traits, becoming an attractive environment for PGPB bioprospection. In the present work, we present and discuss the application of marine PGPB isolated in different classical and novel crop systems as biotools to improve plants' resistance and tolerance mechanisms to adverse cultivation conditions (for e.g. heat, drought and saline stress) as well as potential tools to study the underlying physiological mechanisms improved by this rhizosphere bioengineering.

S.207.4 The photosynthetic efficiency of Thalassia testudinum and abiotic factors associated with the photosynthetic efficiency

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Seagrasses are angiosperms that live mostly in the ocean. Also, they have ecological and economic importance, like having a highly primary production (500 - 4000g carbon m^{-2} year-1) and giving nourishment to fish and other important invertebrates. One of the strategies for evaluating the health of seagrasses is the evaluation of their photosynthetic efficiency. The objective of the study was to obtain the *Fv/Fm* of *Thalassia testudinum* and to analyze the abiotic factors associated with photosynthetic efficiency in seagrasses. In 7 areas of The Gulf of México and Yucatán, environmental parameters (temperature pH, depth, dissolved oxygen, salinity, nutrients in the water column, interstitial water nutrients, type of sediment, and organic carbon) were registered at each site. Plants of *T. testudinum* were collected in 7 areas along the coasts of The Gulf of México and Yucatán during the years 2016 and 2019. They were in dark conditions for less than 24 hours, and with a Pulse-amplitude modulated (PAM) chlorophyll fluorometer, it was possible to register the *Fv/Fm* of the youngest leaves. A PCA analysis was used to establish relations with the photosynthetic efficiency of *T. testudinum. T. testudinum has* an average of 0.72 Fv/Fm ratio. Also, there were significant differences in the areas; Area 5 (San Felipe, Yucatán) presented the lowest *Fv/Fm* ratio (0.61). The most important factors in the PCA were, the *Fv/Fm* ratio of *T. testudinum*, depth, silicates, and dissolved inorganic nitrogen (DIN). Higher values of photosynthetic efficiency are related to a high amount of nutrients and low depths; areas that are low in these parameters will have low photosynthetic efficiency and be vulnerable to seagrasses meadows.

S.207.5 To tree or not to tree? Integrating LCA and ecosystem services to evaluate the sustainability of phytoremediation

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Over the past 30-40 years, urban areas have experienced a considerable shift in their economic activity. Many industrial sites that were once part of the urban centre are abandoned (brownfields), stimulating active discussion on challenges and opportunities for their reclamation and redevelopment. One of the main reasons for the lack of intervention are the high costs for conventional remediation techniques which are also associated with some important environmental disservices (i.e., SOx, NOx and VOC emission). Nature-Based Solutions (NBS), including phytoremediation for urban brownfields, may promote urban renewal, while reducing pressure on surrounding greenfield areas. Despite the high ecological and economical potential, due to some evident constraints (e.g., long operational time frame, plant tolerance to pollution) phytoremediation is still rarely applied on a large-scale. However, phytoremediation may provide multiple benefits in the form of ecosystem services (ES), such as soil and air quality regulation, biomass supply, biodiversity, aesthetics, and human health. Unfortunately, the assessment of ES related to phytoremediation is still incomplete and further research is needed in this regard. The assessment of ES is only partially covered by tools like Life Cycle Assessment (LCA), which provide data about the potential impacts of productions and services. The primary objective of the project is to assess different phytoremediation techniques and their related ES using an LCA approach. This analysis will highlight the most adequate phytoremediation approach providing the most suited ES for a specific area, with a particular emphasis on soil remediation and biodiversity conservation.

In addition, objective tools will be developed to support the fulfilment and validation of guidelines on the use of phytoremediation in urban areas, highlighting benefits and drawbacks of each possible applicable technique to the stakeholders involved. The final aim would be the efficient redevelopment of brownfields, endorsing policies for a sustainable management of these abandoned areas.

S.207.6 The effect of early light and water conditions for the seedlings of chamomille (Matricaria chamomilla L.)

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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.The research is supported by the support of OTKA 143376 application of Hungarian Academy of Sciences.

S.208 UNDERSTANDING FLORAL EVOLUTION ALONG MULTIPLE DIMENSIONS: EMERGING PATTERNS OF MORPHOLOGICAL, SCENT, AND COLOR VARIATION. SESSION 1

S.208.1 Patterns of fine-scale, tissue-specific floral scent in the yucca-yucca moth mutualism.

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Flowers are incredibly diverse, varying across a suite of macro-traits including size, shape, color and scent that are used to advertise rewards to pollinators. However, insect pollinators are usually much smaller than the flowers they visit, meaning fine-scale, or intra-floral, traits are likely significant to pollinator behavior and thus, floral reproduction. Floral scent is predominantly known for its important role in long-range pollinator attraction, with the majority of floral scent analysis conducted at the whole flower or inflorescence level. Getting the pollinator to the plant is of crucial importance to plant reproduction and is the first step in the pollination process, however successful pollination relies heavily upon pollinator behavior once within the flower and is likely highly impacted by fine-scale intra-floral differences in scent chemistry. The existence of floral tissue-specific scent variation has been shown to be present in 14 plant families and the patterns observed thus far are highly variable and species-specific. Intra-floral scent patterns might act as a chemosensory map that guides insects to floral rewards or improves pollination efficiency, but the ecological implications of intra-floral scent variation remain poorly understood. Brood pollination mutualisms, such as the yucca-yucca moth system often involve complex behaviors and a need for the pollinator to distinguish among floral parts, providing an excellent system to elucidate the ecological and behavioral impacts of intra-floral scent variation. Here I analyze the floral scent of tepals verses pistils of five species of *Yucca* that share a common pollinator (*Tegeticula yuccasella*). I describe within-species patterns of intra-floral scent variation, how patterns of intra-floral scent differ among *Yucca* species, and potential implications for pollinator behavior [13].

S.208.2 Testing the sensory drive theory in flower colors and bees: light environment and background are more important than floral color

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The evolution of flower color is commonly shaped by selective pressures exerted by pollinators. The sensory drive theory posits that the evolution of communication signals is determined by the sensory systems of the animals and the habitat conditions in which the signals are received. When applied to pollinators, this theory would imply that some floral colors may have divergently evolved in certain light environments, for example by becoming more conspicuous. Using the Mediterranean vegetation of south Spain, we compared flower color of coastal dune vegetation with open light environment and sandy background with those of closed cork-oak forest with shaded light environment and green leafy background. We hypothesized that, in the visual system of bees, each vegetation should be highly conspicuous in its own light environment and background. Irradiance of each community, reflectance spectra of flowered species and sandy dunes' background were collected. We modelled these data in the visual system of bees to assess conspicuousness differences of each flower community under different light environments. We found that the irradiance of coastal dune with open light environment was four orders higher than light reaching the cork-oak understory and showed differences in the spectral shape. Furthermore, sandy background nearly doubles the reflectance compared to leafy backgrounds, also showing spectral shape differences. In each vegetation type, we categorized flower color as UV$^+$ yellow, UV$^-$ yellow, pink and white. In both communities, all flower colors but UV$^-$ yellow showed significantly higher chromatic contrast in the dunes environment that in the corn oak understory. However, UV$^-$ yellow flowers showed lower in these conditions. Taken together, our findings indicate that open sandy environments favor the conspicuousness of most flower colors and suggests that other selective forces may play a role in the evolution of flower color at the community level.

S.208.3 Integration among phytochemicals cannot explain among-population variation in floral scent in Arabis alpina

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One recent discovery is the presence of variation in floral scent among conspecific populations of plants involved in generalized pollination systems. Often, such variation is taken as evidence suggesting that the floral scent of different populations is moulded in different directions by pollinator mediated selection, due to e.g. variation in local pollinator communities. Pollinators are believed to drive the evolution of floral scent in several systems, and this theory can also be tested for Arabis alpina. However, one possibility is that floral scent may not be the target of selection and that pollinators are not the only agents shaping the evolution of the floral scent chemistry in this system. Many floral scent compounds share biosynthetic pathways with defence compounds. Thus, selection pressures that affect defence compounds could result in indirect selection on the floral scent compounds. Therefore, to determine if floral scent is free to evolve unrelated to other plant compounds it is important to investigate to what degree floral scent compounds are correlated to other plant compounds, especially those involved in plant defence. We extracted floral scent, constitutive foliar volatiles and glucosinolates from 23 populations of the perennial herb Arabis alpina. Thereby, we could assess the magnitude of interdependence among these compounds produced and emitted by different plant tissues. By comparing integration indices, we found that floral scent was largely non-correlated with plant defence compounds in this species, and the geographically variable floral scent variation is thus likely the target of locally divergent selection pressures.

S.208.4 Exploring polyploidy-induced floral scent divergence and its impact on pollination shifts in a Mediterranean carnation complex

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Polyploidy is a significant driver of plant speciation. However, the establishment of neo-polyploids requires a process of ecological divergence to alleviate inter-cytotypic competition. This divergence often encompasses quantitative and qualitative alterations in floral phenotype, potentially affecting pollination assemblage. This phenomenon holds notable significance within the intricate ecological context of the Mediterranean region, marked by its unique climatic nuances and a diverse array of ecological niches. Our objective is to elucidate the foundational mechanisms driving ecological divergence post-polyploidization, using the Mediterranean autopolyploid *Dianthus broteri* complex as a study system. This complex comprises four distinct ploidy levels (2x, 4x, 6x, and 12x) and parapatric monocytotypic populations along an arid gradient in the Iberian Peninsula. Through a multidisciplinary approach involving Reproductive Biology and Chemical Ecology, we identified alterations in the pollinator spectrum and analyzed changes in floral volatilome and transcriptome among cytotypes Our investigation identified varying floral scent profiles and distinct pollinator assemblages among cytotypes. The 12x cytotype, primarily pollinated by hawkmoths, exhibited floral scents rich in ketones, whereas the 2x and 4x cytotypes displayed high visitation rates by bees and floral scent composed by benzenoids, monoterpenoids and sesquiterpenoids. The 6x cytotype showed a floral scent enriched in sequiterpenoids and a generalist pollination by bees, butterflies, and moths. However, experimental sympatry of cytotypes suggested that complete isolation of cytotypes is not automatically conferred by pollinator shifts and may have required further evolutionary adaptations, such as habitat isolation, to diminish the immediate spatial overlap of the neo-polyploids. This comprehensive approach shed light on the mechanisms shaping evolutionary trajectories within the *Dianthus broteri* complex, providing valuable insights into the impact of autopolyploidy on plant speciation and adaptation.

S.208.5 Fragrant Gingers: Ecological and taxonomic insights from floral scents in the genus Hedychium from India and Thailand

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Floral scents play a dual role in a plant's fitness, that is as both an attractant as well as a deterrent. In a community, when congeneric species are in sympatry, competition drives interspecific variations in floral scents. Like any other morphological floral trait, floral scent profiles both qualitatively and quantitatively can be used as a taxonomic character, as they are key traits in many plant-animal interactions. These ecological interactions are often isolating mechanisms driving speciation in many mixed-floral communities. The chemical signatures from floral volatiles can also be used to differentiate taxa within species complexes. These are taxa where the members are not morphologically distinguishable. Here, we first explore the interspecific variations in floral scents among sympatric taxa and secondly, we explore chemicals that may act as signature molecules for taxonomic identifications. To address the above questions, we used the taxonomically complex, fragrant ginger genus *Hedychium* (Zingiberaceae) which is endemic to the Asian paleotropics. A total of 22 species and 12 intermediate forms were sampled from the North-East of India, Western Ghats, and Northern Thailand during two peak flowering seasons. The floral scents were extracted via dynamic headspace sampling and analyzed using Gas chromatography-mass spectrometry (GC-MS). The chemical analysis results revealed that most of the sampled sympatric taxa had their unique chemo space. The intermediates showed a shared profile from both the putative parents suggesting a congruence with what we had known from ecological and morphological data. Our work emphasizes the use of chemical data as critical and complementing to the morphological, ecological, and genetic data in drawing taxonomic boundaries. It also allows us to understand the ecological and evolutionary implications of floral scents among sympatric taxa.

S.208.6 Diversity in reproductive strategies and floral sex allocation in the genus Aeschynanthus Jack (Gesneriaceae)

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Intrafloral protandry is a type of dichogamy where bisexual flowers exhibit male function at the beginning of anthesis and transition to the female phase later. This phenomenon is present in the genus *Aeschynanthus* Jack (Gesneriaceae). Though horticulturally popular, empirical studies on the ecology of the genus are scarce. Here, we investigate the diversity of sexual systems that are present in several species of the Indian *Aeschynanthus*. Our field observations revealed the presence of andromonoecy and variations in forms of andromonoecy among the Indian species of *Aeschynanthus*. Since andromonoecy has been reported in *Aeschynanthus* we explored its nature and efficiency among different species from the North East of India from an ecological perspective. We focused on achieving the following objectives during our study: 1) To investigate the presence of andromonoecy in the genus. 2) To comprehend how the allocation of floral resources (such as floral sex ratio, rewards, and display) is impacted by andromonoecy. 3) To analyze the differences in fitness (such as pollinator visitation and fruit set) among species while considering their reproductive strategies. Out of the four species studied, three were found to be andromonoecious and one was non-andromonoecious. Among the andromonoecious species, taxa with the highest nectar quality (percent sucrose) had the highest male-biased sex ratio and displayed significantly higher fitness. Interestingly, the non-andromonoecious species had similar fitness to this andromonoecious taxa and also had some of the highest nectar quality. Our findings suggest that andromonoecy enables species to improve pollen export without compromising on pollinator attraction, as there is a tradeoff between the proportion of bisexual flowers and nectar quality between species. In this sexual system of protandry and andromonoecy (protandromonoecy), protandry promotes outcrossing while andromonoecy may facilitate better pollen export and efficient resource allocation.

S.209 TROPICAL PLANT EVOLUTION ACROSS SPATIAL AND TEMPORAL SCALES. SESSION 1.

S.209.1 The evolution and distribution of defense traits are shaped by megaherbivores and climate

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The evolutionary arms race between plants and herbivores has led to many adaptations and counter-adaptations in both groups. Plants possess numerous analogous defense structures, such as thorns and spines, that deter predation from large-bodied herbivorous mammals. However, whether herbivory shaped the evolution and distribution of such traits remains unclear. Here, we use a macroecological approach and hypothesize that the evolution and distribution of plant defense traits (spinescence hereafter) is convergent and was shaped by the interaction with medium- to large-sized (i.e., more than 10kg) mammalian herbivores. We focus on the pantropical mimosoid (Mimosoideae, Fabaceae) lineage, including 2338 species (69% of total). We compiled a database of functional traits on growth form, spinescence, leaves, and fruits for all mimosoids. We integrated the mimosoid data with morphological, phylogenetic, and geographical data for 235 extant and 185 extinct species of medium- to large-sized mammalian herbivores, fire regimes, and climate, and applied phylogenetic and structural equation models to identify direct and indirect drivers of spinescence at global and continental scales. Results illustrate the repeated evolution of spinescence across mimosoids, and we show that the global proportion of spinescent species across broad-scale assemblages is strongly associated with species richness of extant and extinct mammalian herbivores and extended periods of drought, whereas fire affected spinescence indirectly, via effects on herbivore richness. Furthermore, we detected biogeographical differences in drivers of spinescence: Extinct herbivore richness was the most important driver in Africa, whereas extant herbivores explained most of the variation in the Americas. Our findings suggest that the environmental correlates of plant defense traits are scale-dependent and that current ecosystems cannot be properly understood without considering past interactions with megaherbivores. We argue that the complex interaction between climate, fire, and the evolution of mammalian herbivores has influenced the evolution and distribution of plant defense adaptations across tropical realms.

S.209.2 Revisiting the patterns of African flora biodiversity using spatial phylogenetics

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The African continent is the second most biologically diverse continent on earth, after South America, harboring a vast richness of animals and over 70,000 known plant species. The African savanna is the richest grassland on earth and the Guineo-Congolian Forest biome is the world's second largest tropical rainforest and carbon sink (after the Amazon Basin). Also, eight of the world's 36 biodiversity hotspots are found on the continent. The unprecedented levels of floristic diversity on the continent indicates that several factors, including ecological, biogeographical, and evolutionary drivers, play important roles. Because of these important historical factors, diversity assessments based on species counts alone cannot reliably describe biodiversity patterns and mechanisms responsible for generating and maintaining them. We conducted spatial phylogenetic analysis of the African vascular plants, leveraging recently accessible georeferenced occurrences and a corresponding time-calibrated phylogeny, using *Biodiverse* software (https://

shawnlaffan.github.io/biodiverse/), to identify areas of significant concentrations of phylogenetic diversity (PD), relative phylogenetic diversity (RPD), phylogenetic endemism (PE), and phylogenetic turnover. We also conducted a categorical analysis of neo- and paleo-endemism (CANAPE). Spatial data for native African vascular flora and a corresponding phylogeny were accessed from open-source databases and published papers. Areas of significant phylodiversity in PD, PE, and RPD were identified using a spatial randomization test. The resulting patterns were compared with climate data to infer biodiversity drivers. We also looked at floristic regions of the continent using a range-weighted version of phyloturnover to evaluate previously published regionalizations. Maps of significant phylodiversity were overlaid on a map of Africa's protected areas to evaluate the congruence of habitat protection and biodiversity patterns. Conservation priorities are given based on these results.

S.209.3 The decline of megathermal forests and fate of tropical forest lineages through the Cenozoic: Insights from palms

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Tropical rain forests and mangroves are much smaller in extent today than in the early Cenozoic, primarily owing to global cooling and drying trends since the Eocene–Oligocene transition. The general reduction of these biomes is hypothesized to shape the diversity and biogeographical history of tropical plant clades. However, this has rarely been examined owing to a paucity of good fossil records of tropical taxa and the difficulty in assigning them to modern clades. Here, we evaluate the role that Cenozoic climate change might have played in shaping the diversity and biogeography of tropical plants through time, by examining the exquisite fossil pollen record for an iconic and ubiquitous component of tropical forests globally: the palms.

S.209.4 Deciphering the complex interactions that shape the genetic diversity of a tropical montane ginger using a genomic approach.

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Widely distributed species often harbour high levels of genetic and phenotypic variations due to their interactions with diverse environmental conditions. This makes them an ideal study group to understand the microevolutionary processes that can lead to speciation. Their wide distribution allows us to investigate the genetic and physical barriers to gene flow across both spatial and temporal scales. Our study focuses on *Hedychium spicatum*, a morphologically variable, widespread ginger found in the understory of tropical montane forests. It is distributed across high-elevational regions of India, Southern China, and Northern Thailand and is found in sympatry with congeners. Ecological studies have shown that *H. spicatum* can interbreed with congeneric, sympatric taxa. This led us to hypothesize that the morphological variation seen in this species could be due to hybridization events. We aim to investigate putative barriers to gene flow in *H. spicatum* across its geographical range. We sampled 12 *H. spicatum* populations and sympatric congeneric species across their distributional range. We used dd-RAD sequencing and SSR markers to investigate the genetic structure of this species using model-based and model-free clustering approaches. We also checked for different genetic isolation models, migration models, demographic history, mating dynamics, and ploidy variations to understand the determinants of the genetic diversity of this species. Our results showed migrations between different geographical regions, and we found evidence of genetic admixtures between *H. spicatum* and its sympatric taxa. We propose that the structure of *H. spicatum* is affected by a combination of factors such as migrations, historical demographic processes, hybridization events, and ploidy variations. Understanding the complex interaction of these factors could be critical in understanding plant speciation mechanisms in the tropics, an area where we still have limited knowledge.

S.209.5 Fossil floras show early diversification in the evolution of Neotropical Rainforests

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Neotropical plant communities are exceptionally diverse and are the result of dynamic processes that include diversification, dispersal, and local/regional extinctions driven by climatic fluctuations and tectonics over the past 66 million years. Two Paleocene floras from northern South America show the earliest evidence of angiosperm-dominated, closed-canopy forests that document the early stages in the evolution of Neotropical rainforests. The Cerrejón and Bogotá paleofloras (58–60 Ma) represent coastal and fluvial environments, respectively, and share similar climatic characteristics and family-level composition seen in living rainforests. Despite overall similarities and shared patterns of low plant richness, these fossil assemblages show contrasting ecologies and composition at sub-familial levels that reflect floristic heterogeneity at a regional scale by the Late Paleocene. Fossil species within dominant and species-rich plant families such as Fabaceae and Annonaceae are typically restricted to each flora, showcasing patterns of diversification in northern South America. This talk revise recent findings within Paleocene floras of Colombia and evaluate the extent to which environmental gradients contributed to the early diversification of Neotropical rainforests.

S.210 SYNANTHEROLOGY RELOADED: RECENT ADVANCES AND THE FUTURE OF EVOLUTIONARY STUDIES IN COMPOSITAE. SESSION 2

S.210.1 Phylogenetic insights into the endemic species of the genus Senecio L. (Asteraceae) in India

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Senecio L. (Senecioneae: Asteraceae) is one of the most speciose genera globally, comprising approximately 1250 species primarily concentrated in southern Africa and South America. The genus is characterized by its remarkable adaptability to varied habitats which is probably the reason for its widespread distribution and high species numbers. The sheer magnitude of species and huge variation has hindered comprehensive phylogenetic reconstruction. For a long period of time phylogenetic studies have revealed the paraphyletic or polyphyletic nature of the genus prompting the need for better sampling as well more sequence markers. However, despite extensive molecular studies on *Senecio* worldwide, the Indian species have remained largely unexplored. In India, the genus is represented by about 53 taxa (47 species and 6 varieties), exhibiting high species diversity in the Himalayas and the Western Ghats. Of the 21 endemic species identified in India, 80% are confined to the Western Ghats. We sampled six species and two putative new species from the northern Western Ghats to study their phylogenetic status. Based on different nuclear ITS and plastid markers (*trnT-L*, *trnL*, *trnK*, *psbA-trnH*), the analysis reveals that these taxa are closely related to *Senecio saxatilis* Wall. placed within *Austrosy-*

notis-Cineraria clade, as identified in Pelser et al. (2007). Furthermore, the study strongly supports the placement of these species under Section *Madaractis* (DC.) Hook.f. represented with species occurring in central Asia.

S.210.2 Biogeography of the Mexico-eastern U.S disjunction in Symphyotrichum

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Biotic disjunctions, the occurrences of related organisms in disconnected areas of the Earth, have attracted scientific attention for past 200 years. Despite being represented in many familiar plants such as bald cypress, flowering dogwood, sweetgum, partridgeberry, etc., the eastern North American (ENA)–Mexican (M) disjunction remains poorly understood. Major outstanding questions include the divergence times of taxa exhibiting the disjunction and environmental/geological processes that may underlie the disjunction. *Symphyotrichum*, one of the most diverse genera in the eastern US, extends across the Americas, the Caribbean, and Eurasia, with several examples of disjunct ENA-M taxa. We performed molecular work using herbarium specimens to sequence accessions representing most of the species-level diversity of broader *Symphyotrichum*. We performed a sequence capture approach on DNA libraries using the Angiosperms353 baitset and used HybPiper to assemble the sequence data. Our phylogenetic analyses used both concatenation in RAxML-NG and coalescence in ASTRAL-III. We used MCMCT$_{\mathrm{REE}}$ to perform divergence time estimation and R package BioGeoBEARS to infer ancestral regions and biogeographic transitions between North America and Mexico. Finally, we used an ancestral niche reconstruction approach in Utremi to test for a role of historical aridification in generating the disjunction. Our molecular data suggest a recent radiation of *Symphyotrichum* at the Plio-Pleistocene boundary (~2.5 mya), with early connections to Mexico in ancestral lineages that closed off shortly after. Several subsequent dispersals to Mexico in the mid-Pleistocene were followed by vicariance across this region. Except for some present-day broadly distributed species, there is a complete lack of movement between ENA and M after 1 mya. A reconstructed disjunct distribution of suitable habitat in Pleistocene climatic models corroborate results from biogeographic modeling and confirm a role for aridification in the North American interior in creating the ENA-M disjunction.

S.210.3 Four or more? Integrative species delimitation of the African daisy complex Dimorphotheca pluvialis-sinuata

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Evolutionary relationships in the South African daisy genus *Dimorphotheca* Vaill ex. Moench. have long been problematic, with historical taxonomy often being based on potentially labile morphological traits. Here we investigate the *Dimorphotheca pluvialis-sinuata* species complex which have historically been separated based on white vs orange ray colour alone; but show widespread variation in ray colour patterns, disc floret sculpturing and fruit characters. We present an integrated taxonomic approach utilising next-generation sequencing genetic data in conjunction with several additional lines of evidence. Plants from 191 populations were sampled from 20 a priori morphotypes which encompassed the range of morphological variation in the complex. DNA of 301 individuals were extracted for genotyping-by-sequencing (GBS) and concatenation and coalescent phylogenetic species delimitation approaches were used to assign individuals to hypothesised genetic species. Support for genetic species was further assessed using surveys of phenotypic trait variation as well as cross-pollination experiments. Results showed strong support for at least four species within the complex; with the previous use of ray colour ineffective in delimiting species. While three putative genetic species can be clearly identified and grouped based on morphological characters, the remaining species encompasses a wide range of diverse morphotypes which exhibit variation on a geographic cline. Phylogenetic patterns suggest this may be due to repeated range expansion and subsequent serial founder effects, and we further assess this using a clinal genomic analysis which incorporated pollinator observations as a potential selective regime. This study provides a framework for untangling complex taxonomic questions and emphasises understanding of evolutionary process in reclassification.

S.210.4 Phylogenomic insights into the Marguerite daisy tribe (Anthemideae, Astearaceae)

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Using targeted high-throughput sequencing of 244 low-copy nuclear genes and capture of 66 plastid genes and including 61 out of 111 genera and all but four of the 19 currently recognized subtribes (Inulantherinae, Lapidophorinae, Lonadinae, and Vogtiinae), our study takes a step further into the intricate evolutionary history of Anthemideae, a remarkably diverse tribe within the Asteraceae family. Our results are largely consistent with previous research but clarify the placement and circumscription of several taxa and reveal compelling incongruences. Some of these clarifications involve longstanding issues affecting some of the 19 currently recognized subtribes, such as the placement of Osmitopsis, the monophyly of Cotulinae, the affinities of Glebionidinae and Santolininae, and the paraphyly of two subtribe pairs, proposed here to be merged: Athanasiinae with Phymasperminae and Matricariinae with Anthemidinae. Among the incongruences, those between nuclear and plastid trees are particularly noteworthy since they challenge subtribal taxonomy and hint at ancient hybridization events. Disparities were also observed between the multispecies pseudo-coalescent (MSC) and maximum likelihood (ML) nuclear trees. Furthermore, our research introduces novel perspectives on the tribe's historical biogeography, supporting three groupings: a Southern African Grade, an Asian Clade, and a Circum-Mediterranean Clade, which shed light on the historical expansion of Anthemideae lineages across different regions. Divergence time analyses underscore the role of Plio-Pleistocene climatic shifts as drivers of rapid radiations within the tribe. By refining the phylogenetic relationships among and within subtribes and by pointing out potential ancient hybridization events, our research highlights episodes that require further investigations, paving the way for a deeper understanding of Anthemideae systematics and evolution.

S.210.5 Palynology of Vernonieae from Madagascar (Compositae)

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One of the largest tribes in Asteraceae, Vernonieae, has proven intractable for taxonomic revision, with more than 1,000 of the ca. 1,500 species being recognised in the genus *Vernonia*. This genus has recently been re-circumscribed to include just 21 accepted species in the Americas, prompting the reclassification of ca. 1,000 species out of *Vernonia*. Much of this work has been completed in the Neotropics, but few studies have been undertaken for the more than 700 species of Vernonieae in the Paleotropics. At least 200 African species remain in *Vernonia*, but due to poor generic delimitation in this tribe, it is unclear to which genus they belong. We have performed the most complete palynotaxonomy study of Malagasy representatives of the tribe Vernonieae to date, which is represented by 90 species, including 39 still placed in *Vernonia*. Pollen grains and micromorphological reproductive characters were analysed under light microscopy and SEM. Our results the eurypalynous status of tribe Vernonieae tribe based on variations in pollen grain size, aperture and ultrasculpture types. Further study that includes more comprehensive molecular sampling of species in Vernonieae is in progress and will be elemental for further understanding the diversity and evolution of pollen within this tribe.

S.210.6 Hyperdiverse but still under-explored: recent and future evolutionary studies in the Compositae of Southern Africa

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The Cape Flora has very high concentrations of species diversity and extremely high levels of endemism in a relatively small geographic area. As for most temperate regional floras, Compositae is the most species-rich family. A number of endemic composite lineages have radiated within (and in many cases, subsequently dispersed out of) the region, after adaptation to the unique edaphic and climatic conditions that characterise the island-like Cape habitats. Most of the taxonomic work on Cape Compositae occurred more than thirty years ago, before the advent of modern methods and resources, and there has been very little evolutionary work on these systems. Here, I present advances in species discovery and in the understanding of speciation processes in the Cape Flora, based largely on our research in two Cape-centred tribes, the Gnaphalieae (everlasting daisies) and the Calenduleae (the African marigolds). These studies make use of herbarium specimens, online databases, and citizen-science platforms; extensive fieldwork; and a range of morphological and molecular techniques, including genomic data, to reconstruct evolutionary relationships, discover new species, and examine the context of diversification. We extrapolate from these results to explore possible implications for future species discovery in other members of the Compositae of this hyperdiverse region.

S.211 EVOLUTION AND DIVERSITY OF CARBON CONCENTRATING MECHANISMS (CCM) IN LAND PLANTS. SESSION 2

S.211.1 Defining the C2 photosynthesis phenotype across diverse plant lineages

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Most plants use only C_3 photosynthesis, which endures high rates of metabolically costly photorespiration under elevated temperatures and dry conditions. However, several plant lineages convergently evolved carbon concentrating mechanisms (CCM; *e.g.*, C_4) to help avoid these photorespiratory costs and consequently boost photosynthetic efficiency under these stressful environments. During the repeated evolutionary transitions from the ancestral C_3 to complex C_4 CCM, evolutionary intermediate C_3-C_4 states arose, many of which use a rare physiology called C_2 photosynthesis. The C_2 CCM is a natural CO_2 recycling mechanism that shuttles the photorespiratory product glycine from mesophyll into bundle sheath cells, where it releases, concentrates, and reassimilates the CO_2 released from photorespiration. Engineering the C_2 CCM into C_3 crops shows promise to increase crop yields, especially under climate change, but achieving this requires a detailed understanding of the complete C_2phenotype across scales, from the sub-cellular to whole-plant. To comprehensively characterise the C_2 phenotype across diverse plant lineages, we quantified ultrastructure, organelle content, and biochemistry of mesophyll *vs* bundle sheath cells, leaf structure, relative growth rate, whole plant resource allocation, root characteristics, drought responses, leaf gas exchange in C_2plants compared with their close C_3 relatives from six plant lineages. C_2 species showed several clear benefits compared to their C_3 relatives under the experimental conditions, including greater biomass, leaf area, and intrinsic water use efficiency, as well as many other phenotypic differences compared to their C_3 counterparts. Our findings clarify the phenotypic changes that accompanied the repeated evolution of C_2 phenotypes in diverse plant lineages, providing critical information needed engineering the C_2 photosynthetic pathway into C_3 crops to achieve food security now and into the future.

S.211.2 Soil organic carbon in tropical Andean ecosystems study methods and approaches: a systematic review

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Soil is the most important carbon (C) reserve in the terrestrial biosphere, soil organic C (SOC) is the result of the balance between the contributions of organic matter to soils and the loss of C through decomposition, leaching and erosion of organic matter, the main source of organic matter is dead plant material from both surface and underground tissues. The potential of soils as carbon sinks has attracted considerable scientific attention in recent years, as an alternative to mitigate warming and which is a key factor for soil health, there are areas that can be strategic to achieve this objective. Like tropical Andean ecosystems with soils that are mostly derived from volcanic ash and important carbon storage and stabilizers, due to their high content of organic matter, these ecosystems present 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 formulated in the review were raised, a gap in knowledge of SOC sequestration in tropical Andean ecosystems has been identified and the methods and approaches for its study must be clarified, understanding that there are various techniques for determining C, but little is addressed from socio-ecological systems and there is diversity of information regarding C models, this research suggests addressing the sequestration of SOC 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 communities in the territories surrounding the conservation of ecosystem services.

S.211.3 Pyrenoid formation and carbon concentrating mechanisms in hornworts: contrasting dynamics but parallel molecular underpinnings

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Biophysical carbon concentrating mechanisms (CCMs) operating at the single-cell level have evolved independently in various lineages of eukaryotic algae and a single land plant lineage, the hornworts. An essential component for an efficient eukaryotic CCM is a pyrenoid, a specialized compartment inside the chloroplast that mainly comprises the CO_2-fixing enzyme RuBisCO. Information on pyrenoid biology and CCM is primarily available for the unicellular green alga, *Chlamydomonas reinhardtii*, suggesting that both pyrenoid formation and CCM is highly dynamic and inducible by low CO_2 concentrations.

In contrast to *C. reinhardtii,* molecular underpinnings, inducibility and dynamics of the hornwort CCM and the pyrenoids are poorly understood. To start investigating molecular underpinnings of the CCM in hornworts we used a combination of methods including (1) protein co-IP of pyrenoid components, (2) localization of candidates homologous to CCM genes in *Chlamydomonas,* and (3) CO_2 assimilation measurements in pyrenoid-bearing and pyrenoid-free species. While we provide evidence that the scaffolding candidate and the RuBisCO co-localize in hornworts like in *Chlamydomonas*, they appear to be less dynamic. We further found that the carbon anhydrase homolog (CAH3) of hornworts is localized to the pyrenoid, while the LCIB homolog is less intimately linked to the pyrenoid than in *Chlamydomonas*. Surprisingly, we observed that pyrenoid formation and subcellular localization of CAH3 and LCIB do not react to changing CO_2 concentrations, darkness or H_2O_2 as it is described in *C. reinhardtii*. Our results imply that the pyrenoid-based CCM of hornworts is characterized by a mixture of *Chlamydomonas*-like as well as hornwort-specific features which is line with their independent evolutionary origin. Furthermore, our study suggests that hornwort CCM may be less dynamic than that of *C. reinhardtii*.

S.211.4 Tree demography driving species composition and carbon stock changes in European forests

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Forest ecosystems play a crucial role in climate change mitigation due to their extensive carbon sequestration and reservoir capacity. Tree species distributions and abundance largely vary across environmental gradients and are expected to change in response to climate change and management. The expected spatio-temporal changes of coexisting species depend on different demographic processes, where tree growth and mortality may follow the same or opposite directions, largely contingent on species strategies to cope with climate change. However, changes in species demographic processes across large environmental gradients remain unexplored. In this study, we aim to investigate changes in species abundance and forest composition considering biomass gains and losses for the main tree species in Europe. We used National Forest Inventories (NFIs) to build species-specific models of biomass gains and losses, considering climate, forest structure, and recent management. Then, we integrated these model's predictions to determine changes in composition and carbon storage under climate change scenarios. We observed that biomass gains and losses generally follow similar patterns, with a high importance of forest structure, climate and recent management driving observed changes. The predicted changes in species and functional composition across Europe under climate change varied across the covered environmental gradient, which is directly linked with the predicted carbon stored. Future work should further explore the potential implications of increased biomass gains and losses under climate change and the potential role of forest management in modifying these trends.

S.212 CLIMATE CHANGE EFFECTS ON ALPINE PLANT SPECIES AND COMMUNITIES: INSIGHTS FROM THE GLORIA NETWORK. SESSION 2

S.212.1 Long-term monitoring of alpine ecosystems

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Naturally treeless by definition, the vegetation covered terrain of the alpine belt amounts to ca. 2 % of all land outside Antarctica. Despite the assumed hostility for life, it embraces an estimated 4 % of all flowering plant species. Habitat diversity created by topography and a microclimate that deviates strongly from what meteorological stations report, are the explanation for this unexpected biodiversity. The habitat diversity across short distances offers unique opportunities to study the long-term effect of contrasting environmental conditions on biodiversity and ecosystem functioning. We present concepts, definitions, challenges and pitfalls in monitoring terrestrial ecosystems and the study of steep gradients of life conditions related to snow duration and length of growing season, with a focus on snowbed and adjacent grassland communities. We provide a synthesis of findings obtained during seven consecutive seasons of monitoring with a standardized protocol, across four monitoring sites in the Swiss and Austrian Alps. We show that plant dry matter allocation is highly conserved across such gradients, tbwhile the ratio of graminoid to herb biomass emerges a sensitive indicator for season length. Microclimate and phenology data will be presented that illustrate the key role of 'timing' for alpine plant life, and underpin the central role of the aerodynamic boundary layer near the ground and exposure for alpine plants. Data from such late successional ecosystems will facilitate projections of the consequences of future changes in season length and they complement findings from early successional systems such as those studied in the GLORIA network. For further reading see: Körner C (2021) Alpine Plant Life, Springer; Körner and Hiltbrunner (2021) Diversity 13:383; Körner et al. (2022) EcoMont 14:48-69.

S.212.2 Using long-term remote sensing series to upscale the vegetation shifts along elevation in the GLORIA network Italian peaks

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Plant species and communities' distribution are remarkably affected by the climate change, particularly in arctic and alpine biomes. In alpine ecosystems, species and communities are shifting upwards due to the temperature increase, seeking for the optimum growth conditions. As a prominent effect, a progressive increase of vegetation cover is leading an alpine greening, with important consequences for the overall plant diversity. Nonetheless, little is known about how this trend may produce different effects along elevation gradients. Innovative upscaling approaches able to link field monitoring evidence to remote sensing data represent a promising tool to get new insights into the ecological mechanisms involved in these changes, and to produce reliable projections over time. This study aimed at parsing the long-term trends of remote sensing-derived vegetation indices in five GLORIA network target regions, located across the Italian Alps and Apennines. NDVI was calculated for each growing season (June-September) in the period 1985-2022, using Landsat 5 and 8 multispectral satellite images of each mountain summit. Linear mixed-effects models were used to analyze the relationships between NDVI, time and climate variables, in different elevation belts. NDVI linearly increased over the last 37 years, but with significant higher increase rates and values at the treeline, lower alpine and alpine zones, compared to the upper alpine, subnival and nival belts. Moreover, NDVI was significantly affected by the interaction between temperature and rain precipitation at lower altitudes. These results provided further evidence of the ongoing alpine greening and showed that vegetation at the treeline is responding faster than the other communities to a warmer and drier climate. Therefore, future scenarios depicting the fate of alpine plant community communities should not neglect for the interplay of temperature and precipitation regimes. Our finding opens future perspectives on the interpretation of GLORIA field evidence, in a continental upscaling perspective.

S.212.3 Results of the 17-year GLORIA survey: Has there been a change in the plant diversity in the mountains of central Spain?

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The environmental particularities of the Mediterranean – a dry season during the vegetative period and a cold season during the rest of the year – make the plausible climate change impacts on the unique Mediterranean summits more severe. A significant number of endemic species, primarily orophytes, are found in this region as a result of the particular conditions that have worked as a selective pressure on plant species. Nevertheless, the biodiversity found in these areas may be in jeopardy as a result of climate change. Dry spells have become more common in central Spain over the last decade, and experts predict that these high elevations will experience even more dry spells as a result of global warming. Our research is centred on identifying the most significant changes in plant diversity that have occurred or are occurring in the summits of the Sistema Central (Sierra de Guadarrama, Sierra de Gredos and Sierra de Béjar) a 300 km mountain range in the centre of the Iberian Peninsula that separates the southern and northern plateaus. This has been accomplished by utilising climatic data derived from GLORIA soil temperature dataloggers and supplementary records from the AEMET (National Meteorological Institute), as well as vegetation data gathered from permanent plots of three surveys of two GLORIA study regions over a span of 17 years (2006–2023). We used multivariate approaches and GLMMs to examine the relationships between diversity patterns and climatic conditions. Here, we go over the main findings concerning species richness, species cover (especially for endemic species and shrubs), colonisation or loss events and how they relate to trends in temperature and precipitation.

S.212.4 Impact of climate change on plant phenology in a Mediterranean mountain (Sierra Nevada, SE Spain) using herbarium specimens

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Mediterranean mountains are extraordinarily diverse and host a high plant diversity, especially of endemic plants. However, these mountain ecosystems are particularly vulnerable to climate change, and significant changes in plant communities and the life cycle of many species are expected. Plant phenology is considered one of the most important bioindicators of climate change, as trends can provide considerable temporal and spatial information on changes in species and ecosystems. This work aimed to analyze the phenological trends of 89 endemic and conservation-important plant species of Sierra Nevada (SE Spain) over period of 187 years. A total of 5,262 records were obtained from herbarium samples. Phenological variability was analyzed considering: altitudinal gradient and climatic data series (temperature and precipitation) extracted from raster layers with temporal climate models from 1950 to 2020. As preliminary results, we found a clear tendency to advance the flowering and fruiting events at the massif scale. And, at the species level, the response was more significant in one than in the others. These results may improve the understanding of phenological changes in endemic plants under the current climate change scenario in a Mediterranean water-limited mountain. Thus, serving as early warning indicators, providing appropriate mitigation and adaptation strategies and measures at the species level. Moreover, the study highlights the crucial role that historical records harboured in herbarium sheets have for monitoring the effects of climate change on biodiversity.

S.212.5 Two Decades of Pollination and Pollinator Studies on the Hengduan Mountains: The Importance of Super-generalist Eusocial Bees

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Mountain ecosystems are natural labs for species evolution providing natural experiments awaiting us to explore. Alpine environments at high mountains are sensitive to environmental changes, plants and their pollinators as well as their interactions at mountain regions are threatened under the current global change and human disturbance situation. Changes of the composition of plants and pollinators at different spatial and temporal scales will reshape the pollination networks, eventually influence ecosystem function and stability. Currently, the topology and structure of pollination on the mountain ecosystem were not fully explored and the spatial and temporal pattern along elevation and factors determining network structures are not fully understood. We selected several typical elevation gradients on the Hengduan Mountain region in southwestern China to study pollination networks by investigating their topologies, structuring mechanisms and spatial-temporal dynamics. We investigated how ecological and historical factors, including functional traits of plants and pollinators, phylogenetic history and environmental factors influence of structure of pollination networks. In this talk, we presented our key findings.1) Compared to other mountain ecosystems, the specialization of pollination networks in our communities was much lower, potentially due to the key roles of super generalists including bumblebees and honeybees. 2) Species abundance, functional trait and phylogenetical history strongly shaped network structures. The matching between insect tongue length and the floral tube/spur length determined the structure and stability of networks. The physical match between floral morph and insects were significantly varied among different insects groups and influenced by elevation. 3) Pollination networks showed a strong spatial and temporal variation. In conclusion, our studies uncover the uniqueness of pollination in the mountains of Southwestern China compared with other mountain ecosystem in the world providing new understanding of plant-pollinator interaction at alpine and subalpine regions.

S.212.6 Differences in seed traits determine 'winners' and 'losers' of climate change in European alpine plant communities.

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Alpine habitats are threatened by climate change because their cold-adapted species are experiencing some of the fastest rates of warming. In response, alpine plants have altered their performance, population dynamics, community structure and geographic distribution, ultimately affecting the functions and services alpine ecosystems provide. Yet, there is a general lack of mechanistic explanations about these complex responses. In this context, application of functional traits, that is morphological, physiological, phenological or behavioural characteristics impacting individuals' fitness, has been considered as a promising approach in assessing climate change vulnerability of alpine plants. In particular, seed traits are expected to have a good predictive power in explaining the observed patterns of alpine species migration, adaptation, and persistence, as seeds are the main plant organ fulfilling these functions. Here, we investigated whether species with contrasting long-term population dynamics differ in their seed traits related to germination, dispersal, and persistence. Specifically, we correlated data on 20-yr population dynamics collected within the GLORIA network (https://www.gloria.ac.at/) for 146 alpine species occurring in temperate, sub-Mediterranean and Mediterranean mountain ranges with seed traits (mass, shape, number, dormancy, germination time, base temperature for germination, anemochory and epizoochroy potential) measured following standardised protocols We revealed that the focal species displayed mountain range-specific changes in abundance, with Mediterranean and sub-Mediterranean ranges having the largest variations. The relationship between seed traits and abundance change were significant only in the sub-Mediterranean ranges. Here, species that increased in abundance exhibited weaker dormancy (e.g. shorter cold stratification period), required higher temperatures for germination, and produced larger seeds, all traits that enable long-distance dispersal and improved performance under a warmer climate. Our results show that seed traits may explain differences in recently observed population dynamics and highlight important insights for assessing extinction risk and predicting future community structure.

S.213 AN UPDATE ON THE PHYLOGENY OF SEED PLANTS. SESSION 2

S.213.1 Seed structure in Bennettites morieri (Bennettitales) and its implications

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Understanding the structure of bennettitalean seeds is important so they can be compared with those of other seed plants, but their interpretation has been controversial for more than a century. A key question is whether or not the integument is surrounded by an envelope, as in seeds of Gnetales and Erdtmanithecales, and hence whether the seeds are, or are not, chlamydospermous. Resolving this question, even in well preserved material, is difficult because the seeds are small and tightly packed in a mass of interseminal scales causing different tissue layers to adhere closely together. Non-destructive reinvestigation of exceptionally well-preserved permineralized seeds of *Bennettites morieri* using three dimensional visualization by synchrotron radiation X-ray tomographic microscopy (SRXTM) indicates the presence of an envelope, as well as two distinctive features seen in several dispersed fossil chlamydospermous seeds; i) closure of the micropyle by radial expansion of the cells of the inner epidermis of the micropylar tube (as also occurs in extant *Gnetum gnemon*, extinct *Protoephedrites* and extinct *Williamsonia*); and, ii) the presence of distinctively angled and radially aligned cells in the apical portion of the envelope (not easily seen in some other permineralized bennettitalean ovules). These results support the hypothesis that Bennettitales, Erdtmanithecales and Gnetales are closely related, and suggest that the ovulate ‘flowers’ of Bennettitales are multiaxial compound heads.

S.213.2 Impact of new taxa and morphological interpretations on seed plant phylogeny and the origin of angiosperms

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Recent discoveries of new fossil taxa, improved data on poorly known fossils, and major reinterpretations of the morphology of several key taxa have potential to strengthen or refute previous hypotheses on seed plant phylogeny. To test the impact of these developments, we have amassed a new data set including *Doylea* (Cretaceous, recently assigned to the mainly Triassic seed fern order Umkomasiales, = corystosperms), *Petriellaea* (Triassic), and *Protoephedrites* (Cretaceous) and substantially redefined many previously used characters. We have revised the scoring of glossopterids in light of evidence that the ovule-bearing structures are axillary cladodes with ovules on the surface facing the subtending leaf and have rescored Bennettitales based on evidence that the ovules are borne on simple sporophylls and lack a cupule, while we interpret *Doylea* as having compound strobili with axillary fertile short shoots bearing ovules enveloped by lobes of the short shoot. Preliminary analyses associate glossopterids with coniferophytes rather than angiosperms, *Doylea* with conifers rather than corystosperms, *Protoephedrites* with Gnetales, and *Petriellaea* and *Caytonia* with angiosperms. The positions of Bennettitales and *Pentoxylon* are particularly unstable, presumably due in part to the uncertain morphological homologies of their reproductive structures. These results are consistent across different methods (parsimony, maximum likelihood, Bayesian inference) and models for character evolution. They may favor origin of the angiosperm leaf by webbing of a pinnately compound or lobed leaf, rather than differentiation of vein orders in a simple taeniopterid- or glossopterid-type leaf, and derivation of the carpel from a megasporophyll with pinnately borne cupules (bitegmic ovule homologs), rather than a leaf plus an axillary cupule-bearing branch.

S.213.3 Embracing uncertainty: the way forward in plant fossil phylogenetics

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Although molecular phylogenetics remains the most widely used method of inferring the evolutionary history of living groups, the last decade has seen a renewed interest in morphological phylogenetics. This has mostly been driven by the promises that integrating the fossil record offers to our understanding of macroevolutionary processes and dynamics, as well as the possibility that the inclusion of fossil taxa could lead to more accurate phylogenetic hypotheses. The plant fossil record presents some challenges to its integration in a phylogenetic framework. Phylogenies including plant fossils often retrieve uncertain relationships with low support, or lack of resolution. This is due to the pervasiveness of morphological convergence among plant organs and the fragmentary nature of many plant fossils, and it is often perceived as a fundamental weakness reducing the utility of plant fossils in phylogenetics. Here I discuss the importance of uncertainty in morphological phylogenetics, and how we can identify important information from different patterns and types of uncertainty. I also review a set of methodologies that can allow us to understand the causes underpinning uncertainty, and how this can help us to further our knowledge of plant fossils. I also propose that a new visual language, including the use of networks instead of trees, represents an improvement on the old visualization based on consensus trees, and more adequately serves phylogeneticists working with plant fossils. This set of methods and visualization tools represents an important way forward in a fundamental field for our understanding of the evolutionary history of plants.

S.213.4 Reassessment of the presumed Phylica inflorescence from Cretaceous amber: Laurales rather than Rhamnaceae

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Cretaceous fossil flowers are highly significant, if not essential, for understanding origin and evolution of angiosperms. Kachin amber from northern Myanmar represents a valuable source of three-dimensionally preserved mid-Cretaceous (approximately 100-million-year-old) plant fossils, including diverse flowers. Systematic placement of early angiosperm fossils is sometimes challenging as they often possess surprising, unique combinations of floral traits which are absent in Cenozoic taxa. Using the published original microXCT data, we reconstructed the fossil inflorescence from Kachin amber previously assigned to the extant genus *Phylica* (Rhamnaceae; Shi et al., 2022), visualized new diagnostic features and reassessed the fossil. The dichasial inflorescence bears bisexual flowers with a spiral phyllotaxis, an undifferentiated perianth with a floral cup, stamens with bilocular valvate anthers and a pair of basal filament appendages, inner staminodes, and a semi-inferior ovary. The characteristic flap dehiscence and the pair of basal staminal glands suggest Lauralean affinities. Using the morphological dataset of extant basal angiosperms by Kvaček et al. (2016) we placed the fossil in the Siparunaceae-Gomortegaceae-Atherospermaceae (SGA) clade of the core Laurales. Our results challenge the notion of the presence of a modern genus of Rhamnaceae in the mid-Cretaceous and are in line with most previous age estimates of Laurales and angiosperms as a whole.

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S.213.5 Paleogenomics reveals angiosperm karyotype evolution during their early history and shows that Amborella belongs in the Nymphaeale

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Chromosome-scale genomes provide a basis for inferring ancestral linkage groups and processes of karyotype evolution. We have reconstructed the karyotypes of numerous representatives of the major groups of flowering plants, using an approach that starts from retained intact chromosomes and syntenic blocks. The results show that the most recent common ancestor of the flowering plants had 16 unique protochromosomes and that nine of these protochromosomes are still retained in at least one extant species without any fusion or fission. Other protochromosomes underwent rare and probably irreversible fusion events, detectable through repeated polyploidizations. Amborella trichopoda shares a unique nested chromosome fusion with Nymphaea colorata, Euryale ferox and other Nymphaeales. Our data also securely resolve the position of the monocots as sister to magnoliids plus eudicots. These findings reject the low ancestral numbers for ancient angiosperms inferred with non-genomic approaches over the past 90 years and have profound implications for the early evolution and biogeography of flowering plants.

S.213.6 Landscape genomic and introgressive hybridization in bur oak (Quercus macrocarpa)

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Quercus macrocarpa Michx. (Fagaceae) is a common, morphologically variable, and geographically and ecologically widespread species in eastern North America. This species is one of more than 16 eastern North American members of the white oak section, *Quercus* sect. *Quercus*. All are capable of interbreeding in sympatry and have been the subject of numerous previous studies, but limited genomic work. It has been proposed that multispecies introgression in the oak syngameon has contributed to the adaptation of eastern North American white oaks including *Q. macrocarpa* to a variety of ecological conditions. To evaluate the pattern of genetic diversity in the species and test for landscape-scale patterns of gene flow, we did genome resequencing across this species and 10 co-occuring species. Our resequencing data includes 693 individuals across the range of Q. macrocarpa, sequenced to an average depth of 21x. Thus far, we have identified approximately 50 highly introgressed individuals with slightly more than a third F1 hybrids, but the remainder showing evidence of introgression back into parental species at around the F2 or F3 generation. Most of the hybridization is concentrated near the boundaries of the parental species. As previously documented, the chloroplast does not appear to correspond with species identity. Interestingly, it also does not seem to strictly correspond to geographical proximity either. *Quercus macrocarpa* exhibits population structure between the northwest, northeast, and southwest regions of its distribution despite its long-range pollen movement. This work is part of a bigger collaboration to characterize the reciprocal influences of environment, migration history, and forest community structure on introgression across the range of *Quercus macrocarpa,* and the potential effects on the organisms who depend on and live with oaks.

S.214 THE ORIGIN AND EVOLUTION OF MODERN PLANT DIVERSITY: INSIGHTS FROM MULTIPLE DISCIPLINES. SESSION 2

S.214.1 Dissecting the impact of mating systems and genetic diversity in Euphrasia: insights into modern plant evolution

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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.

S.214.2 Late Oligocene advent of monsoonal climate and evolution of the evergreen forests in South Asia

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India plays a crucial role in understanding current biogeographical patterns in paleotropical flora, as its vegetation has likely experienced more changes than any other tropical region. This is attributed to the Indian plate traveling a distance of ~9,000 km from the Southern to the Northern Hemisphere. Climatic changes have led to the extension of the majority of the lineages that contribute for its rich diversity of evergreen forests.

However, very little evidence for this rich history comes from the examination of the present-day flora of the Indian subcontinent. Deciphering the story of the origin of the modern-day flora is important for the conservation of this highly biodiverse flora. In South Asia, the evergreen forests are confined to the Western Ghats and northeast India, influenced by the South Asian Monsoon (SAM) or Indian Summer Monsoon (ISM). The evolutionary history and relationship of these evergreen forests with SAM are still poorly known. Here, we present a detailed study on the late Oligocene megafossil record from Makum Coalfield, northeast India, using qualitative and quantitative techniques of paleoenvironmental reconstructions. Qualitative data indicate the presence of mostly megathermal plant families and the dominance of tropical wet evergreen taxa with modern-like floristics diversity. Quantification of climate by using the Coexistence Approach (CA) and CLAMP (Climate Leaf Analysis Multivariate Program) methodologies indicates a tropical warm, humid, and seasonal climate during the late Oligocene. Moreover, leaf physiognomic data obtained from CLAMP indicate the presence of a modern-like SAM during the late Oligocene. Our study suggests that the initiation of modern like evergreen forests and SAM have occurred synchronously during the late Oligocene in South Asia.

S.214.3 How cacti colonized the hyperarid Atacama Desert?

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The evolution of the hydrological niche and its contribution to the biogeographical expansion into hyperarid areas enhance our understanding of how lineages adapt to and occupy some of the harshest zones on the planet. This study focuses on a globose and diverse cactus genus, investigating the evolutionary dynamics of the hydrological niche and its associated functional traits. The study encompasses the genus Eriosyce, distributed along a 2,300 km arid gradient on the Pacific coast of southwestern South America. We reconstructed genomic, time-calibrated phylogenies for Eriosyce, analyzing evolutionary shifts in the hydrological niche and functional traits, together with inferences in the historical biogeography related to the occupation of the Atacama Desert. Phylogenetic reconstructions were based on genomic data obtained from whole genome sequencing. Historical biogeography results were compared with independent geological data on the origins of these deserts. We characterized the water sources used by these plants, differentiating between rainfall, groundwater, dew, or fog, by studying water isotopes (^{2}H and ^{18}O). Variations in niche breadth and isotopic signals were found to be related to the microhabitats occupied and the growth forms of the species. Significant lag times were observed between the colonization of the region and the invasion of hyperarid habitats by Eriosyce subclades, with an inferred historical biogeographical route from less arid habitats, such as Mediterranean central Chile, to the hyperarid desert. The findings suggest that adaptation to extreme environments like deserts, which have been evolving for millions of years, is a slow and complex process. This presents significant challenges for the survival of various species in the face of rapid climate change.

S.214.4 Botany and Geogenomics: constraining geological hypotheses with large-scale genetic data derived from plants

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Decades of empirical research have revealed how the geological history of our planet shaped plant evolution by establishing well-known patterns (e.g., how mountain uplift resulted in high rates of diversification and replicate radiations in montane plant taxa). Under this approach, information is passed from geology to botany by interpreting data in light of geological processes. Instead, in this synthesis, I describe how by integrating natural history, phylogenetics, and population genetics, botanical research can inform our understanding of past geological and climatic processes. This conceptual shift aligns with the goals of the emerging field of geogenomics. In the Neotropics, plant geogenomics is a powerful tool for the reciprocal exploration of two long standing questions in biology and geology: how the dynamic landscape of the region came to be and how it shaped the evolution of the richest flora. I describe what makes some groups of plants excellent model systems for geogenomics research.

S.214.5 The origin and evolution of phytohormone signaling systems driven by horizontal gene transfer

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Plants respond to environmental cues through physiological and developmental changes that are largely regulated by various signaling molecules. The phytohormones strigolactones (SLs) and exogenous compounds karrikins (KARs) are butenolides that influence multiple aspects of plant growth and development. D14 and KAI2 are members of the α/β-fold hydrolase superfamily and act as receptors of SLs and KARs, respectively. In this study, we found that the plant *D14/KAI2* gene family was derived from bacterial gene *RsbQ* via horizontal gene transfer (HGT) during plant colonization of land. The D14/KAI2 and RsbQ proteins share conserved tertiary structures and functional features. We suggest that the acquisition of *RsbQ* by plant cells was fundamental to the formation of a butenolide sensing system, which provided a key innovation associated with the transition of green plants from aquatic to terrestrial environments. Recruitment of additional signal transduction components and gene duplication subsequently led to diverse SL and KAR signaling systems in land plants. This finding highlights the critical importance of HGT in plant evolution.

S.215 FERN AND LYCOPHYTE EVOLUTION: A PHYLOGENOMIC PERSPECTIVE. SESSION 2

S.215.1 Elaphoglossum phylogenomics: perspectives and challenges in the study of one of the most diverse groups of tropical ferns.

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The fern genus *Elaphoglossum* (Dryopteridaceae) is one of the most species-rich and taxonomically complex genera of ferns globally, with over 600 recognized species. Despite extensive taxonomic and systematic studies, numerous species groups within *Elaphoglossum* pose persistent taxonomic challenges and several key evolutionary relationships within the genus remain unresolved. This complexity highlights the significance of improving our understanding of *Elaphoglossum* diversity, given its status as one of the most species-rich, dominant, and frequently collected vascular plant genera in many areas of tropical America, where approximately 500 species of*Elaphoglossum* occur. This presentation introduces the first phylogenomic study of *Elaphoglossum*, including a dataset of more than 230 accessions and target-capture data from around 300 nuclear loci. The resulting phylogenetic hypothesis is largely congruent with those reported previously, but with improved support and resolution, and the recovery of novel clades and previously unsampled taxa. Our phylogenomic analyses also show, for the first time, that reticulate evolution was important and prevalent during *Elaphoglossum* evolutionary history. Integration of our phylogenomic data with information derived from floristic inventories, herbarium specimens, and rigorous taxonomic studies enables a data-driven assessment of the current state of knowledge for *Elaphoglossum*. From this, we highlight persistent challenges hindering the study of *Elaphoglossum* today and identify priorities and research opportunities for future exploration and research of this and other highly diverse and taxonomically complex fern genera.

S.215.2 Diverse origins of horizontal gene transfers in Ophioglossaceae mitogenomes

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Several horizontal gene transfers (HGT) found in ferns are interpreted to significantly benefit their adaptation. As the recent advances of mitogenome sequencing in these plants, more HGT cases are discovered from these genomes. In the fern family Ophioglossaceae, we assessed mitogenome assemblies from all generic representatives, and confirmed numerous HGTs inside their mitogenomes. In the most extreme case, up to one third of mitogenome is HGT-originated. Newly compiled phylogenomic datasets revealed that these HGTs are derived from diverse donors, primarily root parasite angiosperms but also a few from ferns and lycophytes. To evaluate the functionality of these horizontally-transferred genes within the host mitogenomes, we generated transcriptomic data to examine their expression levels and RNA editing patterns. Our novel insights emphasize a unique and unusual evolutionary process by which ferns can acquire a substantial number of foreign genes from angiosperms through plant-to-plant HGTs.

S.215.3 Deciphering reticulate evolution in Isoetes: comprehensive analyses with multifaceted sequencing approaches

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Polyploidy is arguably a dominant force shaping the evolutionary histories of many, if not most, plant lineages. It can fuel evolutionary novelties and, in some cases, facilitate speciation and diversification. Among the free-sporing vascular plants, the lycophyte genus *Isoetes* L. exhibits one of the highest proportions of polyploids, constituting approximately 50% of its species. The globally distributed genus comprises about 250 species, with plants occurring in aquatic environments, fully to partially submerged, and more rarely, terrestrial. Although several phylogenetic studies converge on seven major well-supported clades, the relationships within these clades remain highly unresolved. Since *Isoetes* polyploids mostly have a hybrid origin, polyploidy poses a confounding factor in phylogenetic analyses. In this study, we employed data from multiple sequencing approaches to elucidate phylogenetic relationships and polyploid origins in recently diverged *Isoetes* groups in the Neotropics. Using nuclear datasets derived from double-digest restriction-site associated DNA (ddRAD) and PacBio long-read amplicon sequencing, along with organellar data from skimmed genome sequencing, we showed that while polyploidy evolved early in *Isoetes*, the deep divergences inferred from nuclear and organellar data are identical. On the other hand, relationships in recently diverged groups exhibit strong discordance between organellar and nuclear datasets, reflecting recent hybrid speciation within the genus. Furthermore, ddRAD-Seq data analyses result in well-resolved phylogenetic relationships within the Neotropical species groups. These groups present clear geographical distribution patterns and we discuss the factors that led to their current distribution in the Neotropics. We showcase the robustness of nuclear data in establishing a phylogenetic framework to address evolutionary questions and demonstrate how incongruence between nuclear and organellar data can offer insights into the origin of polyploids. Our findings contribute to a comprehensive understanding of polyploid origins and deepen our insights into the biogeography of the genus in the Neotropics.

S.215.4 Unfurling a reticulate Andean fern clade using phylogenomic methods

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Nearly one-third of fern speciation events involve ploidy changes, compared to 15% in angiosperms, highlighting the unparalleled importance of reticulate evolution in fern diversification. Despite fern diversity peaking in the tropics, few studies have addressed hybridization and polyploidy in tropical fern lineages. *Pleopeltis* is a group of about 100, mostly epiphytic species found throughout the American tropics. Species of *Pleopeltis* occur in a broad spectrum of ecosystems, ranging from pluvial lowlands to dry alpine zones and with a great diversity of morphologies. Hybridization appears to be frequent throughout the group, challenging the delimitation of species and application of names. Evolutionary investigations have been hampered by several polytomies, recalcitrant nodes and short branch lengths in the backbone of the phylogeny, suggesting a possible rapid speciation event. Here, we focus on the Andean *Pleopeltis* species complex, a clade of pinnately divided species found in mid to upper elevations in the northern and central Andes and the putative hybrids between them. Using an integrative approach including geography, morphometrics, spore size and admixture analyses, we developed the first hypothesis of reticulate relationships within this complex and tested this hypothesis using recently developed phylogenomic techniques. Sourced from herbarium specimens and silica gel dried material, we produced DNA sequence data for all members in the Andean *Pleopeltis* species complex using the Genealogy of Flagellate Plants (GoFlag) target capture probe set, and we used a suite of newly developed allele-phasing bioinformatic tools to infer relationships between allopolyploid species and their diploid progenitors in this clade and elucidate the role of introgression and incomplete lineage sorting. This is the first phylogenomic investigation of this genus as well as one of the first investigations of polyploid speciation in a tropical fern clade using modern sequencing and bioinformatic techniques.

S.215.5 A phylogenomic approach for inferring cryptic taxa within the Eurasian allopolyploid fern Polypodium vulgare

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We present a case study using the GoFlag 408 target-capture probe set for ferns to test hypotheses about the progenitors of the allotetraploid fern *Polypodium vulgare* (Polypodiaceae) across Eurasia. Using our recently published SORTER bioinformatic pipeline, we accurately phased homeologs in 65 allopolyploid individuals, allowing us to resolve different progenitor pairs for *P. vulgare* in Asia and Europe, as well as three progenitors in the closely allied allohexaploid *P. interjectum*. We then used by-catch reads to assemble plastid genomes for a subset of samples and generated a time-calibrated phylogeny revealing the maternal progenitors of each polyploid taxon. The results of our combined plastid and nuclear phylogenomic analyses provide support for the segregation of *'P. okiense'* in Asia from *P. vulgare* in Europe. We highlight the effectiveness of the SORTER pipeline to generate allopolyploid datasets for phylogenetic analyses incorporating a large number of samples at varying ploidy levels.

S.215.6 A systematic revision of the lady fern (Athyrium filix-femina) species complex in the Americas

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Athyrium filix-femina (L.) Roth is a terrestrial fern that is widespread in forest regions across the Northern Hemisphere and South America. Despite its prevalence, its taxonomy in the Americas remains unresolved and the evolutionary relationships between taxa remain poorly understood. Uncertainty about whether to recognize a single widespread *A. filix-femina* or several endemic American species has persisted to the present day due to unclear morphological differences between regional varieties and a lack of a comprehensive study across its range. To address this uncertainty, we sampled herbarium specimens from four continents and employed an integrative methodology that combined molecular, morphological, and biogeographic data to examine evidence for speciation, hybridization, and cryptic diversity in this species complex. Our results indicate that there are at least five monophyletic lineages in North America with diagnosable morphology, habitat preferences, and discreet geographic ranges. In spite of many documented hybrids in Asia, we found no evidence for widespread hybridization or reticulation among North American species. In South America, we did not find clear species boundaries defined by morphology, geography or molecular evidence to recognize more than a single species. Allele phasing identified a single putative hybrid from Queretaro, Mexico of unknown origin. Research such as this enhances our capacity to recognize and document American floristic diversity that may be concealed in plain sight and highlights the value of utilizing integrative molecular methods to facilitate biologically accurate classification of plant species.

Symposia Session 13

S.216 COMPARATIVE SPATIAL PHYLOGENETICS OF MEDITERRANEAN-TYPE FLORAS OF THE WORLD

S.216.1 Scaling issues in spatial phylogenetics, in relation to testing hypotheses about biodiversity and its causes

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Newly available distributional data from global museum databasing efforts, rapidly increasing coverage of DNA sequence data, and improvements to computer hardware and software has enabled a new "big data" approach to the application of PD-based metrics and randomization-based hypothesis tests called "spatial phylogenetics." It can be defined most simply as mapping a phylogeny onto geographic space, which can then be used with GIS layers to understand drivers of phylodiversity patterns and for conservation prioritization. Alpha- and beta-phylodiversity can be measured using interestingly different ways of representing branch lengths on a given topology (called "facets." e.g., chronograms, phylograms, or cladograms), and hypotheses about ecology and evolution can be tested using spatial randomization. Scaling questions are present with both the spatial and phylogenetic data. Spatially, what size should be used for the basic spatial units, and how much of the Earth's surface should be studied at once? Likewise, there are similar issues at both the small and large scales in phylogenetics -- what should the OTUs represent, and how much of the tree of life should be studied at once? All these questions involve both theoretical considerations and practical data limits. These scaling issues will be explored using Mediterranean-climate regions as a test case. For example, we compare the results of comparative phylodiversity analyses of monocots alone as compared to results for all angiosperms. We also compare results obtained using different levels of OTUs, different spatial unit sizes, and local vs. global regions.

S.216.2 Spatial phylogenetic patterns in a biodiversity hotspot, the Cape of South Africa

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The Greater Cape Floristic Region (GCFR) of South Africa is a small area found in the southwestern corner of the African continent and comprising an incredible floral diversity (ca 11,500 species, ca 75% endemic). Small-leaved sclerophyllous shrubs and geophytes are the predominant growth forms in the region while tree and annual species represent only a small proportion of the flora. Furthermore, the floristic composition of the region is very distinctive with families such as Iridaceae, Aizoaceae, Ericaceae, Proteaceae and Restionaceae dominating, all of which are minor groups in other floras of the world. Understandably, this diversity has attracted a lot of speculation as to which environmental and/or ecological factors may be the prevailing drivers explaining the uniqueness of the region. This contribution reports on ongoing studies focussing on large-scale spatial phylogenetic patterns within the region. First, we present a spatial phylogenetic analysis using phylogenetic diversity and phylobetadiversity metrics based on a set of species-level phylogenetic trees and fine-scale species distribution modelling comprising all species found in the GCFR. In particular, we investigate the west-east decreasing longitudinal gradient in plant diversity observed in the region, termed the Levyns' Law. We explore the predictions made to explain this gradient by the age and area (i.e., high diversity is the result of biome and climate stability over evolutionary times) and ecological opportunity (high diversity is the result of increased ecological heterogeneity) hypotheses. Secondly, we examine the phylogenetic endemism patterns in the GCFR using Categorical Analysis of Neo- and Paleo-Endemism (CANAPE) to characterize local centres of endemism. We compare these species-level results with preliminary analyses performed at the genus-level to observe the effects of using different taxonomic levels. All these diversity measures are used in concert to try to understand both the origin of this extraordinary biodiversity hotspot and to prioritize conservation efforts.

S.216.3 Comparative Spatial Phylogenetics of Mediterranean-Type Floras of The World: The Case of Chilean Protected Areas

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Determining the factors that explain diversity patterns helps to understand the processes that have shaped different types of biodiversity hotspots. Phylogenetic Diversity (PD) and related evolutionary indicators have been increasingly used to understand patterns of biodiversity distribution and as a tool to aid in evaluating conservation targets. Mediterranean-like climatic areas around the world are characterized as being floristically diverse and vulnerable, and all of them are considered biodiversity hotspots. Central-southern Chile is one of these areas, showing high floral diversity and endemism. In this study, we calculated PD and other related metrics for the Chilean hotspot, identifying several interesting areas (hotspots within a hotspot). In areas such as Mediterranean Chile where lack of locality information is a problem to study biodiversity spatial patterns, species distribution models (SDMs) can be very useful in filling in missing locality information. Using SDMs, we analyzed how protected areas can act as a reservoir of PD in a climate change scenario in Mediterranean Chile, identifying museum-like and cradle-like areas. Randomizations were performed to identify areas in which these metrics departed from values expected by chance, for example identifying places in which phylogenetic overdispersion of taxa occurs. We correlated these areas with parameters such as geodiversity and climatic factors that could influence the spatial distribution of PD. Protected areas in MedChile are expected to harbor more PD than expected in climate change scenarios, but responses of individual areas differ depending mainly on climatic and geographic factors.

S.216.4 Spatial phylogenetics in the western Mediterranean Region: phylogenetic diversity and endemism of the Iberian angiosperm flora

Alberto J. Coello[1,2], Ignacio Ramos-Gutiérrez[2,3], Rafael Molina-Venegas[2,3], Antoni Buira[4], Mario Mairal[5], Pablo Vargas[4], Rosa A. Scherson[6], Brent D. Mishler[7], Juan Carlos Moreno Saiz[2,3], Mario Fernández-Mazuecos[2,3]

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The Iberian Peninsula is one of the main centers of plant diversity in the Mediterranean biodiversity hotspot. The Iberian flora has been the subject of scientific attention for centuries, and biogeographical patterns of plant species richness across Iberia are well known. However, a full understanding of the geographical patterns of biodiversity requires an evolutionary framework, as provided by the field of spatial phylogenetics. Here, we aimed to explore the spatial phylogenetics of Iberian angiosperms, including patterns of phylogenetic diversity and endemism, as a tool to inform conservation actions. We used distribution data from the Atlas of the Vascular Flora of the Iberian Peninsula (AFLIBER) at 10-km resolution and a global species-level mega-phylogeny of seed plants, resulting in a coverage of ca. 60% of Iberian angiosperm species. To analyze spatial phylogenetic patterns, we employed the R package *canaper*, including the mapping of endemism areas according to Categorical Analysis of Neo- and Paleo-Endemism (CANAPE). Uncertainty associated with the phylogenetic placement of unsampled species was addressed using the *randtip* package and compared with results using only sampled species. Our results indicate a concentration of relative phylogenetic diversity (RPD) in peripheral areas of the Iberian Peninsula under oceanic influence. According to CANAPE, areas of super-endemism (with a high concentration of both neo- and paleo-endemism) are found in the Pyrenees, the Balearic Islands and the Baetic Mountains. Areas of neo-endemism are concentrated mostly in the Baetic Mountains and the Balearic Islands, while areas of paleo-endemism are scattered across the Peninsula. The abiotic drivers of these patterns have been investigated using generalized linear models. Based on these findings, we conduct an evaluation of the adequacy of Spanish and Portuguese networks of protected areas to preserve phylogenetic diversity and endemism of the Iberian flora.

S.216.5 The role of traits in community assemblages across Mediterranean-type ecosystems

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Mediterranean-type ecosystems (MTEs) are found in five regions (southwestern Australia; the Cape region of South Africa; central Chile; California; and the Mediterranean Basin). These areas are characterized by warm and dry summers, mild and wet winters, and frequent fire, to which resident plants and animals must be adapted. Floristic diversity and endemism are exceptionally high in all five MTEs. Consequently, all five MTEs have been recognized as global biodiversity hotspots. Studies have suggested that biodiversity in the MTEs is influenced by several eco-evolutionary drivers including high net diversification rates, fire, and geological history. As a result, biodiversity in the MTEs is hypothesized to be strongly coupled with plant traits; thus, understanding patterns of functional diversity can increase our understanding of the biodiversity drivers. We integrated spatial occurrence data for native seed plants, four selected traits, and a corresponding phylogeny for plants of the five MTEs, and employed a novel metric based on phylogenetic diversity (PD) called *trait diversity* (TD), to evaluate and identify areas of significant phylogenetic and/or trait diversity. Areas with different combinations of high or low PD and TD can be used to infer biodiversity drivers and the relative contribution of niche vs neutral processes in these regions. All data used in this analysis were obtained from open access and published empirical studies. The ranges of the plants were restricted to their natural distributions to exclude non-native distributions in other MTEs. We selected four traits that are hypothesized to be associated with the persistence of native flora in the MTEs. Phylogenetic and trait diversity (and spatial randomization hypothesis tests) were computed using *Biodiverse* software (https://shawnlaffan.github.io/biodiverse/), allowing comparison of these patterns across the five global MTEs. Biodiversity in the MTEs appears to be influenced by an unusually complex mixture of past and current biogeographic, ecological, and evolutionary processes

S.216.6 World spatial phylogenetics of the angiosperms

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Spatial phylogenetic analyses combine phylogenies and spatial data at any taxonomic and geographic level. All studies to date have concentrated on either a particular taxonomic group, for example Australian *Acacia*, or the flora of a particular geographic region, for example analyses on the flora of Australia, California, or Chile. The recent PAFTOL angiosperm phylogeny created the opportunity to make a spatial phylogenetic world analysis at the genus level. We cleaned institutional plant records stored in the Global Biodiversity Information Facility (GBIF) to reflect the worldwide native range of each species (over 200000 species), then combined them into the PAFTOL genera. The final spatial dataset contained over 23 million records and was projected using World Mollweide at 50 ×50 km grid cells. The PAFTOL tree and spatial data were combined using Biodiverse to make diversity analyses and randomisations for CANAPE, Relative Phylogenetic Diversity and Phylogenetic Diversity tests. The results of two spatial phylogenetic analyses will be presented, one using a PAFTOL phylogram and one using a PAFTOL chronogram. We also present comparisons of results against climatic variables and the biodiversity hotspots of the world. We particularly focus on the 'Mediterranean-climate' regions of the world and compare the world-analysis results with what has been found previously when analyses have just focussed on one particular area.

S.217 EVOLUTIONARY HISTORY OF ARID FLORAS AND THEIR UNDERLYING BIOLOGICAL SURVIVAL MECHANISMS

S.217.1 Did succulents originate and diversify in response to aridity?

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Succulents have been typically considered the iconic example of arid adapted plants. Although distributed globally, plants possessing the succulent syndrome are assumed to have evolved to adapt to arid climates, because they possess modifications that increase their water use efficiency. Though succulence is considered a classic case of convergent evolution driven by shared environmental drivers, we lack a full understanding of whether the timing and drivers of the diversification of succulent lineages are, in fact, concordant; or even whether their climatic niches are indeed trending towards arid climatic conditions. We present our recent findings about the timing; climatic niches and evolutionary dynamics of major succulent lineages globally. Our analyses reveal different levels of evolutionary synchronicity and relation with aridity. The impact of atmospheric CO2 on succulent macroevolution is varied. While transitions and radiations are especially concentrated in recent time, following a collapse of atmospheric CO2 ~15 Mya, CO2-dependent diversification is not supported in most lineages. With the exception of *Euphorbia*, we find that succulence elevates net diversification, though the effects on underlying speciation and extinction disagree. The phylogenetic distribution of transitions to succulence and rate shift increases suggests these phenomena are decoupled, indicating that succulence might not adhere to a classic key innovation model. The climatic niches of succulents are not differentiated from their non-succulent relatives, but narrower, and contained within the non-succulents', showing no relationship with extreme conditions such as

high aridity or temperatures. Our results reveal the complexity of the succulent strategy, as well as the abiotic conditions and ecological contexts under which the different succulent lineages evolved.

S.217.2 Characterization of drought-resistance traits in the leaf-succulent genus Crassula

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Succulent plants have specialized water-storage tissues with collapsible cell walls that reversibly fold as water is lost. However, the ecophysiological significance of cell wall traits has often been overlooked in succulents. We focused on southern African species of the leaf-succulent genus *Crassula* and used comprehensive microarray polymer profiling (CoMPP) and glycan-binding antibodies to analyse cell wall polysaccharide and glycoprotein content in leaves. We found significant differences in leaf glycomic profiles that can be linked to increased drought resistance in one of the two main growth forms in *Crassula*. Furthermore, some cell wall components correlate positively with increasing aridity, which suggests that they are likely advantageous in terms of arid adaptation. A deeper insight into the relationship between cell walls and the succulent function would be particularly useful given the potential of succulents as natural capital to mitigate the effects of climate change. Numerous hydathodes are another peculiarity of *Crassula* species, foliar structures that are usually associated with guttation. Foliar water uptake (FWU) through hydathodes has long been suspected in *Crassula*, particularly in species that occur in fog-influenced arid habitats in southern Africa. To provide empirical observations linking FWU to hydathodes in *Crassula*, we used the apoplastic fluorescent tracer Lucifer Yellow in combination with different imaging techniques. The resulting images confirm that hydathode-mediated FWU does indeed occur in *Crassula* and is likely widespread across the genus. Surprisingly, FWU is operational in *Crassula* species that occur in rather mesic environments, beyond fog-influenced arid habitats, and even in species with seemingly hydrophobic leaves, in which the hierarchically sculptured leaf surfaces may facilitate FWU thanks to hydrophilic leaf surface microdomains. These findings confirm the ecophysiological relevance of FWU in *Crassula* and reassert the importance of atmospheric humidity for some arid-adapted plant groups.

S.217.3 Evolutionary lessons from the Chihuahuan Desert gypsum endemic flora

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Gypsum outcrops occur in arid and semi-arid regions around the globe, and present a significant barrier to plant growth due to challenging soil nutrient levels (excess sulfur and calcium, minimal nitrogen and phosphorus) and the presence of well-developed soil crusts. Nevertheless, these difficult soils host a wide variety of endemic plants. The Chihuahuan Desert region of Mexico and the USA has the largest known gypsum endemic flora in the world, with over 240 plant taxa known only from gypsum. Ongoing research into the diversification of this flora has revealed a number of repeated evolutionary patterns. For example, the dominant gypsum endemic taxa in the Chihuahuan Desert region typically belong to clades of gypsum endemics that likely originated in the Pliocene or latest Miocene, and that have survived the climatic oscillations of the Pleistocene. Likewise, the dominant gypsum endemic taxa of the Chihuahuan Desert belong to genera and families with many independent evolutionary origins of gypsum endemism, strongly suggesting that preadaptations to life on gypsum exist in these groups. One such preadaptation may be the ability to accumulate sulfur within leaves—an ability that has now been documented in many of the dominant gypsum endemics of the Chihuahuan Desert. The presence of this trait in what are likely the oldest clades of gypsum endemics and some of their closest non-endemic relatives suggests that foliar sulfur accumulation may be one of the driving factors in explaining the historical assembly and evolution of the Chihuahuan Desert gypsum endemic flora. Similar patterns related to sulfur accumulation are also present in the independently derived Spanish gypsum flora, suggesting that this ecophysiological trait may be of global importance in understanding gypsum plant evolution.

S.217.4 Biogeographic and evolutionary history of the Atacama Desert Flora

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Post-Miocene climate history, particularly in arid environments, has emerged as a key factor in shaping species dispersal and diversification. The Atacama Desert in northern Chile, one of the driest regions on Earth, stands out for its presumed Oligocene-Miocene age, as well its unexpectedly high biodiversity and elevated number of endemic species thriving under hyperarid conditions. Contrary to expectations, the extreme aridity of the Atacama predates the estimated divergence times of most extant genera. The initial onset of hyperaridity cannot have been the primary driver of diversification in these extant groups. We argue that recent climatic history, marked by intervals of pluvial and arid phases, especially during the Pliocene-Pleistocene transition, played an important role in shaping the current desert flora. Our research uses next-generation sequencing and molecular clock dating to unravel how this complex biogeographic and evolutionary history was influenced by past climate variability and Andean orogeny. Here, we briefly review our findings on the historical biogeography of selected Atacama taxa and discuss their broader implications for the existing body of knowledge on the Atacama Desert flora. A striking example is the genus *Cristaria* (Malvaceae), an element of the Chilean Mediterranean flora that colonized the Atacama during Pliocene pluvial phases. This led to in-situ diversification likely fueled by repeated introgressions and the emergence of new species. Conversely, the ca. 15 endemic species of *Atriplex* (Amaranthaceae) do not originate from local radiation alone: they arose from multiple colonization events (including by long-distance dispersal) followed by local divergence. The paleoendemic lineage *Huidobria fruticosa* (Loasaceae), on the other hand, appears to have undergone little if any diversification, despite being genetically separated from its closest relatives for about 50 million years. However, our data suggest that its recent population history can be traced to the Pliocene-Early Pleistocene transition.

S.217.5 Dispersal, not vicariance, drives the diversification of native Australian tobacco (Nicotiana section Suaveolentes; Solanaceae) in the arid zone

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For the last six million years, the Australian Eremaean Zone (EZ) has been as dry as today. The flora and fauna of arid regions worldwide, including the EZ, have been hypothesised to have diversified widely before aridification began, in this case 20 Mya, and slowly adapted as aridity developed. Undocumented are more recently arrived plants that developed arid specialisations in situ. Here, we investigate the biogeography and timing of native allotetraploid tobaccos, Nicotiana sect. Suaveolentes, which putatively entered the EZ 5 Mya. The original allotetraploid migrants from South America were adapted to mesic areas of Australia and only recently radiated in the EZ after developing drought adaptations. Based on coalescent and maximum likelihood analyses designed to corroborate timing of the Australian radiation independently, arrival of Nicotiana sect. Suaveolentes occurred approximately 6 Mya, followed by spread via multiple invasions across the EZ from the ecologically highly diverse Pilbara District (Western Australia), which served as a mesic refugium and cradle for adaptations to harsher conditions. These results demonstrate that poorly adapted plant groups can develop novel adaptations that permit them to disperse extensively and rapidly despite the extremes of heat and drought in the EZ.

S.217.6 Comparative evolutionary history of the Australian Amaranthaceae

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The vast arid region covering about 70% of Australian continent remains one of the world's largest and least explored territories. Despite its extremely adverse environmental conditions, this area is rich in xerophytic plant life that has adapted to challenging physiological and ecological constraints. Despite such a high diversity, this flora is thought to have evolved along a similar evolutionary trajectory, known as the littoral connection hypothesis. This hypothesis states that the most recent common ancestors of contemporary arid floral elements arrived in Australia already preadapted to increased aridification and/or salinisation, and were thus able to thrive in environmental conditions that have otherwise driven most mesic floral elements to extinction. Alongside Asteraceae, Fabaceae, and Myrtaceae, Amaranthaceae are one of the species-richest plant families in this arid zone that underwent rapid diversification events. In our studies, we employed various RAD-seq and HybSeq techniques to resolve the phylogenies of numerous recalcitrant groups of xerophytic Australian Amaranthaceae and compare their evolutionary histories. Our analyses focused on understanding the spatiotemporal patterns in these lineages and the underlying biological mechanisms that drove their rapid diversification and survival. Despite their separate arrivals in Australia during the Miocene/Pliocene transition, our analyses unveiled shared spatiotemporal patterns among these groups, lending support to the littoral connection hypothesis. Some lineages exhibited floral exchanges between Australia and South Africa, while polyploidisation, potentially driving speciaton, appeared to be restricted to certain taxa. Future research aims to expand these investigations to other arid-adapted elements in the Australian outback with the main aim to further validate the littoral connection hypothesis and understand the broader role of polyploidisation in the evolution of Australian arid clades beyond Amaranthaceae. Our research sheds light on the evolutionary adaptations of plants in some of Earth's harshest environments, providing valuable insights into the mechanisms driving biodiversity in arid regions.

S.218 THE KEY ROLE OF REFUGIA IN FACING THE GLOBAL BIODIVERSITY CRISIS

S.218.1 Climate Change Refugia Conservation as a 21st Century Solution

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Anthropogenic climate change is posing a serious risk to Earth's biodiversity. As scientists and practitioners, we can document the erosion of our biodiversity, and can model how those changes will increase with each warming increment. However, we can also work together to identify ways to reduce those impacts. Climate adaptation focuses on conducting and translating research to minimize the impacts of climate change, including threats to biodiversity and human welfare. One adaptation strategy is to focus conservation on climate change refugia, areas that remain relatively buffered from contemporary climate change over time and enable persistence of valued physical, ecological, and socio-cultural resources. Climate refugia is a concept that has existed for more than 100 years, originating in the paleontological literature to understand what fostered the survival of disjunct populations despite severe and rapid past climate change events. The refugia concept has captured the attention of scientists, practitioners, and the public more recently, in part because it offers some hope of maintaining current conditions, at least in some places and for the short term. The field transcends disciplines and sectors and intersects with knowledge about other global change stressors like fire, drought, and invasive species to create actionable science that can, in its own small way, address the biodiversity crisis. This talk will synthesize the work that has been to develop and implement the climate change refugia concept and where it is headed in the 21st century.

S.218.2 Karst depressions as past, present and potential future microrefugia

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Karst landscapes cover about 15–20% of the Earth's terrestrial surface, providing high topographic complexity that may facilitate the persistence of plant species despite unfavourable macro-environmental changes. Enclosed depressions (i.e., dolines) are the most common and typical landforms in karst landscapes. Microhabitats in dolines, such as bottoms, north-facing, south-facing, east-facing, and west-facing slopes, may act as microrefugia for many endangered and highly specialized plant species (e.g., species listed in the IUCN regional and/or global Red Lists). Notable examples include *Cerastium dinaricum* (Slovenia), *Dracocephalum ruyschiana* (Hungary and Serbia), *Biebersteinia orphanidis*, *Horstrissea dolinicola* (Greece), and *Magnolia aromatica* (China). Dolines also have the potential to maintain natural and restricted vegetation types (e.g., beech forest patches at low altitudes in Central Europe). Our aim is to provide an overview about the ecological factors of dolines in general, to discuss the mechanisms underpinning their role as microrefugia, and to highlight research priorities that will advance our understanding of plant diversity in dolines. Firstly, we illustrate the importance of geomorphology on ecological factors (such as air temperature, relative air humidity, and soil properties) within dolines, and the long-term stability of these factors. Secondly, we evaluate the effects of these factors on local and regional biodiversity, highlighting the role of dolines as past, present and potential future microrefugia. Finally, we identify key knowledge gaps that need to be addressed to improve our knowledge on the effects of various stressors (e.g., temperature increase, drought, and forestry management) on the refugial capacity of dolines.

S.218.3 Refugia for biodiversity: identification and role in plant persistence

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Mountains are home to a rich biodiversity thanks to the environmental heterogeneity they offer, and considered highly vulnerable to climate change. Indeed, many studies have shown how rapidly mountain land cover is changing in response to both climate change and the abandonment of traditional land uses. However, mountains can also be conceived as mosaics of microclimates that can facilitate the survival of species in the face of contemporary climate change through short migrations, and home to refugia where species withstand climate crisis. In this presentation we combine different approaches to shed light on the characteristics of climatic refugia in the Pyrenean mountain range, as well as their role for the persistence of biodiversity. On the one hand, by deploying numerous small sensors in rough terrain, and thermal images taken from the ground or drones, we identify areas with a narrow thermal range where maximum summer temperatures are damped: climate refugia. On the other hand, based on floristic inventories, we explore what fraction and type of plant diversity inhabits those climate refugia. Finally, from the population monitoring of some unique plants typical of refugia, we demonstrate the environmental stability they offer. The integrity and proper management of mountains, their microclimates and the refuges they shelter, are key to preserving biodiversity in the current climate change scenario.

S.218.4 Not only climatic refugia - the multifaced concept of refugia for the long-term survival of species during the Anthropocene

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The refugium concept in biogeography, evolutionary biology and conservation science has traditionally been associated with glacial and interglacial periods. Particularly, it has been linked to regions or locations with stable climatic conditions over long time in comparison to the surrounding areas. However, over the last decades the massive global environmental changes and the increase of extinction rate of species has led to the need to identify stable areas for species with respect to different environmental factors and temporal and spatial scales. According to this view refugia are landscape elements that remain marginally affected by anthropogenic environmental factors and that subsequently can continue to support native species and community with reference to ecosystem functions, and biodiversity levels. Therefore, depending on the scale, they are location or regions resilient to disturbances and environmental changes. Recent literature has highlighted the existence of Anthropocene refugia or potential areas providing spatial and temporal shelter to species from human activities in the long-term. However, Anthropocene refugia have not been ecologically characterized which is pivotal for recognizing their role in allowing the persistence of species in context of global environmental changes. Works have emphasized the presence of different kinds of refugia for biodiversity such as urban refugia, marine refugia, biocultural refugia, dark refugia, and fire refugia. Therefore, in this work we aimed at reviewing the recent concepts of refugia over different ecological scales and to define their value for biodiversity accounting, landscape conservation and species' evolution as well as identify conservation and management strategies.

S.218.5 Pictorial Conceptualization of Glacial Refuges in the Mediterranean Quaternary

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The importance of glacial plant refugia has been and continues to be a subject that sparks great intellectual excitement and promotes the development of many research activities specifically oriented towards biogeographic, ecological, evolutionary, and conservation biology issues, among others. These investigations aim to address an extensive spectrum of questions that lie on the frontiers of knowledge and have implications in a scenario of climate emergency and biodiversity crisis. It is crucial for society to be properly informed about the conclusions and corollaries arising from all these activities, mostly funded with public money. Scientific illustration and paleoart are essential tools in transmitting the knowledge acquired about refugia to different educational and cultural levels in each social context. Similarly, the pictorial representation, a result of synergy between the artist and paleoecological scientists, provides new avenues of research by highlighting biases, deficiencies, and methodological and interpretative inconsistencies in the study of paleoecosystems. In this poster, we present several paleoartistic proposals for representing glacial refugia in the Mediterranean Basin during the cold Quaternary stages, considering the originality of the depicted communities, the lack of current analogs, their probable landscape structure, and above all, the unique floristic components. The scientific data stem from palynological analyses complemented with other botanical remains and paleoclimatic inferences derived from non-botanical proxies. We put emphasis on hydroclimatic refugia in the driest territories and the evidences in support of these strongholds as reservoirs and sources of biodiversity which favoured the survival of hominins during periods of highly unfavorable climate across most of the European continent

S.218.6 Assessing how climate will change in world's terrestrial protected areas: are they behaving as proper climatic refugia?

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Climatic changes play an essential role in shaping biodiversity. As global climate change accelerates, comprehending its potential impacts on ecosystems and species has become increasingly vital; indeed, climate change is considered a key driver for species extinction. Therefore, climatic refugia will play a crucial role for the conservation of extant biodiversity, and conservation efforts should be directed towards protecting these areas. Protected areas (PAs) are currently regarded as fundamental to ensure biodiversity conservation; thus, evaluating how future climatic change is affecting PAs would be helpful in prioritizing or redesigning the existing ones. Moreover, identifying areas with high climatic stability (i.e., climatic refugia) could also guide the designing of new PAs. This study employs the Climate Stability Index (CSI), developed by Herrando-Moraira et al. [1], to assess the vulnerability of the current network of world's terrestrial PAs to climate change. The CSI originally used an uncorrelated set of the 19 WorldClim bioclimatic variables from present to year 2100 at 2.5 arcmin (ca. 5 km) grid resolution, and here is updated with the latest fourteen general circulation models of climate change at higher resolution (ca. 1 km) of four periods available from WorldClim. This research evaluates the projected climate changes considering the current network of PAs as a whole, but also considering different levels of protection of PAs (e.g. the IUCN six management categories), different biogeographic regions, or different levels of species richness and endemism. The findings will contribute valuable insights to conservation strategies, aiding policymakers and land managers in mitigating and adapting to the impacts of ongoing climate change in the world's terrestrial PAs, ensuring informed decision-making in the face of environmental challenges.

References: Herrando-Moraira, S., et al. (2022). Climate Stability Index maps, a global high resolution cartography of climate stability from Pliocene to 2100. Scientific Data 9, 48.

S.219 BACK TO BASICS: USING MICRO-MORPHOLOGY, ANATOMY AND HISTOLOGY TO INVESTIGATE EVOLUTION IN BRYOPHYTES

S.219.1 The contributions of electron microscopy to bryology

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The 1950s to the early 21st century was the Golden Age of biological electron microscopy: almost every university Biology department had both transmission (TEM) and scanning electron microscopes (SEM). The benefits to bryology have been enormous. In 1952, Manton and Clarke discovered the compound nature of the sperm flagella in *Sphagnum* and suggested it was the same as in algae, ferns and humans. Sectioning then revealed the sperm cytoskeleton, the microtubule spline and multilayered structure. Consequent on meticulous reconstructions, initiated by Carothers spermatozoid ultrastructure now provides a suite of features key to defining the different lineages of land plants and their algal ancestors. Manton was also the first to observe the ultrastructure of hornworts: though disappointed that their cells are basically the same as other bryophytes she illustrated their unique channelled thylakoids. Decades later immunogold labelling confirmed pyrenoids as crystalline arrays of RUBISCO. The same technique has then been used to unravel the unexpected complexities of bryophyte cell walls particularly those of conducting cells, whose unique features had been well documented by Hébant, and stomata. Though TEM has revealed that the structure and biogenesis of oil bodies are unique to liverworts, we have still to solve the mystery of their function. The biggest contributions of SEM have been to illustrating surface and spore ornamentation and the unrivalled beauty of peristomes. Cryo-SEM from the late 1990s added an extra dimension in enabling the observation of bryophytes in different stages of cytorrhytic dehydration and rehydration. In vascular plants intercellular spaces are gas-filled from the outset whereas in bryophytes they are liquid-filled. They remain in this condition in the gametophytes but become gas-filled following stomatal opening in mosses and liverworts. Except for hydroids, bryophyte cells are highly resistant to cavitation. Cryo-SEM also demonstrates that bryophytes have a mixture of hydrophilic and hydrophobic surfaces.

S.219.2 Peristome evolution in the Dicranidae revealed by SEM and histology

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The peristome is considered the most complex and conservative morphological structure in mosses. The arthrodontous peristome is composed of a single, or double, ring of teeth surrounding the opening of the capsule. Peristome characters have long been used for classification at the higher taxonomic ranks, and for understanding evolutionary events across mosses. In the monophyletic Dicranidae, which contain a third of total moss diversity and are characterized by a haplolepidous peristome, the peristome architecture has been found to be informative across the group. A thorough morpho-anatomical investigation of the haplolepidous peristome was carried out across a large sampling in the Dicranidae, using histology and state-of-the-art SEM. The peristome tooth-insertion region, studied with thin longitudinal sections, was delimited, and described. The comparative anatomy of the peristome teeth-insertion region has revealed conserved and variable anatomical features, at the lower levels, that are useful for elucidating relationships in the Dicranidae. The imaging of teeth ornamentations and morphology, using SEM, revealed an unsuspected diversity across the group. The main patterns and traits of ornamentations have been reassessed, and a newly discovered set of shapes and sizes of ornamentations have been redefined. The ornamentations have proven to hold taxon-specific information across and between the various taxonomic ranks. The combination of anatomy and micro-morphology allowed for a global comparison of peristomes in the Dicranidae. This study confirms the taxonomic importance of the peristome at the species, generic and familial level in the Dicranidae. It will allow the use of new diagnostic features for further investigations on the relationships across the Dicranidae, as well as for the establishment of stable characteristics for peristome descriptions.

S.219.3 Evolution and development of water-related traits in the dryland moss Syntrichia caninervis (Mitt.)

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In contrast to vascular plants, most mosses rely on external water transport and absorption over the entire plant surface, a condition known as ectohydry. Morphological characters (i.e., papillae) create capillary pathways or increase the surface area to facilitate water uptake and transportation. As a moss acquires water, small chambers and capillary spaces fill up with water and the moss expands rapidly. Then, a new set of structural features appear, ranging from modifications in their overall morphology to extensive changes of cells in the leaf. The way these features develop over time, function, and/or reflect adaptation to different environmental regimes is an area that remains poorly understood in mosses. This research applies genomics and cutting-edge imaging to (1) characterize leaf development with respect to water-related traits, (2) identify how stages of leaf development facilitate ectohydric capabilities and relate to changes in water conducting cell types, (3) identify gene expression profiles in response to dehydration/hydration cycles in the moss *S. caninervis*. This presentation will describe preliminary data encompassing multiple biological levels of organization (cells, tissues, and organs) along with cutting-edge confocal microscopy to provide a basis for a better understanding of the mechanisms underlying leaf organogenesis, and more broadly how plants evolve complex traits crucial for their adaptation to terrestrial environments.

S.219.4 Complex thalloid going simple: the importance of microanatomic traits in unveiling Dumortiera hirsuta's diversity

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Complex thalloid liverworts (class Marchantiopsida) represent a good example of the importance of microanatomical characters when the macroscopic ones fall short in taxonomic decisions. Some representative microscopic structures showing traits with taxonomical relevance in the group include dorsal epidermis cells, dorsal papillae, hairs, air pore cells, photosynthetic filaments, scales, or rhizoids. *Dumortiera hirsuta* (Sw.) Nees is a widespread pantropical species present also in some temperate regions, characteristically lacking some typical complex thalloid traits, such as air pores or a developed epidermic reticulum. This liverwort displays, nonetheless, a remarkable variation of other microscopic traits. This fact led 18th and 19th-century botanists to describe multiple species that were later synonymized to *D. hirsuta*, concurrently with the lumping trend that thalloid liverwort taxonomy experienced throughout the 20th century. Recently, the likelihood of the ancient multiple-species hypothesis is again being reconsidered according to molecular data. We have chosen this liverwort as a model to study the importance of microscopic characters in Marchantiopsida systematics. For that purpose, the presence or absence of epidermal papillae, the vestiges of epidermal reticulum (in the form of vertical walls on the dorsal epidermis), the morphology of hairs and rhizoids, as well as the morphology and ornamentation of spores, were studied in a selection of *D. hirsuta* specimens, mainly from Europe, Macaronesia, and the Americas. The integration of the morphoanatomical and newly generated molecular data, which is coherent with the multiple-species hypothesis, is discussed together with the next steps to improve our understanding of this lineage.

S.219.5 Fungal symbioses in bryophytes: anatomical insights on the evolution of mycorrhizal associations in land plants

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Light microscope studies, many dating back to the nineteenth century, showed the ubiquitous presence of fungi in many liverworts and hornworts. Their identity and function were unknown. Transmission electron microscopy revealed the endophytes as belonging to a range of major fungal groups; Ascomycota in the rhizoids of Cephaloziaceae, Cephaloziellaceae, Lepidoziaceae, Schistochilaceae and *Mylia anomala* where the fungus induces rhizoid swelling and branching, Basidiomycota in the stems of Scapaniaceae and in the thalli of Aneuraceae, and Mucoromycota (Glomeromycotina and Mucoromycotina) in the Haplomitriopsida, hornworts and many simple and complex thalloid liverworts. The demonstration of healthy fungi in healthy host cells and specialised interfaces comparable to those of mycorrhizal associations in vascular plants, were strongly indicative of symbiotic relationships. Sequencing enabled more precise identification of the fungi. The rhizoid ascomycete is *Rhizoscyphus ericae,* with the exception of *Meliniomyces* in *Mylia anomala*, the same fungi as in ericaceous hair roots. The basidiomycete genus *Serendipita* is found in leafy liverwort families but a later fungal lineage, *Tulasnella,* is the endophyte in the Aneuraceae. Underlying their unusual cytology, also found in some Devonian fossils, the endophytes in the Haplomitriopsida are exclusively members of the subphylum Mucoromycotina whereas hornworts, simple and complex thalloids contain a mixture of Glomeromycotina and Mucoromycotina. From the first establishment of symbiosis, in the Haplomitriopsida, at the foot of the land plant tree, liverwort evolution has witnessed several gains and losses of fungi. Microcosm experiments combined with anatomical analyses are now demonstrating major differences in nutrient exchanges between Mucoromycotina and Glomeromycotina fungi and in their response to elevated carbon dioxide levels on a par with those at the dawn of plant terrestrialisation. Ultrastructural observations of living hyphae in close proximity to *Nostoc* colonies suggest potential plant-fungus-cyanobacterium synergistic interactions in hornworts.

S.219.6 Refining our understanding of hygroscopic movements in moss peristomes using histology

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The peristome in mosses plays a role in spore maturation and release. Arthrodontous peristomes are formed from one or two rings of cell-wall remnants of opposing cell layers that are divided into distinct, articulated teeth. These teeth are reactive to humidity and move in response to changes in the ambient water levels in their immediate surroundings. The hygroscopic movements of the peristome teeth are hypothesised to facilitate spore dispersal. Two main types of response of the peristome teeth to water availability extremes are documented, peristomes that are open when wet and closed when dry versus peristomes that are open when dry and closed when wet. Cell wall deposition patterns on the internal and external faces of the teeth influence the movements based on water diffusion patterns and absorption-loss dynamics. The presence of a hydrophobic substance between the two cell layers of the single or outer ring of teeth has been documented in certain moss species, with several hypotheses proposed to explain its function in the hygroscopic movements and what the substance may be composed of. Histological examination of peristomes from species across the Dicranidae allowed us to clarify the composition of the layer and, when present, clarify its role in the mediation of the hygroscopic movements. Reflections on the responses of peristomes, with and without the hydrophobic layer, revealed a potential link with ecological preferences.

S.220 APG V AND THE CHALLENGE OF TRANSLATING PHYLOGENY INTO CLASSIFICATION WHEN GENE TREES CONFLICT

S.220.1 Nightmare or delight: taxonomic circumscription meets reticulate evolution in the phylogenomic era

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Phylogenetic studies in the phylogenomics era have demonstrated that reticulate evolution greatly impedes the accuracy of phylogenetic inference, and consequently can obscure taxonomic treatments. However, the systematics community lacks a broadly applicable strategy for taxonomic delimitation in groups identified to have pervasive reticulate evolution. The red-fruit genus, *Stranvaesia*, provides an ideal model for testing the effect of reticulation on generic circumscription when hybridization and allopolyploidy define a group's evolutionary history. Here, we conducted phylogenomic analyses integrating data from hundreds of single-copy nuclear (SCN) genes and plastomes, and interrogated nuclear paralogs to clarify the inter/intra-generic relationship of *Stranvaesia* and its allies in the framework of Maleae. Analyses of phylogenomic discord and phylogenetic networks showed that allopolyploidization and introgression promoted the origin and diversification of the *Stranvaesia* clade, a conclusion further bolstered by cytonuclear and gene tree discordance. The well-inferred phylogenetic backbone revealed an updated generic delimitation of *Stranvaesia* and a new genus, *Weniomeles*, characterized by purple-black fruits, trunk and/or branches with thorns, and fruit core with multilocular separated by a layer of sclereids and a cluster of sclereids at the top of the locules. Here, we highlight a broadly-applicable workflow for inferring how analyses of reticulate evolution in phylogenomic data can directly shape taxonomic revisions.

S.220.2 Reconciling gene-tree discordance in classification

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The first four iterations of the APG classification were largely based on sequence data from the plastid genome. Over the past decade, the use of numerous nuclear loci across many taxa has become increasingly common in phylogenetic analyses of plants. In many cases, nuclear and plastid-based topologies for angiosperms agree, providing increased support for inferred relationships. However, in other cases, comparison of nuclear and plastid-based topologies has revealed surprising instances of incongruence at levels much deeper than those likely resulting from recent hybridization or incomplete lineage sorting over recent timescales. These examples of conflict provide important insights into evolution, showing that reticulation has been common and widespread throughout angiosperm evolutionary history. But how best to reflect these examples of deep incongruence in classification, especially in the next APG classification? Various approaches deserve consideration as we attempt to construct classifications that are maximally informative about phylogenetic history. When nuclear and plastid phylogenies conflict, the classification could alternatively follow: (1) the nuclear topology, with symbols indicating where the plastid genome provides an alternative topology; or (2) both the nuclear and plastid topologies by placing a taxon in alternative clades (as allowed under the PhyloCode). Each of these approaches presents challenges. For example, what percentage of nuclear genes would be required for a particular placement to be the favored placement in APG? And what navigation tools might be needed to alert users that a taxon is placed in two alternative groups? A system that provides maximum information and flexibility should be employed.

S.220.3 Whence APG: a short history

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In the middle to late 1990s, as DNA data began to accumulate, it became clear that no modern angiosperm classification resembled the emerging DNA results. In Uppsala, Sweden, Kåre and Birgitta Bremer and their colleagues created a booklet with a new classification based on the DNA results with the idea that it could be used in teaching plant systematics. At that time, several of their PhD students were collecting molecular data in the molecular systematics laboratory at Kew, and on a supervisory visit to Uppsala in 1998 I was shown this teaching booklet. We decided that their largely DNA-based classification should be published. At the time, although molecular systematists were identifying the same clades of families, different order names, formal and informal, were being applied to these, which made communication difficult and was undesirable. We contacted other botanists who were also working broadly on angiosperm phylogenetics, both with DNA and morphological data, to get their input and decided that a new system should be published under the APG acronym, to avoid the situation in which the new classification was authored by one authority. Although the APG classification has gone through some minor changes in philosophy and four updates, with a fifth in progress, the general framework remains unchanged.

S.220.4 Phylogenomics and a revised classification of the Cucurbitales

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Cucurbitales currently includes eight plant families with diversity centers in the Tropics: Anisophylleaceae, Apodanthaceae, Begoniaceae, Coriariaceae, Corynocarpaceae, Cucurbitaceae, Datiscaceae, and Tetramelaceae. These families comprise 109 genera with more than 3,100 species. Morphologically, the taxa of Cucurbitales are rather diverse ranging from the holoparasitic Apodanthaceae, to annual and perennial herbs in Datiscaceae and Begoniaceae, to trees and shrubs in Anisophylleaceae, Corynocarpaceae, Coriariaceae, and Tetramelaceae and finally to woody or herbaceous climbers and creepers in Cucurbitaceae. Based on target-capture and whole genome sequencing data of 125 Cucurbitales samples representing all 102 genera currently accepted in the order, we inferred coalescent species trees and networks. We infer monophyletic and well supported families and tribes. The holoparasitic Apodanthaceae are placed outside Cucurbitales. For the remaining seven Cucurbitales families, the relationships vary. The best supported alternative shows a grade Coriariaceae + Corynocarpaceae, followed by Anisophylleaceae and then the remaining clades, but there is also considerable gene tree and site support for a clade Anisophylleaceae, Corynocarpaceae + Coriariaceae, rest. The woody Tetramelaceae is resolved as sister to the herbaceous families Begoniaceae and Datiscaceae but again there is also considerable gene support for the two alternative combinations within the triplet. Within Cucurbitaceae, there is gene support for different relationships between the tribes but the best supported topology is a clade Actinostemmateae + Gomphogyneae grouping as sister to the remaining tribes. A network analysis revealed ancient reticulation within and between Benincaseae, Coniandreae, and Cucurbiteae, suggesting that Benincaseae are the result of ancestral hybridization between Coniandreae and Cucurbiteae. A similar pattern of reticulation is found between Schizopeponeae and Sicyoeae. Finally, there is evidence for recent reticulation within Coniandreae and within Thladiantheae, indicating frequent hybridization events in the evolutionary history of Cucurbitaceae. We present a revised taxonomic classification of Cucurbitales and discuss the implications for character evolution in the group.

S.220.5 The impact of nuclear data on APG V

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For the past 25 years, the Angiosperm Phylogeny Group has revolutionised the systematics of angiosperms by providing a stable classification system based on robust phylogenetic evidence. This classification has largely been informed by plastid markers. Now, due to advances in high throughput sequencing, the nuclear genome is more easily accessed, allowing us to infer phylogenetic trees from hundreds of nuclear loci. Target sequence capture (e.g. using Angiosperms353 probes) is now routinely used to tap into the nuclear genome, even using DNA from historical collections. These advances, however, demonstrate that the evolutionary history of plants is more complex than the plastid genome suggests, challenging previous classifications. Here, we present novel phylogenetic insights from nuclear data on the circumscription of families, orders and major clades of angiosperms. These insights arise from anuclear phylogenomic research of the Plant & Fungal Trees of Life (PAFTOL) project at the Royal Botanic Gardens, Kew, which has resulted in genome-scale phylogenetic trees including all angiosperm families and nearly 60% of extant genera. Importantly, many relationships by plastid evidence are corroborated, such as the delimitation of major clades, and deep relationships in the ANITA grade, the monocots and the early-diverging eudicots. However, conflict between nuclear and plastid data is evident across the tree, leading to several changes, e.g., the inclusion of Chloranthales in magnoliids; in rosids, the reduction of fabids and expansion of malvids, and the disintegration of the COM-clade; and in asterids, the break-up of orders Aquifoliales, Bruniales and Icacinales. In other groups, like Santales and Brassicales, notable conflicts are observed, but refining family circumscriptions requires denser sampling in those clades. As expected, cytonuclear conflict is evident throughout the angiosperm tree of life. Future classifications must embrace this conflict to ensure that our knowledge infrastructures are consistent with the complex history of angiosperms.

S.221 ATYPICAL SUBSTRATES AS ENGINES FOR PLANT AND LICHEN EVOLUTION I: GYPSUM SOILS

S.221.1 The gypsum outcrops of North America: islands of high floristic endemism and diversity

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Isolated gypsum outcrops along Mexico and southwestern USA are diverse in terms of size and flora. Over 250 plant species restricted to gypsum (gypsophytes) are known there, mostly within the Chihuahuan Desert. The dominant North American gypsum endemics are often physiologically and morphologically highly distinctive from their nearest relatives, and many belong to clades that may have originated several million years ago. Nevertheless, biogeographic patterns of endemism and the ultimate origins of the gypsum flora of North America (including endemic and non-endemic taxa) are poorly known. This is particularly true for the gypsum outcrops in tropical Mexico, which are poorly investigated. Recent efforts showed that the gypsicolous flora of tropical Mexico is highly diverse despite inhabiting much smaller outcrops than in the Chihuahuan Desert. However, no comprehensive studies of diversity patterns, including phylogenetic diversity, have been conducted in North America. Here we use different diversity metrics to analyze the composition of the gypsum floras of North America. We used 6,211 herbarium-based records to estimate the spatial distribution of species richness, endemism, phylogenetic diversity, and phylogenetic endemism. We found that tropical gypsum patches possess a more diverse flora but with significantly reduced endemism as compared to those in the arid regions further north. We detected a mix of Nearctic and Neotropical elements, with the latter especially prominent in western and southern Mexico. Total species richness followed global latitudinal diversity gradients, but remarkable cases of high diversity were identified in the Cuatrociénegas Basin, in the Sierra Madre Oriental at Nuevo León, and in Oaxaca. Categorical analysis revealed examples of neo- and paleo-endemism. Species endemism and phylogenetic endemism are heterogenous throughout the study area, but are higher in the Chihuahuan Desert Region, which may reflect the much greater geographic extent of gypsum outcrops in these areas compared with the tropical patches.

S.221.2 Facilitation in gypsum soils is promoted by homogeneous microenvironmental conditions under the nurses

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Besides the environmental stress in arid and semi-arid regions, gypsum outcrops are a barrier to plant growth due to challenging soil nutrient levels. In such extreme conditions, biotic interactions are highly affected by species traits and micro environmental variability. Studies on facilitation have shown that nurse species alleviate abiotic stress for beneficiary species, but the impact of the micro-environmental variability generated by nurse plants in shaping facilitation outcomes is poorly understood. Here, we assess which traits define beneficiary species and whether nurse and non-nurse species differ in their ability to reduce abiotic stress and its variability under their canopy. We sampled recruits in two gypsum arid and stressful environments in the Cuatro Ciénegas' valley in Coahuila, Mexico. Our aims were to assess i) which species accumulate more juveniles beneath their canopy controlling for their coverage (nurse vs. non-nurse species); and ii) which species benefited from facilitation by determining whether they tend to recruit more species beneath or on the bare ground (beneficiary/non-beneficiary). Then, we compared how nurse and non-nurse species modify the physical and chemical microenvironments underneath their canopy, both in terms of magnitude and variation. Furthermore, comparisons were made between root growth, water retention, and nutrient accumulation in juvenile plants of beneficiary and non-beneficiary species. We found that facilitation is enhanced by species that provide a more homogeneous microenvironment rather than an intense reduction of microenvironmental stress under their canopy. In addition, the juveniles of beneficiary species invest more in root development, accumulate Ca and S in their shoot tissues, and show a higher water content than non-beneficiary species. Our results suggest that the homogeneity of microenvironments plays a crucial role in facilitative interactions, and the juveniles of beneficiary species show a less conservative strategy, investing more in resource acquisition than juveniles of non-beneficiary species.

S.221.3 Mapping gypsophile vegetation in Armenia – solution to former misconceptions?

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Armenia, with an area of less than 30.000 km², is an important biodiversity hotspot with about 3800 plant species and a very diversity of landscapes and vegetation, that ranges from subalpine communities to forests, steppes, semideserts and even a small sand desert. The semidesert belt is very diverse in soil types, including gypsum. However, botanists of the former century have often misclassified plant communities as gypsophile, while in fact dealing with marls and clays. Due to these misconceptions, up to date no detailed map and no complete floristic inventory of gypsum rich soils has been published. Additionally, to the lack of precise data, gypsum outcrops and semideserts as a whole, are not highly valued for conservation by local populations and are highly threatened by destruction and fragmentation, while harboring a good amount of the country's biodiversity. To address this problem, we mapped all gypsum outcrops by satellite imaging (SentinelHub). Within extensive fieldwork we collected soil and herbarium data from all gypsum outcrops in the Republic of Armenia. We created a species inventory for all the species occurring on gypsum and analyzed the soil composition and gypsum content in each gypsum area. Finally, we evaluated current threats to these small and unique habitats and the possibility of their conservation. As a result, we present an updated and corrected critical checklist of plants occurring on gypsum outcrops in the Republic of Armenia and a detailed map of gypsum habitats in Armenia. Finally, we present recent data on the conservation of gypsum habitats and discuss the actual threats to these unique ecosystems.

S.221.4 Secondary metabolic pathways and gypsum endemism

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Gypsum soils are rich in calcium and sulfate, creating a challenge for plant life. Despite these stressful conditions, many gypsophiles (gypsum-loving plants) accumulate high levels of these mineral nutrients in their tissues, particularly in leaves, without suffering toxicity effects. Based on these patterns, we seek to investigate mechanisms, such as assimilation or sequestration, supporting excess mineral nutrient accumulation in plants growing on gypsum. Two secondary metabolites of particular interest are glucosinolates and sulfated flavonoids. These sulfur-rich metabolites are naturally present in taxa common on gypsum (glucosinolates in members of the Brassicaceae and sulfated flavonoids in members of a variety of families but particularly the Asteraceae). Our data suggest that gypsophiles may have higher glucosinolate levels than non-endemics. Similarly, we have data that suggests that plants growing on gypsum produce sulfated flavonoids in flowers and leaves and that the likelihood of their expression may be related to evolutionary history, as some taxonomic groups were more likely to produce these compounds than others. We hypothesize that glucosinolates and sulfated flavonoids may serve as sulfur sinks in gypsophiles and that glucosinolates may also support water uptake in drying soils in these taxa. Future work will investigate how widespread these patterns are in gypsophiles, as well as how plastic these responses are. Identifying the mechanisms supporting plant life on gypsum may help us understand fundamental biological processes such as speciation, adaptation, and how biotic and abiotic factors influence community assembly.

S.221.5 Extreme variability in gypsum lichen species: the case of Squamarina

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The genus *Squamarina* is a predominant component in Biological Soil Crusts (BSC) from gypsum soils in the Iberian Peninsula. It is considered to be well known with only two species cited in this habitat, i.e., S. cartilaginea and S. lentigera. However, the high morphological variability led us to more thoroughly assess the species of *Squamarina* from gypsum soils. Our molecular data revealed the existence of at least five lichen taxa in gypsum soils instead of two. These five taxa were not evenly distributed in gypsum soils in Spain. Subsequent analyses were driven to understand these distributional differences. First, we discovered that these taxa had seven different photobiont haplotypes. Differences in photobiont partner were related with location and lichen species. Functional traits related with water retention were also different in the different locations but not related with the lichen species. Also, traits related with photosynthetic activity were related with location and photobiont haplotypes. These results point out that functional variability in this group is more related to environmental variation and photobiont composition than to lichen species identity.

S.221.6 Bridging Gaps between Mining and Restoration: Insights from Gypsum Quarry Succession

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This research delves into reconciling gypsum mining with sustainable development in a scenario of Global Change. Our research was conducted in a quarry situated within the Protected Area of the Gypsum Karst Natural Park in Sorbas (Almería, Spain). The exploitation of this quarry ceased eight years prior to the initiation of this study, which spans from 2009 to 2024. Ten permanent plots were established there, with dimensions of 20 × 50 m. The presence of perennial vascular plants was documented in these plots over the course of 15 years. Our main objective revolves around monitoring the temporal trajectory of spontaneous succession within the quarry, juxtaposing it with undisturbed shrubland as the reference ecosystem. To this end, we also sampled five similar plots within the shrubland. We hypothesized that a largely predictable convergent successional development will occur, which can serve as a model for habitat restoration. Based on the floristic composition of the plots and the functional types present (based on the degree of gypsophily), we investigated the convergence/divergence of species composition and functional types, characterized by the degree of gypsophily. Non-metric multidimensional scaling (nMDS) analysis was used considering 15 succession points (years) relative to the five corresponding reference points in undisturbed shrublands. Reductions in dispersion over time indicate convergence, while increases signify divergence. Our findings consistently demonstrate a convergent trajectory towards the reference ecosystem, albeit with varying rates of convergence. These results underscore the importance of autogenic succession as a geoecological model to consider for habitat restoration. This research advances our understanding of primary succession dynamics in gypsum quarries after mining cessation, shedding light on the intricate relationship between natural environments and disturbed areas. Importantly, it highlights the fundamental role of scientific knowledge transfer in facilitating effective ecological restoration within gypsum habitats, designated as priority habitats by the EU.

S.222 LET PEOPLE COME TO BOTANY II: IMPROVING FLORA KNOWLEDGE THROUGH INATURALIST

S.222.1 Flora of Russia on iNaturalist: moving forward

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Since 2008, iNaturalist has been crowdsourcing biodiversity observations made by citizen scientists and professional biologists. Thousands of publications have already taken into account these data for use in research, conservation and policy. There are three key themes that iNaturalist embraces: social interaction; shareability of data, tools and code; and scalability of the platform and community. The "Flora of Russia" project on iNaturalist (https://www.inaturalist.org/projects/flora-of-russia) brought together professional scientists and amateur naturalists from all over the country since 9 Jan 2019. The main goal of the project is to maintain crowdsourced data for the national atlas of vascular plants in the absence of an appropriate national platform. By 2023, over 25K+ people were involved in the data collection. Within 5 years, the participants accumulated 3M+ photo observations of 8K+ species of the Russian vascular plants. This constitutes the largest dataset of open spatial data on the country's biodiversity and a leading source of data on the current state of the national flora. The key index of the project is the number of uploaded observations. The project reached 2.5M observations of "Research Grade" quality on 7 May 2023, whereas ca. 0.5M unverified observations make the project's backlog. The Moscow Oblast and the City of Moscow take the lead by the number of observations and observers, whereas Dagestan harbours the highest number of observed species. The Moscow University team of professional botanists leads the expert efforts within the project. About 90% of all project data, are available under free licences (CC0, CC-BY, CC-BY-NC) and can be freely used in scientific, educational and environmental activities. Due to the project, Russia is currently one of top-five countries of the platform by the number of observations and the leading country on iNaturalist by share of records available in GBIF.

S.222.2 The age of colour in alpha taxonomy: new frontiers for online species discovery

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Platforms such as iNaturalist provide botanists with unprecedented, accurate and universal access to information on spatially structured and taxonomically significant colour variation in angiosperms, which was historically inaccessible through herbarium specimens or, more recently, highly dispersed through slide collections and multiple web resources. This wealth of newly and readily available data will accelerate the pace of species description and taxonomic revision of multiple taxa in which flower colour is key to diagnosis. As a proof of concept, I here illustrate the potential of iNaturalist, and other online platforms, to uncover unaccounted or long-neglected taxonomic diversity in three genera of the Iberian Flora. On a more practical side, I present a quick guide for online species discovery using photographic data and introduce a citizen science initiative to map colour variation in iris plants on iNaturalist, championed by the Botanical Society of Portugal.

S.222.3 Citizen science, higher education and iNaturalist: a multifaceted approach for biodiversity conservation in Latinamerican cities.

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University education in Ecuador is conceptualized as a dynamic interplay among academia, research, and societal engagement. Furthermore, academia serves society by providing the information necessary to address problems. Additionally, the dissemination of scientific knowledge to the broader community constitutes an integral facet of university endeavors. Within this framework, to ensure the conservation of biodiversity and its ecological services within cities, multidisciplinary approaches are required to engage the community. This study describes the mechanisms through which these channels of reciprocal enrichment have been cultivated. As an integral component of their academic curriculum, students enrolled in the Biodiversity Engineering program at the Universidad Tecnológica Indoamérica in Quito, Ecuador, actively participated in projects that fostered connections with society. This involvement entailed the practical application of data collection tools, such as surveys, and the utilization of platforms like iNaturalist during various community events. Through these initiatives, a collective repository documenting the city's flora was established, showcasing contributions from both students and citizens. This collaborative effort facilitated the identification of novel findings, including new plant records and endangered species. Furthermore, the outcomes of these projects were disseminated through the creation of posters and other communication materials, as well as environmental education talks conducted in schools and among residents in the neighborhoods where the activities were carried out. In addition to these community interactions, students assumed the role of for articles presented at conferences and subsequently published in scientific journals. This multifaceted approach underscores the university's commitment to knowledge dissemination, practical application, and community engagement.

S.222.4 Using iNaturalist in Plant Research: Strengths and Challenges

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iNaturalist (https://www.inaturalist.org/) self-defined as an "online social network of people sharing biodiversity information to help each other learn about nature", and it is likely one of the largest citizen science web portals of the world as it includes nearly 165 million observations of over 430,000 species produced by a community of almost 2.9 million users by December 2023 (for plants, almost 67 million observations of over 154,000 species by nearly 2 million users). This platform presents some strengths and potentialities such as its usability and low technical requirements, immediacy, open-access, the possibility of interacting with other users, artificial intelligence-aided identification, versatility and the automatic incorporation of the validated records to GBIF. However, there are some features that scientists need to take into account when using data from this science portal in research, making sure that the quality of observations does not limit or hinder its usefulness in plant research. While these are identified, we are providing some suggestions to overcome them and, by doing so, increasing the use and adding value of iNaturalist in plant research.

S.222.5 Contribution of citizen science through iNaturalist to the knowledge of the Mexican Flora

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iNaturalist is an online visual network allowing the interaction between citizens attracted by the natural world, and experts on different taxonomic groups, who would help them to identify the species documented by pictures linked to spatiotemporal data. The platform pursues to promote a connection between people and biodiversity, and to support biodiversity and conservation science. Mexico was one of the first countries to ascribe to this new way of socializing and collecting biodiversity data, under the lead of the Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO), which keeps promoting it. At first, there was some reluctancy from the Mexican scientific community on biodiversity studies, but progressively more researchers have gotten involved in the uploading and identification of observations; and it is becoming more common to find scientific papers benefited by iNaturalist data. The observations have helped to better document the distribution of some species with the addition of unknown localities, and their morphological variation with and increasing number of photographs, long forgotten species have been rediscovered, or even new ones have been named based on clues given by iNaturalist observations. Here we present a revision of the contributions of iNaturalist to the knowledge of the diversity of Lamiaceae family in western Mexico as a case study. A numerical analysis was performed on the comparison of richness patterns revealed in the study area based on two databases; the first downloaded from iNaturalist, and the other assembled from herbarium specimens of more than 20 herbaria. Although the patterns extracted from iNaturalist data are clearly biased in comparison to those obtained from herbarium specimens, the platform helped in adding additional localities and to detect previously unrecorded plants, or even new arrivals in terms of new naturalized species. Recommendations for the use and improvement of iNaturalist impact are also compiled.

S.223 DIVERSIFICATION IN LARGE DOMINANT PLANT LINEAGES: INTEGRATION OF PHYLOGENY, ECOLOGY, PHYSIOLOGY, AND BIOGEOGRAPHY

S.223.1 Evolution in plant function and ecological niches in the oak adaptive radiation inform community assembly at continental scale

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Oaks (genus *Quercus* L) are an important adaptive radiation that includes ecological dominants on five continents with extraordinary diversity and abundance. They are major contributors to ecosystem function, including climate regulation and support of biodiversity in Northern Hemisphere temperate forest systems. Biogeographic history, including past environmental change, have influenced the diversification process and evolution of functional traits. Trait evolution, in turn, has influenced the habitats that the species across the lineage can occupy. Trait evolution in the oaks shows evidence for phylogenetic inertia and adaptation in response to novel environments. We show examples of freezing tolerance and vulnerability to drought as well as chemical and structural foliar traits of leaves as derived from spectral signatures. We test how traits evolved in response to new environmental challenges and whether evolutionary shifts in traits allowed species to colonize new habitats. We show that the coordinated process of diversification in traits and ecological niches explains community assembly processes at continental scale in the Americas. Insights from addressing these questions have far reaching implications for understanding the nature of trait and niche evolution in other lineages across the tree of life.

S.223.2 Ecophysiological adaptations and realized height growth shape Eucalyptus distributions along an Australian rainfall gradient

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Tradeoffs between the energetic benefits and costs of traits can shape the distributions of species and traits along environmental gradients. Here we test predictions based on tradeoffs involving photosynthesis and water loss using survival, growth, and 50 photosynthetic, hydraulic, and allocational traits of ten *Eucalyptus* species grown in four common gardens along an 8-fold gradient in relative moisture supply – as measured by precipitation/pan evaporation (P/E_p) – from mallee to tall wet sclerophyll forest in Victoria, Australia. Phylogenetically structured tests show that most trait-environment relationships accord qualitatively with theory. Most traits appear adaptive across species within gardens (indicating fixed genetic differences) and within species across gardens (indicating plasticity). However, species from moister climates have lower stomatal conductance than others grown under the same conditions. Responses in stomatal conductance and five related traits appear to reflect greater mesophyll photosynthetic sensitivity of mesic species to lower leaf water potential. Our data support adaptive crossover, with realized height growth of most species exceeding that of others in climates they dominate. Our findings show that pervasive physiological, hydraulic, and allocational adaptations shape the distributions of dominant *Eucalyptus* species along a subcontinental climatic moisture gradient, driven by rapid divergence in species P/E_p and associated adaptations over the past 4 million years. Across the entire genus, the rate of net species diversification has increased substantially over this period, especially in areas of low climatic moisture availability, which are often associated with smaller species ranges.

S.223.3 Disentangling the drivers of diversity at multiple taxonomic scales in the rapid radiation of the South African Protea

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The genus *Protea* of South Africa is an iconic plant radiation with remarkable variation in growth form, leaf functional traits, and pollination syndromes. Their center of diversity and center of origin is the Cape Floristic Region of southwestern South Africa, a biodiversity hotspot, and a region characterized by multiple climatic gradients, substantial edaphic heterogeneity, fire-dominated ecosystems, and multiple mountain ranges resulting in both topographic variation and geographic isolation. Here, we synthesize our research on the drivers of diversity in *Protea* across taxonomic scales, asking the extent to which the radiation has been driven by adaptive versus nonadaptive mechanisms. We investigate these questions 1) across the genus in a phylogenetic context, 2) within a restricted clade, 3) across populations within a single species, and 4) between hybridizing species at a single site. We use a variety of approaches, including phylogenomics and Bayesian phylogenetic frameworks, common garden studies assessing trait differentiation and gene expression, in situ measurements of plants growing across climatic gradients, and population genomics tools to assess the roles of geographic and environmental differences. Our findings present a paradox, where we detect trait-environment relationships at multiple scales (suggesting that adaptive processes underlie the radiation) while our population genomic evidence points to a potential role for geographic isolation (suggesting that nonadaptive processes underlie the radiation). Moreover, within a given site, many *Protea* species often co-occur, and co-occurring species often represent wildly disparate morphologies. We attempt to reconcile the roles for these difference mechanisms and point to future work to disentangle the effects of adaptive processes (driven by both biotic and abiotic interactions) as well as nonadaptive mechanisms.

S.223.4 Global drivers of diversification and assembly are spatially structured in the megadiverse Carex (Cyperaceae)

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The processes of speciation and assembly are inextricably linked. Diversification drivers vary among clades and are often determined by the geographic context where speciation is occurring. We should therefore expect patterns of assembly to be influenced by spatially variable speciation dynamics. We use the globally distributed, mega-diverse genus *Carex* (Cyperaceae) to test the hypothesis that both drivers of diversification and assembly are spatially varied, such that observed patterns of phylogenetic diversity and endemism are determined by context-specific physiological traits associated with individual lineages and the ecological conditions of different geographic areas. We used 4.35 million museum records, a global *Carex* phylogeny, historical biogeographical estimations, and rate analyses to test for spatially structured correlations to diversification and patterns of assembly using structural equation modeling. We find that all previously hypothesized drivers of diversification in the genus are associated with elevated speciation rates. However, these drivers have interacted in different combinations in different geographical areas, with no two regions exhibiting the same combination of drivers. This has resulted in spatially varied patterns of phylogenetic diversity and endemism. Our results demonstrate that integrating analyses of diversification and assembly with spatial scaling improves the resolution at which we can understand the origins and distribution of our extant biodiversity.

S.223.5 Diversity and divergence: the ecology and evolution of defenses in the tropical tree genus Inga

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Because plants and their insect herbivores together account for more than half of the macroscopic diversity on land, their interactions play an extremely important role. From an evolutionary perspective, they are thought to be locked in a coevolutionary arms race, in which plants evolve novel defense traits to which herbivores evolve counter adaptations. We discuss evidence for the role of plant-herbivore interactions in shaping the ecology and evolution of *Inga* (Fabacea) a specious tropical tree genus. With a particular focus on the evolution of plant secondary metabolism and ecological significance. To do so we characterized the chemical profile of one-third of species in the genus *Inga* (*ca.* 100) using ultraperformance liquid chromatography-mass spectrometry-based metabolomics and applied phylogenetic comparative methods to understand the mode of chemical evolution. Each *Inga* species contains structurally unrelated compounds and high levels of phytochemical diversity; closely related species have divergent chemical profiles, with individual compounds, compound classes, and chemical profiles showing little-to-no phylogenetic signal; at the evolutionary time scale, a species' chemical profile shows a signature of divergent adaptation. At the ecological time scale, sympatric species were the most divergent, implying it is also advantageous to maintain a unique chemical profile from community members; finally, we integrate these patterns with a model for how chemical diversity evolves. We find that this chemical divergence plays an important role in shaping the community assembly of tropical trees and shaping the host choice of insect herbivores.

S.224 ADVANCES IN FERN ECOLOGY: RESPONSES TO ENVIRONMENTAL AND BIOTIC STRESS FACTORS

S.224.1 Advances in Fern Ecology: a synthesis and future research directions

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In the last decade, studies on fern ecology have overcome many of the historical misjudgments. Some of these preconceptions included the allegedly old evolutionary age of extant ferns, their supposedly low growth rates, low nutrient concentrations, low ability to compete with seed plants, to defend themselves against herbivores, and to withstand environmental catastrophes and anthropogenic disturbances. Furthermore, a high vulnerability of the gametophytic life stage, a low diversity of biochemical compounds, and a reputedly low usefulness for medical or industrial purposes were assumed. We present an overview of the advances in Fern Ecology based on exemplary case studies, which have demonstrated that ferns are much more functionally, ecologically, physiologically, and biochemically diverse than previously thought. In addition, we discuss how the results of current research have changed our perception of the ecological role of ferns in different ecosystems and show how ferns effectively differ from seed plants. Research gaps and open questions are outlined, and future research directions are proposed such as holistic approaches integrating all life stages of ferns, comparative studies between ferns and angiosperms, and conservation approaches to deal with anthropogenic disturbances and climate change. To face these challenges, the future study of fern ecology still requires more inter- and multidisciplinary approaches and intensive collaboration efforts.

S.224.2 Water use efficiency explains differences in global diversity patterns between ferns and angiosperms

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The colonization of land by plants strongly depended on their ability optimize the use of water. Vascular plants have successfully colonized a broad range of habitats, but their diversity is lower under physiologically stressful conditions. Ferns, the second most diverse extant land plant group, exhibits disparate global patterns of species richness when compared to angiosperms. This contrast becomes more evident under water-limited environments, where the diversity of ferns sharply declines. To understand this disparity, we combined greenhouse experiments of water use efficiency (WUE) with studies of global macroecological distribution patterns. In the greenhouse, we compared WUE, quantified as the biomass produced per unit of water usage, of 12 fern and 12 angiosperm species, encompassing both terrestrial and epiphytic ones. We found that among terrestrial species, ferns exhibit lower WUE and consequently higher water loss compared to angiosperms. At the macroecological scale, this is reflected by an increase in the proportion of ferns relative to angiosperms as water availability increases. Conversely, fern and angiosperm epiphytes had a comparable WUE in the greenhouse, which at the macroecological scale is reflected by a constant proportion of fern richness in relation to water availability. These findings reveal the key role of water in shaping the competitive dynamics between ferns and angiosperms, and their diversity patterns. Moreover, it suggests that terrestrial ferns serve as potential early indicators of climate change.

S.224.3 Thermal tolerance and competition of two tropical relict ferns

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Studying the thermal niche of organisms is crucial in the current context of climate change. However, it is a complex task as physiological requirements, species distributions and the modulating factors such as competition need to be analysed simultaneously. We present a study that combines germination experiments along an environmental gradient both with and without interspecific competition, with thermal niche analyses based on estimated climatic data from global distributions. We evaluated the thermal niches by setting up experiments on germination and growth of two fern species: *Culcita macrocarpa* and *Woodwardia radicans*. Both species, which are potential competitors, are tropical relics that share distribution, habitat and exhibit synchronous spore dispersal. Spore germination was compared at eight temperatures ranging from 5 to 35 ºC and gametophyte growth at 10, 20 and 30ºC. Our findings demonstrated that spores of *W. radicans* germinated faster and to a higher percentage, and their gametophytes grew faster than those of *C. macrocarpa*, especially at moderate to high temperatures. Additionally, interspecific competition reduced germination only in *C. macrocarpa*. Besides, our results reveal an exceptionally high correlation between climatic parameters and germination parameters in both species. In the case of *C. macrocarpa*, this correlation increased when examining germination under competition. These findings show the advantages of ferns for culture experiments, and their potential usefulness for tackling many research questions, such as community-level experiments on coexistence, dispersal, effects of community structure on ecosystem functioning or ex situ conservation. These results also hold particular relevance for studying the impacts of climate change even in early life stages, shedding light on how competitive interactions among species can shape their thermal responses and ultimately influence their adaptation.

S.224.4 Nutrient ecology of lithophytic ferns: responses to different substrates

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Many plants grow only on specific soil types. Ferns are no exception. In the family Pteridaceae, many fern species are limited to alkaline limestone or acidic volcanic soils. Although the reasons for soil specialization of plants have received some attention, our knowledge about the consequences of growing on alkaline or acidic substrates is poor. Consequently, we studied the distribution of 19 fern species on 37 sites and the mineral nutrient composition of the shallow soils as well as calcicole (limestone-loving) and calcifuge (limestone-avoiding) fern species in central Mexico, supposing that the former will have higher Ca and lower Al and P concentrations than the latter. All fern species, except the soil-indifferent *Myriopteris aurea,* were restricted to one soil type. As expected, calcicole fern species had higher nutrient contents except for P and Mn, but surprisingly they also contained higher amounts of Al and Fe. This was even more surprising because limestone soils had only higher pH and Ca concentrations, but lower concentrations of exchangeable Fe and P. These results indicate that calcicole fern species possess limited or no mechanism to avoid the uptake of Al but are more efficient in absorbing Fe and P, even when those concentrations are lower than on acidic soils. On the other hand, calcifuge fern species can limit the uptake of Al but are not as efficient as calcicole fern species in absorbing Na, K, Mg, S, and N even if these nutrient elements are available at similar concentrations as on limestone soils. However, there is a considerable variation in the nutrient concentrations of each fern species, which implies that they also differ in their nutrient metabolism independently from the exchangeable nutrient concentrations of the soils.

S.224.5 Haplopteris yakushimensis, a new model for fern independent gametophyte

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In the 1960s, two papers published in the journal *Science* fundamentally altered our understanding of fern gametophytes, giving the concept of 'independent gametophyte' a prominent place in the field of pteridology. Ferns and lycophytes (pteridophytes) stand out among land plants by having two independent phases in their life cycles: gametophytes and sporophytes. Independent gametophytes refer to those long-lived gametophytic populations that extend beyond the geographic distribution of their sporophyte counterparts. Unlike typical cordiform (heart-shaped) gametophytes, independent gametophytes are non-cordiform and some of them can reproduce asexually through gemmae. In this study, we propose to investigate the origin of the independent gametophyte in a rare species *Haplopteris yakushimensis* utilizing an integrated approach including molecular biology, reproductive biology, and ecology. Genetic data reveal that the species comprises two diverged lineages (hereafter α and β) but their sporophytes are morphologically indistinguishable. The distribution of these two lineages is asymmetric, with the α lineage being endemic to Japan, while the β lineage is found in Japan, Taiwan, and Vietnam but persisting solely as independent gametophytes in Japan. This system, featuring two sister lineages with distinct reproductive behaviors (i.e., with and without independent gametophytes), offers a unique opportunity to explore the origins of independent gametophytes. Our preliminary data suggest a complex origin of *Haplopteris yakushimensis*, involving multiple hybridization and polyploidization events. Additionally, both environmental and genetic factors may play roles in shaping the current distribution of the independent gametophytes. Our study is poised to be the most comprehensive in the field and is expected to significantly advance our understanding of gametophyte ecology in general. Furthermore, it will also contribute to the conservation of *Haplopteris yakushimensis*.

S.224.6 Insect herbivory and defense mechanisms in ferns

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For ferns, an abundant component of tropical understories, knowledge about their insect interactions and defense mechanisms is still very limited. Consequently, the ecological and evolutionary drivers of herbivory, as well as the ecological role of ferns in these interactions are overlooked. Here, we investigated fern–insect interactions in three different ecosystems asking the following questions: 1. How do ferns structure their defense mechanism (syndromes)? 2. Does the leaf damage of ferns differ from angiosperms in mangroves? 3. Are there herbivore effects on *Pteridium* after fire events? Our sample included 34 species of ferns from the Atlantic Forest, *Acrostichum aureum* L. (and two angiosperm species) in the mangroves, and *Pteridium* in burnt ironstone campo rupestre. We measured some leaf traits for our first (SLA, water content, trichome density, nitrogen, phosphorus, alkaloids, phenols, saponins, tannins and triterpenoids) and second question (phenols). Leaf damages were estimated by relative leaf area loss per plant and species. All traits were correlated with each other and compared with leaf damages. We identified three different defense syndromes: (I) high nutritional quality combined with a variable trichome density (14 species), (II) low nutritional quality, but high phenol concentrations, and often high trichome density (4), and (III) intermediate nutritional quality combined with a low trichome density or no trichomes (16). Leaf damages ranged between 0 and 32.3% but did not differ among defense syndromes. *Acrostichum aureum* had lower phenol concentrations than the angiosperms mangrove species but was damaged than *Rhizophora mangle*. Postfire resprouts of *Pteridium* were highly damaged by herbivores (almost 75%). We conclude that ferns combine a variety of defensive traits against insects, with a similar resistance against insects, that ferns can exhibit similar damages than angiosperms in mangroves; and that *Pteridium* may constitute a crucial resource for herbivores after fire events.

S.225 FLORAL NECTAR: POLLINATION SYNDROMES, PRODUCTION ATTRIBUTES, REGULATION EVOLUTION. SESSION 1

S.225.1 Floral nectar: cost, regulation and partner manipulation

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Floral nectar is central to most relationships between plants and animal pollinators, and has been the subject of much investigation for a long time. However, much about nectar remains poorly known and understood. We know, for example, costs of floral nectar production to a plant are significant, however, relevant evidence is scant and difficult to interpret. Also unknown is the extent to which plant costs and gains associated with nectar production can be expressed in a single currency such as energy. There is also growing evidence that plants can both secrete and absorb nectar, possibly enabling them to regulate nectar attributes in their flowers and thus manipulate pollinator behaviour to their advantage. In some circumstances, floral nectar may also attract or repulse potential pollinators by virtue of its attributes, but such circumstances are likely rare. In this talk, we present our new findings on cost, regulation and partner manipulation based on the evidence from multiple plant species pollinated by various animal pollinators in Australia and China. By doing a series of floral nectar removal, nectar reabsorption and artificial nectar addition experiments, we provide evidence of simultaneous nectar secretion/ absorption and consequent regulation for sugar volume, sugar concentrations and sugar type. We also show that some floral nectar attributes between neighbouring flowers within an individual plant are correlated in both bagged and open pollination treatments indicating potential partner manipulation.

S.225.2 Color & chemistry: how flowers signal reward quality to pollinators

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The vast majority of flowering plants require animal pollinators for sexual reproduction, and in turn, many animal pollinators rely on floral rewards. Floral colour and scent are the two main signals that plants employ to attract potential pollinators. Our central hypothesis is that flower colour and scent have coevolved with the sensory systems and preferences of pollinators and that those signals convey reliable ('honest') information about a flower's reward. To answer this question, we are trying to determine how flower signals and rewards match pollinator visual systems, ecology, and resource requirements among many independent transitions between pollinators with widely different visual systems, olfactory preferences and/or nutritional requirements. We are collecting and integrating data from a) (micro-) spectroscopy, anatomy, and state-of-the-art optical models to quantitatively understand how floral structure and pigmentation generate visual signals, b) volatile metabolomics to capture and analyse floral scents and c) semi-targeted metabolite profiling to study the nutritional properties of nectar (and pollen). This comparative approach enables identifying how the colour and scent of flowers and the nutritional properties of nectar (and pollen) have co-evolved at a broad taxonomic scale. How plant-pollinator interactions have evolved and shaped biodiversity is a fundamental question in biology and has direct implications for agriculture and species conservation.

S.225.3 Nitrogen at night: do volatile aldoximes serve as index signals of nectar amino acids to hawkmoth pollinators?

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Hawkmoths are important pollinators worldwide, whose powerful dispersal flights can promote gene flow between geographically distant plant populations. That same flight capacity generates high energetic demands, and hawkmoths are known to maximize caloric intake in the face of thermal, osmoregulatory and biophysical constraints. Thus, hawkmoth-pollinated flowers tend to secrete copious quantities of relatively dilute (15-30%) sugar solutions at anthesis, just as they emit strong fragrances known to attract hawkmoths from a distance. One surprising feature of such fragrances is the presence of nitrogenous aldoximes, volatile compounds derived from essential amino acids (LEU, ILE, VAL, and PHE). Aldoximes are uncommon fragrance components in day-blooming plants and are better known for their roles in the indirect defenses of wounded poplar foliage, or as precursors to direct defenses such as mustard oils and cyanogenic glycosides. Nevertheless, they have evolved in dozens of angiosperm families with night-blooming flowers, from Darwin's star orchid to jasmines and gingers. Given that aldoximes are derived from amino acid precursors, we explored their potential to function as volatile "index signals" – unfakeable indicators – of the presence of amino acids in nectar, using the night-blooming flowers of *Oenothera flava* and *Datura discolor* as model systems. First, we tested whether volatile aldoximes are correlated with nectar amino acids, either naturally or under soil fertilizer manipulation, using GC-MS and HPLC, respectively. Next, we designed behavioral assays to test whether flower-naïve hawkmoths (*Hyles lineata*) are attracted to aldoximes derived from LEU and ILE in a nectar-feeding context. Finally, we used behavioral assays to test whether hawkmoths prefer nectars with amino acids, and whether such fortified nectars provide additional fitness benefits to the moths. Our findings suggest an important role for N metabolism as a non-caloric component of floral advertisement and reward in "moonflowers" pollinated by hawkmoths.

S.225.4 Honesty of floral signaling is dependent on neighborhood kinship

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Although pollinators have innate preferences for specific floral signals such as petal color, they can quickly adapt their preferences by associative learning, based on the quality and quantity of rewards (e.g., nectar) provided to them. In this sense, we might expect the local intraspecific neighborhood to have important consequences for an individual plant's optimal strategy of both display and reward. Cohen and Shmida (1993) modelled the association between floral advertisement and reward, with specific attention to flower density. Their model predicts that allocation to signaling traits should be increased when flower density is low, thereby facilitating visibility, whereas allocation to reward should be favored under conditions of high flower density or low visitation rate, thereby capitalizing on favorable pollinator choice. However, to our knowledge, we still lack formal theoretical foundations for predicting the potential kinship effects on the relationship between floral signaling and reward. In our study, we experimentally examined how neighboring kinship affects the relationship between floral signaling and reward. We found that the genetic relatedness of neighbors significantly altered the relationship between floral color and reward quantity. Specifically, plants growing with non-kin exhibited a positive relationship between petal color and nectar production. However, this relationship became negative when plants had no neighbors or when their neighbors were kin. The observed plastic sensitivity to neighborhood composition in the honesty of floral signals might have important effects on pollinator behavior and visitation, with direct and indirect effects on plant reproductive success and mating patterns.

S.225.5 Anatomical, ecological, and evolutionary trends of nectary and nectar traits in Acanthaceae

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Pollinators are linked with plant reproduction and with evolutionary diversification of some clades of angiosperms. Modifications in floral form and function can suggest the best match with different pollinator functional groups implying a positive interaction in reproductive terms. Acanthaceae includes species with diverse floral sizes, shapes and colours that are visited by different pollinators. Previous studies analyzing different floral shapes (floral syndromes) and nectar in Acanthaceae indicated stronger relationships with floral shapes and nectar sugar composition or concentration rather than with phylogenetic trends. Nevertheless, some anatomical nectary particularities may restrict the expression of nectar traits in some groups (clades or genera) although the occurrence of floral form diversification within them. Moreover, nectar secretion patterns may be related with the preferences and needs of different pollinator groups. Thus, the variations in nectary and nectar traits in Acanthaceae may be shaped by a combination of the preferences of the main plant-pollinator interactions (functional or ecological) and/or by the basic anatomy and developmental constraints (phylogenetical) of the flower present in some clades or genus within this family. In consequence, complex trends between nectar and nectary traits could be analyzed using the hypothesis of pollination syndromes but also considering the most accepted hypothetical phylogeny of the family. If nectar and nectary traits are linked with pollinator preferences, associations between floral traits and different groups of pollinators will be stronger than the evolutionary trends within different clades. Species from major clades of Acanthaceae are used to test this hypothesis and predictions. Original data for anatomical features and nectar traits > 20 species distributed among different phylogenetic clades were analyzed. Moreover, a data set from the literature of nectar traits for >100 species were obtained to present a better picture for the family linking developmental, ecological, and evolutionary trends.

S.225.6 Nectar sugar concentration, foraging currencies and floral preferences in bumblebees

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One way in which nectar sugar concentration can contribute to partitioning of pollinator floral preferences is through between-species differences in how viscosity influences rates of nectar transport. However, preferred nectar sugar concentrations may also vary between species depending on the strategy, or 'currency' through which pollinators are optimising their foraging. Here I discuss our recent work in bumblebees investigating both of these factors. Firstly, we investigated how nectar viscosity influences multiple aspects of nectar transport. Secondly, to explore the energetics of foraging, we used a lab-based assay using a biomechanical foraging challenge to test if bumblebees can make a trade-off between nectar valence and the time/energy expended obtaining it. Bee foraging behaviour in this paradigm was in agreement with maximisation of the currency of net rate, but not in agreement with maximisation of the currency of energy efficiency. Given this currency differs from reported results in honeybees, we consider the implications for expected floral preferences between these two important generalist pollinators.

S.226 ECOLOGICAL DRIVERS OF PALM SPECIATION

S.226.1 Can plant-fungal symbioses underpin plant diversity?

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Our understanding of how species originate (speciation) has changed considerably since Darwin's seminal work. One aspect, however, that has been ignored is the role that microbes can play in driving speciation. Here, we propose a new mechanism for the origin of species, whereby coevolutionary divergence in plant-mycorrhizal associations increases local adaptation and leads to the completion of speciation, using one of the most compelling examples of speciation in the face of gene flow as our model system: The *Howea* palms of Lord Howe Island. While it is well known that species can diverge due to geographic barriers such as mountain ridges or oceans, populations can also split in the face of gene flow without geographic isolation, for example through specialisation to habitats or resources. In this context, symbiotic associations that plants have with microbes may be particularly powerful in simultaneously facilitating local adaptation and reproductive isolation leading to speciation. We focus on two sister species of palms (*Howea*), endemic to Lord Howe Island, a remote island in the Tasman sea, and their interactions with arbuscular mycorrhizal fungi. *Howea* palms represent the dominant vegetation on the island. The speciation scenario for *Howea* involves adaptation to different soils, volcanic rocks and calcareous deposits, and associated fitness trade-offs. We hypothesise that soil and soil microbes have affected local adaptation of the ancestral palm population, which in turn led to differences in flowering time, and ultimately promoted speciation. Differing levels of mycorrhizal colonisation and gene expression co-regulated in *Howea* and mycorrhizal associations may have led to the emergence of distinct forms of *Howea* populations occupying different soils. We test these key hypotheses using metagenomics and RNA-seq combined with long-term field experiments on Lord Howe Island.

S.226.2 Climatic-based diversification of a hyperdominant species complex in Western Amazonia and endangered species in the Central Andes

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Landscape reconfigurations in South America have influenced the evolution of tropical plants by triggering diversification through niche partitioning, by facilitating dispersal, or separating ancestral populations. However, the genetic characterization of intraspecific entities or species delimitation remains a primary objective to which we can link the ecological factors that influence their evolution. Using several sequencing technologies and marker types, we assess the genetic variation within two palm lineages growing in two biomes, Amazonia and the Andes; and link the resulting genetic entities to putative environmental conditions that may be acting as selection. *Astrocaryum* section *Huicungo* is a complex of 15 morphologically defined species, the majority of which grow in western Amazonia. We found evidence of cytonuclear discordance where the two major lineages recovered in phylogenetic analyses almost matched. A Bayesian species delimitation test rendered three putative species occupying areas of contrasting geological activity. Preliminary ecological niche modeling show that putative species have different niches characterized by elevation and precipitation seasonality. The case of the Andean palm genus *Parajubaea* is similar in that we found genetic groups occupying different elevations, habitats and geological substrates. The delimitation of two morphologically defined, endemic, IUCN endangered species in Bolivia was challenged by our sequencing data that favored the recognition of three intraspecific genetic groups. Genetic groups showed admixture, no evidence of inbreeding, and we use them to propose management units for conservation. Many palm lineages, especially widespread species complexes, still await an assessment of intraspecific variation or a reconsideration of species limits combined with fine scale niche analyses. High throughput sequencing provides an unparalleled opportunity to unmask genetic differences, which is needed to improve our knowledge of ecological speciation in palms at higher resolutions.

S.226.3 Advances in the study of population dynamics of transposable elements and application to date palm genomics

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Quantifying the factors that drive the accumulation of genetic variation in genomes is essential to understand the rules of life and has widespread applications in agronomy and conservation. However, our understanding of the determinants of genetic diversity is still strongly biased towards the study of point mutations such as single nucleotide polymorphisms (SNPs). More must be done to understand the evolutionary dynamics of structural variation. A common type of such variation includes transposable elements (TEs). These elements are among the most variable genomic features across the living world and can have a dramatic effect on their host's fitness. In this presentation, I introduce some of the most recent advances in our understanding of TEs, adopting a population genetics perspective. I show how combining information about TEs and flanking SNPs may help addressing key questions, such as the distribution of TEs fitness effects. I illustrate the interest of such approaches by applying some of these methods to the date palm (*Phoenix dactylifera*), a keystone species of oasis agrosystems particularly adapted to arid environments, in which recently active TEs account for ~3% of the ~850Mb genome, making them promising candidates to study the bases of (mal)adaptation.

S.226.4 Evolutionary dynamics of central African rain forest plants reveal contrasting responses to past climatic fluctuations

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Central African rain forests are mega diverse and harbor the world's second largest expanse of this biome. Yet, how plant species have adapted to past climate change remains understudied. Palms might not be that diverse in this region, but they are nevertheless omnipresent. Here, we infer the evolutionary and demographic dynamics of three co-distributed palm species using comparative phylogeography based on hundreds of nuclear markers. In addition, we contrast our results with four tree species of Annonaceae, an equally important component on rain forests in Africa. For all species we estimated population variation and the temporal origin of this structure using dated phylogenetic trees. Finally, we explicitly tested how different environmental factors such as soil, climate stability and geography have shaped intraspecific genetic variation in each of our species. Levels of genetic variation varied among palms and Annonaceae, all showing some level of structure. Divergence between populations emerged primarily during the Pleistocene but were rarely concordant. Demographic trends ranged from repeated contraction and expansion to continuous growth. Furthermore, patterns in genetic variation were linked to disparate environmental factors, including climate, soil, and habitat stability. Using a strict refugia model to explain past TRF dynamics in central Africa is too simplistic. Instead, individualistic evolutionary responses to Pleistocene climatic fluctuations have shaped patterns in genetic diversity in central African rain forests. Overall, our results suggest that predicting the evolutionary responses of TRF plant diversity under climate change will be challenging. More emphasis is needed on individual species ecology if conservation of this incredible diversity is to be effective.

S.226.5 The geography of speciation in palms and pines

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Linking phylogenies to the geographical distribution of a lineage allows inferring the geographical mode of speciation. Here, we used the geographical distribution of sister species and their estimated divergence times to infer if there is a predominant mode of geographical speciation (allopatry or sympatry) in two diverse groups of plants from tropical (palms) and temperate regions (pines). We selected two approaches previously used to infer the mode of speciation in vertebrates: 1) the proportion of sister species showing zero and complete range overlap, and 2) a modelling framework that calculates the probability that a sister species pair exists in its current geographical state (i.e., allopatry or sympatry). In contrast to birds, for which the first indicator shows that sympatric speciation accounts for only 5% of speciation events, our results hint towards a greater role of sympatric speciation (ca. 30–45%) in palms and pines. We further find that palms and pines can diverge through either allopatry or sympatry and undergo reverse transitions back to the initial state. In contrast, previous studies showed that the best suited model for primates, amphibians, and birds is one in which species diverge exclusively in allopatry and then undergo an irreversible transition to sympatry. Our work therefore suggests that the sympatric speciation of *Howea* palms might not be an exceptional case, but rather, that sympatric speciation might be an important mode of plant speciation in palms and other plant families.

S.227 THE JOURNAL OF PLANT RESEARCH´S SYMPOSIUM ON BIOTIC INTERACTIONS AND BIOLOGICAL INVASION. SESSION 1

S.227.1 Below- and above-ground mutualisms slows invasion success of alien brooms (Fabaceae) in South Africa

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Mutualisms are thought to be important in the invasion dynamics of alien plant species. There is no guarantee that plants will encounter suitable mutualistic partners in a novel environment. When a mutualistic partner is co-introduced, or is a generalist and easily co-opts mutualists, invasion is more probable. If plants are more specialized in their mutualistic requirements or require multiple mutualistic partners, invasion might be curbed. Most studies consider only one type of mutualistic relationship, but many plant species typically interact with multiple types of mutualists. Therefore, in this study we explore the interactions between two non-native legumes (*Genista monspessulana* and *Spartium junceum*) and their associated below-ground (nitrogen-fixing rhizobia) and above-ground (pollinators) mutualists. We conducted pollinator observations, breeding system experiments and collected root nodules for 16S rRNA gene amplification. Both *G. monspessulana* and *S. junceum* are dependent on pollinators for seed production but are successfully pollinated in South Africa. *Genista monspessulana* is pollinated largely by honeybees and carpenter bees whilst the bigger flowers off *S. junceum* are only pollinated by carpenter bees. Differences in rhizobium associations (nodulation) were much more pronounced. We found *G. monspessulana* populations to be nodulated by at least four distinct lineages of-*Bradyrhizobium*, while for *S. junceum* this was much less. The wider distribution of *S. junceum* compared to *G. monspessulana* likely reflects the differences in propagule pressure (*S. junceum* was a popular garden plant). The inability to nodulate, and relative low rates of pollination of *S. junceum*, suggest it currently poses a much lower risk than *G. monspessulana* in becoming a widespread invasive species in South Africa.

S.227.2 The invasion of X. orientale in Europe and its effect on the native X. strumarium reconstructed on herbarium specimens and garden experiments

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Xanthium orientale, an American species complex presently disseminated across the whole world, was first introduced in Europe via natural fiber trading, as the fruits stick easily to fibers owing to their peculiar spiny diaspores. Various lineages can presently be found in the continent, with *X. orientale* subsp. *italicum* being the first to have been observed in the wild around 1820. The presence of *X. orientale* in Europe has been hypothesized as a contributing factor to the contemporary decline of its indigeneous relative, *X. strumarium*. Herbaria play a crucial role in botany as they offer a wealth of untapped knowledge and a portal into plants' historical past. The potential invasion paths of *X. orientale* subsp. *italicum* were traced using geographic profiling techniques and phylogenomic analyses of herbarium specimens. Moreover, the potential effect of allelopathy and competition for the decline of the native *X. strumarium* were studied through garden experiments. Geographic profiling is a technique initially developed in criminology, and then also applied for imputing biological invasion routes. The inferred spreading point for *X. orientale* subsp. *italicum* was the area close to Pavia or Monzambano. Phylogenetic analyses were conducted on nuclear and chloroplast data using network and ML tree approaches, suggesting a possible area of origin in Texas (US), around the town of Greenville. To test allelopathic effect of *X. oriantale* on *X. strumarium*, we compared germination and growth of seedlings under treatment (watered with *X. orientale* exudates) and control conditions. The presence of a significant effect has been observed on the growth of the two species. Concerning the competition experiments, we used dried biomass, number of burs and bur biomass as measure of fitness, showing a significant effect of the interspecific competition on *X. strumarium*.

S.227.3 Brachypodium distachyon complex associated soil microbial differences across the native and invaded ranges

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In the last few decades, *Brachypodium distachyon* has emerged as a model grass to study fundamental topics in plant biology, including seed development, genomics, plant-pathogen interactions, and root architecture. This temperate grass is closely related to important biofuel crops, such as sorghum and switchgrass. Another research advantage of *B. distachyon* is that there are wild, naturally occurring isolates in its broad native circum-Mediterranean range. Not only are the species of the *B. distachyon* complex found across the native range, but they have been introduced to the US, Australia, China, South Africa and South America, and are invasive in some of these areas, notably Southern California. Although there has been a number of recent research articles on the genomic architecture and microbiome of *Brachypodium* species, there remains a dearth of information on associated rhizosphere microorganisms. In order to better understand the microbial associations of the *B. distachyon* complex, we sampled root, rhizosphere, and bulk microbiomes of *B. distachyon* and *hybridum* across their native and invaded ranges, including 4 countries across Mediterranean Europe, as well as *B. hybridum* from California in the United States. Here we describe the variability in the wild microbiome of this important grass. *Brachypodium hybridum* is a rampant invasive grass across coastal California, and a contributor to fire danger and severity. This data may help us to better understand the invasive qualities of this grass, and potentially could lead to mitigation strategies, which may improve fire conditions in California. Further, we hope that generating model grass microbiome data will contribute to a growing global scientific community working on cereal and biofuels crop genetics, and beyond.

S.227.4 When roses go rogue: Expanding ranges of invasive Rosaceae in South Africa

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Invasive fleshy-fruited Rosaceae are becoming problematic in the grasslands and mountains of South Africa, where they can have severe impacts. Here we review current and ongoing research into the expansion of these species. Plant reproductive ecology experiments have been conducted on a number of the most problematic invasive Rosaceae species. These have included determining seed production, soil seed banks, aviary feeding experiments with frugivorous birds, camera trapping and observations to determine frugivores in the field, and faecal seed counts. To determine altitude and climate impacts on their survival and growth, Rosaceae species were translocated and planted in both natural vegetation and in open top chambers at low and high-altitude sites to represent future climate warming scenarios. Results show that these species produce millions of seeds/m² invasion, which are long-lived in the soil. Fruits are eaten and dispersed by animals and different Rosaceae species appear dependent on different guilds of frugivores. Larger bird species, eland and baboons were highlighted as potential long-distance dispersers. Transplant experiments show that these species are able to survive at high altitudes up to 3100 masl and future climates may favour their spread into mountain ecosystems. These invasive Rosaceae species possess several reproductive traits that make them formidable invaders and difficult to manage. More study is needed to understand all factors involved in exacerbating spread in warmer climate scenarios as climate change experiments suggest the entire altitudinal range of the Drakensberg Mountain system is suitable for the establishment of these invasive Rosaceae.

S.227.5 Plant defense against herbivores of native and non-native populations of Datura stramonium

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Datura stramonium has successfully established in many regions worldwide from its native range in America. Historical accounts indicated that it was introduced to Europe (Spain) after the conquest of Mexico. In the introduced range *D. stramonium* lacks the biotic interactions maintained in its native range opening the opportunity to further evolution. Here, we present field and experimental evidence on changes in plant defense hypothetically promoted by the difference in specialist herbivores between ranges. Results indicate that damage exerted by specialist and generalist herbivores on native and non-native plants differ; specialist herbivores preferred the native plants. There are differences between populations, of both ranges, in resistance to herbivores. The tropane alkaloid scopolamine has a higher concentration on a native population whereas the alkaloid atropine is higher in a non-native population. Analysis of volatile compound emitted by *D. stramonium*, showed that native plants produce a greater number of volatile compounds than non-native plants. Expression of gene *TPS10*, involved in the synthesis of volatile compounds, is higher in artificially damaged plants relative to control plants, and higher in native population and non-native populations. Overall, results suggest quantitative and qualitative change in defense traits between non-native population of *D. stramonium* but most changes are at the population level.

S.227.6 Understanding how to a plague moves: The analysis of the expansion of Cactorum cactorum

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Human activities such as transport, trade and biological control practices have led to the movement of different species, beyond their native distribution regions. Cactorum cactorum is a moth of Argentine origin, which feeds on plants of the genus Opuntia and was introduced for control. After its introduction in the Caribbean, it is considered an invasive species since it has spread to several Islands of the Caribbean, Mexico and the United States. Given the ecological and economic implications that its expansion implies, it is important to know the factors that favor and limit their dispersion. For this purpose, we asked, which environmental factors are correlated with the gene flow and population structure in the native and invaded area? In the invaded area it is observed that trade and hurricanes have promoted gene flow. On the other hand, factors such as seasonality and soil types affect the genetic structure in the native area of C. cactorum. The results show a change in the evolutionary processes affecting native and introduced populations to the extent that the incidence of hurricanes in the Atlantic and the Caribbean promote the expansion and re-entry in Mexico. Given high diversity of Opuntia in Mexico that can constitute potential host plants for C. cactorum, it is relevant the ongoing genetic and ecological monitoring

S.228 TAXONOMY AS OPEN SCIENCE: TOOL SUPPORT TO FACILITATE DATA USE FOR HANDS-ON PRACTITIONERS

S.228.1 Horama ID – making image classification models for species identification accessible to end-users

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Computer vision (CV) has matured as a mobile and user-friendly species identification tool, as demonstrated by apps such as iNaturalist or PlantSnap, which are aimed at the nature-enthusiastic public. However, the CV models of such apps cover taxonomic diversity opportunistically, based on what user-contributed images happened to be available for training the model, as opposed to comprehensive coverage of a taxonomic group. Their scope is primarily the overall appearance of complete, living specimens in their natural environment. If CV is to become the next generation identification tool in taxonomy, field biology, and collection curation, biologists will have to be able to easily train, deploy, and use CV models for anything from dried fruits on a herbarium specimen to pinned insects of their study groups. Specimen collections are increasingly being imaged, and commercial cloud services allow users without expertise in AI research to train models. The main remaining bottleneck is getting species identification models into the hands of end-users. We present Horama ID, a system for the storage and deployment of image classification models for species identification. It consists of a server where contributing taxonomists can upload the model, metadata such as its title and description, who created it, acknowledgements, and a title image, as well as a table of species profiles including profile images and external weblinks, e.g., to eFlora profiles. The Horama app displays the list of models available on the server and allows the user to download them individually and switch between them. The camera page of the app displays live updates of identification estimates. The user can tap suggested names to see species profiles and compare them against the specimen. Horama ID gives taxonomists the opportunity to develop CV models as part of their studies in the confidence that they can become available to end-users.

S.228.2 ParseGBIF: data and an interactive database for visualising and prioritising plant occurrence data

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Global and national initiatives to halt the loss of plant diversity require adequate knowledge of species and their occurrences. Such knowledge can be currently characterised as poor and very uneven (Oliver et al. 2020). For example, in GBIF the plant diversity of the Amazon Forest biodiversity hotspot is documented by an average of 10 to 14^2 occurrence records per 100 km². In contrast, the Mesoamerican biodiversity hotspot in Costa Rica is documented by 10,539 records per 100 km² (GBIF). Despite this, there are few tools to visualize knowledge gaps or to prioritize how they should be filled. We have developed such a tool, Prioritization Resource for Information-driven Species Monitoring (PRISM) for doing so at the regional, national, or subnational level. PRISM aims to support the prioritization of areas for data acquisition based on local priorities. To do so we have, 1) developed a workflow, ParseGBIF (Melo et al. 2023), to assemble a baseline of occurrence records, 2) used the baseline to characterize sample effort and gaps in occurrence data at high resolution, and 3) overlayed these with key biodiversity, conservation and ecosystem services layers to support the prioritization of areas for data acquisition, at the regional, national, or subnational level through an interactive database.

References: Oliver et al. (2021) Global and national trends, gaps, and opportunities in documenting and monitoring species distributions. https://doi.org/10.1371/journal.pbio.3001336. GBIF, biological collections occurrence data, accessed January 16 2023. Hendrigo Alves de Melo et al. (2023). https://doi.org/10.21203/rs.3.rs-3579370/v1

S.228.3 Improving access to biodiversity data: leveraging digital tools and global information standards

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Herbaria represent vast repositories of data that have the potential to contribute to research across biological disciplines. The value of herbaria and the data of the specimens within depends largely on the accessibility and quality of this information. As collections become more widely available through large-scale digitisation initiatives, it is integral to develop tools that can help researchers and curators access, review, assess, and annotate specimen data and related information with ease. Additionally, as specimens are included in nomenclatural and taxonomic events, digitised collections and data repositories must reflect these changes rapidly to ensure the most accurate distribution of information. Here, we trialled the tool Echinopscis, an "extensible notebook for open science on specimens" (Nicolson & Lucas, 2022). Echinopscis has provided researchers and curators with a new and effective way to access specimen determinations within other institutions across the globe and has been used to facilitate note-taking and data tracking. Curators of herbaria are limited by resource availability and level of training, meaning that curation standards vary within herbaria and differ greatly between herbaria. Institutions, researchers, curators, and collectors have different methods of recording data in the field, in the herbarium, and in the digitisation process. Small variations in the presentation of data can have vast impacts on how data is sorted and accessed digitally. In a time marked by worldwide open access information sharing, there is a vast need for more global standards in herbarium curation. Here, we present recommendations for global standards in data recording and identify opportunities for the development of new tools to assist and facilitate the curation process within herbaria.

S.228.4 New advances in the development of echinopscis, an extensible notebook for open science on specimens

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Botany can claim to have led the way in the mobilisation of specimen metadata through digitisation. Botanical research groups also were central in the development of e-taxonomic systems to apply this digital information in networked research activities. With the subsequent growth of the open science movement, many generic research tools and working practices have become available. We highlight tools and platforms which can be adapted for use to realise the vision of e-taxonomy and to enable researchers to easily access and use the wealth of data that is now available online. The "echinopscis" project is an experiment in creating an extensible notebook for open science on specimens, built on the generic note-taking software Obsidian. In contrast to early centralised e-taxonomic systems it operates on a local set of files stored in plain text (Markdown) format, enabling the user to have confidence about long term access to their data. It facilitates access to many of the components of the digital extended specimen, including literature, nomenclature, taxonomy, specimen metadata, images, and descriptive data. These data can be further contextualised through access to information stored in Wikidata, which supplies identifier mappings and can act as a broker between different information systems. The use of open data formats and generic data reconciliation standards should allow wider participation in the project and help to cement open science principles in the process of botanical taxonomy.

S.228.5 The digital extended specimen network: from manual links to machine-action accelerating network generation

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With advancing digitization of natural science specimens, e.g. preserved in herbaria and paleobotany collections, bio- and geodiversity researchers are increasingly working with digital representations of collection specimens and related digital-born data. Dedicated and enthusiastic, they are embracing and developing digital tools and platforms to infer novel discoveries and support conservation decisions to address the biodiversity crisis. Research that is meeting today's questions and challenges increasingly relies on high-quality, multidimensional datasets that are seamlessly integrated across sources and datatypes. Accordingly, on-site digital infrastructures are currently more and more integrated with online resources and functionality. These developments have led to the concept of the Digital Extended Specimen (DES), which describes how a diversity of Findable, Accessible, Interoperable and Reusable (FAIR) data from disparate sources can be linked and integrated into analysis pipelines. Recognizing that large-scale, fair and equitable technical linking needs to be community-driven and requires social connections, networks of trust, and community acceptance, the International Partners for the DES (IPDES) were formed. Since 2020, the informal group brings together individual scientists, representatives of international, national and regional organizations, and stakeholders from different backgrounds. It provides a forum for exchange and coordination to foster and expand on community-driven successes to connect people, data, tools, and working practices. We present insights from a community workshop in 2023 that explored data linking, and we reflect on the rapid developments over the past months towards linked resources. The workshop revealed several difficulties in extending existing natural history specimens, including lack of automation and lack of pertinent data. One year later, we address the questions: where are we now? Do we have everything we need, or are there gaps? Importantly, do we address the concerns and expectations of both the communities of tool and infrastructure providers and end users?

S.229 UNDERSTANDING FLORAL EVOLUTION

ALONG MULTIPLE DIMENSIONS: EMERGING PATTERNS OF MORPHOLOGICAL, SCENT, AND COLOR VARIATION. SESSION 2

S.229.1 Pollen release dynamics in morphologically distinct buzz-pollinated Melastomataceae flowers

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Flowers that are buzz-pollinated have evolved restricted, poricidal anthers that are most effectively pollinated by bees rapidly vibrating the stamens to extract pollen. This functionally specialized pollination strategy has evolved repeatedly in approximately 8% of angiosperms, and dominates in the plant family Melastomataceae, with around 96% of species exhibiting buzz pollination. Within Melastomataceae, a vast diversity of anther shapes and configurations have emerged and have been equated to an 'adaptive plateau' of morphologically successful phenotypes. In this study, we explore the biomechanics of different anther structures and their effects on pollen release dynamics. Using CT scans and artificial buzzing experiments of morphologically distinct Melastomataceae species, we relate vibration parameters (frequency, amplitude, and number of pulses) and anther structure to pollen release rates. We present results from convergent and divergent anther types found in different genera across three different Melastomataceae communities. We then interpret these results in their pollination-ecological context, i.e., whether Melastomataceae species visited by a larger diversity of bee species also show high pollen release rates across a larger range of vibration parameters. This work is done with the aim of contributing to the field's understanding of the evolution and functioning of stamen trait diversity and subniche partitioning within the buzz-pollination syndrome, as well as to pinpoint potential evolutionary trajectories towards convergent or divergent floral phenotypes.

S.229.2 Flower trait evolution and pollination sharing in a community context

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Pollination involves the transfer of pollen from anthers to stigmas. Indeed, pollination is a "messy" process shaped by the fit between flowers and pollinators, the contact with reproductive organs along the body of pollinators, pollinator preferences, and the plant's breeding system. In addition, pollination interactions are often generalized, leading co-flowering congeners to share pollinators, creating selective pressures based on reproductive costs. If costly, the evolutionary consequences of pollinator sharing should be reflected in patterns of variation in reproductive organs to reduce interspecific pollination and reproductive interference. Here, I investigate variation in pollinator fit, pollen pick-up, and deposition in allopatric and sympatric populations of *Linum suffruticosum* with other *Linum* species. The study aims to understand if floral variation can be attributed to local patterns of pollinator sharing, reducing interspecific pollen transfer. Observations in different localities, floral measurements to measure morphological overlap between species, and quantitative analyses of reproductive costs through interspecific hand pollinations were conducted. Results revealed that the size and identity of the most important pollinator explained floral trait variations. The morphological overlap of *L. suffruticosum* flowers with co-flowering species varied depending on the identity of the co-flowering species. While post-pollination incompatibility maintains reproductive isolation, conspecific pollen-tube formation decreased after heterospecific pollination. In co-flowering sites, conspecific pollen-tube formation was lower than in single-species localities. Overall, the results suggest that trait variation in *L. suffruticosum* corresponds to the most important local pollinator, and incomplete pollinator partitioning may lead to interspecific pollination with associated reproductive costs. These costs may drive selection favoring reduced morphological overlap with co-flowering congeners, potentially leading to the evolution of pollination ecotypes.

S.229.3 Floral allometry and its relationship with pollinators along an altitudinal gradient of the tropical Andes of Bolivia

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Flower traits have been shown to be related to breeding systems (outcrossing vs. selfing), pollinators and can vary along environmental gradients. Environmental variation along altitudinal gradients is commonly associated with changes in the diversity of plants and animals, making them ideal systems to study variation in flower traits and its relationship with pollinators. We measured flower traits of 20 plant species and observed their pollinators (flower visitors that touched reproductive parts of the flower) along an altitudinal gradient (1000-4500m) in the tropical Andes of Bolivia. Flower traits included flower size, entrance diameter, flower length and anther-stigma distance. In particular, we compared allometries of stigma-anther height and flower size traits along the gradient. In this study we test the hypothesis that anther-stigma correlations is stronger at higher altitudes, assuming that at higher altitudes the conditions are harder, pollination is less reliable and therefore selfing plants species would be more common. We tested whether allometric slopes for fit traits (anther-stigma height) differ from those for flower size traits and among pollination systems. We expect to find a shallower allometric slope for fit traits than size traits. Additionally, we tested whether anther-stigma height correlations are related to more generalist plant species or a particular guild of pollinators.

S.229.4 The importance of your neighbors: co-flowering community effects on pollination and reproductive success of deceptive orchids

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Interactions for pollinators among co-flowering species are common and can modify plant reproductive success and ultimately natural selection on floral traits. However, studies considering the effects of the whole co-flowering community are still rare. Food-deceptive orchids provide suitable models to test for community effects on plant fitness as they often depend on rewarding co-flowering species to attract pollinators. Novel statistical approaches such as hierarchical latent-variable joint models now allow testing the influence of multiple co-flowering species on plant reproductive success. Here, we used two food-deceptive orchids *Dactylorhiza majalis* subsp. *lapponica* and *D. majalis* subsp. *majalis* to address the effects of the co-flowering community on pollination and plant reproductive fitness. We implemented the Hierarchical Modelling of Species Communities (HMSC) framework by fitting hierarchical latent-variable joint models with relative pollination success and fruit set as response variables. Together with phenotypic traits, we included the animal-pollinated co-flowering species in the community of each orchid as model predictor by using a reduced-rank regression approach in HMSC. Our results revealed that the animal-pollinated co-flowering community affected both pollination success and reproductive fitness via fruit set. Moreover, for *D. lapponica*, we found that the effect of animal-pollinated co-flowering species was strong even after accounting for effects of non-animal pollinated species in the community. By using a reducing-rank regression approach within the HMSC framework, we yielded new insights on the biotic factors influencing pollination and reproductive success of deceptive pollinated species. This approach can be extended to other pollination systems and plant communities and highlights the importance of considering the whole co-flowering community to understand the ecology and evolution of flowering plants in multispecies communities.

S.229.5 Flower size, thermal plasticity and local

adaptation under climate change

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Increasing average temperatures as well as more frequent extreme weather events caused by climate change are likely to affect plant-pollinator interactions around the globe. The ability of plants to adapt their reproductive strategies to new environmental conditions is crucial for their survival. Temperature-induced changes in the floral phenotype might negatively affect visitation rates and potentially hinder plant sexual reproduction and reduce fitness. At the same time, phenotypic plasticity may improve plant fitness under fluctuating environments. We used *Hypericum perforatum* to assess the effect of temperature on floral and flowering traits using a common garden full factorial setup. Contemporary and historical seed accessions, collected across the native distribution of the species, were grown under four temperature treatments. We tested for differences in population-level floral plasticity between temporal (ancestors vs. descendants) and geographical (trailing, core, and leading part of the distribution) origins to reveal potential changes in plasticity over the last decades and how these vary across space. We compared local adaptation of ancestral and descendant populations in a reciprocal transplant experiment across the European native range of the species. Our results show that higher temperatures are associated with a reduction in flower size and flower display and an earlier onset of flowering. Ancestral and descendant populations differed in flower thermal plasticity, which may have played an adaptive role over the last decades. Additionally, a reduction in fitness linked to a smaller flower size, display or earlier flowering onset could highlight detrimental effects of higher temperatures on plant sexual reproduction. Lastly, in our reciprocal transplant experiment, individuals from descendant populations flowered earlier than their ancestral counterparts, indicating potential rapid adaptive evolution to a warmer climate. Understanding evolution of thermal plasticity and floral adaptation to higher temperatures will improve predictions on how plant-pollinator interactions may respond to climate change.

S.229.6 Floral trait integration and potential for reproductive interference in North American Lobelia (Campanulaceae)

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Tight integration of floral traits may constrain floral diversity among closely related species and influence mechanisms of pre-mating reproductive isolation as well as the potential for reproductive interference when close relatives co-occur. Here, we present a detailed analysis of floral morphology in *Lobelia* sect. *Lobelia* (Campanulaceae). This monophyletic clade comprises 25 eastern North American species with a diversity of breeding systems, from obligate inbreeding to bee and hummingbird pollination to gynodioecy. Even though *Lobelia* sect. *Lobelia* species are phenotypically and ecologically similar, largely cross-compatible in the greenhouse, and frequently sympatric, hybrids are rarely observed in the wild. We measured 40+ morphometric characters on preserved flowers from across the ranges of 19 species, including samples from allopatric and sympatric populations and greenhouse-grown hybrids. A single principal component explained more than half of the variation in overall flower size and showed strong phylogenetic compared to geographic structure. Species exhibit distinct floral forms that fall along three continuous axes of floral shape: shorter, wide corolla tubes accommodating bumblebee access; long, narrow tubes associated with hummingbird pollination; continuous length variation with medium-sized tubes, with the smallest borne on selfing species and larger flowers associated with visits by small bees and butterflies. While the sex organs of all species show the form typical of the *Lobelia* "pollen pump," their lengths and angles within the flower differ in ways that should affect the likelihood of interspecific pollen transfer. Individual metrics of size and shape show different patterns of inheritance in hybrids, with most matching one of the parents and only some traits showing intermediate values. We interpret these patterns in light of effects on reproductive dynamics, isolation and interference where these congeners occur in sympatry.

S.230 BENEFICIAL PLANT-MICROBE INTERACTIONS. SESSION 3

S.230.1 Dynamics of microbial communities associated with Pisum spp. (Fabaceae) across plant growth stages and microhabitats

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The discovery of the holobiont in plants (host plant-microorganism association), particularly in angiosperms have revolutionized our understanding of the effects on the physiology and ecology of associated plants. The plant-microorganism interaction is governed by a 'chemical dialogue' via the production of exudates by the plant which selects and recruits bacterial communities which, in return, produce metabolites which facilitate the acquisition of nutrients and help promote the growth of the host plant. Symbiotic relationships between plants and microorganisms are the most documented, such as *Rhizobia* strains associated with root nodulating legumes that facilitate N uptake. Beyond these associations, non-symbiotic bacteria also impact their host. Significant gaps persist in understanding these complex microbial associations and require holistic approaches at different temporal and spatial scales. In this study, we conducted a greenhouse experiment to characterize the microbial communities associated with *Pisum* throughout its developmental cycle and in four compartments or microhabitats provided by the host plant. Microbiomes from four compartments of 144 plants from four different *Pisum* genotypes (*Pisum fulvum*, *P. sativum* subsp. *abyssinicum*, *P. sativum* subsp. *elatius* and *P. sativum* subsp. *sativum*) were sampled at three distinct developmental stages, representing a total of 456 microbial communities. These microbiomes were analyzed using full 16S rRNA gene PACBIO sequencing and phylogenetically-corrected statistical analyses. Our results suggest that the plant-associated microbiome composition and structure evolved throughout the plant's developmental cycle, likely in response to differential nitrogen and carbon allocations during vegetative, flowering, and seed-filling stages. The different microhabitats offered by the plant acted as ecological filters, influencing the composition of bacterial communities. Finally, bacterial communities associated with peas exhibited differences based on the genotype of the host plant. These findings enhance our understanding of the dynamics of bacterial communities and the host's influence in shaping this process.

S.230.2 Whole-soil microbial communities from shaded coffee plantations and montane forest fragments offer similar benefits to coffee and

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Soil microbial communities are among the most species-rich components of terrestrial ecosystems and can influence plant productivity and quality by establishing direct interactions with plant roots (pathogens, parasites, root herbivores, mycorrhizae) and by locking or liberating nutrients into the soil. However, agricultural practices such as tillage and fertilization can reduce soil community diversity in general, reduce mycorrhizal inoculum potential, or modify the abundance of soil microorganisms such as arbuscular mycorrhizal fungi (AMF). In this study we exposed seedlings of coffee (*Coffea arabica*), and three native shade tree species (*Albizia carbonaria, Cordia alliodora* and *Inga densiflora*) to contrasting soil types and sterilized vs. whole-soil live microbial communities from long-term fertilized shaded coffee plantations and montane forest fragments in Colombia. Surprisingly, plants showed a limited response to contrasting soil types, but benefited from live soil microbial communities, and their growth differed across varied combinations of soil type and inoculum source. Fast-growing plant species (*A. carbonaria* and *C. alliodora*) benefited the most from inoculation with live soil organisms, but *A. carbonaria* benefited the most from soil microbes coming from shaded coffee plantations. In contrast, shade-tolerant species (*C. arabica* and *I. densiflora*) performed similarly across different live inoculum sources, but growth of *I. densiflora* with a live inoculum was higher in soils containing higher organic matter, and N and P contents. AMF colonization varied across species, being the lowest in *C. arabica*, but similarly high for plants inoculated with soils coming from shaded coffee plantations and forest fragments. These results suggest that agricultural systems that maintain intermediate plant diversity and employ low soil disturbance, despite fertilization, maintain soil microbial communities similar to those present in more diverse natural habitats.

S.230.3 A small signal peptide modulates root hair growth in response to fungal ethylene emissions

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In nature, plants and microorganisms communicate with each other by exchanging different signaling compounds including volatile compounds (VCs), some of which have biostimulating properties. In Arabidopsis, VCs from the fungal phytopathogen Penicillium aurantiogriseum promote growth, photosynthesis and root hair (RH) proliferation and hyper-elongation through mechanisms involving ethylene, auxin and photosynthesis signaling. A striking alteration in the proteome of roots of fungal VCtreated plants involves strong up-regulation of RALF22. To test the possible involvement of the RALF22 in the fungal VC-promoted RH changes, we characterized the RH responses of ralf22 and fer-4 plants impaired in RALF22 and its receptor FERONIA to VCs emitted by P. aurantiogriseum. We found that these plants were unresponsive in terms of VC-promoted RH elongation and proliferation. Unlike in WT roots, fungal VCs did not enhance the transcript levels of RALF22 in roots of fer-4 and ethylene- and auxin- insensitive mutants, and those of RH-related, ethylene-responsive genes (e.g. RSL2, RSL4, RHD2, PRX1 and PRX44) in ralf22 and fer-4 roots. Finally, we identified ethylene as the bioactive fungal VC, as VCs of ΔefeA strains of P. aurantiogriseum cultures impaired in ethylene synthesis weakly promoted RH proliferation and elongation in exposed plants. Collectively, our results demonstrate that RALF22-FERONIA complex is a key determinant of the ethylene, auxin and photosynthesis signaling-mediated RH response to fungal ethylene emissions.

S.230.4 The use of compost improves biodiversity in the bacterial community of the rhizosphere of tomato plants

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Certain bacteria form symbiotic relationships with plant roots in the rhizosphere and on the rhizoplane and endosphere of the roots, leading to improved plant nutrient uptake, enhanced productivity, and resilience to abiotic stresses and pathogens. However, soil biodiversity is nowadays endangered and reduced by modern agricultural practices, having a severe impact on soil structure and plant productivity. Soil microbiota is the source from which plants recruit bacteria species to interact with. A community of bacteria in the soil and the rhizosphere is necessary to allow correct plant nutrition, and development, and to help the plant to cope with environmental and biotic stresses. Among all the strategies to sustain soil biodiversity, biofertilizers, substances containing beneficial microorganisms that enhance plant health and growth, offer a potential remedy. Among these, compost, a product of controlled aerobic decomposition of organic materials carried out by microorganisms, stands as a promising solution. Recognized in agriculture for being rich in organic matter and nutrients, compost's unexplored potential as a microbial inoculum for enriching the soil and fostering plant health necessitates further investigation. This work revolves around the study of compost and its role as a source of beneficial microorganisms, aiming to elucidate its capacity to enrich microbial communities in soil and the rhizosphere. Additionally, the study seeks to isolate and characterize the culturable bacterial diversity within compost and assess its ability to promote plant growth. This research contributes to understanding sustainable agricultural practices and soil ecosystem health, aligning with the EU's 2030 sustainable development goals.

S.230.5 Halocnemum strobilaceum as new source of potentially plant growth promoting endophytic bacteria

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In recent years, several efforts have been made to enhance the salt-tolerance of plants, as salinity stress is one of the major abiotic stresses threatening crop production in arid and semi-arid regions. Also, soil salinization is expected to increase due to climate change and increased irrigation practices. Recent research has shown that bioaugmentation of crops with halotolerant bacteria isolated from halophytic plants can alleviate salt stress and promote plant growth. *Halocnemum strobilaceum* is a widespread hyperhalophyte desert plant known for its antioxidant, antimicrobial, insecticidal and phytoremediation properties. However, it is critically endangered in Spain. Whereas most of the studies focus on rhizospheric bacteria, little is known about how endophytes help halophytes to cope with salt stress. In this work we study the diversity of endophytic bacteria of *Halocnemum strobilaceum* from arid areas of Murcia and Almeria, Spain. In total, 79 endophytic bacterial strains were isolated from the aerial parts of this halophytic plant on tryptic soy Agar supplemented with 0.5 M NaCl to ensurance their salt tolerance. They show in vitro plant growth promoting (PGP) properties as phosphate solubilization, siderophore production, auxin IAA production, biofilm formation, and enzimatic activities as protease or cellulase. We also carried out 16S rRNA gene sequencing and found several isolates could be new potential species of Halomonas and Kushneria, a relatively novel and small genera. We selected three best strains based on their PGP properties and set up a greenhouse trial with *Medicago sativa* under 100mM NaCl salinity stress to test the consortia capacity in mitigating salt stress.

S.230.6 Defining a forest by the fungi: "mycorrhizal spillover" effects on nutrient cycles, soil microbiomes, and plant community dynamics

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Arbuscular mycorrhizal (AM) and ectomycorrhizal (ECM) tree species tend to differ across a multitude of

traits beyond the structure of the root symbiosis, including leaf and root chemistry, litter decomposability, carbon allocation to mutualistic fungi, and protection from root pathogens. Here we explore how, as foundation species, the mycorrhizal type of dominant trees also has a profound "mycorrhizal spillover" effect on soil biogeochemistry and the soil microbiome, resulting in different stresses experienced by all members of the plant community. We present evidence that, compared to soil in forests dominated by ECM tree species, soils in forests dominated by AM tree species have increased soil mineral nutrient availability, greater abundance and diversity of plant pathogens and AM fungi, and lower abundance and diversity of ECM fungi. Although we discuss some context-dependency of these patterns, they seem to be consistent even across a continuous gradient of mycorrhizal dominance (i.e., 0 to 100% AM basal area), and for individual species (e.g., for AM plants surrounded by increasing dominance of ECM trees, and vice versa). Based on these patterns, we describe a new hypothesized framework of additive and interactive effects of mycorrhizal spillover. These mycorrhizal spillover effects shift the strength and direction of plant-soil feedback and conspecific density dependence in predictable ways, which has implications for our understanding of future plant community and evolutionary dynamics.

S.231 TROPICAL PLANT EVOLUTION ACROSS SPATIAL AND TEMPORAL SCALES. SESSION 2

S.231.1 Do reticulate relationships between tropical trees drive diversification?

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Radiations that generate species-rich clades are fundamental in the evolution of diversity. Hybridisation can facilitate radiations through transfer of adaptive variation, catalysing rapid divergence. Much of the hyperdiverse neotropical tree flora was generated by radiations, but the influence of hybridisation on their evolution remains unexplored. Rainforest tree communities are subject to relentless insect herbivory, such that co-occurring tree species differ significantly in herbivore defence chemistry, with 'rare' defences most effectively overcoming local herbivores. Chemical defences show evidence of divergent evolution between sister species of *Inga,* a chemically diverse genus of >300 rainforest trees that typifies rapid neotropical tree radiations. Thus, here we ask whether hybridisation catalysed the rapid radiation of *Inga* through passage of 'rare' herbivore defence traits. We use phylogenomic approaches to first understand whether reticulation preceded rapid diversification in *Inga,* and hence whether hybridisation may underlie this radiation. Then, using whole-genome resequencing of >520 *Inga* accessions comprising >40 species, we ask whether hybridisation facilitates the transfer of linkage blocks containing 'rare' chemical defence loci between species. Overall, we aim to assess whether ecological divergence facilitated by transfer of adaptive variation through hybridisation helped to generate the unmatched diversity of rainforest trees.

S.231.2 Contrasting diversity and biogeographic patterns in the forest-savanna transitions of Africa.

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In tropical Africa, forests and savannas are the two most widespread biomes and potentially represent alternative stable states with a divergent species composition. Transition zones between the two biomes are thought to be floristically impoverished, with fewer representatives from each biome. Further, the evolutionary dimension of diversity has received limited attention, despite its importance for understanding the biogeographic history of biomes. Here, we quantified species richness and several measures of evolutionary diversity in 1º grid cells, using ca. 300,000 occurrence records of trees and shrubs combined with biome affiliation data for 3203 species. We found that assemblages in transition zones hold fewer woody species than assemblages in forest and savanna zones. However, transition zones hold more phylogenetic diversity than expected given their species richness, whether one considers forest and savanna assemblages separately or together. We also show that the Congo Basin forests have low levels of phylogenetic diversity, given the number of species, and highlight south-eastern African savannas as a centre of savanna woody species richness and phylogenetic diversity. Regions with high phylogenetic diversity, given the number of both forest and savanna species, were centred around the Dahomey Gap and Cameroon, mainly in transition zones. Overall, our study shows that even if floristically impoverished, transition zones hold unexpectedly high evolutionary diversity. This suggests that they are important centres of evolutionary innovation and diversification and/or serve as evolutionary crossroads, where lineages that diversified in contrasting environments coexist within a single area.

S.231.3 Insight into biodiversity formation in Amazonia: phylogeny and evolution of the fern genus Adiantum

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The tropics are home to high species diversity, but our understanding of the formation, evolution and distribution of that diversity is still limited. This hampers the targeting of conservation efforts, especially in such megadiverse environments as Amazonia. Here we focus on unraveling the evolutionary diversification of the fern genus *Adiantum* in Amazonia. The genus has approximately 225 species distributed worldwide, and ecological inventories have found it to be one of the most abundant and diverse fern genera in Amazonian rain forests, making it an ideal example group. However, the species delimitations, phylogenetic relationships, and niche evolution of *Adiantum* remain poorly understood. By applying advanced bioinformatics techniques and integrating information from molecular (chloroplast and nuclear data), morphological and environmental data, we aim to elucidate the phylogenetic relationships of *Adiantum* in Amazonia and to explore to what degree the diversification of *Adiantum* species is related to niche evolution, dispersal limitation and hybridization. The results will not only improve our understanding of the biodiversity of *Adiantum* itself but will also contribute to understanding the formation of biodiversity in the Amazon region in general.

S.231.3 Understanding the evolutionary and biogeographical history of the enigmatic pantropical family Putranjivaceae

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Tropical ecosystems are recognized as one of the most biologically diverse regions on Earth. The "odd-man-out" pattern proposes that Tropical Africa is less diverse than both Neotropics and Tropical Asia. Although this is true for many vascular plant groups, this is not the case for the pantropical family Putranjivaceae. It is a complex and species-rich group that includes two genera: *Putranjiva* (4 spp., restricted to Asia) and *Drypetes* (219 spp.). Asia contains the greatest number of species belonging to *Drypetes* (113 spp.), followed by Africa (86 spp.) and significantly less in America (20 spp.). The high number of African species recently described indicates that the diversity of Putranjivaceae on this continent has been underestimated. The evolutionary and biogeographical history of the Putranjivaceae has never been studied due to the lack of both an updated taxonomic scheme (the only extant infrageneric classification of *Drypetes* was published in 1922 by Pax & Hoffmann) and a comprehensive phylogeny for the family. Herbaria store vast collections of plant specimens accumulated over several centuries, and recent advances in DNA extraction methods and sequencing techniques allow researchers to include degraded DNA in their studies. We aim to analyze ~200 herbarium specimens, accounting for over 90% of the Putranjivaceae family's diversity, to reconstruct their phylogenomic relationships. Target capture sequencing combined with genome-skimming (HybSeq) is favored due to its compatibility with old herbarium material and ability to produce numerous low-copy nuclear orthologs and organellar DNA. This study will advance understanding of the evolutionary history of Putranjivaceae and demonstrate how a strong phylogenomic hypothesis can inspire and direct future taxonomic research, support species identification and elucidate important inquiries regarding their evolution and biogeography.

S.231.4 Sapotaceae across time and space: a taxonomic and historical biogeographic perspective

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Sapotaceae is one of the most important plant families in the world. With around 1,250 species and 62 genera, Sapotaceae is a pantropical family, and is usually restricted to lowland tropical rainforests. However, the taxonomy of the family is unstable and lacks in information of this ecologically important groups of angiosperms in the tropics. Many incongruences between phylogeny and classification in Sapotaceae have been noted, as well as alternative topologies for species-level phylogenies. Here, we generate a higher sampled Sapotaceae phylogeny and, for the first time, we aimed to determine the geographical origin of the pantropical family and the roles vicariance and dispersal have played in shaping its modern distribution. We used target sequence capture data from the Angio353 probe for 199 taxa. The concatenated maximum likelihood molecular phylogeny was constructed using IQ-TREE (v. 1.6) considering GTR+G and partition models, and 1000 bootstrap replicates. Dates of diversification events were estimated using two fossils and the penalized likelihood approach (treePL). The subsequent dated phylogenies were compared and analysed for biogeographical patterns using BioGeoBEARS. The phylogeny moderately recovered the three subfamilies of Sapotaceae, showing relatively high support for Sapotoideae but not for Chrysophyloideae. The phylogeny shows inconsistencies with the current morphological classification. Our results indicate that the ancestral range of the family was in East Asia ca. 84 - 80 Mya, with dispersal to South America and Africa. Chrysophylloideae had a early diversification in Africa ca. 71 - 57 Mya, with subsequent dispersal to the Neotropics (two events) and Australasia (singles event) during the Palocene and Eocene. Sapotoideae had an early diversification in Africa ca. 71 - 50 Mya, with migration to Australasia and North America during the Eocene. Those results are somehow congruent with previous studies. Long-distance dispersal has been an important mechanism for range expansion in Sapotaceae.

S.231.5 Berries on bellflowers: diversification patterns in one of the fastest Andean plant radiations

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The centropogonids within Lobelioideae (Campanulaceae), consist of *Burmeistera* H.Karst. & Triana, *Centropogon* C.Presl, and *Siphocampylus* Pohl, stand out as one of the rapidest plant radiations in the Neotropics. Remarkably, this alliance gave rise to approximately 550 species in less than three million years. Traditionally, fruit traits were employed to distinguish genera within centropogonids, where *Siphocampylus* is identified by capsules, and *Burmeistera* and *Centropogon* by berries. Inflated berries are a distinctive feature of *Burmeistera*, representing a third of its species diversity. Our study compares inflated and fleshy berries in *Burmeistera*, examining differences in elevation, as well as the evolution of morphological, ecological, and geographical traits. This analysis, conducted within a phylogenomic framework, provides insights into how these factors have influenced the diversification of *Burmeistera*. Our findings indicate that inflated fruits evolved multiple times in the phylogeny of *Burmeistera* species, with inflated and fleshy berries occupying distinct adaptive regimes, particularly concerning elevation. Moreover, the diversification patterns in *Burmeistera* varied among species distributed in the Chocó biogeographic region, exhibiting a comparatively reduced frequency of inflated berries. We propose that studies focused on the conservation of often overlooked taxa, like *Burmeistera*, could significantly impact the preservation of severely threatened cloud forest ecosystems.

S.232 GENOMICS

S.232.1 Ancient DNA recovered from lake sediment with Angiosperms353 shows plant composition shifts with paleoclimate

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Humans have steadily been in Southern California for 14,000 years. Despite this legacy of human presence, studies showing the historical composition of the organisms that cohabited this Southern California with humans are scant. Sedimentary ancient eDNA can be used as a tool to reconstruct thousands of years of plant and mammal presence records and may present a more sensitive spatiotemporal scale than pollen records. We sequenced the mammal and plant DNA present in a sediment core from Lake Elsinore, spanning 24,000 years of natural history and 10,000 years of human settlement. Preservation of environmental DNA is poor in warm climates, so we tested the Angiosperms353 Target Capture Kit's effectiveness in increasing the proportion of diagnostic plant sequences for ancient metagenomic samples. We find that the Angiosperms353 libraries have a greater proportion of reads mapped on average, and a greater plant target richness. From the target capture data, we seek to trace ethnobotanical families, like Rutaceae, Fagaceae, and Apiaceae, to characterize the landscape around the time of human arrival to understand some of the challenges and opportunities presented to early inhabitants. Further, we associate characteristic environmental changes, like shrubland dominance and absence of widespread taxonomic groups, with a newly reconstructed charcoal history, suggesting that humans have been ecosystem engineers via controlled use of fire for thousands of years. This project validates the preservation and recovery of ancient eDNA using Angiosperms353 in warm-climate sediment cores from southern California, which can be a tool that helps define the role of humans in shaping California's ecological history.

S.232.2 An update on plant genome size diversity: contributing towards a comprehensive understanding across angiosperms

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Research into genome size evolution in angiosperms has increased significantly, uncovering a huge diversity across different taxonomic lineages. Despite the efforts made and the vast amount of data generated (> 10,000 species), which have been carefully collated onto the plant DNA C-values database (http://data.kew.org/cvalues/), many taxonomic families are still lacking a single estimate. Certainly, such taxonomic gaps are particularly notable in angiosperms, where nuclear DNA contents are only available for about 3,000 genera out of ca. 13,000 genera currently recognised, and over 10,000 species (ca. 2.5% of the ca. 352,000 species recognised). At the family level, this translates into estimates for 270 families out of 417 (*sensu* the Angiosperm Phylogeny Group IV), i.e., nearly 65% of the currently accepted diversity. With the already available data, we have been able to unveil a staggering diversity of nuclear DNA contents in angiosperms that spans up to 2400-fold. Notwithstanding, the question still remains as what is the extant diversity of genome sizes in angiosperms? And what is yet to be uncovered? In order to bring further robustness to our current understanding of angiosperm genome size diversity, we set up an initiative aimed at filling most –if not all- the taxonomic caveats, starting at the family level. The unceasing production of novel genome size data, complemented with an increasingly robust understanding of the worldwide distribution of organisms, has opened unprecedented prospects for investigating the role of genome size in shaping and influencing the survival of extant biodiversity. Our goal is to produce at least one estimate per each accepted family (122 families represented so far, i.e., 94%), focusing our efforts on those lineages largely understudied, and interpret these data within an evolutionary context, investigating the existing links between the patterns and processes shaping extant plant genome diversity.

S.232.3 The Sapria himalayana genome provides new insights into the lifestyle of endoparasitic plants

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Sapria himalayana (Rafflesiaceae) is an endoparasitic plant characterized by a greatly reduced vegetative body and giant flowers; however, the mechanisms underlying its special lifestyle and greatly altered plant form remain unknown. To illustrate the evolution and adaptation of *S. himalayasna*, we report its *de novo* assembled genome and key insights into the molecular basis of its floral development, flowering time, fatty acid biosynthesis, and defense responses. The genome of *S. himalayana* is ~ 1.92 Gb with 13,670 protein-coding genes, indicating remarkable gene loss (~ 54%), especially genes involved in photosynthesis, plant body, nutrients, and defense response. Genes specifying floral organ identity and controlling organ size were identified in *S. himalayana* and *Rafflesia cantleyi*, and showed analogous spatiotemporal expression patterns in both plant species. Although the plastid genome had been lost, plastids likely biosynthesize essential fatty acids and amino acids (aromatic amino acids and lysine). A set of credible and functional horizontal gene transfer (HGT) events (involving genes and mRNAs) were identified in the nuclear and mitochondrial genomes of *S. himalayana*, most of which were under purifying selection. Convergent HGTs in *Cuscuta*, Orobanchaceae, and *S. himalayana* were mainly expressed at the parasite–host interface. Together, these results suggest that HGTs act as a bridge between the parasite and host, assisting the parasite in acquiring nutrients from the host. Our results provide new insights into the flower development process and endoparasitic lifestyle of Rafflesiaceae plants. The amount of gene loss in *S. himalayana* is consistent with the degree of reduction in its body plan. HGT events are common among endoparasites and play an important role in their lifestyle adaptation.

S.232.4 Extreme chromosome copy number variation and unusual suite of transferred sequences characterize mitogenomes of Gastrodia

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The evolution of heterotrophy in plants has induced dramatic genomic alternations, such as for plastids, where extensive gene loss and size reduction are widely reported. Analogous to plastids are several extreme modifications discovered in mitochondrial genomes (mitogenomes) of parasitic plants. However, whether trophic reliance on symbiotic fungi (mycoheterotrophy) similarly results in mitogenomic alternations remains largely unknown. We present a comprehensive mitogenomic study for mycoheterotrophic plants based on 11 *de novo* assemblies of *Gastrodia* (Orchidaceae). These mitogenomes contain multiple chromosomes, range from 0.56 to 2.1 Mb in size, and exhibit several features are rarely, if ever, observed among other plants. Specifically, variations in chromosome copy number are universal, and in two assemblies, a chromosome exists at approximately 15 times higher abundance than the conspecific average, resulting in the most extreme chromosomal copy number variation among any mitogenomes so far. Insertions from plastid and fungal genomes are unexpectedly scant, in contrast to those potentially rampant, species-specific, non-coding sequences transferred from the nucleus and distant plant taxa. Yet, despite the 3.8-fold size variation and highly variable intergenic sequence components, these mitogenomes harbor an ordinary complement of genes and introns, and exhibit moderate substitution rates of coding sequences, with no genes acquired via horizontal transfer. Taken together, our findings suggest a minor role of mycoheterotrophic lifestyle on mitochondrial coding sequences, but the extreme copy number variation across mitochondrial chromosomes and unusual combinations of transferred sequences set new benchmarks for architectural and content variation seen in plant mitogenomes, and hints at unexplored mechanisms governing mitogenomic evolution of these extraordinary heterotrophic plants.

S.232.5 Reciprocal gene loss after whole-genome duplications contributes to species diversity in mangrove plants

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Whole-genome duplications (WGDs) are prevalent and provide extensive material in plant evolution process. The extensive gene loss and biased retention of duplicated genes after WGDs were proposed responsible for the environmental adaptation and species diversification, but the mechanisms are still rarely uncovered. In mangroves that inhabited intertidal environments independently from inland ancestors, we found the clades experienced WGD events had higher species diversity. We choose *Avicennia* genus, a typical mangrove clade with specified phenotypes and a high species diversity, to explore the possible molecular mechanisms of WGD in promoting species divergence. We first assembled seven high-quality mangrove genomes of the *Avicennia* genus using PacBio Single-Molecule Real-Time sequencing. Then, we identified two recent WGD events in *Avicennia*. The more recent one is *Avicennia*-specific, coinciding with the genus's origin approximately 46 Mya. The WGD retained gene duplications are involved in high salt tolerance and nutrient absorption, contributing to the genus' adaptation to intertidal environments. We test the role of reciprocal gene loss (RGL) in the rapid species divergence of the *Avicennia* genus. Combined with gene collinearity and phylogenetic analyses, we accurately identified RGL events among these species. Interestingly, a few RGLs between sister species are closely related to reproduction process, such as pollen tube invasion of the stigma. Further functional studies suggested that RGLs may cause reproduction isolation between sister species. In summary, our study uncovered the role of WGD in environmental adaptation and provided evidence that RGL after WGDs may be a potential speciation mechanism in mangrove plants.

S.232.6 Phylogenetic Analysis of Marchantia Species in Sri Lanka Based on rbcL, psbA, and ITS2 Sequences

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This study presents the first comprehensive phylogenetic analysis of *Marchantia* species in Sri Lanka using nucleotide sequences from three distinct genetic markers: *rbc*L, *psb*A, and ITS2. The aim of this research was to elucidate the evolutionary relationships among different *Marchantia* taxa within the Sri Lankan context, providing valuable insights into the genetic diversity and evolutionary history of these liverworts. A total of 20 *Marchantia* samples representing diverse geographical locations across Sri Lanka were collected and analyzed. DNA was extracted, and the targeted regions (*rbc*L, *psb*A, and ITS2) were amplified through polymerase chain reaction (PCR). Subsequent sequencing and alignment were performed to construct phylogenetic trees using MEGA version 11.0.13. The resulting trees were then subjected to bootstrap analysis to assess the robustness of the inferred relationships. Our phylogenetic analysis revealed distinct clustering patterns within the *Marchantia* species sampled from

Sri Lanka. The utilization of multiple markers (*rbc*L, *psb*A, and ITS2) provided a more comprehensive understanding of the evolutionary dynamics, offering insights into both conserved and variable regions of the genome. Furthermore, the study identified potential cryptic species and clarified the taxonomic relationships among *Marchantia* populations in Sri Lanka. The implications of these findings extend beyond the realm of taxonomy, contributing to our understanding of the biogeography and evolutionary processes shaping the diversity of *Marchantia* in this region. This research not only adds to the growing body of knowledge concerning liverwort evolution but also underscores the importance of incorporating multiple genetic markers for a robust phylogenetic inference. The insights gained from this study have implications for conservation efforts and provide a foundation for future investigations into the ecological and physiological adaptations of *Marchantia* species in Sri Lanka.

S.233 FROM MULBERRIES TO FIGS: STUDIES IN THE EVOLUTION OF MORACEAE

S.233.1 Revisiting C.C. Berg's and E.J.H. Corner's treatments of Moraceae: morphology and its role in the evolution of the fig family

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The diversification of angiosperms poses an intriguing evolutionary puzzle that has been attributed to the origin of the flower. Pollinator-mediated selection stands as a key force driving the astonishing diversity of floral forms observed in angiosperms, but its role in the diversification of Urticalean rosids has been neglected. Utilizing the Moraceae family as a model system, we aim to investigate how changes in floral traits have influenced its floral disparity and the emergence of unique clades, such as the figs. This pantropical, monophyletic family boasts a remarkable floral diversity across its 46 genera and ca. 1,200 species. Despite the family's extensive morphological diversity, limited studies have explored the role of floral traits in its evolution and diversification. Previous classification schemes by C.C. Berg and E.J.H. Corner, primarily based on morphology, led to conflicting taxonomic circumscriptions due to the family's homoplasious nature. Recent advances in molecular techniques and phylogenomic analyses have unveiled deep-seated relationships among Moraceae tribes, shedding light on the evolution of floral structures and reproductive mechanisms. The time is now ripe to revisit Berg's and Corner's treatments of Moraceae. Leveraging the latest phylogenomic study in the fig family, we applied model-based phylogenetic comparative methods to translate hypotheses of morphological evolution under pollinator-mediated selection. We inferred ancestral character states and conducted trait-dependent diversification analyses based on a literature review and a comprehensive Moraceae dataset of 529 species. Understanding the intricate web of factors influencing the diversification of Moraceae remains a dynamic area of research, offering crucial insights into the macroevolutionary trajectories of one of the most diverse groups of angiosperms.

S.233.2 An updated classification of Moraceae supported by stable phylogenomic hypotheses

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The Moraceae is an ecologically and economically important family with a worldwide distribution centered in the tropics. Notable species include species of *Ficus* (figs), *Artocarpus* (breadfruit and jackfruit), *Morus* (mulberries), and others. Classification within the family based on morphology has led to instability over the past century due in part to the difficulty in distinguishing preserved ancestral or convergent characters from truly plesiomorphic characters. Historical classification systems have particularly disagreed on the importance of stamen position, which may be straight or inflexed in bud, the latter a notable adaptation to wind pollination. Inflorescence architecture varies widely from spicate inflorescences in the Moreae to the closed syconium of *Ficus* or the flattened disc of *Dorstenia*, yet differences in the individual flowers may be more cryptic. Two decades of molecular phylogenetic analyses, the most recent incorporating hundreds of genes as well as analyses of introgression, have clarified evolutinoary relationships and transitions within this family. After reviewing the current state of phylogenetic reconstructions and the morphological traits that characterize the major clades, this paper will propose a comprehensive updated classification of Moraceae that is consistent phylogenetic reconstructions but morphologically tractable. The author hopes that this updated classification will provide stability for further work on Moraceae and bring formal taxonomic names in line with phylogenetic evidence.

S.233.3 Syncarpous fruits from the Early Oligocene Capella Flora in Queensland, Australia suggest affinities to the Moraceae

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Fruits composed of a many individual fruitlets that are united into a complex structure are described as a syncarpium or a sorosus. Syncarpia occur in diverse and phylogenetically unrelated families, such as in the monocots Araceae, Bromeliaceae, Cyclanthaceae, Pandanaceae, and dicots Balanophoraceae, Bataceae, Chloranthaceae, Cornaceae, Moraceae, Rafflesiaceae, Rubiaceae and Urticaceae. Permineralised fruits from the Oligocene Capella locality in Queensland consists of many fruitlets, and the seeds occur in the upper portion of each fruitlet. The fruitlets form connate radiating segments, which are interpreted as being derived from the perianth. These radiating segments extend from the centre to the margin of the fruit and adjacent perianth apices appear to be fused apically, forming an irregular pentagonal-hexagonal imbricate surface which shows no consistent phyllotactic pattern. It was possible to exclude the monocot families and Balanophoraceae because the arrangement of seeds in the fruits of these families typically exhibit a regular phyllotaxy, which is less evident in the Pandanaceae. The structure of the fruit and seed shape in the fossil differs from that in Rafflesiaceae. The fossil also has a complex internal structure consisting of thin connate radiating elements that are closely aligned and in this respect the fossils differ from the internal fruit morphology of Cornaceae, Chloranthaceae, Rubiaceae, Bataceae and Urticaceae. Comparison of character traits across these families suggests that these fossil syncarpous fruits are considered to have affinities with the Moraceae. While most fruits in Moraceae are syncarpous the fruit morphology of genera in the family is highly diverse, although five-sided fruits are not currently known. The connately arranged fruitlets and pentagonal-hexagonal external appearance suggests that the closest affinities of these fossils lie with the Artocarpeae.

S.233.4 Exploring evolution of breeding systems in Moraceae within the context of correlated character traits

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Monoecy, the presence of discretely sexed flowers on the same individual, and dioecy, the presence of only unisexual individuals, are both relatively rare breeding systems among angiosperms (Renner 2014) but yet are the only breeding systems, with few exceptions, found among the roughly 1200 extant members of the Moraceae family. Dioecy, in particular, has long been considered as an evolutionary endpoint due in large part to the perceived reproductive hurdles such a breeding system presents in plants. But there is an increasing body of evidence that dioecy can and will revert to other breeding systems, demonstrating lineage extinction is not a foregone conclusion. With this increasingly accepted, exploration into the surrounding factors is merited. Using an updated molecular phylogeny, the evolutionary patterns of these breeding systems within Moraceae are contextualized through their relationships with character traits chosen either for their long association with dioecy or for their potential to contribute to resilience in the face of habitat disruption or periods of low reproductive success. Evaluating these factors in tandem will reveal key evolutionary milestones and adaptive connections which enabled Moraceae to diversify into the ecologically important family it is today.

References: Renner, S. S. 2014. The relative and absolute frequencies of angiosperm sexual systems: Dioecy, monoecy, gynodioecy, and an updated online database. American Journal of Botany 101:1588–1596.

S.234 THE EVOLUTION AND BIOGEOGRAPHY OF APOMICTIC PLANTS. SESSION 1

S.234.2¡1 Female-male crosstalk affects male meiosis and pollen development in sexual and apomictic Limonium species

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Breeding systems were extensively studied by Baker, who has been influential in the development of evolutionary and biogeographical hypotheses for Plumbaginaceae, as in *Limonium* (sea-lavenders). This genus is a remarkable case-study as apomicts have a large general distributional success, although most of the relevant questions were not yet answered which hampers an understanding about apomixis origins. *Limonium* species present a polymorphic sexual system associated to flower polymorphisms such as ancillary pollen and stigma and/or heterostyly, under sporophytic control that prevents self and intramorph mating. Most sexual and apomict species are self-incompatible, the first usually form meiotically reduced embryo sacs and viable pollen. While apomicts can originate unreduced embryo sacs and pollen ranging from low to high fertility or it is not produced at all. To explore the mechanisms beyond these reproduction modes, ovule transcriptome profiling of sexual and apomict species was carried out. Our investigations revealed several novel challenges, among which female-male interactions associated with reproduction modes.

S.234.2 Apomixis and polyembryony in plants of Cerrado, the Neotropical savannas in Central Brazil

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Polyembryony involves multiple, either sexual or asexual embryos in the same seed. Asexual embryos are commonly the result of apomixis processes. Although sexual systems and monoembryony predominate among Cerrado plants, the Neotropical savannas in Central Brazil, recent studies have shown increasing numbers of apomictic species, many of them polyembryonic. Here we surveyed the polyembryony among Cerrado plants and connected its occurrence with apomixis. We compiled records of embryonic patterns - monoembryony or polyembryony (216 species) and breeding systems (139 species) from literature, and also gathered original data (91 species). We observed the rate of polyembryony either by dissecting seeds or evaluating the emerging seedlings per seed after germination experiments. Plant species were classified as exhibiting monoembryony, low polyembryony (<5%) or higher polyembryony rate (>5%). Polyembryony was observed in 72 species (31.8%). Surveyed species were either self-incompatible (66 species; 47.5%), self-compatible (33 species; 23.7%), apomictic (28 species; 20.1%) or dioecious (12 species; 8.6%). Among apomictic species, 89.3% (N = 25) were polyembryonic. Percentage of polyembryonic seeds ranged from 0.09% to 98.4%, with sporophytic apomicts exhibiting usually higher rates of polyembryony. Polyembryony and

apomixis in Cerrado plants seem to be linked to dioecy and polyploidy, and widely distributed woody species. Although apomixis and polyembryony are common in taxa such as Bignoniaceae, Fabaceae, Malvaceae and Melastomataceae, we did not find any clear phylogenetic signal for the distribution of these traits. Polyembryony rate higher than 5% proved to be a good indicator of apomixis. However, polyembryony was absent in some apomictic specie and, in several cases, was even linked to sexual reproduction. Polyembryony associated with apomixis seems to be a common reproductive alternative in savanna plants rather than a reproductive abnormality. Moreover, these traits will be important for plant conservation strategies in this threatened biome. Acknowledgments: We acknowledge CAPES, FAPEMIG and CNPq funding.

S.234.3 Multiple origin of widespread apomictic Hieracium halleri: phylogenomic and cytogenetic evidence

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Hieracium s.str. (Asteraceae) is a highly diverse genus that occurs in a wide range of environments, from lowlands to the alpine zone. It is known for its notorious taxonomic complexity, caused by widespread past interspecific hybridisation. This process has been closely linked to polyploidisation and apomixis, which has ensured the persistence of otherwise sterile hybrids. As a result, *Hieracium* is the largest apomictic-sexual genus among angiosperms, whose diversity is dominated by apomictic polyploid species. However, very little is known about the evolutionary and biogeographical history of these apomictic polyploids. We aim to decipher the evolutionary history of the alpine apomictic species *H. halleri*, which probably arose from hybridisation between *H. alpinum* and *H. intybaceum*. We also ask if *H. halleri* originated only once or if it is of recurrent hybrid origin. To achieve these aims, we combined cytogenetic (*FISH* and *GISH*), flow cytometric (assessment of mode of reproduction), and molecular (RADSeq, cpDNA) approaches. This multidisciplinary approach is applied to plants collected across the range of the species, which shows a large disjunction between the Alps and the Western Carpathians. We found that despite strictly apomictic mode of reproduction, *H. halleri* is cytogenetically variable taxon, both in chromosome number (prevailing are triploids, tetraploids are very rare) and karyotype pattern (variation in number and positions of 5S rDNA, 45S rDNA and HintCL-82 repetitive DNA clusters, and unbalanced translocations). Prevailing triploid *H. halleri* cytotype contains two genomes of *H. alpinum* and one genome of *H. intybaceum*, the pattern explaining the much closer morphological affinity of *H. halleri* to *H. alpinum*. Furthermore, cytogenetic and phylogenomic data indicate multiple origin of *H. halleri*. To conclude, multiple hybridisation events, post-hybridisation chromosomal rearrangements, and migration to the Western Carpathians have shaped molecular and biogeographic histories of this species.

S.234.4 Evolution and biogeography of the Ranunculus auricomus complex in marginal areas: from the Mediterranean to the circumarctic

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Young species complexes represent prime subjects for the study of speciation, hybridization and range expansion. The apomictic mode of propagation sometimes expressed in such groups can exacerbate the morphological and taxonomic complexity characteristic of hybridizing species complexes, as well as facilitating rapid expansion into new habitats. We focus on the facultatively apomictic *Ranunculus auricomus* complex in order to investigate the evolution, biogeography and taxonomic status of geographically marginal populations of this young (<1 mya) and rapidly radiating group. At the southern and northern edge of the groups range apomixis is the primary mode of propagation, with sexual reproduction occurring only rarely. Taxonomically, *Ranunculus auricomus* agg. is composed of a handful of sexually reproducing basal lineages occuring in temperate Europe, which through repeated hybridization have begotten manifold polyploid apomictic lineages. Given this, we also examine the patterns of ancestry in marginal areas, utilizing phylogenomic methods including subgenomic phasing. At the southern periphery we find no additional sexually reproducing species, supporting the recognition of many newly described apomictic hybrid taxa in the region as nothotaxa. In the circumboreal-circumarctic zones we focus on a particular morphogroup, typified by the diminutive *Ranunculus monophyllus* Ovcz. Individuals included in this morphogroup exhibit dwarf growth, high ploidy levels (4x-6x) and obligate apomixis. In order to test the plasticity of traits distinguishing *R. monophyllus* from other morphogroups, we conducted climate chamber experiments which showed little phenotypic plasticity in key morphological traits in response to temperature. We conclude that dwarf growth is adaptive and evolved multiple times during colonization of Northern marginal areas. Biogeographical analyses of the whole complex based on phylogenomic data will show the expansion of the *R. auricomus* complex in space and time, contributing to our understanding of geographical parthenogenesis.

S.234.5 Evaluating a drought-driven hypothesis for the origin of obligate apomixis in ferns

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Obligate apomixis -- asexual reproduction by seed, spore, or egg -- has evolved repeatedly across the tree of life, in diverse organisms ranging from animals (such as reptiles, insects, and fishes) to angiosperms and other plants. Despite its many origins, and the intriguing ecological and evolutionary parallels among them, little is known regarding the causes and long-term consequences of this heritable reproductive syndrome. Some studies suggest that drought, or periodic water limitation, could be key to driving the repeated evolution of obligate apomixis. To evaluate the drought hypothesis, we are uniting genomic, spatial, environmental, and life history data (across multiple evolutionary and ecological scales), leveraging ferns as a model system. Current estimates indicate that 10–30% of ferns exhibit obligate apomixis, which has evolved repeatedly in xeric and monsoonal environments around the world. Dry environments impose major constraints on plant life histories and the fern life cycle is especially vulnerable. In this study, we focus on North American desert ferns, integrating reproductive traits (karyotype, gametophyte development, and spore size/number), climate and microhabitat, and phylogenomic data to specifically ask: Does environmental niche predict obligate apomixis or its constituent traits in desert ferns of North America? This work aims to further bridge generational gaps in technical expertise among next-generation researchers for a variety of cutting-edge and classical approaches, stimulating interdisciplinary student-driven research that emphasizes the value and relevance of museum specimens for addressing fundamental biological questions.

S.234.6 The origin and evolution of apomixis-related chromosomes in Boechera (Brassicaceae)

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The genus *Boechera* (Brassicaceae) comprises approximately 480 genetically distinct taxa, predominantly distributed in North America. Characterized by a basic chromosome number of $x = 7$, the genus includes diploid sexuals ($2n = 14$), diploid apomicts ($2n = 14, 15$), and triploid apomicts ($2n = 21, 22$). The extensive morphological diversity within the genus arises from frequent hybridization among diploid species, leading to the emergence of apomictic diploid hybrids. Triploids have independently arisen through hybridization between sexual and apomictic diploids. Notably, apomictic *Boechera* plants feature two heterochromatic B-like chromosomes (Het and Del). With a small genome size, close evolutionary ties to Arabidopsis, and the coexistence of diploid sexual and apomictic lines, *Boechera* stands as a unique model system for exploring genomic changes associated with apomixis. This study, employing cutting-edge cytogenomics and phylogenomics approaches, delves into the genome structure and evolutionary dynamics of sexual and apomictic *Boechera* plants. By unveiling the origins of chromosomes linked with apomixis, our findings contribute valuable insights into the broader cytogenetic foundations of apomixis, advancing our understanding of reproductive strategies in plants.

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S.235 INTEGRATING ECOLOGY INTO MACRO AND MICROEVOLUTIONARY STUDIES PROBLEMS AND OPPORTUNITIES IN CURRENT AND PAST DATA SOURCES

S.235.1 Ecological and evolutionary drivers of current plant diversity in North America

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The North American continent is characterized by striking diversity in climate, geology, and soil, which have together shaped patterns of plant diversity. With nearly 40,000 species of seed plants and >20% of the world's seed plant flora, North American plant communities differ in species richness, phylogenetic diversity, and their resilience in the face of climate change. Analyses of eco-evolutionary dynamics have demonstrated processes of community assembly and species diversification that have contributed to geographic structure of plant diversity at continental, regional, and local levels. For example, differential patterns of species diversification and temporal impacts of community assembly appear to have led to distinct patterns of phylogenetic diversity in eastern versus western North America. Moreover, biodiversity hotspots were identified in Mesoamerica, central Mexico, California, and Florida, with corresponding centers of endemism in Mexico, the southwestern USA, and the southeastern USA. Ongoing studies are integrating traits, phylogenies, and distributional data to forecast risks and resilience – both phylogenetically and regionally – in the North American flora. The North American Coastal Plain, a global biodiversity hotspot that encompasses the southeastern USA and extends from Texas to the northeastern USA, is a composite of areas of paleo- and neoendemism, which in some cases correspond to regions of significant habitat heterogeneity. Environmental gradients in temperature and precipitation have shaped plant distributions across the hotspot, producing a patchwork of lineage-based adaptive zones. Many rare lineages converge in Florida, where areas of high and low phylogenetic diversity are in close juxtaposition and regions of high endemicity correspond to key structural features such as ridges and river valleys. These nested analyses at multiple geographic scales promise new perspectives for conservation.

S.235.2 The splendid isolation of the South American continent for angiosperms: tempo, rates and the role of distance and temperature

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South America was an island continent separated from other landmasses by large open seas for more than 50 million years. It was only when the Isthmus of Panama emerged from the sea, about 3 Mya, that South America came into contact with North America and the Great American Biotic fauna Interchange (GABI) began. The long-term confinement of South American mammals resulted in the evolution of an exceptional endemic fauna, giving rise to the so-called "Splendid Isolation" diversification pattern proposed by Simpson. Nonetheless, whether this model can be extended to explain the outrageous diversification of the Neotropical angiosperm flora remains uncertain. It is unclear whether the isolation of South America was as strict for plants as it was for other groups of organisms, or whether angiosperms were able to disperse from other landmasses uninterruptedly during the isolation. It remains to be clarified as well, to what extent the arrival of new colonizers contributed to the extraordinary diversification pattern observed in the Neotropics today. To understand the effect that the disconnection of South America had on the evolution of the Neotropical flora, in this study we reconstruct the global biogeographic history of angiosperms and examine the proportion of dispersal events into and out of the Neotropics that occurred throughout the Cenozoic. We also investigate whether abiotic factors such as geographic distance or temperature directly affected dispersal opportunities into the Neotropics. Given the higher dispersal capacity of plants than animals, we hypothesize that the "Splendid Isolation" model will not hold for the Neotropical flora, and that several dispersal events between the Neotropics and other continents will be recovered during the Cenozoic.

S.235.3 Reconstructing past niches: the link between quantitative paleobotany and phylogenetic reconstructions

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A comprehensive understanding of the ecological niches occupied by the ancestors of today's plant clades is essential for elucidating the evolutionary pathways that have shaped contemporary diversity. Integrating present-day observations with fossil records is crucial for studying these niches accurately. However, incorporating fossil information into phylogenetic ancestral reconstructions is challenging due to the limited direct information on the ecological niches of fossilized plants. Our work reviews the primary uses of fossils in niche reconstructions and identifies significant gaps in fossil knowledge. Deep time reconstructions often rely on morphological analyses of fossils due to difficulties in obtaining niche information from ancient specimens. Traits of extant plants like stomata, growth rings, tracheid size and thickening types, or foliar architecture (e.g. CLAMP) have proven to be indicative of present climatic conditions and in some cases are utilized for paleoclimatic reconstructions. However, the use of plant traits is based on inferences made on certain groups of extant plants and loses its applicability in deeper time as the taxonomic and atmospheric differences become so great that the comparison is unreliable (e.g. studies stomatal density in Carboniferous Pteridosperm leaves do not show consistent results). Additionally, the use of traits of the plant taxa themselves could lead to circular reasoning. Alternative methods, such as isotopic analyses and sedimentology, offer additional evidence on the abiotic conditions in which the plant fossilized evidence but face limitations in data scarcity. Our review examines plant traits, sedimentology, and stable isotope data from 15 fossil taxa (spanning from 470 to 100 Ma) that are commonly used to calibrate the land plant tree. This forms the basis for developing a methodological framework to infer the ancestral niches of the main clades of extant land plants, ensuring consistency and comparability in future research.

S.235.4 Plant palaeoecology of the Late Cretaceous in Central Europe and its bearing on angiosperm dispersal

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Early angiosperms and their environment are frequently discussed topics in palaeobotany. However, detailed reconstructions of their environment are not always available. In the present study we reconstruct five major terrestrial palaeoenvironments, some dominated by angiosperms, from the Cenomanian Peruc-Korycany Formation of the Bohemian Cretaceous Basin in Central Europe. The present taphonomic studies are based on long term observations of plant macro-, meso- and microfossils providing detailed information about plant communities during that time period. The environmental conditions and plant communities, ordered from sea inwards, are reconstructed as follows: 1) Salt marsh environments dominated by cheirolepidiaceous conifer *Frenelopsis alata*, 2) Coastal wetlands dominated by cupressoid conifers (typically *Cunninghamites lignitum*), 3) Meandering rivers characterised by lauroids (*Myrtophyllum geinitzii*), 4) Braided rivers dominated by lauroid angiosperm *Mauldinia bohemica* (with *Eucalyptolaurus* sp. foliage), 5) Upland vegetation characterised by fern prairies. This study shows a diversity of angiosperms in alluvial plains, with prevailing lauroids and platanoids. The reconstruction of the upland vegetation, interpreted as fern prairie shows also a diversity of ancient angiosperm groups with particularly affinities to ANA group and Chloranthaceae. Comparisons of the Late Cretaceous (Cenomanian) palaeonvironments with the Early Cretaceous (Barremian-Albian) palaeoenvironmental conditions from the Lusitanian Basin in western Portugal shows remarkable and interesting differences. In the Early Cretaceous environments, angiosperms are interpreted as herbaceous and shrubby plants growing in disturbed habitats. While in the Late Cretaceous angiosperms were already part of canopy forming arborescent and shrubby vegetation in alluvial plains of both meandering and braided rivers.

S.235.5 A pipeline to include the species climatic heterogeneity and the complexity of the world's climate in ancestral reconstructions

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Current approaches that integrate climatic niche in evolutionary studies often fail to consider the climatic heterogeneity of species, the climatic context in which they live and the complexity of the World's climate. Indeed, evolutionary studies often resort to climatic classifications to deal with the World's climatic complexity or to summary statistics to address the heterogeneity of the species climatic preferences. In this study we evaluate the impact of using different types of climatic data (discrete and continuous) and comparative approaches (character state, quantitative and probabilistic) to reconstruct climatic niche evolution in the Asian Palmates of Araliaceae, an example of the tropical-temperate diversity pattern. We used phylogenomic reconstructions, worldwide point-occurrence database of the Asian Palmates and five classification schemes of the World's climate. We used discrete categorization of genera (tropical or temperate) for the character state reconstruction and the first axis of a climatic PCA for the continuous-based reconstructions, using summary statistics for the quantitative approach and the complete climatic space of each genus for the probabilistic one. The character state and the quantitative reconstructions using maximum and minimum values were inconclusive. Instead, we disclosed a general preference of the Asian Palmates ancestors for the subtropical and tropical climatic transition when using the mean and median values. The probabilistic approach allowed us to uncover the narrow ancestral climate niches of the ancestors in comparison to the broad niches of the extant genera. We propose the probabilistic approach at least for lineages with high climatic heterogeneity or living in highly heterogeneous regions. However, since the precision of this probabilistic approach is highly dependent on the accuracy of the distribution data, we also provide a pipeline to consider climatic heterogeneity and the complexity of the World's climate for ancestral reconstructions in lineages in which the knowledge of species distribution is poor or biased.

S.235.6 Phylogenetic diversity and regionalization of root nodule symbiosis

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Among the most vexing questions in legume biogeography is why non-nodulating and facultatively nodulating legumes, i.e., those that do not or need not engage in RNS with rhizobia, are preponderant in the tropics, whereas extratropical areas have almost entirely nodulating legumes. Understanding the environments associated with loss of symbiosis would yield more precise insight into the ecological function that nodulation confers in natural ecosystems. Here we determine centers of species richness (SR), relative phylogenetic diversity (RPD) and centers of paleo- and neo-endemism, and regionalizations of phylogenetic diversity in the mimosoid clade of the legumes to understand the distribution and environmental associates of mimosoids lacking RNS (root nodule symbiosis). We built a phylogenetic tree of 1313 species and high-quality species distribution models for 1128 species representing the phylogenetic breadth of the mimosoid clade to identify the geographic distribution of RNS. Centers of significant RPD and endemism were identified using a randomization approach, the latter using CANAPE. Phylogenetic regionalization used a distance-based phylogenetic beta-diversity approach. We recognized nine areas of contiguous high SR as distinct SR hotspots. Non-RNS species occur mainly outside hotspots but are closely correlated with high RPD. Absence of RNS was best predicted by high precipitation, and represents multiple independent phylogenetic assemblages in different biogeographic areas. SR hotspots are partly incongruent with centers of RPD and phylogenetic endemism. Lineages lacking RNS, likely to represent loss of symbiosis, are distributed in SR hotspots in Africa and the Americas, belong to biogeographically separate species assemblages, and are, in most cases, associated with relatively moist tropical environments with low temperature seasonality and high available soil nitrogen.

S.236 EVOLUTIONARY TRENDS IN SKY-ISLANDS: NEW INSIGHTS IN THE SEARCH OF MAJOR BIOGEOGRAPHIC AND PHYLOGEOGRAPHIC PATTERNS

S.236.1 Niche conservatism prevails in repeated long-distance colonization of Madagascar mountains by the genus Helichrysum (Compositae)

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Madagascar is a world's biodiversity hotspot, showing exceptionally high levels of species richness and endemism. Despite the island's prolonged geographic isolation (150 to 160 Ma from Africa, 84 to 90 Mya from India), most of its extant endemic plant species are the result of recent long-distance dispersals, mainly from continental Africa. The genus *Helichrysum* is a relevant study-case to explore the evolutionary and biogeographic history of Malagasy flora because it represents one-fifth of the Compositae species of the island. We generated a time-calibrated phylogeny of 350 *Helichrysum* species (including 60% of the Malagasy endemics) based on target-enrichment DNA sequence data and conducted ancestral range estimation analyses. Our results reveal at least six independent dispersal events to Madagascar from African regions since the Pliocene. Notably, Madagascar was colonized at least twice by lineages originating from the Tropical Afromontane region, leading to significant subsequent radiations in the island's highlands and mountains. The southern African montane grasslands have also played a key role in Madagascar's colonization, originating at least three clades on the island, one of which notably diversified. *Helichrysum mahafaly*, endemic to the arid SW region of Madagascar, was inferred to originate from an ancestor coming from the arid region of SW Africa. The similarity of habitats between source and colonized areas suggests the prevalence of niche conservatism, a common phenomenon in allopatric speciation following the colonization of a newly isolated region. Our results underscore the affinities between continental Africa and Madagascar's montane floras. The main radiations of *Helichrysum* in Madagascar's mountains occurred within the last 2 My, coinciding with a transition towards a cool, arid climate and the expansion of open habitats, and were likely driven by a combination of allopatric and ecological speciation.

S.236.2 Evaluating the role of evolutionary processes in the differentiation of Dendrosenecio species from Mount Kenya

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Mountains are dynamic regions that undergo tectonic, erosional and climatic processes over a short geological time period. These processes make mountainous regions highly heterogeneous environments with a wide variety of topographic features. Such habitat heterogeneity and dynamics generate increased opportunities for lineage differentiation through ecological adaptation, geographic isolation and secondary contact. The afroalpine vegetation belts on the top of the East African mountains are highly isolated both geographically and ecologically, which makes them a great system to study evolution and speciation. The genus *Dendrosenecio* evolved independently in four geographically isolated afroalpine mountain groups, mainly as a consequence of reduced gene flow between these mountain groups. At the same time, populations of different *Dendrosenecio* species are sometimes found in sympatry, which could be evidence for ecological speciation. In this study, we focus on two sister species, *D. keniensis* and *D. keniodendron*, that likely evolved on Mount Kenya and show clear differences in morphology, flower phenology, reproduction and ecology. These species can be found growing sympatrically, and the existence of a hybrid zone has been reported. We employed vegetation plot information and dd-RADseq data together with population genomic tools to evaluate the extent of habitat differences, genetic differentiation, and the demographic processes involved in the divergence between these two species. In particular, habitat similarity between the two species on Mount Kenya were analysed, genetic differentiation between them was evaluated, and ecological speciation was tested against geographic speciation followed by secondary contact. Vegetation plot data showed a negative relationship between both species, genetic differentiation supported two well differentiated groups, and demographic modelling supported a speciation-with-gene flow scenario. Taken together, these results suggest that ecologically mediated speciation occurred between these two *Dendrosenecio* species from Mt. Kenya.

S.236.3 Pleistocene climatic cycles, landscape dynamics and the late rise of sky island vegetation in the Alps

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How past orogeny, landscape dynamics and climate change drove the emergence of species-rich mountain floras remains poorly understood. Here, we aim to uncover how the physical history of a range influences the assembly of its biodiversity in the context of the European Alpine sky island (ASI) flora. Using newly sequenced chloroplast genomes for 96% of the flora, we reconstruct a time-calibrated phylogenetic tree to infer temporal changes in assembly rates. We show that the majority of the flora assembled via colonisation rather than diversification, and experienced high rates of extinction over the course of its evolution. The accumulation of extant lineages was decoupled from major orogenic events, such as the initial uplift of the Alps and the later rise of the peripheral massifs. Most ASI lineages instead originated within the last 5 Myr. The Quaternary climate oscillations had the strongest impact on colonisation and diversification rates, which increased substantially during the Pleistocene glacial cycles. A search of existing biogeographic literature showed that many ASI lineages originated locally in Europe, rather than through long distance dispersal from temperate Asian ranges. We conclude that the ASI flora consists of a continuous subset of the European flora, potentially filtered by the ability to disperse into the sky islands after the disturbance of the Pleistocene glacial cycles. Our findings contradict established theories of Alpine plant biogeography, likely because by analysing the entire flora we include species-poor lineages that comprise an overlooked, but important, component of the flora.

S.236.4 Post-glacial expansion patterns and hotspots of intraspecific diversity for high elevation plants in the Pyrenees: a multi-species

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The urgent need for preserving biodiversity is beyond any doubt. However, not all components of biodiversity are usually taken into account. For a long time, conservation efforts have targeted ecosystems or species; in recent years, a new focus has been put on cryptic intraspecific diversity on the gene level. In mountain ranges of the temperate regions, intraspecific diversity has been strongly determined by the Pleistocene glaciation cycles. We here focus on the Pyrenees, a hotspot of plant diversity in western Europe with more than 4,300 plant species, but still lacking an assessment of intraspecific diversity features. We aimed to reconstruct the response of alpine plants to the last glacial period and to identify areas of high intraspecific phylogenetic endemism, which are ultimately of special interest for conservation. For this purpose, we used a multi-species comparative phylogeography approach combining molecular data (RADseq) and retrospective as well as prospective distribution modelling of species and intraspecific lineages. Our results show a highly structured distribution of intraspecific diversity, which allows to formulate the first molecular-based hypothesis of glacial refugia for alpine plants in the Pyrenees. Refugia of calcicolous species were in weakly glaciated ranges south of the main chain, while silicicolous species show a pattern of multiple geographically incongruent genetic groups, indicative of species-specific reduced size refugia and nunatak survival. The easternmost Pyrenees emerge as a common refugium for most of the studied species and contain high levels of phylogenetic endemism, rendering them an area of major interest for conservation of intraspecific diversity.

S.236.5 Interglacial refugia shape the distribution of apomict allopolyploid Hieracium halleri on European 'sky-islands'

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Interglacial refugia serve as counterpoint to glacial refugia for cold-adapted species widely distributed during the glacial maxima but forced to retreat due to changing climatic conditions and increasing competition from new immigrants during interglacial periods. European 'sky islands' function as climate refugia for many hybridogeneous species whose origin might be clouded by demographic processes like founder effect, bottleneck, selection and genetic drift. Yet in allopolyploid apomictic species, i.e., hybridogeneous species which reproduce by seeds without fertilization, severe gene flow reduction and few meiotic rearrangements, preserve the progenitor genotypes and therefore allows for exploring previous contacts and subsequent local extinctions of their parental lineages. We explored the origin, genomic composition and post-polyploidization population dynamics of the apomict *Hieracium halleri* (triploid and tetraploid) that evolved through hybridization between diploid *H. intybaceum* (2n=18) and diploid or triploid *H. alpinum* (2n=18, 27). We aimed to investigate the tempo of recurrent establishment of asexual cytotypes of *H. halleri*, elucidate whether the differences in evolutionary histories of these cytotypes is reflected in their genetic variation, morphology, recent distribution, and ecology. The genetic structure of hybridogeneous apomictic species and its progenitors was explored using RADseq loci. For the allopolyploid apomicts, haplotypes were obtained with alignment-based phasing that segregated data originated from the parental subgenomes. We performed chromosome scale assembly of one of the progenitors (*H. alpinum,* genome size ~ 4G) and created a pseudoreference for the other by RAD loci concatenation. The repeated independent polyploidization events were dated using whole plastome and Hybseq low-copy nuclear genes alignments. We also presented the read-mapping approach method to identify subgenomes in hybrid. Thus, an integrative approach allowed us to decipher evolutionary history and biogeography of this widely distributed apomict.

S.236.6 Frailejones in Sky Islands: insights into their evolution, biogeography, and conservation

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Páramos, located above the timberline in the Tropical Andes, are remarkable examples of sky islands, and are often considered the world's most diverse and fastest evolving ecosystems of the high elevations. Frailejones (common name here referred to all the species within the Espeletiinae, Asteraceae), are the most representative plants of the páramos. With circa 144 recognized species, most endemic but locally abundant, these plants are a model to understand not just biogeographic and phylogenetic patterns in sky islands, but also their conservation challenges under the pressing world's environmental crisis. We present the state-of-the-art regarding our knowledge on these aspects. The most recent insights into their phylogeny using *Hyb-Seq* on 1269 nuclear loci, support the hypothesis of two large clades (i.e., Venezuelan and mainly Colombian clades), radiating in the last 2.5 Ma, from Venezuela into Colombia and more recently into Ecuador. The support for the previously established genera is conflictive, exacerbated by the frequent interspecific hybridization. Regarding their conservation status, our most recent conservation risk assessment for Colombia suggests that 55 (61%) of the 90 species found in the country are under threat, and 40 (45%) species are endangered. *In-vitro* and *in-situ* propagation of some of these species is underway. Based on a comprehensive dataset of georeferenced records (5,560 records for 138 species), we implemented the Important Plant Areas (IPAs) approach, using units of analyses of 100 km^2. We identified 176 potential IPAs using the distribution of records of globally threatened species (including 59 species), and 51 potential IPAs when considering species richness (including 76 species). We assessed gaps based on currently established protected areas and found that only 27% of the potential IPAs are within those areas, and 73% face significant human disturbances. These results inform priorities for conserving these keystone species for the páramos of the northern Tropical Andes.

S.237 ATYPICAL SUBSTRATES FOR PLANT AND LICHEN EVOLUTION II: ULTRAMAFIC SOILS

S.237.1 Investigating the diversity and function of microorganisms in serpentine and non-serpentine soils across California

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Serpentine soils, characterized by high heavy metal levels and magnesium-to-calcium ratios, exert selective pressure on plants and microorganisms. While some plants are endemic to these soils, most struggle to survive. Our research revealed that serpentine-indifferent plants, thriving on both serpentine and non-serpentine soils, may be sustained by their association with locally adapted plant growth-promoting bacteria. The role of microorganisms in supporting plant diversity and ecosystem services is being explored, and characterizing taxonomic and functional microbe diversity on and off serpentine soils is crucial. Our project aimed to identify taxa associated with serpentine or nonserpentine soils, characterizing microorganisms' plant-growth-promoting properties across California. Shotgun metagenomic sequencing and physiological assays were conducted on soil samples from 23 sites. Kaiju and MEGAN6 were used for taxonomic classification and functional analysis. After removing contaminants, 41,326 taxa were identified, with similar abundance and alpha diversity across serpentine and nonserpentine soils. Soil chemistry and location significantly shaped bacterial and eukaryotic communities, not archaeal ones. Random forest analysis highlighted features like Mesorhizobium, Rhizobium, and Pontibacter in nonserpentine soils and Nitrosophaera and Pontibacter in serpentine soils. Preliminary functional analysis revealed Ni/Fe subunits and siderophore production functions. Siderophore production was influenced by nickel presence, with higher levels in serpentine soils. Approximately 50% of microorganisms from both soil types fixed nitrogen, and 20% solubilized phosphorus. This study enhances our understanding of nutrient cycling in metal-rich, drought-prone soils, impacting plant-microbe interactions, agriculture, and bioremediation. The findings inform conservation policies, aiding efforts to preserve unique soil ecosystems and their microorganisms.

S.237.2 How ultramafic soils can affect plant-herbivore interactions

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The unique features of atypical substrates such as ultramafic soils can have important effects on organismal interactions and may provide stimulating avenues for research. Some ultramafic soil plants (metal hyperaccumulators) have extraordinarily elevated metal concentrations (most often nickel). Hyperaccumulated nickel can defend plants against some (unadapted) herbivores and therefore act as an elemental chemical defence. Elemental defences differ from more widely studied organic chemical defences because the toxin is absorbed from the soil (rather than being constructed from photosynthetic products) and an elemental defence cannot be obviated by breaking it down into constituent parts (which is one way that organic defence chemicals can be detoxified by herbivores). But some herbivores (such as the heteropteran *Melanotrichus boydi*) have apparently evolved metal tolerance and thus can feed with impunity on nickel hyperaccumulators. Elemental defences may even benefit plants that accumulate elements at levels lower than hyperaccumulation thresholds, especially if elemental defences and organic plant defences have additive or synergistic joint effects. This aspect of elemental defences needs further investigation. Plant-herbivore interactions may also influence the color of plant species growing on ultramafic soils. For example, there is a striking correspondence between substrate color and seed coat or leaf colors of some California serpentine plants, suggesting that visual apparency of these plants to herbivores may drive evolution of traits such as seed coat or leaf color. Visual apparency may be an under-studied aspect of plant-herbivore interactions on serpentine and other atypical soils.

S.237.3 The diversity of mineral nutrition in a diverse shrubland on ultramafic soil is revealed through community ionomics

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High species richness is observed in some shrublands growing on infertile substrates. Mineral nutrients may be the main limiting resources in such ecosystems and underground interactions between plants are probably a key to understand their diversity. Here we tested whether there was a nutritional differentiation between plant species co-occurring in a shrubland in an edaphically extreme environment. We designed a 20 × 20 m plot in a diverse shrubland ("maquis") on ultramafic (infertile) substrate in New Caledonia. We sampled all 475 plants taller than one meter and we characterised their ionome (22 elements). A total of 37 species were recorded, including a few abundant species and many rare species, representing all major types of mycorrhizal symbioses, nitrogen-fixing plants (actinorhizal but not Fabaceae), cluster rooted and parasitic plants. Both nickel- and manganese-hyperaccumulating species were present in the plot. Using hypervolume approaches, we observed limited overlap in the ionome of the 10 most abundant species. The functionally most distinct species were also the rarest ones in the plot. A diversity of nutritional strategies was represented in the plot, as indicated by the diversity of root symbioses and differences in leaf ionomes. These special nutritional traits associated with adaptation to the infertile substrates meet the expectation of the theory of the Old Climatically Buffered Infertile Landscapes (OCBIL). Our results suggest that partitioning into different biogeochemical niches, including highly specialised ones, could explain the coexistence of a large number of species in this shrubland on infertile substrate.

S.237.4 Ophiolitic substrates as drivers for reticulate evolution in Armeria (Plumbaginaceae)?

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Ultramafic substrates can play a role in fostering ecological adaptation and microevolutionary dynamics. The Italian endemic *Armeria denticulata* complex includes two species (*A. denticulata* and *A. saviana*): the former is a serpentinophyte endemic to Tuscany and western Liguria, the latter grows on limestone/jasper in a small area of southern Tuscany. Intriguingly, also northern Apennine populations of *A. arenaria* subsp. *praecox*, a subspecies otherwise endemic to western Alps, grow on ophiolites. Finally, the central-southern Italian endemic *A. gracilis* is strictly linked to limestone. We aimed at understanding whether substrate specificity and/or hybridization-introgression promoted speciation in the *A. denticulata* complex, despite similar ecological conditions failed to cause speciation in the nearby *A. arenaria*. We extracted DNA from two populations of *A. arenaria* subsp. *praecox*, three of *A. denticulata*, one of *Armeria saviana*, and one of *A. gracilis*. Sequencing was conducted using genome skimming on a NovaSeq sequencer, gathering about four Gb of sequence information per sample. After quality trimming of the reads, we performed reference-based assembly of plastomes (152kb) and nrDNA (ETS+ITS+rRNA regions, 12kb altogether) to infer phylogenies. The genomic data were complemented by a morphometric study using a Principal Component Analysis (134 individuals × 27 characters). Phylogenomic results suggest that *A. saviana* may have a homoploid hybrid origin involving *A. denticulatas*.str. (pollen donor) and *A. gracilis* (ovule donor), whereas a population of *A. denticulata* from inner Tuscany (Monte Ferrato) could have originated from an introgression/hybridization event between *Armeria denticulata* s.str. (pollen donor) and one of the haplotypes found in *A. arenaria* subsp. *praecox* (ovule donor). This is supported also by morphometric results, which highlight positions of the putative hybridogenic populations somehow intermediate between the putative parents in the morphospace. In summary, our results suggest that substrate specificity and hybridization/introgression prompted microevolutionary processes.

S.237.5 Exploring Nutritional Strategies in the Rich Gypsophile Flora of Mexico

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The accumulation of mineral elements in the leaves, such as S, Ca, Mg, and Sr, has been proposed as a set of important traits in gypsophile plants to cope with the edaphic and hydric stress posed by gypsisols. Mexico hosts the richest gypsophile flora globally, primarily concentrated in the Chihuahuan Desert and the Sierra Madre Oriental, although gypsum soils are scattered throughout the country. However, many functional aspects related to the adaptations of this flora remain unknown in this biodiversity hotspot, including those associated with the accumulation of the mentioned key mineral elements. To explore nutritional strategies, soil (15) and foliar (30) samples from two species of *Selaginella*, four ferns, and 24 angiosperms were collected on gypsum soils from the Valle de Tehuacán, the Sierra Madre Occidental (Colima and Jalisco), the Sierra Madre Oriental, and the Chihuahuan Desert. Of these species, 19 are considered gypsophiles, and 11 are gypsovags (Ortiz et al. 2023). Our initial hypothesis proposed that nutritional patterns are similar among Mexican plants growing on gypsum compared to those known in the Spanish gypsicolous flora, thoroughly investigated from this point of view. Our results confirm the high values for foliar mineral contents, typical of gypsophiles and some gypsovags (Merlo et al. 2019). These findings align with the high gypsum contents of Mexican soils; in 2/3 of the cases studied, gypsum contents were higher than 90%. However, we found notably high values for S, Ca, Mg, and Sr in some of foliar samples collected in Mexico. These results are not only consistent with those found for the Spanish flora, but we also extend them to the case of ferns and lycophytes, which are studied here for the first time.

References: Ortiz-Brunel, J.P. et al. 2023. https://doi.org/10.3390/d15040522. Merlo, M.E. et al. 2019. https://doi.org/10.1016/j.ecolind.2018.10.001.

S.238 NEW INSIGHTS ON BIG PLANT GENERA 1: DIVERSITY & DISTRIBUTION

S.238.1 The history of the colonization of the Southern Hemisphere by the megadiverse genus Carex L. (Cyperaceae)

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Carex (>2,000 spp) diversity is not equally distributed across the continents. This cold-adapted genus was originated in E Asia during the Eocene, from where it expanded and diversified across the Northern Hemisphere. The colonization of the Southern Hemisphere (SH) happened from the Miocene onwards. Remarkably, the resulting diversity levels in each of the landmasses are very different. South America (SA) and New Zealand (NZ) harbor the largest diversity compared to Africa and Australia. Here we perform a continental-level comparison of *Carex* evolutionary history in the SH. Results indicate that all the areas were recurrently colonized by different lineages. N to S migrations happened repeatedly from the Miocene to the Pleistocene, suggesting that no single bioclimatic event or colonization route were the triggers of the dispersal events. The number of groups in these areas increased towards the late Miocene, pointing that the Neogene global cooling facilitated colonization. Most lineages appear to be ecologically pre-adapted to SH cold/temperate climates, since little differences in the bioclimatic niche is observed compared their sister groups. Africa, NZ and SA displayed a few large in-situ radiations, which entailed to some extent niche diversification. Most diversity in NZ was explained by extensive radiation of two clades, which seemingly have had a competitive exclusion effect preventing the establishment or diversification of other lineages. SA diversity is equally due to in-situ diversification and also to a number of poorly diversified groups. The higher connectivity of SA with the Northern Hemisphere, and the larger available area for *Carex* to diversify, explains these differences. In turn, the relatively low diversity in Australia and Africa appears to be due to the limited ecologically available area in these landmasses. Essentially the differences respond to the huge *Carex* diversity and its diverse natural history, involving different taxonomic groups, geoclimatic events and colonization routes.

S.238.2 Systematics and evolution of the Euphorbiaceae giants (Croton and Euphorbia): recent findings, new insights, and current challenges

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The family Euphorbiaceae includes two of the most-species rich genera of flowering plants: *Croton* (~1,300 species) and *Euphorbia* (~2,060 species). *Euphorbia* is clearly defined by its highly specialized and unique inflorescence, the cyathium, while *Croton* is distinguished by a suite of morphological features. Taking their global distributions together, species of both or either of these genera are present in almost all biomes of the world. Many species are important for a variety of traditional human uses and for the development of products in the pharmaceutical and other industries. Numerous weeds and pioneer species are present in both genera, while ornamentals of high commercial value are common in *Euphorbia*. A robust phylogenetic framework is available for *Euphorbia* based on both Sanger sequencing and genomic data. Many of the recent advances in the systematics of *Euphorbia* have been focused on groups or species complexes distributed in Eurasia, Macaronesia and Africa. Unlike *Euphorbia*, phylogenetic relationships within *Croton* remain largely unresolved at deep and shallow nodes, but preliminary analyses using genomic data (HybSeq) show promising results for resolving the genus backbone as well as species relationships within its main clades or sections. Recent developments in our knowledge of *Croton* include the discovery of new clades, clarification of phylogenetic relationships and taxonomy of important sections, and the increasing incorporation of anatomical characters and development approaches in morphological studies, including both vegetative and floral structures. These have provided new insights into the evolutionary success of *Croton* in arid or seasonally dry habitats, and into the evolution of chemical and physical defenses against herbivores and pathogens. Major gaps in the biological knowledge of the two genera are highlighted, including suggestions for key questions to be addressed in future studies.

S.238.3 Why we recognize big genera? The birth of a big genus, Miconia (Melastomataceae)

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The tribe Miconieae (Melastomataceae) comprises ca. 1,900 species of Neotropical mostly shrubs and trees. For most of the 20th century between 17 and 22 genera were accepted in most treatments, and another ca. 12 were often recognized in the tribe. Phylogenetic analyses, first with a few genes and more recently with hundreds of genes, recover *Miconia* (the largest genus with close to 1,100 species in its old definition), as paraphyletic with all other genera embedded within it. Moreover, only four traditionally recognized are recovered as monophyletic, with some, like *Leandra* and *Ossaea*, recovered in at least a dozen clades each. A search for diagnostic characters that would allow recognition of a manageable group of smaller genera have proven futile due to a series of factors: 1-node stability and support, 2-changes in resolution with the addition of taxa, 3-well conserved and diagnostic characters being impractical for taxonomy (e.g. micromorphological features of seeds or internal anatomy), 4-well-defined and supported groups contain many taxa with reversals to plesiomorphic conditions rendering diagnostic characters unusable, and 5-well-supported and diagnosable clades are embedded in larger grades. Based on these factors we have proposed an expanded *Miconia* as the only genus in the tribe. *Miconia* s.l. is the seventh largest genus of flowering plants, and notably the only one among the 10 largest whose native range is restricted to the Neotropics. Recognizing *Miconia* s.l. highlights an extraordinary radiation that occurred in a relatively short amount of time. While the advantages of recognizing a single genus outweigh the disadvantages, this decision has some drawbacks. These include the size, making it unwieldy for monographic work, and subsumation of endemic genera that may impact their utility in conservation. We discuss how these issues are shared among megadiverse genera and address different strategies for tackling them.

S.238.4 Ancient origin and recent diversification of a giant genus: Evolution of Philodendron (Araceae) in the junction zone of Central & South America

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With >600 currently accepted species and an estimated total of 1500 species, *Philodendron* is the second largest aroid genus and one of the most diverse genera in Neotropical rainforests. It originated 29 Mya in the pan-Amazonian rainforests and diversified more intensely from the Late Miocene onwards, coinciding with the rise of the Andes and the formation of the Isthmus of Panama. Being South American in origin, the genus colonized Central America only relatively late from the Pliocene onwards. Nonetheless, the region is one of the centers of diversity and endemism of *Philodendron*, harboring >120 known species in Central America and Mexico. In all available molecular studies, however, representation of species from this region has been poor. In order to understand the evolutionary origin of the high Central American diversity, we used an exhaustive species sampling and a combination of three non-coding plastid regions (petD, rpl16, and trnK/matK). The phylogenetic results support 12 geographically well-defined clades in the large subgenus *Philodendron*, 10 of which consist of species from the Amazon, the Andes, and the Chocó Biogeographical Region. The vast majority of species from Central America, southern Mexico and the Caribbean were found in two distinctive and diverse Central American clades, apart from five smaller subclades and several single, rather widespread species nested within the South American clades. This pattern suggests at least nine colonization events in the region and several rapid radiations, especially in the Talamanca Mountain range and along the Isthmus of Panama. In summary, *Philodendron* has proven to be an ideal model group to study the historical biogeography and evolutionary processes of big plant genera in the Neotropics, the most diverse phytogeographic realm.

S.238.5 Twenty years of big genera

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Big plant genera are often considered the final frontier of plant systematics. Their size means that they are difficult to study in their entirety and as a consequence the taxonomy, systematics, evolutionary history, and ecology of these genera are poorly known. It is now 20 years since the last review of the history and concepts of big plant genera, when 57 such genera were recognized. There has been a proliferation in plant bioinformatics and taxonomic databases over the past 20 years, including the World Flora Online and Plants of the World Online. Here we review the current number, size, and geographic distribution of big plant genera based on the current data. We recognize 87 big plant genera, an increase of 30 genera, that collectively include 25% of all plant species. Of these genera, 28-29 are considered "megadiverse" with >1000 species each and account for 13% of all plant species. We discuss, with examples, the mechanisms behind the changes in the number and size of big and megadiverse genera since 2004. We compare the distribution of species in big plant genera to the distribution of flowering plants as a whole to demonstrate that big genera have diversified through the temperate and tropical regions of the world but are over-represented in temperate regions.

S.238.6 The evolution of Impatiens: phylogenomics and biogeography

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The *Impatiens* genus is well known to vary excessively, presenting extensive modifications in floral structure among its 1200 species. Most *Impatiens* lineages radiated just within the last 3 million years, indicating that these disparate floral forms can evolve rapidly, even among closely related taxa. Phylogenetic relationships in the genus have historically been difficult to intuit based on morphology, given numerous occurrences of convergent evolution, but also difficult to determine based on molecular characters, due to issues such as incomplete lineage sorting and hybridization. We present results of the first target enrichment approach to *Impatiens* phylogeny, using Angiosperm353 loci. In our tree with over 325 individuals from 250 taxa, we focus on resolving the phylogenetic relationships among African taxa, with a fine-grain focus on the endemic-rich Eastern Arc Mountains of Tanzania and Kenya. We also recovered plastomes for these samples and estimated the chloroplast phylogeny; we found several instances of discordance with the nuclear phylogeny. In the nuclear phylogeny, we found that endemic-rich clades generally diversify within mountain units in the Eastern Arc Mountains. This indicates ecological speciation in this case, and the important role of limited dispersal ability in *Impatiens* diversification. Conversely, we found the opposite pattern in the bird pollinated endemic-rich clades. However, the pattern for bird-pollinated taxa is not present in the chloroplast tree.

S.239 MTZ FLORAS, A WARNING LIGHT OF GLOBAL CONSERVATION FUTURE

S.239.1 Contrasting patterns for endangered flora revealed by 60-year land-use change analysis

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Land-use change analysis is widely accepted as a biodiversity conservation tool. However, it has seldom been used in the context of endangered plants. Our aim is to accurately quantify changes in land cover over the last 60 years in a selection of 58 populations of 43 Spanish threatened plants. Consequently, we explain how these changes correlate with major trends in biodiversity conservation such as human demography, ecological gradients or the spatial distribution of plant threats. A semi-automatic classification methodology has been used to identify land-cover changes by comparing aerial photographs from 1956 to 2019 in an established radius around field plots. Secondly, information from field plots and external databases was analyzed using GIS layers and PCA statistics. Land-use changes have been extensive throughout the sampled threatened plant populations. On the one hand, we find species inhabiting mountain areas, which are less prone to land-use changes because human activities are limited. On the other hand, species that have their habitats in coastal and/or urbanized areas. Hence, land-use changes define two groups in the endangered flora: a first group is related to high human densities, low elevation settings and low in situ protection, while a second group is related to the cessation in human pressure, protected area establishment and increase in forest cover. Based on our research, it can be concluded that passive rewilding is not the solution to conservation problems for plants, and could be counterproductive. Urban land-use changes present a more urgent issue, especially for those endangered plants in coastal areas. Finally, high herbivore density and richness compromise endangered plant populations growing at high elevation in protected areas.

S.239.2 Quantifying the potential niches of endangered plant species for improving reintroduction success

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One of the most severe threats to global biodiversity is land-use changes. Reintroduction is a major conservation tool, but its success relies on accurate estimation of the species niche. While niche modeling has been used to predict the distribution of plants, it has been rarely used as a tool for predicting reintroduction success. We aim to examine the possible use of niche modeling for improving endangered species reintroduction success and thus contributing to plant conservation efforts. The East Mediterranean basin is a hotspot of plant diversity, but due to dense population and massive urbanization, only a small fraction of the natural areas remains, challenging the finding of appropriate sites for reintroduction. Moreover, habitat suitability is rapidly changing with global climate change. We used species distribution models (SDM) to estimate the potential niche for reintroduction of endangered species based on known sites of occurrence. Reintroduction field experiments in natural reserves and agricultural land are currently performed for five endangered endemic plants- *Rumex aeroplaniformis, Verbascum berytheum, Salvia eigii, Onosma gigantea*, and *Vicia esdraeloninsis*- representing two endangered habitats: Loamy soils in valleys and coastal sandy soils. For those species, we also predicted future potential distribution using future climate projections. For all species, the model predicts a general decline in the potential distribution, particularly in the suitability of current population sites.

S.239.3 Composition, diversity and productivity of ruderal vegetation in Mediterranean peri-urban greenspaces

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Urban ecosystems are experiencing a significant growth worldwide. Cities include areas that provide important ecosystem services such as carbon sequestration and maintenance of biodiversity. In a context of global warming, it is necessary to increase knowledge on ecosystem services provided by Mediterranean urban greenspaces. Our study was focused on spontaneous vegetation in four periurban greenspaces located in Madrid (Spain). We aimed to analyse the composition, diversity and productivity of four plant community types widely extended in Mediterranean urban areas, namely annual graminoid grasslands, annual herbaceous communities on slope roadsides, perennial herbaceous communities and perennial graminoid grasslands. Plant species composition, productivity, diversity, cover of growth forms and functional groups were determined in 3 plots x 4 plant-communities x 4 greenspaces = 40 plots analyzed. We used generalized linear model to determine the influence of the community type on vegetation variables. We performed a cluster analysis by unsupervised agglomerative classification, to test numerically the vegetation types and to identify their diagnostic, characteristic and differential species. Our results showed that perennial herbaceous communities had a significant lower species richness in comparison to the other communities but a lower Shannon index and higher biomass when comparing them with herbaceous communities on slope roadsides and perennial graminoid grasslands. Besides, annual grasslands showed a significant higher abundance of individuals. Regarding functional groups, a significant higher cover of mucilage-accumulator plants was detected in the perennial herbaceous communities and of Sulphur-accumulator plants in the annual herbaceous communities on slope roadsides. The agglomerative classification identified two sub-communities within the vegetation type on slope roadsides. We conclude that plant productivity, diversity, and cover of functional groups and their associated ecosystems services, are unevenly distributed throughout urban greenspaces. Furthermore, their management should be addressed to preserve those vegetation types that better support biodiversity and carbon storage.

S.239.4 Regional application of a global conservation approach: spatial patterns of EDGE angiosperms in the Iberian Peninsula

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Determining the species or regions to prioritize for preservation stands as a key topic in Conservation Biology. Traditionally, this assessment relies on specific criteria such as the threat risk to a particular taxon or the richness of species for defining protected areas. However, incorporating an evolutionary variable into these analyses can be achieved through the utilization of mega-phylogenies. The EDGE (Evolutionarily Distinct and Globally Endangered) metric combines how evolutionary unique a species is, along with how likely it is to become extinct. Thus, a comprehensive global EDGE analysis allows the creation of a priority list, offering a quantitative measure of the importance of preserving each individual species. The Iberian Peninsula is a major center of plant richness and endemism within the Mediterranean hotspot, and the recent publication of the AFLIBER atlas with the distributions of all Iberian angiosperms using a 10 km grid, enabled the use of an EDGE analysis for the first time for a regional flora. We then determined which areas presented a higher conservation value, calculated as the sum of the EDGE scores of all occurring species in each area. Lastly, a prioritization list of areas for preservation was established using complementarity methods, maximizing EDGE conservation in a minimum area. Many selected areas were located in coastal or mountainous enclaves, often absent from national networks of protected spaces.

S.239.5 MTZ (MTE, Mediterranean type zones) floras, a warning light of global conservation future

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MTZ combines three main aspects basic in conservation science, biodiversity, threats and knowledge. It is one of the richest and highly diverse biome in the Globe, the most if we consider area extension. In addition, the MTZ floras are extensively studied and well known. Finally, MTZ has been for long, one of the more intensive conservation scenarios. We address two major points: **First, we review major current drivers of threats. We provide an update on some of the most acknowledged plant conservation problems,** such as land use changes (urbanization), fire, or herbivory. We also review the red list plants assessments in MTZ. **Then, we carry on a future prospect of conservation mediterranean plants, addresing future scenarios of conservation efforts.** More specifically, we question: are different MTZ areas responding differently to common conservation challenges? For that we explore trends in extinction rates and threatening processes, delineating what types of plants are becoming more threatened and why. This will allow us to identify possible conservation gaps in plant conservation. We also deal with future trends in protected areas: National Parks, microrreserves and urban areas in relationship with plant conservation.

Finally, we introduce flora rewilding as a restoration approach for plant conservation. We identify some current and future projects. We propose some tools for a global system of plant biodiversity and conservation monitoring in the five MTZ.

S.239.6 200 years evolution of an urban remnant habitat

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Urban biodiversity is originated by the curse of urban history, biogeographical context, and disturbance regime. Therefore, several species groups and functionalities conform present urban biotas, conforming a mixture of novel ecosystems and remnants of natural habitats. Recently, urban settings have been considered perfect scenarios to develop nature conservation and restoration actions. However, because of this mixed origin and rapid changes, the frontier between nature and cultural conservation may be fuzzy and true conservation measures could be mistaken for traditional horticultural practices. The study of the evolution of remnant natural habitats immersed in the urban matrix can contribute to clarify future trends of urban biodiversity conservation. We hypothesized that urban remnants evolve differently than the rest of urban green habitats by maintaining, not also more species diversity, but also better functionality. Further, they may respond in different ways to urban perturbations. Our main objectives are: (i) To record gain and losses for native and non-native plants for a 200-year period in a remnant habitat, Casa de Campo (Madrid), and to compare it with the rest of urban green habitats.

(ii) To study rare- common species conformation during this period. (iii) To study functional diversity and functional spectrum. By compiling plant records from different inventories performed in Casa de Campo and Madrid during the last 200 years, we recorded losses and gains of species (discovery and extinction rates) in both Casa de Campo and the rest of the city and simulated how different scenarios of plant species change may affect functional diversity in the remnant habitat and its surroundings.

S.240 INTERDISCIPLINARY APPROACHES IN THE VISUAL ARTS AND THE BOTANICAL SCIENCES

S.240.1 "Iconotypes" at the Natural History Museum Vienna and the importance of color systems, such as those utilized by Ferdinand Bauer

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Aside from the more commonly selected herbarium specimens for this purpose, a botanical illustration, in particular a historical one, can also serve as type for the name of a taxon. Although the term "iconotype" is not formally used in the International Code of Nomenclature for Algae, Fungi, and Plants, it is generally understood to be an illustration that serves as the type for the name of a taxon. For example, the lectotypes of many Linnaean binomials are illustrations. When a type specimen is lost or destroyed, illustrations prepared from the original material can be candidates for types; such illustrations are obligate lectotypes when all other original material has been lost. The Archive for the History of Science at the Natural History Museum Vienna holds many such "iconotypes." These include illustrations used in Jacquin's, Schott's, and others' taxon descriptions. Use of illustrations as types is facilitated if they were made using standardized coloration. An outstanding example of this is the work of Ferdinand Lucas Bauer. Bauer's pencil field-sketches, now almost all at the Natural History Museum Vienna, were the bases for colored illustrations (mostly now at The Natural History Museum London), some of which are types. The drawings are important, as they include information omitted from the final, colored illustrations, such as collection localities, dates, and additional detailed sketches of descriptive morphological characters. The field drawings enabled Bauer to produce colored plates of exceptional aesthetic and scientific quality by employing numerical and other codes, which indicate the hue, brightness, opacity, and texture of particular parts of the living organism.

S.240.2 Botanical motifs in the visual arts in China: an alternative look at nature

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It is well known that plant elements (flowers, leaves, fruits, but also whole plants) are a recurring motif in the different expressions of visual art (mainly painting, ceramics, sculpture and architecture) in most cultures and civilizations. In the case of East Asian countries (China, Korea and Japan) botanical motifs have an even more evident weight in their art, mainly due to the dominant religion and philosophy (mainly Taoism, Buddhism and Shintoism) in which nature and respect for it is a common thread of many of their principles. In this contribution we are focusing on the case of China, a place where "artistic botany" reached its maximum expression thanks, most likely, to the astonishing wealth of plant species and different landscapes that the country houses. This great diversity may have constituted a substrate and at the same time a catalyst for the rooting of beliefs and precepts in harmony with nature and, in turn, a source of inspiration for artists. Some examples of plant motifs used profusely in Chinese visual art will be presented, corresponding to various historical periods, including Buddhist, Taoist and Confucian symbols. These will be used as vehicles through which we analyze China's flora from a scientific point of view, both in aspects of diversity and conservation. Finally, the possibilities offered by the resurgence of Buddhism and Taoism in China for the conservation of its biodiversity will be also discussed.

S.240.3 Kaleidoscope Science: using herbarium specimens, scientific illustrations, and printmaking to provide a holistic perspective on na

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Transdisciplinary approaches to science, specifically science/art, increase student learning and engagement and retain underrepresented groups in STEM, and using art to engage the public has been the source of many broader impacts. An area of transdisciplinarity that is understudied and underutilized is embracing our "transdisciplinary self". People are multifaceted, from their biology to their culture. However, we often find ourselves in a self or socially enforced silo. This is common in science, where specialization isolates disciplines, ways of thought, and collaboration. Instead of dividing ourselves into categories like "scientist," "artist," "student," "gamer," "teacher," we should be embracing all of them to inform our "transdisciplinary self." By bringing our whole selves to our research, outreach, and teaching, we produce more meaningful outcomes. Through my experiences leading National Science Foundation funded science art outreach projects, conducting scholarship of teaching and learning research, and developing my artistic practice, I understand that by being our transdisciplinary selves, we make science art that achieves more than just communication. To accomplish this, I worked with Visual Arts faculty at the University of Wyoming to develop a project that exemplifies the idea of the transdisciplinary self. Kaleidoscope Science is a science art outreach project using photo processes and printmaking to showcase the complexity of native organisms. These organisms are viewed through many lenses to generate a holistic perspective of their ecology, natural history, traditional knowledge, and other perspectives. To highlight the different aspects of each organism, we pair a screen print designed in a certain color/set of colors with a corresponding perspective and expert narrative. The final product is similar to Andy Warhol's "*Self Portrait*," and can be used in schools, institutions, and by researchers to gain insightful perspectives on organisms and the complexity of research, themselves, and the benefits of the transdisciplinary self.

S.240.4 Personal practices in the integration of art and science

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Unification of art and science has largely been accepted in the scientific community as a way for scientists to hone in on communication skills and be able to share their science more broadly. However, I argue that there are greater implications integrating art and science process. During this presentation will share how it became essential for me to make art to explore my personal experiences alongside my work crafting my dissertation. For example, through this process I found the ways that looking at my emotional experience and personal growth with a scientific attention to detail and curiosity allowed me to overcome difficult interaction; to take ownership for my emotions rather than attempting to control the emotions of others. I share the how I consciously bringing my heart into science helped me find (or rise again after failing to find!) the notoriously elusive plants I study while navigating summers in the Rocky Mountains from Idaho to New Mexico solo. Finally, I share how devoting my final field season to water color portraits of my study group taught me more about the environments I studied than past seasons driven by my rush to collect data. By allowing awareness of my emotions to be present in science, I found I was able to connect to my work more honestly and with less resistance to failed expectations. Most importantly, I found beauty in and purpose for my unique strengths. Without taking into account emotional reality, science will perpetuate the disconnect between humans and the natural world that is made undeniable in the depletion of our world's soils, dramatic loss of biodiversity and in the always rising rates of depression and anxiety. However, if we embrace and move forward without rejecting any parts of ourselves, we can mend our relationships by connecting to human creativity.

S.240.5 How Do We Learn to Love Learning? Using Art and Creativity to Facilitate Paleobotanical Outreach

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What makes an educational experience memorable? How can education be individually relevant to students while maintaining quality and consistency? Can we as educators utilize our distinctive experiences to inform more effective communication? Developing outreach and teaching materials and habits is a lifelong and adaptive learning process, often through which we reach a main goal of scientific communication. In this discussion, I explore relevant methods incorporating interactive creativity used to foster engagement and understanding between scientist and audience, be that in the classroom or other settings we find ourselves in. I include my experiences in these roles and discuss responses to and results from different creative learning experiences I have facilitated throughout my time as an educator, and directions of interest for future work. As scientists and educators, we are situated where our connections to both roles require us to explore the most effective ways to communicate concepts to colleagues, students, and the general public. In recognizing the role our own perspectives and skills play in our teaching and communication, it is increasingly possible to utilize those differences to teach in a unique and effective way.

S.240.6 Field Notes

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The of this talk have been collaborating formally as artist (RD) and writer (AH) for more than 20 years. We have published a book and several illustrated natural essays together, and we have a book in press. We are currently working on a series of paintings and essays based on the lakes of Northern Wisconsin, supported by a multiyear residency through the Drawing Water Program at UW Madison's Trout Lake Station. We collaborate at the interface between art, literature, science, and natural history. Our work is in part documentary: we take great pleasure in seeing and recording what the natural world presents us, then sharing it in our own ways. We each see an organism from a different angle, see something the other could not have. The collaboration moves beyond documenting and telling *about*, however. It also informs our individual work in art, education, and science. For Andrew, writing mediates between subjects of inquiry in the field and herbarium—a weevil escaping from an acorn, an early-emerging false rue anemone—and the processes that connect individual organisms. Sentences convey information, but they also give form to understanding. The writing is the thinking, not simply an account of thoughts. For Rachel, photographing plants, fungi and insects is a first step to discovering the formal in the natural. Painting, drawing, natural dyes, and printmaking are ways to distill the shapes of plants, the light reflected off the water, mosses seen through a magnifying lens, and lichens into patterns. The rearrangement of shapes from the landscape with colors found in nature engages and feeds her as an artist. Our talk will illustrate how this collaboration both reveals and exists in parallel with the natural world, while presenting our understanding of how integrating art, science, and natural history has changed our respective practices.

S.241 ECOSYSTEM GENOMICS: ELUCIDATING THE GENETIC DRIVERS OF NUTRIENT FLUXES IN BRYOPHYTE DOMINATED COMMUNITIES

S.241.1 Mosses as hosts to nitrogen-fixing cyanobacteria: abiotic and biotic controls

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Nitrogen (N) fixation by moss-associated cyanobacteria is the main source of new N in pristine ecosystems such as arctic tundra, boreal forests, and tropical cloud forests. While we have a good understanding of individual factors (e.g. temperature, humidity) that drive this ecosystem process, we still lack a comprehensive framework that can answer key questions in biogeochemistry, symbioses and ecophysiology research. Here, I present N fixation data from various environmental gradients (and thereby the combined effects of various factors), ranging from altitudinal to nutrient availability gradients, as well as moss hosts to synthesize current knowledge on moss-associated N fixation. For instance, N fixation decreased with elevation along a tropical forest mountain, linked to sharp declines in air temperature, relative humidity as well as shifts in bacterial communities associated with mosses. Nitrogen availability or pollution is another key driver of moss-associated N fixation, with inhibiting effects along natural N fertility gradients as well as in laboratory settings. In contrast, heavy metal pollution seems to be less detrimental. Whether moss host or the habitat drives bacterial communities on mosses, and thereby, N fixation rates, is an ongoing debate, and I bring new data to the debate.

S.241.2 Variation in volatile organic compound emissions and nitrogen fixation rates from subarctic cryptogams and associated microbes.

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Cryptogams can be significant emitters of volatile organic compounds (VOCs). VOCs are highly reactive, can considerably affect atmospheric chemistry and lead to positive and negative climate feedback. Simultaneously, cryptogams associate with microbes, especially nitrogen (N)-fixing cyanobacteria. Cyanobacteria can contribute to N-budget of the plant host as well as of the ecosystem. Besides their contribution to the N cycle, these microbes could contribute substantially to VOC emissions measured from cryptogams. However, their contribution has not been assessed to date, and a potential link to N fixation, albeit plausible, is similarly unknown. In this study, VOC emission and N fixation rates of several cryptogamic species were measured. Four moss species (*Hylocomium splendens*, *Sphagnum spp.*, *Pleurozium schreberii*, *Polytrichum commune*), three lichen species (*Peltigera aphtosa*, *Nephrona arcticum*, *Cladonia spp.*) and one liverwort species (*Lophozia lycopodioides*) from subarctic tundra were investigated before and after removal of associated microbes. Removal of associated microbes was done by surface sterilizing. VOC emissions were measured using real time PTR-ToF-MS and GC-MS. N fixation rates were measured using the acetylene reduction assay (ARA) as a measure of nitrogenase activity. Results revealed statistically significantly lower N fixation rates in washed compared to control condition in *Hylocomium splendens* and *Polytrichum commune*. Of all cryptograms in this study, N fixation rates were highest in the lichens *Peltigera aphtosa* and *Nephrona arcticum* and lowest in the liverwort *Lophozia lycopodioides* but without significant differences between control and washed condition. This lack of effect to surface sterilization on N fixation could be due to various reasons such as cyanobacteria residing safely within the plant cell or generally low colonization of some species. Preliminary data shows VOC emission rate and blend differences among cryptogam species as well as a positive link to N fixation rates.

S.241.3 The molecular ecology of moss–cyanobacteria symbioses

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Cyanobacteria are oxygenic photoautotrophs that are widely known for releasing potent toxins in water bodies, contributing to global oxygen production and playing an important part in the evolution of life on the planet. Nevertheless, nitrogen-fixing cyanobacteria also perform a vital ecological role in the nitrogen cycle of several aquatic and terrestrial ecosystems, either as free-living organisms or in symbiotic relationships. Several plants from tropical, temperate and boreal environments were shown to recruit cyanobacteria as epiphytic symbionts when going through nitrogen starvation. This includes mosses, non-vascular plants that are usually found in moist and shaded areas. These bryophytes can be responsible for up to 100% of primary production in some pristine northern ecosystems, in which 50% of the nitrogen input may derive from moss–cyanobacteria associations. Moss–cyanobacteria interactions have consequences on a global scale, since northern environments sequester 20% of all the carbon generated by forests in the world and stock at least 32% of global terrestrial carbon. Nevertheless, few is known about how mosses can influence the physiology and nitrogen-fixing activities of these microorganisms. Information is also lacking about the importance and dynamics of moss–cyanobacteria interactions in tropical ecosystems and how they will be directly or indirectly affected by climate change. In this presentation, I explore advances on the molecular aspects of ecological interactions between mosses and cyanobacteria in northern and tropical ecosystems. Our results suggest that mosses from different environments are potentially capable of manipulating the morphophysiology of cyanobionts to increase their N fixation rates, but without necessarily giving cyanobacteria something in return.

S.241.4 The evolutionary origin of gene networks regulating mutualistic plant-microbe interactions

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It was proposed that the molecular network enabling and controlling intimate plant-microbe symbiotic interactions could have evolved from a general starvation response. Molecules released during starvation by the host plants could have been recruited by microbes to recognize the plant host and the ancestral starvation network of the host plant could have been extended with components enabling proper control of the symbiotic interaction. Nevertheless, this hypothesis remains largely untested because information on the consequences of nutrient starvation is mainly available for vascular plants but missing for most non-vascular plant lineages. Here we investigated this hypothesis by exploring gene expression changes during nitrogen starvation in the two major lineages of bryopyhtes, hornworts and liverworts, capable of establishing intimate symbiotic interaction with cyanobacteria. By conducting comparative analyses with symbiotic and non-symbiotic vascular as well as non-vascular plants we found that the global gene expression response to nitrogen starvation is highly conserved across bryophytes and vascular plants. Furthermore, we observed little difference in response to nitrogen starvation in symbiotic and non-symbiotic species and between species establishing symbiosis with AM fungi, nodule forming bacteria or cyanobacteria. These observations suggest that the nitrogen and general nutrient starvation response is highly conserved across the two major lineages of land plants the vascular plants and the bryophytes and likely represents a starvation response inherited from their common ancestor. While the overall starvation response was conserved, we were also able to identify pathways and molecule groups only induced in the cyanobacteria-hosting bryophyte species implying their potentially role in attracting the symbionts in the initial phase of the symbiosis. Overall, our results are in line with the proposed hypothesis and suggest that regulatory gene networks governing the intimate symbiotic interaction between plants and microbes have likely evolved from a conserved starvation response involving few regulatory changes.

S.241.5 A laboratory-to-field approach for determining the genetic and environmental factors underlying mutualism within a Sphagnum peatland system

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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.242 DYSPLOIDY, DIPLOIDISATION AND DIVERSIFICATION: IMPACT OF POST-POLYPLOID GENOME RESTRUCTURING ON SPECIES AND TRAIT DIVERSITY. SESSION 1

S.242.1 Post-polyploid diploidization and diversification through dysploid changes

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Whole-genome duplications are pervasive across land plant phylogenies, with pronounced frequency in ferns and angiosperms. These duplications have been instrumental in propelling the evolution of key innovations, fostering diversification within numerous angiosperm clades and lineages. Notably, diversification is not instigated by genome doubling itself. Instead, the differentiation of primary polyploid populations, facilitated by various processes, culminates in post-polyploid genome diploidization. Structural diploidization orchestrates a gradual reversion of the polyploid genome to a functionally diploid-like state through frequent chromosomal rearrangements, giving rise to dysploid changes. These alterations, in turn, hold the potential to induce reproductive isolation among post-polyploid offspring, significantly contributing to speciation and cladogenetic events. This intricate interplay between genome dynamics and evolutionary outcomes underscores the importance of understanding the role of post-polyploid diploidization in shaping plant diversity.

S.242.2 Recurrent polyploidy, dysploidy, genome restructuring and ecological success in Sporobolus sect. Spartina (Chloridoideae, Poacea)

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Polyploidy and genome evolution are particularly well documented in the grass family (Poaceae), although the accumulated knowledge is concentrated in subfamilies containing important crop species such as rice (Oryzoideae), maize, Sorghum (Panicoideae) or wheat (Pooideae) and related species. In contrast, one of the largest, and highly variable subfamily (notably with regard to base chromosome number and ploidy levels), Chloridoideae, is still underinvestigated. We focused on the large *Sporobolus* genus where various basic chromosome numbers are recorded (n=7, 8, 9, 10). In this genus, S. sect. *Spartina* (Schreb.) P.M.Peterson & Saarela is a monophyletic clade that represents an iconic model system in evolutionary ecology. It contains several species that are considered as ecosystem engineers on coastal saltmarshes, and

some of them are highly invasive, having expanded on different continents. Of particular interest is the textbook example of neopolyploidy involving hybridization in Europe between the native *Sporobolus maritimus* (presumed hexaploid with 2n=60) and introduced American *S. alterniflorus* (2n=62) during the 19th century. Genome duplication of the sterile hybrid *S. x townsendii* (2n=62) resulted in the successful allopolyploid species *S. anglicus* (2n=124). We conducted comparative analyses involving newly *Sporobolus-Spartina*assembled genomes and related grass genomes. We show how two successive whole genome duplication events (WGD1 & WGD2) have shaped the mesopolyploid parental genomes (chromosomal repatterning, repetitive sequence dynamics) following the diversification of the *Sporobolus- Spartina* clade in the last 20 MYs. Descending dysploidy appears to have resulted in a new base chromosome number following WGD1, which allowed us to revisit ploidy levels of the derived species. We also show how chromosomal restructuration accompanied divergence between *S. maritimus* and *S. alterniflorus* (2-5 MYA) during the speciation process and resulted in an additional chromosome pair (2n=60+2) in *S. alterniflorus*, and discuss consequences of these dramatic genome changes on species distribution and ecology.

S.242.3 Cyto-phylogenomics of the Brachypodium grass complex unveils different pre- and post-polyploidization descending dysploidy trends

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Descending dysploidy may be considered as one of the mechanisms that convert polyploids into functional diploids. However, karyotypes resulting from this mechanism can also be present in neopolyploids and diploids. The model grass genus *Brachypodium* contains up to 21 recognized species showing a remarkable descending dysploidy and various ploidy levels. We performed an extensive cyto-phylogenomic study of its 14 worldwide distributed perennial species and minor satellite taxa. Genome size, chromosome number, and comparative-chromosome-barcoding analyses across 147 populations revealed previously unknown cytotypes for several species and characterized the karyotypic profiles of their constituent genomes. A *Brachypodium* supertree showed the participation of ancestral 'orphan' progenitor genomes in American *B. mexicanum*, ancestral and recent 'orphan' and 'extant' progenitor genomes with diverse basic chromosome numbers or karyotype structure in the aridic-to-mesic Mediterranean and Western European lineages (*B. retusum*, *B. boissieri*, *B.* phoenicoides, *B. rupestre*), and intermediate-recent 'extant' progenitor genomes in currently diploid core-perennial mesic lineages (B. arbuscula-2x, B. sylvaticum-2x, B. pinnatum-2x). Phylogenetic inference suggested the rapid evolution of distinct descending dysploidy trends from ancestral (x=10) or intermediate (x=9) karyotypes to different sorts of derived karyotypes (x=8, x=6, x=5). Our hypothesized scenarios indicated that some of the descending dysploidies preceded both ancestral and recent polyploidizations (x=10->x=8[genome A2], x=10->x=9[G], x=10->x=5[D], x=9->x=8[E1], x=9->x=5[E2]) as these unique karyotypes correspond to orphan diploid progenitor genomes of current Brachypodium polyploids, while others likely occurred after the polyploidizations (x=8[A2]+8[E1]+5[E2]->x=8[A2]+6[E1']+5[E2]; x=9[G]+5[E2]+5[E2]->x=8[G']+5[E2]+5[E2]), as they correspond to rare orphan subgenomes of some allopolyploids. Our analysis uncovered another recent descending dysploidy (x=9[G]->x=8[G*]) occurring in parallel in closely diverging diploid lineages. Most of the descending dysploidies detected in Brachypodium resulted from nested chromosome fusions, while just a few were caused by telomeric fusions. The different combinations of these 'orphan' and 'extant' dysploid genomes originated diverse phenotypic differences among species and cytotypes.

S.242.4 Phylogenomics and biogeography of Nicotiana section Suaveolentes

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For the last six million years, the Australian Eremaean Zone (EZ) has been as dry as today. The flora and fauna of arid regions worldwide, including the EZ, have been hypothesised to have diversified widely before aridification began, in this case 20 Mya, and slowly adapted as aridity developed. Undocumented are more recently arrived plants that developed arid specialisations in situ. Here, we investigate the biogeography and timing of native allotetraploid tobaccos, Nicotiana sect. Suaveolentes, which putatively entered the EZ 5 Mya. The original allotetraploid migrants from South America were adapted to mesic areas of Australia and only recently radiated in the EZ after developing drought adaptations. Based on coalescent and maximum likelihood analyses designed to corroborate timing of the Australian radiation independently, arrival of Nicotiana sect. Suaveolentes occurred approximately 6 Mya, followed by spread via multiple invasions across the EZ from the ecologically highly diverse Pilbara District (Western Australia), which served as a mesic refugium and cradle for adaptations to harsher conditions. These results demonstrate that poorly adapted plant groups can develop novel adaptations that permit them to disperse extensively and rapidly despite the extremes of heat and drought in the EZ.

S.242.5 Comparative genomics of woody bamboos using a novel Arundinaria gigantea genome

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Giant rivercane (*Arundinaria gigantea* (Walter) Muhl., Poaceae) is a woody bamboo species native to the eastern United States. Prior to European colonization, large stands of giant river cane—called canebrakes—formed unique ecosystems across the Southeast. However, these ecosystems have undergone significant reduction, diminishing to a mere fraction of their original size. This decline has resulted in the dwindling or extinction of multiple species that depended on canebrakes for survival. Moreover, giant river cane holds considerable significance in the cultural practices of numerous Indigenous Peoples, making it both a cultural and ecological keystone species. As a member of the tribe Arundinarieae, *Arundinaria* shares a polyploidy event with other temperate woody bamboo species and is part of a complex subgenomic history associated with multiple polyploid events and reticulate evolution across the bamboos. In this study, we present the first chromosome-scaffolded genome of *Arundinaria gigantea*. Using this genome and other available bamboo genomes, we characterize variation in how shared and different polyploid events have diploidized in the bamboos. We consider patterns of transposon diversity, retention of paralogs, differences in post-polyploid tandem gene duplications, structural changes, and homoeologous exchange, and examine how they influence overall subgenome contribution to genes associated with potentially adaptive phenotypes. Given the uniquely high discrepancy across bamboos for flowering cycle times, we focus on genes identified through transcriptomes generated from floral and fruit tissue taken at various developmental stages to investigate how these genes have evolved across different bamboo lineages. Finally, we discuss the future of how the *Arundinaria* genome will be used to assess genotypic and phenotypic diversity across populations of giant river cane in efforts to restore these lost ecosystems and promote the protection of threatened species and Indigenous cultural practices.

S.242.6 Genomic changes between early generations of allopolyploids show diploidization and increased progeny fitness in Tragopogon

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Recently formed allopolyploids *Tragopogon mirus* and *T. miscellus* (Asteraceae) and their diploid parental species, *T. dubius*, *T. porrifolius*, and *T. pratensis*, offer an opportunity to study the earliest stages of allopolyploidy. This study is the first large-scale common-garden and genotyping experiment to assess genomic and phenotypic trait variation in the North American *Tragopogon* allopolyploid complex from both natural and synthetic lines. We conclude that polyploidization contributes to larger progeny and therefore improved establishment of the young plant, as well as the already known gigas effect observed in mature polyploid plants, resulting in increased competitive ability. Natural populations as well as the three generations of resynthesized allopolyploid lines examined here generally showed minor phenotypic trait differences, indicating that any trait differences due to polyploidization were seen in the very first generation after allopolyploidy had occurred and did not change much in subsequent generations after polyploid formation. Likewise, we detected evidence of diploidization via gene loss and as well as gene silencing in the first generations after polyploid formation and repeated across different lineages. We observed increasing gene loss and silencing over several generations of synthetic polyploids and even more in the natural polyploids approximately 45-50 generations old. Both genomic and expression changes are maintained and continue to accumulate over subsequent generations at a steady rate over time, with gene loss occurring at a greater magnitude and rate than gene silencing over the same time period. Gene silencing does not seem to be a prerequisite for gene loss, and the two processes may operate independently of each other. Our findings confirm McClintock's hypothesis of genomic and transcriptomic shock following hybridization, but in this case following allopolyploidization. Together, these results further demonstrate the dynamic nature of polyploid genomes shortly after their formation.

S.243 THE JOURNAL OF PLANT RESEARCH´S SYMPOSIUM ON BIOTIC INTERACTIONS AND BIOLOGICAL INVASION. SESSION 2

S.243.1 Traits of co-occurring native and non-native plants in invaded communities

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Many plant species of European origin have been introduced to North America. Many of these introduced species are highly competitive, and have displaced endemic native plant species. However, in most invaded communities, non-native species co-occur with some native species. We investigated the role of non-native plant species in the functional assembly of putative donor and recipient communities by conducting coordinated floristic surveys and analysis of plant traits related to competitive ability in California and Spanish grasslands. While in Spain, all species were native, in California, half species were non-native. All non-native species found in California grasslands were native in Spain. Many non-native species were more abundant in the Californian invaded grasslands than in the communities of their putative Spanish native range. Invaded California grasslands were more similar in species composition to Spanish grasslands than some Spanish grasslands were among themselves. In California, non-native species had more resource acquisitive traits than co-occurring native species. In Spain, species that invaded California were also more acquisitive than species not known to be invasive somewhere. However, trait differences were not as large as in the introduced range of California indicating that they might have increased their competitive ability. This might also reflect preadaptation of the entire species pool to the management practices that have taken place in Europe for millennia. Trait differences between native and non-native species were also dependent on environmental conditions indicating that niche differentiation is subject to the influence of abiotic and biotic filters encountered in the new region of introduction. Our results show that differences between co-occurring native and non-native species are context dependent and that a correct interpretation of filtering processes in community assembly requires a biogeographical perspective.

S.243.2 Buzz pollination in invasive plant populations

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Plant populations that colonise and spread beyond their native range might face reproductive challenges arising from the scarcity of con-specific mates and suitable pollinators. For this reason, it could be expected that outcrossing plants with specialised pollination syndromes should be at a particular disadvantage compared to similar species with generalised pollination or capable of shifting to autonomous self-pollination. Here, I discuss the case of species that have managed to successfully colonise and spread beyond their native range despite having a functionally specialised pollination system that relies on vibration-producing bees to release pollen, i.e., buzz pollination. Buzz pollinated plants usually have tubular-shaped anthers that open only through small apical gaps or pores (poricidal anthers). Reducing pollen limitation in successful invasions of buzz pollinated plants could be facilitated by modification of poricidal anthers to release pollen in the absence of pollinators, thus promoting autonomous selfing. Alternatively, buzz-pollinated plants may be able to recruit taxonomically different, but functionally similar types of buzz pollinating bees in the introduced range. Buzz pollinating bees are geographically widespread and can adapt behaviourally to deploy vibrations in many types of flowers. Thus, we expect that invasions of buzz pollinated plants often occur by recruiting non-native buzz pollinators rather than by transitions to increased autonomous selfing.

S.243.3 Adapting plant genetic diversity to climate change along a continental latitudinal gradient

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Climate change, including increased temperature and altered precipitation, is likely to advance spring phenology and cause poleward range expansions of many plant species but also herbivores. This is likely to profoundly alter both abiotic and biotic natural selection on – and evolution of – plant traits in local plant populations. We used latitudinal gradient across the continental Europe as a 'space-for-time approach' to mimic future climates, i.e., current southern ecosystems represent the abiotic and biotic conditions of more northerly habitats in the future. Genotypes of the woodland strawberry (*Fragaria vesca*; Rosaceae) originating from this gradient were replicated to five separate experimental sites placed across a north-south latitudinal gradient within Europe. Additionally, at each site, half of the plants were exposed to a drought treatment. By using this framework, we studied biotic and abiotic natural selection on plant traits. Herbivore pressure was higher at mid-latitudes compared to the extremes of the latitudinal distribution of *F. vesca* in Europe. In the Arctic, *F. vesca* genotypes from southern and central Europe had delayed flowering onset compared to when they grew at more southern sites. However, northern *F. vesca* genotypes showed remarkable flexibility in their ability to time flowering onset according to local conditions. Plants subjected to drought experienced more herbivory, accelerated flowering in most of the sites, and grew larger and produced more fruits and runners at some sites. However, at the driest site, there was a decrease in fruit production and chewing damage. Indication of a trade-off was found between reproduction, growth, and defense at several of the sites, being evident almost only under drought. Our results provide timely insights on how plant adaptationsS. to climate change should be studied in combination with plant adaptations to biotic interactions, which also are affected by changing environments.

S.243.4 The specialized buzz pollination syndrome poses a partial barrier to plant invasions

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The missed mutualist hypothesis proposes that when a species is introduced into a new range it may leave behind its mutualistic partners, which can lead to reduced fitness and prevent the species establishing and becoming invasive. Further, it has been hypothesised that specialist mutualisms are likely to impede invasion success due to the difficulty of attracting new specialist partners. The buzz-pollination syndrome encompasses specialised floral traits that restrict pollen access and requires a specialised bee behaviour for efficient pollen extraction. Yet, many invasive plants globally exhibit the buzz pollination syndrome. We used the buzz-pollination syndrome as a model to test the hypotheses that: (1) plant species exhibiting specialised pollination syndromes are underrepresented as invasive species, (2) species with specialised pollination syndromes that have become invasive can reproduce in the absence of specialist buzzing pollinators. Our review of global invasive species found evidence for buzz-pollination in 1.8% (82/4,630) of invasive angiosperms, which is an underrepresentation of the proportion of angiosperms that are estimated to exhibit this syndrome (6-10%). Most invasive buzz-pollinated plants are genetically self-compatible (97%), but only 43% can set fruit in the absence of a pollinator. We undertook assessments of the breeding system and pollinators of a highly invasive weed across the world's tropics, *Senna obtusifolia*, in its native and invasive ranges. *Senna obtusifolia* is self-compatible and can set seed in the absence of pollinators. An analysis of the behaviour and pollen loads of floral visitors demonstrated that the specialist behaviour is not required to extract pollen from *S. obtusifolia*, depicting alternative foraging behaviours can be used to extract pollen from plants that exhibit the buzz-pollination syndrome. This is important where buzzing pollinators may be absent or not attracted to newly introduced plant species, potentially enabling invasions for plants that exhibit the specialised buzz-pollination syndrome.

S.243.5 What processes maintain the species diversity of annual plants in arid environments?

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Arid regions support diverse floras of annual plants. Such regions are characterized by highly variable rainfall. The flexibility of the annual plant life cycle is suited to such variable conditions because annual plants can take advantage of short periods of rainfall to germinate, grow and set seed. A striking feature of such annual plant communities, however, is high levels of temporal variation in species composition. This variation can be traced to species-specific germination requirements, especially sensitivity to temperature when rain falls, which differs between species. More than 70 years ago it was suggested that temporal changes in composition have an important role in maintaining the species diversity of these systems. These annual plants are generally assumed to compete intensely for soil moisture and nutrients, but temporal variation in composition means that the various species are competing for these resources at different times. Many observations and experiments have confirmed these patterns, yet definitive tests that temporal variation maintains diversity is lacking. Such tests use covariance measures to test whether temporal patterns in germination and growth do, over time, intensify average intraspecific competition relative to interspecific competition, thus promoting species coexistence. However, such systems are commonly subject to high levels of seed predation from rodents, ants, and birds, which can limit competition, undermining temporal variation as a coexistence mechanism. Species-specific patterns of seed predation, however, provide an alternative diversity maintenance mechanism, yet studies of seed predation patterns are too limited to support this mechanism. Quantitative coexistence theory suggests observations, experiments and statistics that would provide strong tests of these hypotheses, and quantify their relative and absolute contributions to species coexistence. The evidence from the existing literature on these hypotheses will be reviewed, including evidence from biological invasions. Suitable studies for strong tests of the various hypotheses will be proposed.

S.244 METHODS IN INTEGRATIVE TAXONOMY: BRIDGING THE PHYLOGENY TO CLASSIFICATION GAP. SESSION 1

S.244.1 New approaches for machine-learning-based integrative taxon-omics in plants

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Species are the central units for taxonomic research and measuring Earth's biodiversity. Recent findings in evolutionary genomics are raising awareness that what we call species can be ill-founded entities due to solely morphology-based or regional species descriptions. This particularly applies to plant groups characterized by intricate evolutionary processes such as hybridization, polyploidy, and/or apomixis. Here, challenges of integrative taxon-omics, that is genomics combined with morphological, ecological, and other datasets, become apparent: (i) different favored species concepts (e.g., genetic vs. morphological concepts), (ii) missing appropriate analytical tools for intricate evolutionary processes (which often hurt assumptions of popular MSC-based models), and (iii) highly subjective ranking and fusion of datasets for final taxonomic treatments (e.g., whether genetics or morphology is taxonomically most important). Now, integrative taxon-omics combined with machine learning (ML) under a unified species concept may enable systematic data integration and thus reduce subjectivity in species classification and delimitation. Recent ML applications predominantly rely on deep learning, which represents automated feature extraction and learning based on artificial neural networks (ANNs). We introduce supervised (with labeled training datasets) and unsupervised (only using the inherent structure of testing datasets) ANN approaches that fuse genomic information with other sources (e.g., 'genomics', 'genomics+morphology', 'genomics+morphology+ecology', etc.) using integrative taxonomic datasets. Accuracy scores, confusion matrices, and bootstrapping techniques were applied to evaluate results. In addition, strategies to visualize highly important features within ANN classification or clustering processes ("XAI") and current ANN limitations will be discussed. Integrative taxon-omics based on ML may help classify or delimit species less subjectively as well as more reliably and rapidly than traditional methods do, and thus may help to revise and unravel plant diversity also on a global scale.

S.244.2 Integrative taxonomic approach in unravelling the Systematics of Machilus glaucescens and M. macranthus (Lauraceae) from India

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The Asian genus *Machilus* (Lauraceae - wild relative of avocadoes) is widely distributed in South and Southeast Asia. The systematic profiling of the group has suffered from the lack of integrative taxonomic approach across the distributional range, including India. Historically, the taxonomic revision of *Machilus* in the Indo-Burmese region (Chakrabarty et al. 2022) did not improve the taxonomy and distribution. In this study, we used integrative taxonomic approach to delineate taxonomy, distribution, and phylogenetic relationship of *Machilus macranthus* Nees, (endemic to the Western Ghats-Sri Lanka hotspot), and *M. glaucescens* (Nees) Wight, (Indo-Burma region). We integrated morphological, molecular (nuclear and chloroplast), and distribution data to elucidate the systematic relationship. We collected individuals in flowering and fruiting from Assam, Meghalaya, and Mizoram of the Northeastern region of India and Western Ghats of south India. We sequenced the collections using two nuclear markers (*ITS* and *LEAFY*) and one chloroplast marker (*trnL-trnF*) for the phylogenetic analysis. We further explored 27 morphological characteristics for cluster analysis and extensively mapped the distribution of the species through primary and secondary sources. Cluster analysis using morphological characters, the distribution range as well as phylogenetic relationship confirms that *M. macranthus* and *M. glaucescens* are two distinct species and reflected two distinct distributional ranges. The phylogenetic result also supports the hypothesis that both are two distinct species. Our integrative taxonomic approach proved to be better to understand the systematics of species belongs to *Machilus* genus and could shed light on the origin and biogeography of the genus *Machilus* in the Asiatic region.

S.244.3 A primer on integrative taxonomy

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The concept of "integrative taxonomy", until then restricted to define terminology the fields of psychology and business, was first introduced into biodiversity research in 2005, by the North American zoologist Benoît Dayrat, about twenty years after the onset of molecular phylogenetic research. Dayrat recognized a deep division between the field of molecular phylogenetics, which had developed new methods to test species boundaries, and the field ot traditional taxonomy, which appeared to rely on typological approaches. He defined "integrative taxonomy" as the "*... science that aims to delimit the units of life's diversity from multiple and complementary perspectives (phylogeography, comparative morphology, population genetics, ecology, development, behaviour ...*" While Dayrat's argument focused on species delineation and the development of solid taxon concepts at the species level through multiple lines of evidence, integrative taxonomy has since then been expanded to encompass taxonomy at all hierarchical levels, with the aim to bridge the gap between molecular phylogenies and their translation into formal, stable classifications. Other terminology developed for this purpose includes "polyphasic taxonomy" and the "pluralistic species concept". Here, we redefine integrative taxonomy to encompass the following four components: (1) a molecular phylogenetic framework; (2) quantitative assessment and integration of non-molecular data (phenotype, ecology, behaviour, distribution, etc.) into this framework; (3) formal implementation of the results in a revised classification; and (4) providing revised identification tools reflecting the new classification. Using this strict definition, many works claiming to do "integrative taxonomy" actually fail to do so, either lacking a quantitative integration of non-molecular data or a revised formal classification. Methods for quantitative integration of non-molecular data are briefly outlined.

S.244.4 Cryptic Beauty Revealed: Quantifying Phenotypic Variation in Two Vicariant Ophrys aveyronensis Populations via Image Processing

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Studying phenotypic differentiation is essential in understanding population divergence and the traits involved in the speciation process. Detecting slight phenotypic variations is difficult at first glance, especially when species have a disconnected spatial distribution or conceal cryptic taxa. To examine this, we implemented image-based analyses in conjunction with a simple machine learning algorithm to distinguish between two vicariant population groups within an orchid species complex acknowledged for its resistance to differentiation using conventional morphological criteria: *Ophrys aveyronensis*. Our all-encompassing approach involved three primary stages: (i) Capturing and measuring 109 individuals in their natural habitat, (ii) extracting morphometric, colour and colour pattern information from field photographs and (iii) utilising random forest algorithms for classification, the amalgamation of field and image-derived data resulted in an identification accuracy rate of 95%, highlighting the efficacy of our multidimensional approach. It is worth noting that the variables pinpointed by the random forest algorithm for distinguishing between the two population groups differed from those typically proposed in current literature. This captivating discovery emphasises the demand for inventive techniques that go beyond traditional standards in phenotypic differentiation studies. Our outcomes demonstrate the capacity to augment taxon identification through combining field-captured images with machine learning classification methods. Furthermore, they draw attention to potential traits for future eco-evolutionary investigations, offering valuable observations into the complex interplay of phenotypic variations within intricate species. This study not only aids in improving taxonomic methodologies but also highlights the significance of advanced analytical tools in enhancing our comprehension of species differentiation and evolutionary mechanisms.

S.244.5 Exploring the diversity of Wetmoreana lichens (Teloschistaceae) using an integrative taxonomic approach

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The genus *Wetmoreana* includes saxicolous, crustose-lobate to squamulose species with bright orange anthraquinones, often producing vegetative propagules such as isidia, papillae, schizidia or soredia. It is known throughout the Americas, Africa and Asia. The origin of the genus is unknown, but the highest diversity occurs in South America, perhaps indicating this continent as the centre of its diversification. The genus was studied using quantitative integrative taxonomy methods to resolve its delimitation and explore its taxonomic diversity at the species level. As a result, the number of taxa within *Wetmoreana* increased from four to sixteen, including six newly described species, as well as six species newly transferred to this genus. Among the latter are some species for which DNA sequences are as yet unavailable. Their classification within *Wetmoreana* was tested using a quantitative approach based on phenotypic traits combined with the evaluation of phylogenetic signals by means of phenotype-based phylogenetic binning. Clade distinctiveness of all recognised taxa at the generic, specific and intra-specific levels was assessed by a multi-response permutation procedure (MRPP). The taxa of interest mainly represent poorly studied South American species and are characterized by a certain variability in phenotypic traits. Such variable taxa pose a challenge to taxonomists, and our results confirm the usefulness of statistical methods in assessing such difficult species complexes.

S.244.6 Anarchy to Harmony: Redbud (Cercis spp.) as a case for integrative taxonomy

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The genus *Cercis*, like many genera, is fraught with taxonomic controversy. Circumscriptions of species, subspecies, varieties, and forms of North American taxa are hotly debated in taxonomic and horticultural literature. Common garden assessment of phenotypic variation and documentation of the genetic basis of phenotypic variation can inform taxonomic circumscription. We investigated published delimitations for North American *Cercis* taxa through analysis of phenotypic variation among specimens growing in a common garden (JC Raulston Arboretum, North Carolina State University). In addition, we leveraged an available breeding population for genomic estimation via GWAS and for phenotypic traits that have been used to distinguish *Cercis canadensis* var. *canadensis* and *Cercis canadensis* var. *texensis*. By combining phenotypic information with an understanding of the genetic basis of key taxonomic traits, we illustrate how a pluralistic and integrative approach to taxon delimitation can yield rigorous and reproducible species and infraspecific taxonomic concepts.

S.245 FLORAS AND DIVERSITY OF EASTERN ASIA. SESSION 1

S.245.1 Moscow Digital Herbarium and Atlas of the Russian Flora initiative

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A web-resource, the Moscow Digital Herbarium (https://plant.depo.msu.ru/), was launched by Lomonosov Moscow State University in October, 2016 for publication of specimens imaged and databased in the Moscow University Herbarium (MW). From 2015 to 2018, a commercial partner scanned 93% of the regular herbarium collections at 300 dpi and 100% of the types at 600 dpi. Since 2019, Moscow Digital Herbarium became a consortium of Russian herbaria with nine active members (MW, MHA, IRKU, KUZ, TUL, TULGU, KULPOL, TKM, MAG). As of August 2023, database contained 1,266,139 specimens with 1,244,376 images covering 36,171 species of vascular plants and bryophytes. These data are available in GBIF as nine independent datasets and updated in a weekly synchronization mode. Gradually, we started to publish extended metadata on our portal, like full transcriptions of labels and georeferences, i.e., the coordinates of collection sites for each specimen. Two thirds of records (890,356 specimens) are currently georeferenced and 600,424 specimens have complete label transcriptions. Atlas of the Russian Flora is a new initiative for producing grid maps of native vascular plants of the country. This initiative is integrated into the Moscow Digital Herbarium and employs different data sources merged into a single FLORUS dataset. Ca. 6.5M+ records (700K grid records) were used to produce 9,885 grid maps with 100×100 km squares. This dataset includes precleaned GBIF data (including data from the Moscow Digital Herbarium), complete data from the Flora of Russia project on iNaturalist, as well as previously unpublished records. The taxonomy is given against the Catalogue of Life associated with the accepted names in the Moscow Digital Herbarium. Acknowledgments: The work was supported by a grant from the Russian Science Foundation (project No. 21-77-20042, https://rscf.ru/en/project/21-77-20042/).

S.245.2 Invasive alien flora of China: An update

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China is the largest country in eastern Asia and contains habitats that range from cold temperate to tropical rainforest. The Chinese have a long history of plant cultivation and domestication. Although most cultivated plants in China are native species, many are non-native plants introduced throughout Chinese history for food, medicine, horticulture or ornamental purposes. The Catalogue of Alien Plants in China records a total of 14,710 alien plants. Among these, some, such as corn and potato, are used as food to meet the demands of China's large population. Non-native plants that have established populations and colonized local environments are called naturalized plants. Previous studies indicate that the number of naturalized plant species in China ranges from 861 to 933. Of those, between 126 to 402 have been designated as Invasive Alien Plants. In China, invasive plants have been detrimental to the conservation of biodiversity and native ecosystems, particularly since the 1990s. Thus, it is critical to use multidisciplinary, nation-wide approaches to investigate invasive plants in China. Here we present an analysis of 403 invasive plant species based on the Alien Invasive Flora of China and other recently published works.

S.245.3 An overview of current checklist of vascular plants in Mongolia

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In this study, we critically revised and updated the checklist of native vascular plants of Mongolia. The checklist comprises 3,041 native vascular plant taxa (2,835 species and 206 infraspecific species) from 653 genera and 111 families, including 7 lycophytes, 41 ferns, 21 gymnosperms, and 2,972 angiosperms. In the angiosperms, we identified the 14 families with the greatest species richness, ranging from 50 to 456 taxa. Species endemism is also noted here; 102 taxa are endemic to Mongolia, and 275 taxa are subendemic that co-occur in adjacent countries. Since 2014, a total of 14 taxa have been described new to science based on morphological evidences. Moreover, five genera and 74 taxa were newly added to the flora of Mongolia. Based on our critical revisions, names of three families, 21 genera, and 230 species have been changed in comparison to the previous checklist, "Conspectus of the vascular plants of Mongolia" (2014). We revised the checklist of Mongolian vascular plants provided by Urgamal et al. (2014), which included 3,127 taxa, belonging to 683 genera and 112 families. There were 3,069 native taxa from 682 genera and 110 families listed by Urgamal et al (2014) and the current checklist has been shortened and comprises 3,041 native vascular plant taxa from 653 genera and 111 families. There are 10 families with a high species richness (> 10 genera / > 94 species): Asteraceae (85 genera/456 species), Fabaceae (24/328), Poaceae (58/229), Rosaceae (28/168), Ranunculaceae (20/156), Brassicaceae (51/138), Cyperaceae (10/131), Lamiaceae (22/103), Caryophyllaceae (20/97), and Amaranthaceae (34/94). At the genus level, 10 genera represent a high species richness (> 40 species): *Astragalus* L. (127 species), *Artemisia* L. (103), *Carex* L. (99) *Oxytropis* DC. (97), *Potentilla* L. (75), *Saussurea* DC. (55), *Taraxacum* F.H.Wigg. (53), *Allium* L. (50), *Salix* L. (42), *Ranunculus* L. (41).

S.245.4 Global National Management List of Invasive Alien Plants: Key Species and Policy Analysis

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Invasive alien plants (IAPs) pose a major threat to biodiversity and ecosystems worldwide. The recent adoption of the Kunming-Montreal Global Biodiversity Framework sets an ambitious "Target 6" for tackling invasive alien species. Our study provides a comprehensive analysis of the current national management list of IAPs. It aims to answer the questions for achieving this target: Which species are priority IAPs/potential IAPs/should be eradicated or controlled in priority sites? How to manage IAPs to achieve the target? 107 countries/union were analyzed, and only 26 of them have officially released national management IAPs lists. 65% of them are legal documents while 35% are only official lists. These countries/union span six continents. France, South Africa and Argentina have more than 300 IAPs, while Slovakia only has seven IAPs. Based on all of the lists, 1316 taxa were compiled, belonging to 683 genera and 149 families. The families with the most taxa are Poaceae (159) and the genera with the most taxa are *Prosopis* (29). 104 taxa distributed in at least three continents and listed in four or more countries/union were considered as the priority IAPs in our study. We also found species exchanged between the Eastern and Western Hemispheres have been a major pathway enabling plant invasions worldwide. For potential IAPs, we suggested the long-distance pathways between the Eastern and Western Hemispheres should be a top focus for prevention and pathways management. Aquatic IAPs are recognized as top priorities for prevention and control in island nations and other vulnerable sites. Additionally, our study revealed that most countries/union lack concrete control and management measures. This indicates that significant improvements are still needed to align IAPs lists and policies with the called for Target 6.

S.245.5 Diversity, taxonomy and evolutionary history of the ferns Hymenophyllaceae in China: a phylogenetic and biogeographic approach

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Hymenophyllaceae, encompassing over 600 recognized species, are useful as indicators of the threatened humid forest environments at a pantropical scale. Emerging at least in the early Triassic and maybe in the Paleozoic, the family has ancient origins and displays a worldwide distribution resulting from significant diversifications and potential vicariance events since the Mesozoic. The taxonomic stabilization at family level is necessary and a prerequisite for biogeographic research, providing insights into its evolutionary history, including diversification patterns and processes. With nearly 1/3 of the world's species, Asia would likely be the origin area of certain lineages. Furthermore, China would host approximately 70 species of Hymenophyllaceae, representing over 10% of the total family diversity, making it a potential key area for biogeographic studies at an Asian and global scale. Therefore, an updated revision of Hymenophyllaceae diversity and taxonomy in China appeared essential and has yet to be conducted. For this purpose, a first step was to revise the list of names, descriptions and a representative sample of specimens in the collections, including types, with the aim to provide an updated list of valid Chinese taxa and their verified synonyms, and to generate an online identification key. In a second step, we acquired DNA sequences for many Chinese specimens, used *rbcL* to reconstruct phylogenies for Trichomanoideae (6 genera in China: *Abrodictyum*, *Callistopteris*, *Cephalomanes*, *Crepidomanes*, *Didymoglossum*, *Vandenboschia*), and *rbcL* combined with *rbcL-accD* and *rps4-trnS* for the genus *Hymenophyllum*. With these datasets and by conducting dating and biogeographical analyses, we tested species hypotheses, and the role of China in the assembly of the family biodiversity, especially in Asia, was explored and is discussed. Hymenophyllaceae are emblematic and indicators of fragile and threatened wet habitats. This taxonomy work is thus integral to a conservation and decision support perspective.

S.245.6 Advancements in Chinese plant names index: a comprehensive overview

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China's plant biodiversity, boasting 38,844 species, ranks among the highest globally. Since 2000, it consistently reports 220 new vascular plant taxa annually, with notable changes in names and national-level records. Despite most findings being published internationally, some, particularly from regional and university sources, lack representation in global databases. To address this, a systematic review of Chinese plant nomenclature literature since 2000 has been undertaken. This effort has resulted in annual plant species name indices and the Chinese Plant Names Index (https://cpni.ibiodiversity.net/) database, hosting 16,495 entries from 7,565 publications. This platform aims to fill the gap for species excluded from international databases, facilitating convenient access to plant name data for taxonomic revision and research citation. The comprehensive initiative extends beyond plant names, compiling data on 3,305 to avoid hip homonymity and enhance research accuracy. Additionally, information on 7,458 Chinese plant collection sites, with historical and contemporary spellings, aids precise referencing for researchers. The systematic organization of China's plant taxonomy documents not only advances botanical research but also contributes to the conservation and sustainable use of the country's abundant plant resources. In summary, the project addresses the underrepresentation of Chinese plant species in global databases by systematically organizing and disseminating information on plant taxonomy, aiming to enhance accuracy in botanical research, citation, and ultimately support the conservation and sustainable utilization of China's diverse plant resources.

S.246 RANUNCULALES: FROM MORPHOLOGY TO PHYLOGENOMICS AND EVO-DEVO

S.246.1 RanOmics: genomic tools for studying evolutionary innovations on the molecular scale in Ranunculales

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One of the central goals of evolutionary research is to understand how changes in gene regulatory networks lead to the origin of novel, complex traits, or, in short: How do evolutionary novelties arise? Ranunculales are early branching eudicots that comprise extremely morphologically diverse species and they are special because several morphological novelties evolved repeatedly, and novel floral traits emerged. I introduce the RanOmics project, aimed at uncovering gene regulators modules required for the emergence of novel, often convergently emerging traits. We have sequenced the genomes in reference quality of several Ranunculales and the transcriptomes of several species from homologous tissues and comparable developmental stages. I provide the state of the art of this project with the first comparative analyses of the genomes. The RanOmics project provides the genetic resources for the Ranunculales community and all researchers interested in studying comparative genomics, evolution of gene regulatory networks, and origin of novel traits.

S.246.2 Petal evolution and morphogenesis in Ranunculaceae

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Ranunculaceae comprise *ca.* 2500 species that display a broad range of floral diversity, particularly at the level of the perianth. Petals, when present, are often referred to as 'elaborate' because they have a complex morphology. In addition, the petals usually produce and store nectar, which gives them a crucial functional role in the interaction with pollinators. Its morphological diversity and species richness make this family a particularly suitable model group for studying the evolution of complex morphologies. For this purpose, we scored and analysed traits that characterize in detail the complexity of mature petal morphology in 32 genera (out of *ca.* 55), and used an already published robust and dated phylogeny of the family to conduct ancestral state reconstruction. Furthermore, we described petal development using high resolution X-Ray computed tomography in six species with contrasting petal forms. Our results suggest a flat and shortly clawed ancestral petal for the entire family, and for the ancestors of all tribes except Adonideae. Elaborations would have therefore evolved independently in different lineages, with some convergences in shape. To further explore the morphogenesis of elaborations, we focused on the spurred petals of Staphisagria picta. We described the cellular characteristics (volume, sphericity, orientation in space) of the developing spur using a newly designed automated method to analyse in a three-dimensional space images generated using confocal microscopy. Our results show that spur development is marked by an early phase of dominant cell proliferation, followed by a phase of dominant anisotropic (directional) cell expansion. The acquisition of the spur's curvature seems to be achieved by a complex interplay of anisotropic cell elongation and cell division, both mechanisms being unevenly distributed among the different parts of the spur.

S.246.3 Curiouser and curiouser: mechanisms underlying spur development and diversification in Aquilegia

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The lower eudicot model system *Aquilegia* possesses several morphological features that can shed light on the evolution of novelty, particularly in the context of complex organ form. We have been studying several key aspects of the *Aquilegia* flower but will focus today on the three-dimensional petal nectar spur. We have found that *Aquilegia* petal spurs initiate due to a localized region of cell division. This lays the ground pattern of the spur, which is then realized through anisotropic cell elongation. Diversification of spur morphology has involved multiple factors, including heterochronic shifts that generate much longer, narrower cells; differences in cell numbers around the radial axis of the spur and along its length; and independent control of both cell division and elongation on different surfaces of the spur, which generates curvature. We are now combining transcriptomics, candidate gene approaches, and QTL mapping to explore the genetic architecture of spur development and understand its evolution.

S.246.4 Dissecting the genetic and developmental basis of petal spurs in Aquilegia using QTL, hybridization and phylogenomics.

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The origin of nectar spurs is associated with the adaptive radiation of the columbine genus, *Aquilegia*. Dissecting the genetic and developmental mechanisms of nectar spur development specifically and petal morphology generally is thus important for our understanding of the origin of novel traits. Recently, a key gene in *Aquilegia* spur development, *POPOVICH*, was identified using hybridization between a natural spurless species, *A. ecalcarata,* and a spurred relative exemplifying the utility of natural variants. I outline our ongoing efforts to identify additional potential genes for spur and petal development using natural variation in the closest relatives of *Aquilegia*, *Semiaquilegia* and *Urophysa*. There have been recent discoveries of rare species of *Semiaquilegia* with novel petal shapes and we have been able to produce intergeneric hybrids between some of these species and *Aquilegia,* which offers a new research avenue. *Urophysa* consists of two species, *U. rockii,* which produces small petals with very short spurs and *U. henryi*, which in one accession produces small flat petals and in another produces small cupped-shaped petals but no spurs. Thus, QTL analysis from hybrids among these species will also likely aid in finding candidate genes involved in petal shape. Finally, we are developing genomic assemblies of both *Semiaquilegia* and *Urophysa* to facilitate the identification of genomic features unique to *Aquilegia* and thus potentially being involved its adaptive radiation.

S.246.5 Developmental genetics of floral traits associated with wind pollination in Thalictrum

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Wind pollination has evolved repeatedly in flowering plants, yet the developmental genetics of floral traits associated with this pollination mode remains elusive. *Thalictrum* (Ranunculaceae) have transitioned repeatedly between insect and wind pollination and exhibit intermediate floral morphs with mixed pollination, providing an ideal system to test the correlated evolution of floral morphology, developmental genetics and pollination mode. Prior data broadly supports the existence of detectable flower morphs from convergent evolution to wind pollination in *Thalictrum*, consisting of small, inconspicuous, and mostly dioecious flowers with extended stigmatic surfaces on long styles or dangling stamens. *MIXTA* family transcription factors are known to modulate the differentiation of cellular outgrowths (conical cells and trichomes) on the epidermis of land plants and were tested here as potential candidates for the longer stigmatic papillae and extended stigmas found in wind-pollinated species. A single copy ortholog from diploid *T. thalictroides, paleoMIXTA* (*TthPMX*), was functionally characterized via targeted gene silencing and overexpression, followed by comparative transcriptomics to investigate the gene regulatory network. The reduction in stigmatic papillae length under targeted gene silencing and their extension under over-expression suggest that *TthPMX* has a novel role in promoting stigmatic papillae cell elongation. Elevated expression of specific *PMX* paralogs in carpels of polyploid taxa further suggests that duplications in *PMX* may have facilitated the evolution of the long stigmatic papillae found in plumose stigmas of wind-pollinated species.

S.246.6 Ranunculaceae: from Morphology to Phylogenomics and Evolutionary Developmental Biology

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Ranunculaceae exhibits a remarkable diversity in genome size, floral morphology, and secondary metabolites. How these characters evolved, and to what extent the changes of genome size have contributed to the evolution of other characters, however, remain largely unclear. Here, by sequencing the genome of *Nigella damascena* (genome size about 10 Gb) and the transcriptomes of the other 51 species representing 37 genera of the 14 tribes, we: 1) constructed a robust and well-represented phylogenetic tree with time calibration of the Ranunculaceae, and detected two gene flows that have resulted in nuclear-cytoplasmic incompatibility; 2) explored the processes and general patterns of the evolution of genome size and other important characters; 3) revealed the mechanisms underlying the diversification of flowers in basic structure, petal shape and several phytochemical traits, and 4) discussed the roles of the changes of genome size in plant evolution.

S.247 FLORAL NECTAR: POLLINATION SYNDROMES, PRODUCTION ATTRIBUTES, REGULATION EVOLUTION. SESSION 2

S.247.1 Nectar secretion mechanism in a monocot Roscoea (Zingiberaceae)

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Nectar serves as a reward offered by flowers to pollinators, facilitating the success of sexual reproduction. Consequently, nectar holds indispensable biological significance in plant reproduction and evolution. Despite the characterization of nectar function and composition, the mechanism of nectar secretion has remained unclear. To elucidate the probable mechanisms governing nectar secretion, we selected two *Roscoea* species as model: the outcrossing species *R. cautleoides*, secreting nectar from its nectaries, and the autonomous selfing species *R. schneideriana*, no nectar. We first conducted a comparative study for microstructure, nectary size and nectar volume were recorded in the field. Nectary location, external form and internal structure were observed by paraffin section staining method. Subsequently, we performed an intricate assembly and annotation of the *R. cautleoides* genome, employing multi-omics techniques, facilitating an analysis of the molecular mechanisms in the nectaries and doing identification of target genes crucial for nectar secretion. Ultimately, we delved into the gene structure, function and evolution of these essential genes. Here, we found that the nectaries of *R. schneideriana* possess significantly reduced volume and deteriorated internal structures, compared to *R. cautleoides*. Multi-omics correlation analysis identified one gene that is specifically highly expressed in the nectaries of the *R. cautleoides*, which is critical for nectar secretion in *Roscoea*. These results provide an important basis for revealing the differences of floral characteristics, pollination mechanism and breeding system, as well as the mechanism of nectar secretion between outcrossing and selfing species in *Roscoea*. Characterization of this target gene regulating nectary production has provided new insights into understanding of the mechanism and evolution of nectar secretion in plants.

S.247.2 Predicting pollination syndromes along an altitudinal gradient of the tropical Andes of Bolivia

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Pollination syndromes refer to a set of flower characteristics, including flower structure, color, fragrance, and rewards, which have developed through interactions with a particular category of animal pollinators. The predictive power of pollination syndromes regarding actual plant-animal interactions has been constantly debated. Here we tested this prediction power in 30 plant species occurring along an altitudinal gradient (1000-4500m) in the tropical Andes of Bolivia. We measured flower traits, flower morphometry (size), signal (color, shape) and reward traits (nectar). In addition, we observed the pollinators (flower visitors that touched reproductive parts) corresponding to different pollinator guilds: bees, flies, wasps, beetles, butterflies and birds. Using the flower traits, we classified the plant species into a particular pollination syndrome. Later based on the most legitimate and abundant pollinators, we confirmed or rejected the predicted syndrome. Along the altitudinal gradient we expect to find different conditions related to both specialist and generalist strategies of pollination. If so, then we expect an accurate predictive power of the pollination syndromes in the specialist systems only.

S.247.3 The challenge of nectar production in Mucuna (Fabaceae): from anatomical to ecological traits

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The genus *Mucuna* (Fabaceae) shows explosive flower opening and an impressive radiation involving different pollinators. The aim of this study was to verify how anatomical and ecological traits affect the dynamics of nectar production in the genus *Mucuna* which have a diversity of vertebrate pollinators. *Mucuna japira* (pollinated by birds) inflorescence bears 12-21 yellow flowers, which are in anthesis for seven days, whereas *M. urens* (pollinated by bats) inflorescence bears 36-54 greenish flowers, but only 1-3 flowers are in anthesis simultaneously, that last one night. Related to floral morphology, the reproductive organs are enclosed in the keel, being released after explosive flower opening. At the tip of the keel, the petals are stiff and united, which probably act as support to trigger flower explosion. In the non-lignified part of the inner epidermis occur entwined secretory papillae, which keep the petals firmly united. Both species had constant nectar sugar concentration (ca. 10% for *M. japira* and ca. 16% for *M. urens*) and secreted high volumes of nectar (ca. 340μl per flower for *M. japira* and 310μl per flower for *M. urens*), during five days for *M. japira* and six hours for *M. urens,* but nectar production stops immediately when flower opening mechanism is triggered. Nectar resorption occurred in both species since there is no longer any chance of flower being pollinated. Both species of *Mucuna* are dependent on their pollinators to produce fruits and seeds, but they have different strategies to promote the necessary interaction with birds or bats, especially related to nectar and flower traits. Also, anatomical traits can mediate pollinators visitation as secondary wall thickenings of the inner mesophyll exist only in *M. japira* flowers, which are more difficult to open than those of *M. urens*.

S.247.4 Challenges and rewards of measuring selection on nectar

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The importance of nectar in plant-pollinator interactions and the diversity of animal pollinated flowers has long been appreciated. However, nectar traits have generally been neglected in estimates of natural selection in populations. While researchers appreciate that nectar may be a target of selectin in populations, it can be a challenging trait to quantify in the numbers necessary for phenotypic selection studies. Here I outline some of the challenges and opportunities for studying selection on nectar. I also outline lessons we've been learning as my lab attempts to fill this important gap in our understanding of the evolution of floral traits. I'll show that nectar can be but isn't always a target of selection. Abiotic conditions can also change selection patterns on nectar. Quantifying selection on nectar traits may be particularly important to understand the impacts of our changing climate on floral evolution. Nectar can be a plastic trait influenced by current conditions, many which are changing, such as temperatures and water availability. Therefore, understanding the relationship between phenotypic plasticity and natural selection will be particularly important for furthering our understanding of the evolution of nectar.

S.247.5 Identifying and measuring the role of natural selection in the evolution of floral nectar attributes: Avoiding the pitfalls

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Determining how floral nectar attributes have evolved and continue to evolve is important and necessary for understanding, managing, conserving and manipulating plant biology. However, there are several pitfalls that can and do arise along this path. One pitfall is the assumption, often implicit, that plants evolve nectar attributes to benefit their animal pollinators, rather than themselves. Instead, floral nectar should be viewed as an evolutionarily stable strategy with fitness outcomes clearly identified for both plant nectar production and pollinator behaviour. To suggest that pollinators preferentially visit or revisit individual plants on the basis of their nectar attributes is similarly problematic because pollinators are generally unable to assess nectar attributes of a flower (volume, concentration, composition) without probing it and removing its nectar and unlikely to remember and preferentially revisit or avoid particular plants based on encountered nectar. Another pitfall is to argue, also often implicitly, that a plant population or species has certain nectar attributes because these attributes benefit the population or species rather than an individual plant. There are also problems with attempts to measure what has been termed 'phenotypic selection' by observing correlations across individual plants between some measure of plant reproductive fitness (e.g., seed set) and various phenotypic traits, possibly including nectar attributes. In addition, measurements of 'phenotypic selection' sometimes omit consideration of male function reproduction which should be half the story. A final pitfall may arise when attempts are made to determine the nature and extent of natural selection in relation to nectar attributes through experimental manipulation because such experiments may not leave everything else unchanged. Determining how floral nectar attributes evolve will therefore require a carefully developed approach with much care given to avoiding the pitfalls described above. However, this may not be easy, especially given how easy it is for these pitfalls to arise.

S.248 EVO-DEVO

S.248.1 Perianth evolution in Ranunculales

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As sisters to all other eudicots, members of the Ranunculales are pivotal to understanding the evolution of their perianth, and the homology of petals that can be of bracteal or staminal origin. However, recent ancestral character reconstructions suggest that the most recent common ancestor (MRCA) of Ranunculales and several families, including Berberidaceae, had not two but three series or whorls of perianth, and that the innermost was petaloid. To assess perianth organ evolution and homology between extant lineages and the MRCA of Ranunculales, we thus re-evaluated floral development in two genera of Berberidaceae with several whorls of perianth becoming increasingly petaloid toward the center of the flower. However, only the two innermost persist at anthesis in *Nandina* and four in *Vancouveria*. Using scanning electron microscopy, we confirmed that in both genera, the outermost whorls of sepals are all caducous. In addition, in *Nandina*, the two whorls of petals are not delayed in development and interpreted as the two innermost whorls of increasingly petaloid sepals, similar to those persisting in *Vancouveria*. Primordia at the base of some stamens of *Nandina* that we interpreted as being homologous to those regularly found in two whorls around the stamens in *Vancouveria* were also documented but they vanish during development whereas in *Vancouveria*, while they are typically delayed in development and form modified and nectariferous petals. Our study suggest that like in *Vancouveria*, the MRCA of Berberidaceae and Ranunculales as a whole likely had a perianth differentiated into outermost and innermost more or less petaloid sepals, and more or less modified and nectariferous petals. As such, their flowers thus had petals of both bracteal and staminal origins at anthesis, supporting the hypothesis of a fading-border ABC model determining floral organ identity and petaloidy in the basalmost eudicot lineage.

S.248.2 New floral organs in Amaranthaceae: ontogeny and gene function

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Most eudicot angiosperms have flowers with four types of floral organs arranged in concentric whorls - sepals, petals, stamens, and carpels -. However, throughout the process of evolution, flower morphology has evolved, resulting in a variety of modifications such as the origin of new or the loss of existing floral parts, changes in the function of floral organs, and others. In Amaranthaceae, androecial tubes occur with appendages known as 'pseudostaminodes', alternating with the stamens. The characterization of the pseudostaminodes has been controversial with different definitions found in literature. However, a recent floral ontogenetic study based on scanning electron and light microscopy suggested that pseudostaminodes are a new category of floral organs called 'androecial appendages'. Two types of appendages were identified: appendages on the androecial tube and appendages on the filaments. To test this hypothesis and further clarify the nature of the androecial appendages, an RNA-seq study was conducted in order to obtain transcriptome sequences. Bioinformatic analyses were then performed to determine differentially genes expressed in these new floral organs, and their possible functions.

S.248.3 Developmental analysis of Ophrys sphegodes labellum helps to unravel the secrets of sexual mimicry

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The orchids of the genus *Ophrys* represent an excellent system to study pollinator-driven speciation. These orchids have a particular pollination strategy that involves the attraction of the males of one specific species of insect, mimicking the pheromone and the appearance of the conspecific females. After landing on the flower, the deceived male starts to perform a "pseudocopulation", which leads to removal of pollinia. Different species of *Ophrys* typically attract different species of insects due to the perfection of the decoy. Thus, if two orchids vary enough in their floral traits to attract different species, the genetic flow between them is interrupted, promoting plant differentiation and speciation. However, until now we lacked an understanding of the mechanisms behind the development of the floral traits employed in the mimicry. In this study, we investigate the *Ophrys sphegodes* labellum, the highly specialized petal responsible for pollinator attraction, in order to uncover the genetic basis of these floral traits. We used a combination of microscopy, micro-computed tomography, and photography to describe the morphology of the labellum during the development. We delineated, for the first time, seven distinct developmental stages, which will be pivotal for subsequent studies. We also found three main cell types that are localized in three different areas of the labellum. With this knowledge in hand, we created the first expression atlas of labellum stages and tissues by RNA-Seq, so as to be able to uncover the genes involved in pollinator-relevant traits of the labellum. These results will facilitate future detailed evo-devo studies between *O. sphegodes* and other *Ophrys* species with different pollinators.

S.248.4 Knockdown of floral symmetry in Fedia graciliflora

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Shifts between radial symmetry (actinomorphy) and bilateral symmetry (zygomorphy) in flowers have occurred multiple times independently within angiosperms. These morphological shifts are commonly associated with increased pollinator specialization and speciation rates. The CYCLOIDEA (CYC)-like genes have been shown to shift their expression dorsally independently in nearly all shifts to bilaterally symmetrical flowers examined. Three core eudicot clades of CYC-like genes have been identified: CYC1, CYC2 and CYC3, with only CYC2-like genes being shown to have a role in floral symmetry. We use the non-model plant, Fedia graciliflora (Caprifoliaceae) to examine the effect of CYC2 as well as CYC3 paralogs on floral shape and symmetry. F. graciliflora have strongly bilaterally symmetrical flowers with morphologically distinct dorsal (upper), lateral, and ventral (lower) petals and only two functional stamens. Fedia is nested within the Valerianella, a group with pseudo-radially symmetric flowers with three functional stamens, providing a model for studying the evolution of strong bilateral symmetry and teasing apart the effects from each paralog. Here we used Virus-Induced Gene Silencing (VIGS) to knockdown each of the paralogs separately: FgCYC2A, FgCYC2B, FgCYC3A, and FgCYC3B. The down-regulated plants were assayed using geometric morphometrics combined with tools of multivariate statistical shape analysis to quantify shape changes, using a combination of landmarks and semilandmarks to precisely capture in high detail the corolla outline. Using canonical variate analysis (CVA), we are able to statistically model the morphological effect of lower expression of each paralog. These analyses indicate that each paralog plays a slightly different role in patterning floral symmetry, both in location and size of petal lobes. Additionally, here we show evidence for the first time that CYC3, despite having lower expression in general, also patterns corolla shape.

S.248.5 Genetic basis underlying heteranthery in Melastomataceae.

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Melastomes are well known for their striking diversity in stamen morphologies. The variously modified connective appendages and heteranthery (stamen dimorphism) occurring within this family of ca. 5800 species, has fascinated botanists for more than two centuries. A variety of functions associated with pollination have been discovered for these staminal traits over the years. Although most species are buzz pollinated, repeated evolutionary shifts in staminal traits have often been linked to pollinator shifts and suspected of causing diversification in the family. The evolutionary lability of the connective morphology and heteranthery within several clades lead us to hypothesize that these traits might be controlled by relatively simple genetic mechanisms. We aimed to test this hypothesis by using a comparative transcriptomics approach and selected two closely related *Arthrostemma* species with different degrees of heteranthery for our studies. Suitable developmental stages for transcriptomic comparisons were identified and RNA was extracted by dissecting and separating the two stamen whorls. Differential expression analyses were done to compare the gene expression profiles of the tissues from the two whorls of stamen within and between species at different developmental stages. Further analyses of the differentially expressed genes to identify candidate genes/groups involved in pedoconnective development and heteranthery are underway. We hope to gain a better understanding of the genetic basis behind this phenomenon of heteranthery and associated staminal traits to use as a substrate for future evolutionary studies in melastomes and other angiosperm families showing heteranthery.

S.248.6 Using Lonicera (Caprifoliaceae) as an evo-devo model clade to study floral and extrafloral fusion and shape.

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Diversification in plant form commonly arises from changes in regulation of rates of tissue growth and location of tissue boundaries. *Lonicera,* with roughly 140 species, displays considerable variation and multiple independent transitions in floral symmetry; length of floral whorls; and fusion of petals, ovaries, extrafloral bracteoles, and leaves. We have used target enrichment to sequence twenty candidate genes and a microRNA (across most of the species) that are known to underlie these traits in core eudicots and/or angiosperms. In addition to genic coding sequence, we also targeted potential upstream and downstream regulatory regions to examine changes in transcription factor binding sites across the group that correlate with morphological shifts. Our key initial focus examined the role of *CUC* (*CUPSHAPED COTYLEDON*) in frequent shifts in fusion of leaves, bracteoles, and ovaries across *Lonicera*, with independent shifts recreating the same structures repeatedly. *CUC* is a NAC1a transcription factor that has been shown to affect organ boundaries in leaves and floral organs. We previously used genomic skimming and transcriptomic datasets to infer the phylogenetic history of *CUC* across *Lonicera*, and our findings suggest that there has been a duplication of *CUC2* and a genomic loss of *CUC3*. This is the first known case of loss of *CUC3* in any angiosperm group, and it is correlated with a marked increase in transitions in extrafloral fusion across the Caprifoliaceae. We further show that both *CUC2* paralogs in *Lonicera japonica* and *L. sempervirens* are more highly expressed in corolla lobes than in the corolla tube, suggesting a function of *CUC2* in separating tissues in *Lonicera* flowers. Using our target enrichment dataset, we discuss changes in the *CUC2* binding elements that correlate with morphological shifts. We further use this dataset to examine the larger gene regulatory network that includes *CUC*.

S.248.7 Documenting developmental transitions and studying targeted gene expression in the gametophyte of ferns: *Adiantum raddianum* and *Anemia villosa*

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Ferns constitute the second most diverse lineage of vascular plants on Earth, surpassed only by angiosperms. In most recent phylogenies, ferns appear monophyletic. In both ferns and lycophytes, gametophytes and sporophytes can grow independently as multicellular haploid and diploid bodies, respectively. Gametes are generated through cellular differentiation in the haploid gametophyte, which by itself a product of spore germination. After fertilization, the zygote develops into a new sporophyte. In comparison to angiosperms, few developmental studies have focused on ferns, and the studies made have emphasized morphological diversity and gene expression data in the sporophytic phase. For instance, several studies have addressed the expression of identity and leaf development genes, as well as reproductive transition genes in fronds and during sporangia formation. Similar analyses are lacking in the haploid phase: the gametophyte. This study standardized spore germination and gametophyte growth in *Adiantum raddianum* and *Anemia villosa*. Morphological changes and developmental timing were documented for all haploid stages, from spore germination to zygote formation. Successful optimization of RNA extractions from tiny individuals allowed expression analyses for *LEAFY (LFY)* and *Phosphatidylethanolamine Binding Protein (PEBP)* genes. These gene lineages control the reproductive transition in angiosperms, and are hypothesized to play similar roles in ferns, due to their wide expression in fern sporophytes, especially in sporangia throughout their maturation. Our data shows active expression of *LFY* and *PEBP* homologs in fern gametophytes. We discuss the specific expression patterns and their putative functions in spore germination, gametophyte growth, or the formation of antheridia and archegonia and gametogenesis in early diverging vascular plants.

S.249 PHYLOGENETICS AND PHYLOGENOMICS. SESSION 1

S.249.1 Phylogenomics of angiosperms based on mitochondrial genes: new insights into deep node relationships

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Angiosperms are the largest plant group and play an essential role in the biosphere. Phylogenetic relationships of many families and orders remain controversial despite 30 years of study, and, in an attempt to address these, we performed the most extensive sampling of mitochondrial genes to date. We reconstruct a seed plant phylogenetic framework based on 41 mitochondrial protein-coding sequences (MTCDSs). The results for major clades of angiosperms have moderate to strong support (>70% bootstrap) for more than 80% of the nodes and strong support for monophyly of most orders. Eight major nodes were supported in this study, including three paraphyletic ANA grade (Amborellales, Nymphaeales, and Austrobaileyales) and five major core angiosperm branches. Chloranthales and Ceratophyllales are placed sister to the eudicots, whereas the monocots are placed sister to the magnoliids. A new order, Huales, was proposed to establish to accommodate phylogenetic isolated Huaceae. Our results indicated that mitochondrial genomic data were effective at resolving deep node relationships of angiosperm phylogeny.

S.249.2 Glue them all: innovative recycling genomic sequencing resources using universal Angiosperms353 probe sets

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With the continuous advancement of sequencing strategies, high-throughput sequencing (HTS) technologies have developed as one of the most important tools in plant phylogenomics. Target capture sequencing, particularly hybridization target enrichment sequencing (Hyb-seq), is a crucial HTS sequencing strategy known for its flexible probe design, which has been becoming a standard method of phylogenomics. The widely used universal Angiosperms353 probe sets (Angiosperms353) play a pivotal role in Hyb-seq and have increased applications in recent years. We have comprehensively assessed the potential application for Angiosperms353 by combing a large amount of literature and empirical datasets. We found that RNA-seq strategy captures the highest number of Angiosperms353 genes, and then followed by whole genome sequencing and genome skimming strategies; increasing sequencing depth leads to higher yields of captured genes; and no obvious bias was observed for the yields of Angiosperms353 across all angiosperm groups we tested. Hence, based on the knowledge acquired above, we used Angiosperms353 extracted from genome resequencing data, and attempted to build a phylogeny for all the seed plants, as well as phylogenomics of Elaeagnaceae and Rosaceae. In the era of genomics with large volumes of HTS data, our works demonstrate the practical application of Angiosperms353 by innovatively recycling vast genomic sequencing resources, maximizing genomic data sharing and utilization.

S.249.3 Phylogenomic insights into the evolutionary history of evergreen broadleaved forests in East Asia under Cenozoic climate change

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The evergreen versus deciduous leaf habit is an important functional trait for adaptation of forest trees and has been hypothesized to be related to the evolutionary processes of the component species under paleoclimatic change, and potentially reflected in the dynamic history of evergreen broadleaved forests (EBLFs) in East Asia. However, knowledge about the shift of evergreen versus deciduous leaf with the impact of paleoclimatic change using genomic data remains rare. Here, we focus on the Litsea complex (Lauraceae), a key lineage with dominant species of EBLFs, to gain insights into how evergreen versus deciduous trait shifted, providing insights into the origin and historical dynamics of EBLFs in East Asia under Cenozoic climate change. We reconstructed a robust phylogeny of the Litsea complex using genome-wide single-nucleotide variants (SNVs) with eight clades resolved. Fossil-calibrated analyses, diversification rate shifts, ancestral habit, ecological niche modelling and climate niche reconstruction were employed to estimate its origin and diversification pattern. Taking into account studies on other plant lineages dominating EBLFs of East Asia, it was revealed that the prototype of EBLFs in East Asia probably emerged in the Early Eocene (55–50 Mya), facilitated by the greenhouse warming. As a response to the cooling and drying climate in the Middle to Late Eocene (48–38 Mya), deciduous habits were evolved in the dominant lineages of the EBLFs in East Asia. Up to the Early Miocene (23 Mya), the prevailing of East Asian monsoon increased the extreme seasonal precipitation and accelerated the emergence of evergreen habits of the dominant lineages, and ultimately shaped the vegetation resembling that of today.

S.249.4 New genetic markers for phylogenomic studies in Amaranthaceae sensu stricto

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Amaranthaceae *sensu stricto* form a monophyletic group within the Amaranthaceae (including Chenopodiaceae) comprising 80 genera and 900 species. Amaranthaceae *s.s.* are found predominantly in tropical and subtropical regions worldwide. In Australia 10 genera with together ca. 190 species occur, spread across the entire continent including also arid biomes. Current phylogenies are insufficient to understand the complex evolutionary history of the lineage which is challenging due to three whole genome duplication events, rapidly diversified sublineages and an unusual high number of widespread, often introduced weedy species. This rules out a genome skimming approach and suggests target capture methods as the more appropriate approach. We identified a new genetic marker set universally applicable across the entire Amaranthaceae *s.s.* lineage. The baits are based on 28 transcriptomes and a reference genome of *Amaranthus hypochondriacus.* A total of 10,612 orthologous and low-copy genes were identified in a previous comprehensive transcriptomic study and compared with the output of MarkerMiner. Following the genome reference, 73,262 exons were split and filtered based on criteria including a minimum length of 800 bp, less than 50% missingness per sequence, more than 2% informativeness, a minimum of 75% pairwise identity, and a requirement of at least 15 sequences per alignment. The remaining 2,561 exons were manually checked to ensure the quality of the loci. The final probes target a total of 884 nuclear loci and 1.7 Mbp. Based on this set of carefully selected loci, we reconstruct the evolutionary history of the entire Amaranthaceae *s.s.* lineage with the first aim to investigate the origin, age and spread of Australian lineages of Amaranthaceae s.s.

S.249.5 Ecological and historical factors underlying the uneven diversification of firs in the Northern Hemisphere

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The Northern Hemisphere represents the largest landmass and harbors the most diverse temperate biomes on the Earth. Notably, species richness is unevenly distributed across regions in the Northern Hemisphere, which is much higher in East Asia than in North America and the Euro-Mediterranean region. However, the possible factors underlying this pattern remain to be explored. *Abies* (Pinaceae) represents one of the most species-rich genera of conifers, which is consistent with the general biodiversity uneven patterns of the Northern Hemisphere, and once used as an important ecological proxy in estimating climate changes. Therefore, *Abies* is an outstanding lineage to explore the evolutionary force underlying the heterogeneity of species diversity in the Northern Hemisphere. In this study, we used the next-generation sequencing approach Hyb-seq to obtain nuclear conserved ortholog loci, and to reconstruct a robust phylogeny of *Abies* with maximum likelihood and coalescent analysis. The multi-peak Ornstein-Uhlenbeck model and BayesRates revealed the significant correlation between diversification rate changes and niche shifts, that the ecological environment plays an important role in firs diversification. We also conducted multiple regression analyses and simultaneous autoregressive and the results indicated that the *Abies* species richness negatively responds to warmer temperatures and lower precipitation, which prefers seasonally moist and cool temperatures. The estimated time of speciation rate change and major niche shift in the East Asia clade coincides with the Asian monsoon strengthening caused by orogenic events in the Himalayas and Hengduan Mountains. We proposed that the significant transition from arid to humid and cool climates in large areas of East Asia as well as the diverse mountain environment in the Himalayas and Hengduan Mountains, has triggered an acceleration of Abies diversification. Our results unraveled that the net diversification driven by specific environmental factors is responsible for the fir diversity anomaly in the Northern Hemisphere.

S.250 LET PEOPLE COME TO BOTANY: NEW METHODS TO ENGAGE PEOPLE WITH PLANT DIVERSITY. SESSION 2

S.250.1 Sowing the Seeds: Citizen Science and Mobile Apps in Education and Beyond

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Over the last decades, there has been a sharp decline in global biodiversity. Land-use change, habitat fragmentation, and climate change are key human-induced causes contributing to the current biodiversity crisis. However, public awareness of the biodiversity crisis is low, particularly for plants, creating a barrier to their conservation. Moreover, in a world where a large part of the human population lives in urban areas, the contact of people with nature is declining, a tendency that will be exacerbated in the future. Indeed, many have highlighted the "extinction of experience" — a term for the growing alienation between people and nature — as the primary cause of this lack of public awareness of the biodiversity crisis. In this work we show how citizen science and mobile apps can be used as educational tools to raise awareness about plant diversity among students and the broader public. We examine the outcomes of three BSc-level formal education activities as well as two informal education initiatives. We discuss the potential of these approaches as educational and outreach tools and show that citizen science and mobile apps are remarkable tools for connecting students and the public with nature and engaging society in environmental challenges such as biodiversity conservation. We also explore the need for developing metrics to determine the real impact of these new approaches and propose some of them, such as an increase in the number of students in Flora disciplines and master's theses, plant conservation activism and observations in iNaturalist by former students.

S.250.2 Green roofs in continental climates: what makes them different?

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Green Roofs (GRs) are Nature-based Solutions that provide habitats and support biodiversity in cities. While GRs number is rapidly increasing, their ecological characterization is still poor. In particular, while all GRs are seeded or planted with plant mixtures, the development of plant communities on GRs has rarely been investigated. To unravel relationships between GRs vegetation and structural and environmental factors, this study examined 75 GRs in the city of Ingolstadt, Germany. A comprehensive sampling was carried out in the summer of 2023 within plots of 1 m^2 located in the centre of each GR. GR size, height, soil depth, age and management regime were considered as predictor variables. The plant taxonomic diversity of the roof communities was calculated using Hill numbers. The main drivers of species composition were identified through a Non-Metric Multidimensional Scaling (NMDS) and selected variables were used to fit a Redundancy Analysis (RDA). GLMs were then fitted to model diversity indices and bryophyte coverage across GRs in relation to selected factors. Differences in bryophyte coverage according to management type were also assessed with a Kruskal-Wallis test. The NMDS showed that the most influential variables on GRs plant communities are age, soil depth, mowing and weeding practices (9% of the variance explained in the RDA). Plant diversity tends to increase with increasing soil depth and GR height. Bryophyte cover decreases with increasing soil depth. In addition, bryophyte cover is significantly different between unmanaged and regularly mown or weeded GRs. Our study shows that plant communities of GRs are affected by several roof variables, and that soil depth, roof height and management strongly affect plant communities developing on the roofs. The results may provide useful insights for more environmentally and financially sustainable design and management of GRs.

S.250.3 The time for species knowledge is now!

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How can we spark people's interest for the fascinating world that is Botany? The climate and the biodiversity crisis are the main focuses in both education and media. But are we prepared to tackle these important issues? To understand biodiversity, or the loss of biodiversity, it is essential to also know the building blocks of biodiversity – species! There has never been a time when species knowledge has been more important than now! How do we spread our knowledge inside and outside the classroom? As a botanical garden, we have a broad platform for communication of botanical knowledge. People arrive happy and excited and (most often) by their own choice, that's a good start! We also have strong presence on social media. By combining the digital content, podcast and personal interaction in the garden at events, lectures and guided tours, we can reach a mixed target group. This is where we can spread and encourage interest in species knowledge; give people the information they didn't know they wanted. We present challenges and new possibilities on how people can interact with botany!

S.250.4 Surveying the scope, success, and challenges of plant conservation community science

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Since the end of the 20th century, volunteerism has become a major component of biological conservation worldwide. Interacting factors including limited funding, availability of technology, and public interest present a unique opportunity for conservation scientists and practitioners to benefit from larger datasets with broader spatial and temporal reach than possible with professionals alone. Volunteer monitoring efforts can be considered a part of the wider, growing field of community science (a.k.a. citizen science). In tandem with benefits to science and conservation, volunteers gain hands-on research experience, scientific knowledge, outdoor opportunities, and community. While adoption of community science in plant conservation appears to be increasing over the last 30 years, the landscape has remained largely undefined. To better understand the current status of community science in plant conservation, we conducted an assessment of community science projects that conduct rare plant monitoring. Through online research and targeted outreach, we surveyed 19 project managers in the United States and Australia and close to 300 volunteers from five unique projects. We documented a spectrum of project models, bounded by semi-autonomous surveys and monitoring directly supervised by researchers. We found that volunteers contribute tens of thousands of hours to monitoring rare plants annually, representing hundreds of thousands of dollars of in-kind donations. Despite project success documented through longevity, number of volunteers, and the amount of data collected, persistent challenges including data quality, data security, and project management limit establishment of new projects and the potential of existing projects. This assessment has led to the founding of the Rare Plant Community Science Network with the goal of "improving rare plant monitoring and conservation through sharing and collaboration between community science programs." The network currently represents 38 programs spanning four countries (Canada, U.S., Australia, and South Africa) and three continents.

S.250.5 Botanical diversity and conservation strategies in the Colombian Caribbean: the critical role of local herbaria

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The Colombian Caribbean stands out for its immense biological richness, evidenced by diverse flora and the presence of numerous endemic species. This presentation outlines the current state of knowledge about this flora and highlights the scientific value of botanical collections in the region. The Colombian Caribbean flora faces significant threats, primarily due to anthropogenic factors such as deforestation, urbanization, and agriculture. Key mountainous regions like the Sierra Nevada de Santa Marta and the Serranía de Perijá host a unique diversity of plant formations, including the valuable páramos. In parallel, the extensive plains of the Caribbean, which make up the majority of the region, are home to equally important ecosystems such as dry tropical forests. These plains, along with the mountainous zones, form a mosaic of habitats that underscore the rich biodiversity of the Colombian Caribbean. The fragmentation and systematic destruction of these ecosystems have drastically reduced their extent, leaving less than 8% of the original dry tropical forests. This alarming situation underscores the urgency of implementing effective conservation strategies. In this context, botanical collections become critically important. The local herbaria, like the one recently established at the University of Cartagena, are fundamental for preserving knowledge of the regional flora. These centres serve as vital resources for research in taxonomy, diversity, evolution, and ecology. Beyond their academic value, the herbaria play an essential role in education and raising awareness about the importance of local flora conservation. Conservation efforts through these herbaria are a vital step towards understanding and protecting the unique biodiversity of the Colombian Caribbean. Interinstitutional collaboration and continuous commitment to botanical research and conservation are key to tackling environmental challenges and preserving this valuable natural heritage.

S.250.6 Scientific common names (SCNs) for selected medicinal plants: an improved botany communication method

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New ‘scientific’ common nomenclatures were constructed in line with the root meanings of scientific names. Based on this study, 563 novel, scientific common names (SCN) have been created for 181 medicinal plants belonging to 79 families, in relation to their binomial nomenclature for the first time. The newly established common names have the benefit of making scientific knowledge simpler. Newly formed SCNs can be used as templates for the naming of other living things and for the creation of new, scientific local names in other languages. New ‘scientific’ common nomenclatures were constructed in line with the root meanings of scientific names. Based on this study, 563 novel, scientific common names (SCN) have been created for 181 medicinal plants belonging to 79 families, in relation to their binomial nomenclature for the first time. The newly established common names have the benefit of making scientific knowledge simpler. Newly formed SCNs can be used as templates for the naming of other living things and for the creation of new, scientific local names in other languages. The construction of new SCNs followed the etymologies of scientific terms. This study led to the creation of 563 new common names for 180 medicinal plants from 80 families, which were previously unknown in relation to their binomial nomenclature. The primary benefit of the recently established common names is that scientific data is presented in clear, concise language that is easy to understand. On the basis of this, it is advised to review plant common names. These new SCNs can be used as templates to generate similar names for other living things.

S.251 ECOPHYSIOLOGICAL CHALLENGES IN THE ANTHROPOCENE. SESSION 2.

S.251.1 Functional traits and soil water availability shape competitive interactions in a diploid-polyploid complex

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Although polyploid species become successfully established in the short term, only a few persist in the long term. Interaction between polyploids with their ancestral cytotypes in secondary contact zones can contribute to these extinctions. Environmental factors as water availability and functional trait divergence may influence this competitive interaction.We conducted a greenhouse competition experiment with four cytotypes (2x, 4x, 6x, and 12x) of Dianthus broteri under two contrasting water regimes. We estimated niche and fitness differences and predicted the pairwise competitive outcomes. Additionally, we explored the influence of functional traits (SLA, AN, Fv/Fm, and iWUE) on competitive interactions. Water availability modified the competitive dynamics between cytotypes and predicted competitive exclusion. Under high water availability, cytotypes with lower ploidy levels (2x and specially 4x) exhibited the greatest competitive abilities while under low water availability, the higher level cytotypes (12x, 6x) overcompeted. These differences in competitive outcomes were explained by functional traits related to competitive effects (SLA) and competition tolerance (AN, Fv/Fm, and iWUE). Our study emphasizes that the long-term fate of polyploids largely depends on water availability, with polyploids having a competitive advantage in arid environments and highlighting the role of functional traits in shaping the competitive dynamics between cytotypes.

S.251.2 Inter- and intraspecific variability in leaf minimum conductance (gmin) in vascular plant species across five biomes

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Leaf minimum conductance (g_{min}) represents the vapor diffusion conductance through the surface with closed stomata, encompassing cuticle and "leaky" stomata. It stands as a critical functional trait defining the dehydration rate after stomatal closure and its capacity to overcome long-lasting droughts and heatwaves. While other traits related to drought resistance (e.g., wilting point, embolism vulnerability) are known to vary with climate, the climate-dependent variation in g_{min} remains poorly understood, despite being recognized to display significant interspecific variability and plasticity to growth conditions. Our study encompasses a diverse array of over 300 species growing under natural conditions, including angiosperms, gymnosperms and pteridophytes, as well as various growth forms—from trees to herbs—and leaf habits. To capture the interspecific variability and plasticity in g_{min}, we sampled plants from more than 50 locations spanning a steep mean annual temperature and precipitation gradient in Europe, ranging from 2.4 to 19.6 °C, and 250 to 2200 mm, respectively. Sampling was conducted on current-year, sun-adapted leaves during the summer of 2023. Measurements also included leaf dimensions, stomata distribution, trichome presence, and leaf dry mass per area. This broad sampling allows to explore the extent of g_{min} variability and its potential correlations with climatic conditions across five biomes in a large spectrum of plant diversity. In order to explore intraspecific variability, we selected four widely distributed species representing different ecological strategies—*Quercus ilex* (evergreen angiosperm), *Ailanthus altissima* (deciduous angiosperm), *Pinus halepensis* (evergreen gymnosperm), and *Pteridium aquilinum* (fern)— and measured them in over 10 locations. Results showed a strong intra- and inter-specific variability in g_{min}, as well as significant plasticity. This study provides valuable insights into the adaptive responses of plants to climate, enhancing our understanding of the functional significance of g_{min} in the context of climate change adaptation.

S.251.3 Stomata are driving the direction of carbon dioxide induced water-use efficiency gain in selected tropical trees in Fiji

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To date, the effects of decadal scale rising atmospheric CO_2 concentration on plant gas-exchange characteristics in the tropics are largely unknown. This research provides a rare insight on the little-known long-term impact of rising atmospheric CO_2 on plant water-use and conductance of tree species in Fiji. Our study focuses on five tree species from the South Pacific Islands, a region that is particularly vulnerable to the impact of global warming. This is the first known study on the long-term physiological response of native plants to climate change in the region. Studying this long-term trend using herbarium records is challenging due to trait intraspecific variation. We assessed the impact of atmospheric CO_2 concentration rise of about 95 ppm (1927–2015) on intrinsic water-use efficiency (iWUE) and theoretical maximum stomatal conductance of five tropical tree species in Fiji using isotopic composition and stomatal traits of herbarium leaves. Empirical results were compared with simulated values using models that uniquely incorporate intraspecific variation of empirical maximum stomatal conductance responses and specimen- or species-specific parameterization. While the magnitude of iWUE and maximum stomatal conductance response is species-specific ranging from strong to negligible, our findings indicate that the impact of stomata on determining the direction of iWUE response becomes apparent in situations where there is a consistent trend in photosynthesis. Generally, a stronger increase in iWUE was accompanied by a stronger decline in maximum stomatal conductance. This study demonstrates that incorporation of adaptations in maximum stomatal conductance, via changing size and/or density of stomata, in simulation is necessary for assessing an individual species iWUE response to changing atmospheric CO_2 concentration.

S.251.4 The role of the plants' defense dimension on shaping abiotic stress tolerance of woody plants

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Plants are members of a biodiverse community where interactions can either benefit or negatively impact plant fitness. Herbivore insects (negative interaction) exert a strong selective pressure on plant defensive strategies. At the same time, the production and maintenance of defenses is energetically costly and depends on habitat quality, including resource and non-resource stress levels. Accordingly, under high herbivory pressure, plants allocate resources to defense against phytophagous insects, possibly limiting resource allocation to tolerate abiotic stressors. In other words, biotic and abiotic stress tolerance can exhibit a trade-off. In that context, we aim to elucidate the role of biotic stress (defense dimension) on shaping a species abiotic tolerance syndrome. The so-called Stress Tolerance Space (STS) was recently described as a trade-off model defining the limits of ecophysiological tolerances of Northern Hemisphere woody plants towards four major abiotic stresses (shade, drought, cold and waterlogging). A plant tolerance to a given abiotic stress is constrained by other co-occurring abiotic and biotic factors and, therefore, the integration of key ecological dimensions with the STS model would allow to disentangle the multidimensional nature of woody plants' adaptations to abiotic stress. To that end, we have compiled data on traits related to the feeding ecology (e.g., feeding guild, hostplant specialization) of 6000 species of phytophagous Lepidoptera and Hymenoptera associated with the woody plant species under study within the abovementioned STS model. By exploring how insect feeding traits distribute within the STS, we provide evidence of a complex association between particular sets of feeding traits and specific stress tolerance strategies in woody plants of the Northern Hemisphere, thereby gaining insights about the significance of the biotic-abiotic stress tolerance trade-off.

S.251.5 The above- and below-ground segregation of functional space of oak seedlings responds to native habitats

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Seedling growth and morphology reflect functional responses to habitat because their establishment relies on the development of resource-acquiring organs and their capacity to respond to the environment. Oak species contribute significantly to above-ground biomass and biodiversity in Northern Hemisphere Forest ecosystems. Although morphological and physiological differentiation has been studied in oaks, it is necessary to conduct studies to analyze the ecological strategies at the seedling stage. In this study, we conducted an experiment under controlled conditions to assess how interspecific variation in functional traits of oak seedlings varies in relation to their native climates. We selected three oak species from dry lowland forests and three from mesic highland forests of Mexico. We analyzed the trade-offs among leaves, stems, and roots that drive functional differentiation between dry and mesic oak species. We examined trait-by-trait relationships, constructed interaction trait networks, and then quantified the overlap of functional space at both the species and environmental group levels. Our results showed significant differences among environmental groups, primarily in leaf carbon:phosphorus ratio, stem water content, and biomass allocation. Oak species from dry environments allocate biomass to roots to obtain water and nutrients as a drought adaptation. Meanwhile, mesic oak species allocate more biomass to leaves, with higher leaf nitrogen and phosphorus concentrations and stem water content. Both environmental groups showed trait-by-trait relationships; however, we found that the pattern of coordination of traits was different between the dry and mesic oaks. This supports the idea that the selective value of the same traits differs under different environmental conditions. Finally, we found significant segregation of the functional space among species in the same environmental group, highlighting the diversity of ecological strategies in oaks. Variations in plant functional traits and different elemental compositions among oak species promote diversity in ecological strategies.

Symposia Session 15

S.252 THE EVOLUTION AND BIOGEOGRAPHY OF APOMICTIC PLANTS. SESSION 2

S.252.1 Phylogenomics and morphometric-environmental modeling unraveled reticulate polyploid evolution of the Ranunculus auricomus complex

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Hybridization, polyploidization, and/or apomixis represent important evolutionary forces of plant speciation. However, consequences of partly overlapping, intricate evolutionary processes are still poorly understood for non-model, neopolyploid plant groups. Analytical challenges are attributable to high heterozygosity, low genetic divergence, and missing information on progenitors species, ploidy levels, and reproduction modes. To tackle this, we selected the large European *Ranunculus auricomus* species complex, comprising five newly circumscribed sexual species and >800 polyploid taxa/morphospecies. Subgenomic (97,312 RAD-Seq loci, 576 nuclear genes, and 71 plastid regions), flow cytometric leaf/seed (1,474/1,075 screened individuals), geometric morphometric (1587-1880 landmarked individuals per trait), and abiotic environmental datasets were collected from 75 polyploid apomictic taxa and four putative sexual progenitor species. In this talk, an innovative taxonomic workflow will be presented, which includes phylogenomic tree, structure, network, and SNP-origin analyses, and genomic-morphometric-environmental multivariate modeling. Results consistently showed polyphyly and only 3–5 supported groups instead of 80 polyploid morphospecies. Each group contained an extant sexual progenitor species, and surprisingly, one group possessed a yet unknown (probably extinct) progenitor. Combined multi-genomic analyses demonstrated predominantly allopolyploid origins, each involving 2–3 different diploid sexual progenitors, potentially during interglacial periods. Young allotetraploids showed subgenome dominance and non-hybrid SNPs, suggesting substantial post-origin (e.g., hybrid segregation) and little lineage-specific evolution. Sexual progenitors occupied a much smaller range in southern and central Europe, whereas three-times more heterozygous polyploid and predominantly obligate apomictic derivatives expanded their range towards northern and northeastern Europe characterized by more temperature variable habitats. Allopolyploid apomicts, compared to their diploid sexual progenitors, resemble a mosaic of new, more stress-tolerant genotypes with morphologically intermediate to transgressive biotypes often outside the progenitor's ecological niches, explaining the observed geographic parthenogenesis scenario. The joint evaluation of phylogenomic, cytological, morphological, and ecological data supports a revision of the purely descriptive, subjective traditional morphological classification.

S.252.2 Integrative taxonomy studies to disentangle Hieracium tenuiflorum Arv-Touv. (Asteraceae) diversity in Italy

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Hieracium L. has extreme morphological variation caused by complex reproductive strategies, interspecific hybridization and polyploidization. The genus includes few sexual diploids and numerous apomictic polyploids (Mraz & Zdvořák 2019). Taxonomy and systematics of this group are extremely complex and poorly investigated. *Hieracium. tenuiflorum* Arv.-Touv. belongs to *H. murorum* L. group (sect. *Hieracium*), and occurs in Alps and Apennines, where it grows in forest margins and along roadsides between 200-1800 m a.s.l. Currently, there are 6 subspecies ascribed to *H. tenuiflorum*. Most of them were originally described for Italian localities across the Alps. However, the current classification for these taxa is based only on morphology and information on current distribution, ploidy level or genetic diversity is lacking. To disentangle the taxonomic diversity of the species, we used an integrated taxonomic approach, including nomenclatural investigation on herbarium specimens, morphometry, chromosome counts, genome size estimation and molecular systematics. Recently collected plants from *loci classici* of *H. tenuiflorum* subspecies and from different localities in Alps and Apeninnes were investigated. These studies revealed a high variability in ploidy level in *H. tenuiflorum*. For the first time, at least three diploid *H. tenuiflorum* populations were reported in the Southern Alps. Morphometric analyses showed morphological differences between subspecies despite morphological clusters mainly overlapped, suggesting high morphological similarity. Finally, we performed molecular investigations using three plastid intergenic spacers (trnH-psbA, trnT-trnL, and trnV-ndhC) and ten nuclear microsatellites to evaluate the phylogenetic relationship between sampled populations.

References: Mraz, P., & Zdvořák, P., (2019) *Ann. Bot.*, 123(2), 391-403.

S.252.3 The hybrid origins of African forage crop grasses in the genus Urochloa (Panicoideae, Poaceae)

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African grasses in the genus Urochloa (Brachiaria) have been recognised for their forage crop potential as early as the 18th century. Three closely related African species (U. brizantha, U. decumbens, and U. ruziziensis) dominate Urochloa breeding and are hybridizied to produce the world's most commercially important tropical forage cultivars. These three grasses form a naturally occurring species complex characterised by diverse ploidy levels, overlapping morphologies, and sexual and asexual reproduction. The reticulate evolution of U. brizantha, U. decumbens and U. ruziziensis, and their phylogenetic relations within Urochloa remain unclear. Elucidating this history will greatly benefit future breeding projects. We inferred a species level phylogeny for Urochloa using target enrichment and RNA-seq data from Kew Herbarium and Centro Internacional de Agricultura Tropical (CIAT) accessions. Additionally, we estimated ancestral states for important forage traits using our phylogeny. Finally, we investigated reticulate evolution in U. brizantha, U. decumbens, U. ruziziensis and their closest wild relatives using phylogenetic networks and fluorescent in-situ hybridization (FISH). Our analysis revealed the independent evolution of five forage clades across Urochloa. Urochloa brizantha, U. decumbens, and U. ruziziensis form a well-supported clade with two wild relatives, U. eminii and U. oligobrachiata. Phylogenomic networks and FISH analysis confirm that U. brizantha and polyploid U. decumbens are hybrid species that share at least one parental lineage. Further, diploid U. decumbens and polyploid U. decumbens belong to separate lineages, which is supported by morphological data, chloroplast phylogenies, and previous population genetic and cytological work. We found evidence of reticulate evolution between polyploid U. decumbens and the lineage containing diploid U. decumbens and U. ruziziensis. The reticulate evolution of U. brizantha is more complex as diploids and polyploids share a single origin. Our study demonstrates that multiple lines of evidence (morphological, phylogenetic, cytological) are required to disentangle highly reticulate species complexes.

S.252.4 "Pseuds corner" – morphometrics and distribution of Dryopteris pseudocomplexa and Dryopteris pseudodisjuncta in the UK and Ireland

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The scaly male ferns of the *Dryopteris affinis* (Lowe) Fraser-Jenk. complex cause problems for taxonomists because of their hybrid origins and partly apomictic, partly sexual methods of reproduction. The work presented is part of a larger study of this complex in the UK and Ireland, combining morphometrics and flow cytometry. *Dryopteris pseudocomplexa,* previously known informally as 'morphotype Arranensis', was published by Fraser-Jenkins as a subspecies of *D. cambrensis*, with records on Skye, Arran, and two locations in Ireland. In 2016 it was discovered to be a fertile tetraploid. It was published by Sell as a species. There are also reports of a similar fertile tetraploid taxon from the Härz mountains, the Vosges, and from Romania. *Dryopteris pseudodisjuncta* was first discovered in the UK in 2008, in Kirkbean Glen, Scotland, where there are also records of *D. pseudocomplexa.* It has subsequently been found on Arran and at Strome ferry, Scotland, where *D. pseudocomplexa* is also recorded, and in Cumbria and Somerset. *D. pseudodisjuncta* is a triploid apomict, and also produces male gametes that can hybridise with sexual species. Results of the morphometric analysis, and the current distribution of these two taxa in the UK and Ireland will be presented, together with identification guides to distinguish these taxa from other scaly male ferns. Samples for DNA sequencing from this study will be provided for a study led by Michael Kessler, Zurich, which may reveal whether these two taxa are related. Alternatively, they may occur together because of their preference for an Atlantic climate.

S.252.5 The cost of co-occurrence: pollen from apomicts negatively impacts the fitness of sexuals in an open-pollinated common garden

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Diverse factors have the potential to explain geographical parthenogenesis, the tendency for related sexual and apomictic forms to occupy distinct ranges. Apomicts are expected to have a colonization advantage relative to obligately outcrossing sexuals, but if this advantage is purely demographic, we might expect sexuals to 'catch up' over time and colonize sites where apomicts have established. Where this is not the case, it could reflect ecological and/ or additional life history divergence that precludes coexistence. Asymmetrical reproductive interference is an additional or alternative mechanism that may prevent invasion by sexuals into apomictic sites, through the action of pollen from apomicts reducing the reproductive fitness of sexual outcrossers. *Townsendia hookeri* (Asteraceae) includes obligate apomictic autotriploid and sexual outcrossing diploid populations that display a classical pattern of geographical parthenogenesis along the eastern slope of the Rocky Mountains, from Colorado, USA to British Columbia, Canada. The two forms overlap in range in southern Wyoming, but co-occurrence is rare. Transplants across the range reveal that sexuals can persist in sites occupied by apomicts. We measured the strength of reproductive interference (RI) by analyzing progeny produced in a mixed, open-pollinated common garden located in the zone of range overlap. Seed set of sexuals declined as a function of their proximity to apomicts. We used genomic markers (SNPs) to infer the parentage of progeny arrays from sexual maternal plants, using the programs BORICE to estimate the mating system and HIPHOP to determine parentage. We detected low levels of hybrid formation, and, contrary to previous interpretations from controlled crosses, no evidence of induced selfing. Our findings point to significant negative impacts of co-occurrence via RI, even though sexuals were roughly equal in number to apomicts in our garden. This suggests that, in some cases, reproductive interference may be key to explaining geographical parthenogenesis.

S.252.6 Deconstructing apomixis in angiosperms: from macroecological patterns to microevolutionary processes

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Mapping the geographical distribution of phylogenetic traits helps visualize macroecological patterns (above species regional level) and understand how long standing microevolutionary processes (below species level) shape evolution. These processes are determined by mutation, genetic drift, gene flow, non-random mating, and natural selection, leading to the patterns we see today.

We reviewed global occurrences of apomictic species and mapped them according to the Tree_of_Life 3.0. Apomixis (asexual seeds), develops by sporophytic (adventitious embryony) or gametophytic (apospory or diplospory) pathways. Almost 1500 species show evidence of apomixis and c.230 species have anecdotal evidence of apomixis. Most apomicts occur in Asteraceae, Rosaceae and Poaceae, and 6 families have at least 50 apomictic species whose distribution varies significantly among continents. A correlation between developmental phenotypes among apomictic species and families suggests developmental constraints on phenotypic variability, adding to the recognized association between apomixis-derived biodiversity and general biodiversity.

To bridge the gap between microevolutionary processes and macroecological patterns and understand the role of apomixis in speciation, we took Paspalum intermedium a grass species with sexual diploids and apomictic tetraploids ecologically differentiated along a latitudinal gradient in South America– and use population-level genomics (Genotyping-by-Sequencing), reproductive and environmental/occurrence data (Ecological-Niche-Modelling) to assess microevolutionary processes. Diploids are genetically less variable than tetraploids and shows a narrow diploid gene pool from which tetraploids arise in P.intermedium. STRUCTURE analysis shows three consistent K values that relate to ploidy states, lineage ancestry and ecological attributes. Principal component and minimum spanning network analyses support a narrow cluster of diploids, and more diverse tetraploid lineages differentiated by geographic region (North/Centre/South) and cytotype co-existence (sympatry/parapatry/allopatry). Reproductive mode ratios (sexual/apomictic) associate to environmental variables and within population clonal diversity in marginal areas.

Our analyses suggest that differences in gene flow conditions promote intraspecific geographic/genetic differentiation within and between cytotypes, supporting early steps of speciation.

S.253 HABITAT-BOUND BRYOPHYTE EVOLUTION

S.253.1 Haplotype variation in mosses bound to niche adaptation

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Thanks to molecular information, numerous new bryophyte species, both morphologically recognizable and cryptic ones were discovered during the last decades. Some of the new species are restricted to specific habitats, but what about haplotypes, haplotype groups, or lineages within species? Haplotype variation within bryophyte species was often used to infer migration routes of populations, population histories, and similar aspects. Much less often the focus was on correlations with habitat or potential niche adaptations or intraspecific habitat diversification. Still, we should expect these to occur when different populations adapt to environmental conditions and sometimes as part of speciation. By not considering this aspect, we may draw incorrect conclusions regarding which factors explain observed patterns of bryophyte haplotype variation and thus, predictions in species/haplotype response to climate change. Here we explore whether certain haplotypes, haplotype groups, or lineages in mosses are or may be associated with specific environmental niches, sometimes contrasting this with geographical patterns. Further, we discuss how correlations between haplotypes and habitat parameters could be explored in greater detail in the future, including important caveats – for example, factors like the number of samples and sampling strategies.

S.253.2 Disentangling habitat adaptation in species of Sphagnum magellanicum complex in North America

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Evolutionary drivers play a pivotal role in shaping biodiversity and influencing how species adapt and change over time. The process of habitat adaptation and evolution helps species better fit their environments, increasing their chances of survival and successful reproduction. *Sphagnum* species are remarkable in their ability to construct and modify their own niches, which are often well differentiated among species. Nevertheless, the scarcity of morphological characters that separate the species poses a challenge in identifying ecological traits crucial for understanding their evolution and systematics. A current contentious topic revolves around the classification of the widely distributed *S. magellanicum* into several morphologically indistinguishable taxa. The recent addition of two newly described species brings the count of North American species to four: *S. diabolicum*, *S. divinum*, *S. magniae*, and *S. medium*. *Sphagnum*, especially the *S. magellanicum* complex, has been developing as a model group for ecological genomics. To explore differences among these cryptic species in microhabitats and climate niches, we developed barcode markers and used RADseq analyses on 808 collections from 119 sites across eastern North America. Microhabitats, classified by hydrology and shade, alongside hierarchical modeling of species communities, were assessed for niche variation among species. Surprisingly, *S. diabolicum* showed not significant responses to any variable, whereas the other complex members exhibited diverse responses. Climatic variables strongly influenced *S. magniae* but less so for *S. diabolicum, S. divinum*, and *S. medium*. Micro-habitat variables minimally affected occurrence variation for all species, whereas random variables (sample and locality) explained significant variation for *S. diabolicum, S. divinum*, and *S. medium*. These results suggest that there are still unmeasured but important ecological traits impacting species occurrence. Our findings underscore the intricate interplay between species and their environments, emphasizing the varying impacts of climate and local factors on *Sphagnum* species.

S.253.3 Parallel evolution in the genus Ulota (Orthotrichaceae, Bryophyta) under hyper-humid oceanic climates of the southern hemisphere

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The subfamily Orthotrichoideae, comprising 14 genera and approximately 360 species, plays a significant role in epiphytic communities within temperate regions and high tropical mountains worldwide. Four genera notably contribute to the subfamily's diversity, accounting for around 94% of its species: *Orthotrichum* (ca. 110 taxa), *Zygodon* (80), *Lewinskya* (75), and *Ulota* (70). The latter genus boasts a subcosmopolitan distribution but stands out for its greatest diversity in the hyper-humid oceanic-temperate climates of the southern hemisphere. In western Patagonia, thriving within these conditions, Valdivian temperate forests and Magellanic subpolar forests host 23 recognized *Ulota* species so far. All these species are endemic to the area, exhibiting remarkable and rare dispersion-related adaptation patterns that could have emerged during radiative processes. Many species show adaptations that limit spore release, such as oversized endostome segments or capsule mouth contraction. Moreover, large spores are very common, and among Patagonian *Ulotae* the abundance of spores with endogenous germination (multicellular spores) stands out. Despite being an uncommon feature in the genus, this trait has appeared in up to six species in Patagonia. Large and heavy spores as those found here might face challenging long-distance dispersal. Arguably, both climatic preferences and dispersal limitations could be linked to an evolutionary pressure for spores to remain within favorable locations, particularly in this territory where strong winds can transport propagules to adverse environments, including the nearby ocean. In addition, rapid germination significantly aids the establishment of new individuals in similar and suitable conditions. These adaptations, whether occurring as syndromes or in isolation, are also observed in other regions, such as Australasia, China, or Japan. Current data suggest that this intercontinental pattern might reflect parallel evolution that arises from homoplasy, which is common in the family.

S.253.4 Habitat-bound evolution in epiphyllous leafy liverworts of the Lejeuneaceae

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The leafy Lejeuneaceae is the largest family of liverworts with some 1.900 species in 88 genera and comprise a high morphological and ecological diversity in tropical and sub-tropical ecosystems. Most species have an epiphytic lifestyle with a rather large proportion of species adapted to epiphyllous microhabitats. Specific characteristics of epiphytic and epihyllous Lejeuneaceae are, among others, a small size, rhizoid discs, inflated leaf lobules and a short life cycle. The evolution of these epiphyllous and epiphytic lineages with their morphological and life history traits, as well as habitat transitions from terrestrial to epiphytic within the Lejeuneaceae is still poorly understood as a well-supported backbone phylogeny is lacking for this family. Beside exploring large Sanger-Sequencing datasets of nuclear and plastic markers, we use nuclear target enrichment data based on the GoFlag probe kit to untangle the evolutionary history of Lejeuenaceae that started during the Jurassic and Cretaceous. Our study will give novel insights into the evolution of potential habitat-bound life-history traits associated with the independent colonization of unstable epiphyllous habitats by several Lejeuneaceae lineages.

S.253.5 Effect of niche on the epiphytic bryophyte community in a tropical rainforest of the Amazon

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This study evaluated the presence and distribution of epiphytic bryophyte species in a vertical gradient based on the influence of niches associated with a tropical rainforest in the Colombian Amazon. The vertical gradient evaluated included 16 phorophytes and 16 decaying fallen logs. Each fallen log was considered as a zone (Z1), and in the case of the phorophytes six height zones (Z2 - Z7). Each zone (Z1 - Z7) was surveyed in a 10 cm2 plot, for a total of 192 sampling units (96 for phorophytes and 96 for logs). The taxonomic and floristic composition yielded a total of 120 bryophyte species, corresponding to 81 liverworts and 39 mosses. Species richness and diversity was quite similar between fallen logs and phorophytes; however, differences in species composition were evident. Of the total number of species identified, only 44 species were shared between fallen logs and phorophytes. Of the shared species, 16 were widely distributed, occurring in almost all height zones of the phorophytes, suggesting a wide tolerance of the species to changes in microclimatic and physical conditions of the environment and substrate; 20 species were restricted to the first zones of the tree, without reaching the canopy, and finally, eight species were shared between fallen trunks and the phorophytes. Species were identified as being distributed in a free vertical zonation pattern along the host trees. By comparing the data obtained with regional studies, it could be confirmed that the niche assemblage is driving the species composition of epiphytic bryophyte communities at local and regional scales.

S.253.6 Epigenetic and transcriptomic changes of amphibious liverwort Riccia fluitans during transformation from land to water form

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Amphibious plants, adept at thriving in the transition zone between terrestrial and aquatic environments, exhibit remarkable adaptability by adjusting their morphology and physiology to fluctuating environments. *Riccia fluitans*, an aquatic liverwort, serves as an excellent example. This species can grow as floating mats in water or on moist land, demonstrating its versatile adaptability. In our study, we employed genomics and transcriptomics approaches to shed light on the molecular mechanisms that underpin this adaptation. To assemble and annotate the *Riccia* genome, we utilized nanopore-based native DNA and RNA sequencing, nanopore full-length cDNA transcript sequencing, Illumina-based RNA-seq and DNA-seq of paired-reads, and Hi-C libraries. The genome of *Riccia fluitans* was 448 Mbp, scattered over 8 chromosome-scale contigs. Interestingly, the genome size was double that of Marchantia polymorpha, mainly due to the expansion of transposons. By comparing the water and land forms of *Riccia fluitans*, we identified over a thousand differentially expressed genes involved in a variety of biological processes. Our analysis of alternative splicing (AS) revealed over 800 splicing events with significant inclusion levels that differentiated the water and land forms. The majority of these events were classified as intron retention (RI), followed by alternative 3′ splice site (A3SS) and alternative 5′ splice site (A5SS). The least frequent AS events were exon skipping (SE) and mutually exclusive exons (MXE). We also applied native, direct RNA sequencing to identify m6A sites along the transcriptomes of both water and land forms. This revealed 152 methylated sites across 110 genes in the water form and 25 modified sites across 18 genes in the land form. Interestingly, even among the shared genes (16), different adenosines were methylated in the compared ecotypes. This study thus provides a comprehensive insight into the molecular mechanisms underlying the aquatic adaptation in *Riccia fluitans*.

S.254 NEW INSIGHTS ON BIG PLANT GENERA 2: GENOMICS & TRAIT EVOLUTION

S.254.1 Discovery of a major gene behind prickles, an important plant innovation, in Solanum (Leptostemonum Clade)

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Solanum is one of the largest genera in the plant kingdom with approximately 1,250 species. The largest monophyletic group within *Solanum* is the Leptostemonum Clade, with more than 500 species. A distinctive characteristic of this clade is the presence of epidermal prickles on vegetative organs; these are a synapomorphy of the Clade and represent a single origin evolutionary innovation in the genus. Prickles have been lost independently in several taxa. In cultivated species, breeders favored selection of prickleless (*pl*) materials during crop domestication. Interspecific mapping populations between *pl* eggplant (*Solanum melongena*) and wild prickled species revealed that the *pl* phenotype is recessive and consistent with one Mendelian locus. Advanced backcrosses of prickle-bearing wild species into the *S. melongena* background pointed to a region at the end of chromosome 6 containing the causal genetic locus. Fine mapping of the region narrowed the causal interval to a 600 kb genomic region containing 13 annotated genes that included a *LONELY-GUY* (*LOG*) cytokinin biosynthesis gene harboring a splice-site mutation. Other prickleless cultivated eggplants were found to have either splice-site mutations (*S. macrocarpon*) or a deletion (*S. aethiopicum*) in this gene, identifying it as *PL*.

Sequencing of *PL* in prickleless species from the Leptostemonum clade revealed 15 independent mutations (i.e., frameshift, splice-site, TE insertion, and deletion alleles). The key role of *PL* in the development of prickles was further confirmed by CRISPR-Cas9 gene editing of *PL* in the prickly Australian wild species *S. cleistogamum* and *S. prinophyllum*, which recapitulated the phenotype. Our results indicate that *PL* may have had a major role in the evolution of an adaptive morphological novelty in the Leptostemonum Clade, as well as serving as a key genetic target during multiple instances of crop domestication.

S.254.2 Exploring the evolutionary history of Carex (Cyperaceae) with new insights from geometric morphometrics

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Carex, with over 2000 species and a cosmopolitan distribution, is the second largest genus within monocots. The Global *Carex* Group, a research consortium established in 2013, has produced a series of publications addressing the systematics and evolution of this giant genus. As a result, a robust phylogenetic backbone at the subgeneric level and a sectional classification framework for *Carex* are now available. In this work, we have doubled previous genomic species sampling and obtained a well-supported Hyb-Seq phylogeny for all subgenera and represented groups, except for the subgenus *Carex*. For the first time, we applied geometric morphometrics to nutlet (achene) shape across all *Carex*, allowing the reconstruction of ancestral achene shape and its comparison among lineages. This exploration will be informative about the anatomical diversification of the genus during its global expansion. Our work, by identifying synapomorphies of the organ likeliest to be preserved in the fossil record, will also help in the identification and subsequent incorporation of previously unassigned fossil records of *Carex* in divergence time estimation. Furthermore, we explore the potential correlation of achene shape and ecological requirements. Therefore, our results could potentially help to understand the possible triggers of radiation events and the factors influencing the expansion and settlement of the different *Carex* lineages.

S.254.3 Genome dynamics across mega-diverse taxa: the role of changes in repetitive DNA on Begonia evolutionary radiations

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Understanding the drivers of species diversity and rapid radiations has always been a major goal in evolutionary biology research. *Begonia* is one of the most species-rich angiosperm genera with over 2000 pantropically distributed species currently identified. Recent work on *Begonia* provides a robust phylogenetic background for the analysis of evolutionary patterns across various radiations in the group, and suggests that speciation in *Begonia* is not only driven by adaptive processes, but rather by a “random walk”. This group exhibits large variation in chromosome number and genome sizes across the genus, and previous genomic studies also confirm abundant and recent transposon activity in some *Begonia* species.

We have analysed patterns in TE content and activity of all main radiations within Begoniaceae using the five previously published *Begonia* genomes and seven new genome assemblies. We show that *Begonia* species show more complex, repetitive and dynamic genomes overall than their close relative, the monotypic *Hillebrandia sandwichensis* and identify repeat families recently expanded in species from two different highly speciose South-East Asian sections and in two large Neotropical radiations. We examined in detail two of these parallel radiations represented by two highly species-abundant sections, one in SE Asia and the other in the Neotropics. Results show recent LTR and wide satellite DNA expansions across very recently diverged species, in contrast with their species-poor, closely related clades. The genomic analysis of *Begonia heracleifolia* accessions showing variable genome sizes revealed a markedly higher satellite repeat and LTR-Gypsy content in the accessions with larger genome sizes, associated with the expansion of a few abundant repeat lineages. We finally identify an association between changes in genomic repeat content and genetic barriers to reproduction within this species, directly linking expansions of repetitive DNA to the process of genetic isolation and speciation.

S.254.4 Adaptive evolution of stomatal cluster and hypodermis in Asian Begonia

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With more than 2,000 species exhibiting striking morphological variation, the mega-diverse genus *Begonia* has emerged as a fascinating system for studying plant speciation. Many explanations, such as genome size variation, polyploidization, hybridization, and geographical isolation, have been proposed as the potential drivers for its high species richness. However, few studies have studied the role of phenotypic variation has played in facilitating ecological adaptation and triggering speciation. One unique morphological anatomic feature in some *Begonia* species is the presence of stomatal cluster and hypodermis that are beneficial for growing in arid habitats; however, the evolutionary importance of these anatomical traits has never been investigated under a broad phylogenetic context. Based on a highly resolved phylogenomic tree of Asian *Begonia* reconstructed using target capture data, phylogenetic comparative analyses of three characters (i.e., singular vs. clustered stomata, absence vs. presence of hypodermis, and epiphytic vs. lithophytic vs. terrestrial) were conducted. Our study demonstrates strong and significant phylogenetic signals in all three characters and reveals high concordance between both leaf anatomical traits with habitat preference, implying a high degree of phylogenetic niche conservatism in *Begonia*. However, the transition from singular to clustered stomata had occurred mainly in the common ancestors of *B.* sect. *Baryandra* and *B.* sect. *Jackia* distributed mainly in limestone karsts of the Philippines, Malaysia and Indonesia, respectively. Considering the biogeographic origin mainly mediated by long-distance dispersal in *B.* sect. *Baryandra*, our findings suggest that, after the common ancestors of *B.* sect. *Baryandra* dispersed to the Philippines, the possession of stomatal cluster and hypodermis could have facilitated the successful colonization to the limestone habitats throughout the archipelago. By integrating multiple data sets, our study demonstrates how phenotypic variation and ecological adaptation could have triggered an exceedingly high speciation rate in the megadiverse *Begonia*.

S.254.5 Homoplasy in the evolution of the New World clade of Astragalus (Fabaceae)

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With more than 3,000 recognized species, *Astragalus* L. (Fabaceae) is possibly the most species-rich genus of seed plants. With limited exceptions, the species recognized two decades ago have still been found to be part of one large *Astragalus* s.s. clade after subsequent phylogenies using small and large numbers of loci. These phylogenies have been relatively successful at identifying major clades within the genus especially for Old World species, where about 5/6 of the species richness of the genus is found. However, the phylogeny of the New World clade (informally called Neo-Astragalus) has proven more difficult to resolve. Neo-Astragalus has about 400 species in North America and 100+ species in South America that all have chromosome numbers in an aneuploid series (n = 11, 12, 13, 14, 15), in contrast to the euploid chromosome numbers predominant in the Old World (n = 8, 16). I speak about the origin of the aneuploid series and chromosome number evolution in Neo-Astragalus as well as the paralogy that hinders phylogenetic inference within the clade. In addition to the variable structure of Neo-Astragalus nuclear genomes, plastid genomes in the clade have also undergone numerous rearrangements, some of which are shared by multiple species through homology and others shared through homoplasy. I also examine rates of homoplasy in morphological characters within Neo-Astragalus and Astragalus as a whole and discuss how this may have influenced the number of species assigned to the genus.

S.255 SEEDS, SALINITY AND SURVIVAL: A FUNCTIONAL PERSPECTIVE

S.255.1 Seed germination and seedling establishment strategies under salt stress

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Salinization is a serious agricultural and environmental problem worldwide that impacts crop production and natural ecosystems. Germination and seedling establishment is the prerequisite for species growing in saline environments. Thus, germination responses to salts have received considerable attention. The influences of salts on plant growth including germination include osmotic effects, ion effects and nutrient deficit. Therefore, germination strategy under salt stress should be considered based on these aspects of saline effects. We designed a series of experiments using grassland species and crops to study the related questions. We found that the osmotic effect was not the predominant effect under NaCl stress because the hydrotime model cannot predict germination of barley and grass species well. Then we proposed a salinity model which can better fit germination of these species under NaCl stress. The ion effect was adverse to germination only at high salinity, with sodium as an osmotic regulator to promote germination percentage and speed of barley at low and intermediate salinity. An experiment testing germination tolerance of 12 halophytes to salt type NaCl, Na_2SO_4 and $NaHCO_3$ showed species-specific responses to different salts and they were either salt tolerators (high germination at high salinity) or avoiders (high recovery germination when salinity alleviated). Bigger seeds had higher salt tolerant capability at high salinity. Further analysis with mixed salts revealed that the most closely related salt parameters with germination and seedling growth was Na^+ concentration, not pH. Diluted salt solutions should be considered to conduct recovery germination experiments, rather than distilled water based on our study. We found that proper N application may aid seedling establishment of grass species in saline soils, which denoted nutrient deficit effect of salts. These results help to understand plant adaptation in saline environments and provide important information for salt tolerant species/crops breeding.

S.255.2 Variability in seed salinity tolerance in an island coastal community

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Many coastal plant species have adaptations that enable them to exist in higher saline conditions. However, rising sea levels, increased frequency and intensity of storm surges, and increased drought due to climate change are anticipated to increase the level of salinity to which coastal plants are exposed. Although some species may be able to tolerate these changes, salinity tolerance is highly variable across species and ontogenetic stage. Coastal ecosystems are critical for the welfare Hawaiʻi's residents, providing sustenance, stabilizing shorelines, and promoting economic and cultural well-being. Understanding how increased salinity will affect Hawaiian coastal plants is important to effectively manage and conserve these critical ecosystems. To improve our understanding of coastal plant species tolerance to projected increases in salinity exposure at the early ontogenetic stage of seed germination, we tested the effect of salinity (0, 10, 20, and 35 ppt total salinity of unfiltered/untreated seawater), then tested for resilience by rinsing seeds and sowing with freshwater. We included 17 native and 3 non-native species in our study. Although salinity tolerance varied considerably among species, salinity exposure generally reduced and delayed germination. The greatest effects were detected at higher salinity levels. Recovery germination overall was higher for seeds that had been exposed to higher salinity. None of the factors we explored emerged as predictors of salinity tolerance except seed mass, which tended to enhance germination at higher salinity. Species responses to salinity exposure indicate high vulnerability of coastal systems to increased salinity stress, and variability among species could lead to shifts in community assembly and composition under sea level rise. These results can help guide coastal ecosystem conservation and restoration management decisions in the face of climate change.

S.255.3 Effect of Ibuprofen on the germination niche of halophyte species

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Salt marshes are habitats of high ecological value and conservation concern worldwide. Recently, pharmaceutical pollution has become a further human-induced risk for these already-threatened environments. While the effects of pharmaceutical pollution were investigated on some fishes and invertebrates, they are largely unexplored for wild plants. This research investigated the effect of ibuprofen, one of the most commonly detected pharmaceuticals in surface waters, on seed germination of salt marshes plants. Adverse effects of this emergent contaminant can affect species population dynamics and, consequently, the integrity of salt marsh plant communities. We explored the germination requirements of *Juncus acutus, Limonium vulgare, Sarcocornia fruticosa, Tripolium pannonicum*. Then, seeds of the best germinating species *(Juncus acutus* and *Limonium vulgare)* were exposed to increasing concentrations of ibuprofen (0, 2, 20, 200, and 2000 μgL^{-1}), both alone and under saline conditions (NaCl 513 mM). Recovery tests were performed to investigate seeds' ability to recover after salinity and Ibuprofen stress. In *J. acutus*, ibuprofen slightly decreased the germination percentage and increased the standard deviation around the mean values. Ibuprofen also increased the germination time and synchrony, although not significantly. *L. vulgare* showed a less linear trend and non-significant effects. Recovery tests showed that, although with fluctuating patterns, seeds of both species can recover from salinity, also when exposed in combination with Ibuprofen. This research for the first time empirically tested the effect of ibuprofen on the germination of wild species. Furthermore, it provides relevant insight to understand plant dynamics and their responses to emerging human-induced threats, such as pharmaceutical contamination.

S.255.4 Saline Challenges: A Hydrotime Modeling Perspective on Germination Patterns in Mangrove Species under Differing Sodium Chloride Co

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The study focused on investigating the impact of salinity on the germination of selected mangrove species; Aegiceras corniculatum, Acanthus ilicifolius, Pemphis acidula, Sonneratia caseolaris, and Allophylus cobbe, emphasizing the critical adaptations these plants undergo during germination to thrive in the challenging interface of salt and freshwater. The study explored the relationship between water potential in the growth medium and the germination rate by applying a hydrotime model. Seed germination was studied under various temperatures (15, 25, and 35 °C) and varying sodium chloride concentrations. The germination patterns of different mangrove species were analyzed, with a specific examination of whether these patterns align with the hydrotime model. Effects of salinity on cotyledon emergence were also evaluated for A. corniculatum. Temperature was identified as a critical factor affecting seed germination, particularly of S. caseolaris and P. acidula. Moreover, an interaction effect of temperature and medium osmotic potential was evident on seed germination. The research unveils distinct salinity tolerance levels among the tested species, with A. corniculatum (a viviparous species) exhibiting the highest tolerance, followed by S. caseolaris, A ilicifolius, P. acidula, and A. cobbe. A. corniculatum, showed a delay in cotyledon emergence from radicle emergence, showing epicotyl dormancy and significantly fewer days to emerge cotyledon in higher osmotic potentials when compared to lower osmotic potentials. A. ilicifolius was the only species conforming to the hydrotime model, with a determined threshold water potential of −1.8 MPa. Overall, the findings revealed that the studied mangrove species exhibit facultative halophytic behavior, capable of germinating across a wide range of saline environments. Salinity can influence the duration of epicotyl dormancy of A. corniculatum. While the application of a hydrotime model was limited for mangroves due to deviations from model criteria, the research enhances our understanding of the intricate adaptations enabling mangroves to thrive in extreme conditions.

S.255.5 Are there different germination patterns along the saline gradient in the co-occurrent halophytes in Mediterranean saltmarshes?

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Soil salinity is one of the most relevant drivers leading to plant zonation in Mediterranean saltmarshes, where germination is a critical stage in the life cycle of many halophytes. The study of how salinity allows the germination and establishment of halophytes in saline environments is a relevant first step to disentangle the assembly processes in theses habitats, where sympatric species occupate separate ecological niches as a result of adaptive differentiation along the salinity gradient. In this framework, the main goal of this study is to assess if the co-occuring halophytes in Mediterranean saltmarshes show different germination patterns along the salinity gradient. Experiments were conducted considering the seeds of perennial co-occuring species in Mediterranean saltmarshes (*Arthrocaulon macrostachyum*, *Salicornia fruticosa*, four sympatric *Limonium* species -*L. caesium*, *L. cossonianum*, *L. delicatulum*, and *L. supinum*- and *Lygeum spartum*) and the whole salinity gradient of these habitats (0–6% NaCl). Our results suggest that the successful establishment of halophytes depends on the germination strategy which implies a rapid germination velocity when the soil salinity decreases, shaping the plant asssembly within the saline habitat. According to the obtained results, two different germination strategies have been defined which favour the adaptation of different halophytes species under favorable conditions. Certain species can germinate along a wide salinity range (e.g., *S. fruticosa*, *L. cossonianum*), whereas others are characterised by high germination at low-medium salinities and a reduced germination after high salinity exposure (e.g., *A. macrostachyum*). These findings provide evidence to shed light on the local assembly processes of halophytic communities and its particular zonation.

S.255.6 Seed germination responses of annual back dune species to current and future climatic scenarios

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Plant species living in coastal sand dunes face survival challenges from harsh environmental conditions like high soil temperature and low water availability that climate changes could exacerbate. The regeneration of annual plant species depends on seeds; thus they may be particularly vulnerable to climate-induced environmental changes. We studied seed responses of annual dune species to environmental cues in the laboratory, with the aim of identifying the thermal and water potential germination limits, as these could be critical to forecast the germination risk. We sampled characteristic annual species in Mediterranean back dune grasslands: *Festuca fasciculata* (Poaceae), *Marcus-kochia ramosissima* (Brassicaseae) and *Silene canescens* (Caryophyllaceae). Fresh and after-ripened seeds were exposed to different temperature and light regimes. To explore water stress responses, seeds were exposed to different water potential levels. After-rip-ening overcame dormancy allowing for germination responses at most temperatures and light conditions in *F. fascitulata* and *S. canescens*. *M. ramossima* had very low germination under all treatments except when exposed to GA3, thus this species probably exhibits deeper dormancy compared to the other two annuals. While *F. fasciculata* exhibited broader temperature and water potential germination niches (Psib50 = -0.83) compared to *S. canescens* (Psib50 = -0.24), the former species exhibited a thermal germination risk compared to the latter, which did not exhibit a risk. Whilst light positively affected seed germination under no water stress, a negative effect was detected when seeds were exposed to water stress, indicating photoinhibition of seed germination under these conditions for all species. In conclusion, we found common responses among phylogenetically distant species (*F. fasciculata* and *S. canescens*) concerning the environmental cues examined. In particular, seeds can integrate water and light signals from their environment to modulate their germination responses to avoid the risk of seedling mortality that may occur in water stress scenarios.

S.257 PLANT AWARENESS DISPARITY RESEARCH (PAD) AND CHALLENGES IN SCHOOL EDUCATION

S.257.1 Assessing Plant Awareness - a tool for science and school

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Since the early 20th century, biologists have bemoaned the lack of interest in plants and their neglect in education. Wandersee and Schussler (2001) defined this phenomenon as 'plant blindness' and challenged educational practitioners and researchers to investigate the causes and reform plant pedagogy. The next step in development was to redefine the condition as 'plant awareness disparity' to address the ableist connotations of the original term and to examine its components through the lens of the new definition. Following this line of thought, plant awareness, a novel perspective in contrast to deficit-oriented studies, encompasses visual perception, knowledge of and attitudes towards plants. Perceptual attention involves focusing mental resources on plants compared to other environmental elements. Attitude, a stable evaluation of a phenomenon, includes components such as perceived importance, appreciation, and preference for plants. Focused attention, positive affect and motivation contribute to an individual's interest in plants, whereas negative attitudes often arise from misconceptions about plant vitality. While various studies have examined these components individually, a comprehensive understanding of plant attitudes requires measurement tools that capture multiple dimensions and ensure internal consistency and structural validity. This oral presentation aims to promote a common understanding of plant awareness by exploring its conceptualisation and measurement methodology. The measurement tool we have developed will be examined in detail, as it is the first tool to go beyond self-report items. This includes an exploration of its development, overarching objectives, and the results of an expert-led validation of the Delphi technique. The in-depth examination of this measurement tool provides valuable insights into the complexities of plant awareness and highlights the evolving landscape of research in this area.

References: Wandersee JH, Schussler EE (2001). Towards a theory of plant blindness. Plant Science Bulletin 47, 2–9.

S.257.2 Plant awareness in Spanish formal education: an analysis of new curricula and innovative experiences at initial teacher training

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Plants constitute a highly diverse taxonomic group with fundamental ecological functions, which is currently undergoing a dramatic biodiversity loss. It is thus essential to promote their knowledge and appreciation through formal education, particularly during educational stages that are compulsory for all citizens. In Spain, plants are studied along primary (6-12 years) and compulsory secondary education (12-16 years). An analysis of the new competence-based Spanish curricula (2022) was conducted by identifying all plant-related text fragments and classifying them into a system of categories; the results will be presented and discussed to highlight both the strengths and weaknesses of the new curricula regarding plant contents teaching. Furthermore, and basing on the fundamental role that teachers play for the introduction of new perspectives in societies, two educational experiences aiming to promote plant awareness in Spanish pre-service teachers will be presented. The first one had two fundamental pillars: (1) the use of an organic garden as a real-world context where students could establish direct interactions with alive plants and develop attachment to them, besides learning about plants that are useful (thus facilitating authentic learning: linking new knowledge to prior knowledge and noticing the relevance and applications of their learning); (2) the use of a teaching-learning strategy largely based on drawing to promote observation, and including a seminar on botanical illustration, drawing sketches from nature, or designing mind maps. The didactic sequence included other science activities and contents, with the overall objective of integrating plant-related contents and promoting plant awareness. The second one constituted a refinement of that first experience, in which some new and relevant elements were included, such as a test that was purposely designed to assess students' perception of plants both at the small and medium-scales, as a measure of plant awareness. Results of both experiences will be also presented and discussed.

S.257.3 Reverting plant blindness: challenging civic epistemologies through education

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In the realm of plant sciences, both classical and contemporary experiments have unveiled a level of complexity in plant behavior surpassing conventional perceptions held by the general public. Beyond their fundamental ecological roles, plants exhibit intricate behaviors akin to those observed in higher animals. Positioned as scholars within the academic sphere, we bear the responsibility of disseminating this knowledge widely throughout society. This dissemination contributes significantly to the evolution of our shared "civic epistemologies"—the processes through which knowledge is cultivated and authenticated within a given society, ultimately influencing public engagement and decision-making. This oral presentation, framed under the overarching theme of "Plants and Society," showcases recent educational initiatives that effectively mitigate students' cultural "blindness" towards plants. Commencing with an exploration of its historical context, I introduce the concept of plant blindness—a term coined in 1999 by botanists and educators James Wandersee and Elizabeth Schussler. Subsequently, an examination of "civic epistemologies" in the context of plants will ensue, drawing insights from the scholarly contributions of Sheila Jasanoff. The presentation will proceed to scrutinize three experiments in higher education (Brenner, 2017; Bonser et al., 2013; Nyberg y Sanders, 2013). Leveraging common technologies such as smartphones, these experiments have demonstrated efficacy in heightening students' awareness of plant behavior and ecological significance. Following this, I contemplate the implications of these experiments in challenging preconceived civic epistemologies. Additionally, a conclusive sociological study by Katherine Mach and colleagues (Mach et al., 2020) will be presented to underscore the imperative for a collective "coproduction" of knowledge across diverse educational levels, ensuring heightened applicability. Confronting the urgent challenges posed by climate change necessitates an imperious call for societies to cultivate a more widespread dissemination of plant-related knowledge within the public domain.

S.257.4 Revisiting the term 'plant blindness' with community INCLUSION AND GROUND-SOURCED ALTERNATIVES

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When first identified in 1998, the construct of 'Plant Blindness' captured public attention and summarized botanists' frustration with people's inattention to plants. The term grew in popularity over two decades and continues to be regularly invoked outside the United States, with visual cognition explanations as the root cause for the observed plant perception biases. With increasing awareness of the need for respectful communication for supportive and inclusive societies, researchers appropriately revisited the concept and recommended a new title of 'Plant Awareness Disparity.' Their goal of moving away from ableist language to describe this cognitive inattention toward plants is noble and forces reexamination of the language we use. While we applaud efforts to encapsulate public botanical inattention through considerate terminology, we propose that the journey to rename 'Plant Blindness' has not reached its natural community-based conclusion. We suggest that inclusive nomenclature *for the community* must arise *from the community*. We present our current research-based efforts to identify a ground-sourced alternative to 'Plant Blindness,' through which we invite participation of diverse voices to identify a ground-sourced alternative.

S.257.5 Plant awareness in children's picture books

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In this contribution I theorise the importance of children's picture books as spaces for interaction and awareness with plants. I reflect on the new and more traditional genres within children's literature and how plants have been used (and abused) within them before critically reviewing a selection of popular children's fiction found in the five most popular supermarkets in England. One in five children's books in the UK are purchased at supermarkets and the selection of books in this study includes some of the most well-known and current popular titles. Following content analysis of a sample of these books (for audiences of ca. 5-10 years old) I highlight how plants are being represented in different ways, who (if anyone) is seen as responsible for these plants, what the impact of the plants are to the story, and how accurately they are represented (both through text and illustration). I then consider the potential impacts these representations may be having on young audiences and the challenges children's and illustrators are faced with. Final comments will suggest ways in which teachers and teacher trainers might choose and use books in order to support young people navigate plant awareness.

S.258 PHYLOGENOMICS AND ADAPTIVE EVOLUTION OF THE WOODY PLANT GENUS RHODODENDRON

S.258.1 Pervasive hybridization during evolutionary radiation of Rhododendron subgenus Hymenanthes in mountains of southwest China

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Radiations are especially important for generating species biodiversity in mountainous ecosystems. The contribution of hybridization to such radiations has rarely been examined. Here, we use extensive genomic data to test whether hybridization was involved in evolutionary radiation within Rhododendron subgenus Hymenanthes, whose members show strong geographic isolation in the mountains of southwest China. We sequenced genomes for 143 species of this subgenus and 93 species of four other subgenera and found that Hymenanthes was monophyletic and radiated during the late Oligocene to middle Miocene. Widespread hybridization events were inferred within and between the identified clades and subclades. This suggests that hybridization occurred both early and late during diversification of subgenus Hymenanthes, although the extent to which hybridization, speciation through mixing-isolation-mixing or hybrid speciation, accelerated the diversification needs further exploration. Cycles of isolation and contact in such and other montane ecosystems may have together promoted species radiation through hybridization between diverging populations and species. Similar radiation processes may apply to other montane floras in this region and elsewhere.

S.258.2 Genomic insights into spatiotemporal evolution and adaptive evolution of the species-rich cosmopolitan plant genus Rhododendron

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Evolutionary radiation is a widely recognized mode of species diversification, but its underlying mechanisms have not been unambiguously resolved for cosmopolitan plant genera. The factors that enable certain species-rich plant genera to adapt to diverse environments and achieve global distribution are still not fully understood. *Rhododendron*, as the largest genus of woody plants in the Northern Hemisphere, presents an exceptional system for investigating the genomic mechanisms driving evolutionary radiations and the capacity to adapt to a wide range of habitats. Here, we reconstructed the first completely resolved and dated phylogeny of *Rhododendron* and found that most extant species originated by evolutionary radiations when the genus migrated southwards from circumboreal areas to tropical/subtropical mountains. We also found rapid increases of both net diversification rate and evolutionary rate of environmental factors in the Miocene, indicating that ecological factors have triggered the evolutionary radiations. Furthermore, we have accomplished high-quality, chromosomal-level genome assemblies of nine species and revealed diverse adaptive strategies employed by *Rhododendron*, particularly the adaptation to alpine and subalpine habitats by expansion/contraction of gene families involved in pathogen defense and oxidative phosphorylation, genomic convergent evolution, gene copy number variation, and a high percentage of private genes. The adaptation to high altitudes is further supported by our population genomic analysis of *R. nivale*, a species representing the highest altitudinal distribution within the genus and based on comprehensive range-wide sampling. Moreover, using metabolomic, transcriptomic, and genomic analyses, we have identified the genes involved in the biosynthesis of anthocyanins and carotenoids. This study provides a good example of integrating phylogenomic and ecological analyses in deciphering the mechanisms of plant evolutionary evolutions. It holds considerable significance in enhancing our understanding of plant adaptive evolution and offers valuable insights for improving flower colors in this important horticultural plant genus.

S.258.3 Genomic adaptation and future responses of an alpine rhododendron species in the eastern Hengduan Mountains

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High-altitude plant species have shown local adaptations to specific environments, such as low temperature, drought, ultraviolet radiation, and short growing season. In the face of climate change, alpine specialists are more likely to experience range contractions and evolutionary risks. To quantify such adaptation as well as vulnerability, we sampled 15 populations of an alpine Rhododendron (*R. intricatum*) with a large elevational range (3000 m - 4500 m) in the Mt. Gongga region of the eastern Hengduan Mountains in southwestern China. Using a whole-genome re-sequencing dataset, we performed genotype-environment association (GEA) and gene ontology (GO) enrichment analyses to explore its adaptation signature along elevation. Using inferred outlier SNPs (single nucleotide polymorphisms), we then modeled genetic turnover in a multidimensional climate space and estimated genetic offsets under climate change. The genomic data showed no significant geographic structure, while GAE tests revealed a large number of outlier SNPs associated with elevation. Among the inferred significant SNPs, GO enrichment analysis revealed a strong functional tendency associated with reproductive processes such as pollination and signaling. The current genetic turnover shows strong signals along climatic variables related to precipitation seasonality and extremes, which is consistent with a northeast-southwest geographic separation of the population. Meanwhile, such turnover signals would lead to remarkable risks at high elevations with intense precipitation changes in the future. Together, we highlight the genomic mechanisms underlying local adaptation at high altitudes. More importantly, we show that predicting climate vulnerability from both evolutionary and ecological factors reveals population-level risks to climate change in a mountainous region.

S.258.4 Exon and exon-flanking regions sequence assembly from deep genome skimming data for Rhododendron phylogenomics

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Using the deep genome skimming (DGS) data to assembly target nuclear orthologous genes for phylogenomics has recently become attractive, but little practical exploration has been done for herbarium specimens. Sequences flanking target genes are useful for phylogenetic inference of shallow taxonomic levels, while it is underutilized in studies possibly due to its finite recovery. We evaluated the optimal sequencing depth and performance for recovering target nuclear gene from specimen accessions, by subsampling genome sequencing data (10×, 15× and 20× sequencing coverage) with *Rhododendron* as example. To explore whether the sequence recovery of target exons and their flanking regions improved or not, we utilized exons only or allowed intron-containing sequences (supercontigs) as reference for read sorting in assembly process using HybPiper, respectively. Additionally, phylogenetic analyses were conducted to test the phylogenetic utilities of plastomes and the captured nuclear exons and their flanking sequences. Our results showed that DGS can be well applied for herbarium specimens to recover large number of nuclear genes, and the optimal sequencing depth for high-quality gene assembly from specimens was ~15× coverage. Further analyses suggested that the adoption of supercontigs as reference can capture more higher-integrity target exons and flanking regions, and can be used as an alternative to increasing sequencing depth to improve sequence recovery in the case of limited sequencing data. The high-integrity nuclear sequences recovered here and plastome sequences recovered robust phylogenetic relationships in *Rhododendron*. It is also noteworthy that the recovered non-targeted exon-flanking regions showed great promise for shallow-scale phylogenetic relationships. The exons and flanking regions captured by adding introns into references for assembly shed new light on resolving interspecies relationships by using DGS data which recover high-integrity target nuclear genes and their flanking regions for phylogenomics of an expanding sampling covering both the extant and the natural history collections.

S.258.5 The migration history of Kamchatka rhododendron (Therorhodion camtschaticum s.l.) - twice towards eastern Beringia

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Therorhodion is a small genus including three species – *T. redowskianum* with an Asian-restricted range and two amphiberingian taxa *T. camtschaticum* and *T. glandulosum*. The Kamchatka rhododendron

(*Therorhodion camtschaticum* s.l.) is a small cold-resistant arcto-alpine shrub species with a controversial intraspecific taxonomy and a wide distribution range covering northern Eurasia and North America within Beringia. Russian taxonomists recognize one species with two subspecies, whereas two distinct species are recognized in North America following a broader species concept. We set out to unravel the taxonomic relationships within *Therorhodion* and the likely dispersal route/s of *T. camtschaticum* and *T. glandulosum*. First, we look at the overall phylogeny and recover strong molecular support for *Therorhodion* as the sister clade to *Rhododendron,* and within *Therorhodion* three strongly supported monophyletic clades representing three species are inferred. Next, we assess the level and distribution of diversity in the two closely related amphiberingian species within the native species range. The degree of differentiation we found is consistent with the species rather than subspecies status of the taxa studied. Two genetic lineages reflect the migration pathways of species from western Beringia to eastern Beringia. A northern pathway for *T. glandulosum* from northern East Asia (Okhotsk seashore, the Kolyma region, Chukotka, central and northern Kamchatka) to the Seward Peninsula in northern Alaska. A southern pathway for *T. camtschaticum* from the southern part of western Beringia (the Sikhote-Alin ridge, Sakhalin Island, the Kuril Islands, and southern Kamchatka) to the Aleutian Islands and the seashore of southeast Alaska. We inferred a divergence of *Therorhodion* from *Rhododendron* in the late Paleocene with the Asian-restricted *T. redowskianum* diverging during the middle Miocene, supporting an Asian origin for the genus. Demographic analysis using nSSR data inferred a divergence time between *T. camtschaticum* and *T. glandulosum* in the Pleistocene at 1.52 Mya.

S.258.6 Phylogenomic and morphological insights into ploidy and the radiation of Rhododendron subsect Lapponica in the Hengduan Mountains

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Understanding the evolutionary history in the genus *Rhododendron* (Ericaceae) is a difficult but important enterprise. The genus is iconic, both in horticulture where their charismatic flowers and hardy growth habits are highly valued, and as a prominent element of the North Temperate flora. In addition, polyploidy is highly desirable in rhododendron breeding and occurs naturally among multiple groups within the genus. The alpine group, subsection *Lapponica* remains somewhat of a mystery to 'rhody' enthusiasts. While some of the species in the group display consistent morphological identity across their geographic range, many taxonomic characters hold little value for delimitation. Additionally, we have uncovered a pattern where polyploids are more frequent than previously thought. Here, we present DNA relationships among samples from China and botanical garden material that test hypotheses about species boundaries in *Lapponica*. In tandem, using morphological data from flowers and leaves, we compare phenotypes to one another in an effort to understand where variation is most informative for species identification. Finally, we combine the two approaches together to provide our first look at the complicated and beautiful evolutionary history of *Rhododendron's* 'Hardy Mountaineers.'

S.259 USING PLANTS FOR RESTORATION, CONSERVATION AND MANAGEMENT OF FRESHWATER HABITATS

S.259.1 Macrophyte-based solutions: Environmental drivers, potential and limitations of aquatic plants as key actors in ecosystem restoration

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Freshwater biodiversity is collapsing globally. Urgent and effective actions are essential to address this crisis within-a-crisis. In Europe, for example, most up-to-date data show that climate change is a growing threat (1), mainly due to increased drought and decreased precipitation, while agricultural activities, land abandonment and urbanization (2) are the main pressures on habitats and species of conservation concern. Natural wetlands emerge as the best sites for preserving adequate levels of aquatic and riparian vegetation and associated biota; however, especially in the lowlands, pristine wetlands and aquatic ecosystems have almost completely disappeared. Therefore, actions are needed to maintain, on the one hand, and recreate, on the other hand, an extensive network of wetlands capable of preserving acceptable levels of aquatic/wetland vegetation diversity and functioning. Understanding the eco-functional responses of macrophytes to ecological/anthropogenic pressures and local effects of the climate crisis is, then, crucial to achieving this fundamental goal. Findings gathered over the past two decades on diverse and complex wetland systems located in overexploited Italian lowlands confirm the key contribution made by natural sites in maintaining vegetation diversity in highly compromised riverine settings. This also suggests a direct effect of interannual and seasonal dynamics of water-level changes on observed vegetation patterns. In addition, progressive loss of hydrological connectivity and herbivory have been shown to massively affect macrophyte establishment and growth processes, especially in the very early stages of development and recovery of an impaired waterbody. Building on this evidence and delving into major international experiences in wetland restoration and enhancement, the aim is to outline the potential and limits of using macrophytes as nature-based solutions.

S.259.2 Big plans for small pools: a morphological typology for in situ conservation and management of the seasonal rock pools of Malta

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The seasonal freshwater rockpools (SFRs) of Malta constitute an Annex I ‘priority’ habitat (3170*) and function as a network of ecological islands supporting phytocoenoses that differ from those of the surrounding habitat matrix. The plants in these biotopes range from obligate aquatic species to amphibious species, to terrestrial species tolerant of saturated soils. Management, conservation, and restoration of SFRs provides unique challenges as the occurrence of these species is influenced by the integrated effect of multiple factors including the depth of water and sediment. Relatively small changes, on a scale of 1 cm, in the topography of the pool basin can modify the hydroperiod characteristics of the affected segment of the pool, leading to replacement of a plant assemblage by another. This study therefore aimed to guide management initiatives by proposing a morphological typology of SFRs, based on a sample of 170 pools from 12 pool landscapes. A preliminary hierarchical cluster analysis optimised by k-means partitioning suggested four morphoclasses of pools, each with their own indicator species. Morphoclass I: deeper pools with a low surface area to volume ratio and a thick sediment layer**;** Morphoclass II: shallow pools with a low surface area to volume ratio and thin sediment; Morphoclass III: shallow pools with thick sediment and variable surface area to volume ratio; Morphoclass IV: shallow pools with thin sediment and a very high surface area to volume ratio. The species with the highest indicator values (*Elatine gussonei*, *Ranunculus saniculifolius*, *Lythrum hyssopifolia*, and *Zannichellia melitensis*) generally have very high specificity for the SFR habitat and were associated with different morphoclasses. As such, management plans for these habitats should take these variations into account so as to assess the effectiveness of restoration programmes against a realistic benchmark for each morphoclass.

S.259.3 Pyrenean mountain wetlands: assessment of main threats and restoration actions to improve their conservation status

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Pyrenean mountain wetlands are unique ecosystems that face several threats (overgrazing, dam regulation, drainage, tree encroachment, etc.), which keep them away from a favourable conservation status. To help tackling the main management challenges, since 2014 we have assessed (and monitored) the condition and primary threats of Pyrenean wetlands through extensive field sampling. Our findings revealed overgrazing as the predominant disturbance, affecting 24% of these wetlands. Dry spells and water table drawdown were also of primary importance and affected habitats differentially. Dam regulation and pine encroachment had intermediate importance, whereas other threats were less relevant. Consequently, we initiated pilot restoration experiments involving plant transplantations or removals to address these challenges. To mitigate overgrazing, we set up 14 exclusion fences -both permanent and temporary-, where, through passive restoration, we observed a significant recovery of plant cover, particularly on pugged soils. Plant community composition showed a slow trend from pioneer to late-successional wetland specialists. Fostering this natural process, we undertook active restoration on four wetlands by the transplantation of selected specialist species (*Carex nigra*, *Valeriana dioica*, etc.). To counteract the effects hydroelectric regulation, we performed the initiation of two wetland habitats on the shores of a decommissioned reservoir by transplanting sedges (*Carex rostrata*) and peat mosses (four species, including vulnerable *Sphagnum magellanicum*). Although restoration was successful for both habitats, dry spells affected severely sphagnum hummocks, whereas wet sphagnum carpets endured unaltered. As for encroachment, we set up a pine clearcutting action, which will expectedly lead to a rise of the water table by a reduction of tree transpiration, and to the removal of negative shadowing on wetland-specialists. The knowledge gained from the successes -and failures- of our pilot restoration experiments can be used to guide management decisions for improving the conservation status of mountain wetlands.

S.259.4 The wetland of the "Climate-friendly Parks" - a project in the city of Reggio Emilia (Italy)

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Within the framework of the European project "Life CityAdaP3," the municipality of Reggio Emilia, in Italy, is implementing a project known as "Climate-friendly Parks." This initiative aims to mitigate the urban heat island effects and enhance the overall environmental quality. Among the foreseen interventions, particularly interest is focused on "Marco Biagi Park". This represents a first experimentation of the *adaptive* park model application. The model is based on the introduction in an urban green area of four main *landscape environmental devices,* including the micro-forests (as described by "Miyawaki method"), rural hedges, trees in row and multispecies meadows. Moreover, the project has foreseen the realization of an artificial pond with a lateral runoff, which exploits the possibility of deriving water — in the summer —from the nearby irrigation channel (managed by the local "Consorzio di Bonifica"). The landscape environmental devices and the wetland area share common objectives, including the mitigation action on the microclimate, biodiversity conservation, improvement of air quality and the usability for social activities. Particularly attention has been focused on the plant species selection for the wetland, which involves non-rooting and rooting hydrophytes (for example *Lemna minor*, *Callitriche palustris*, *Mentha aquatica*, *Nymphaea alba*, *Nuphar lutea*, *Nasturtium officinale*); proceeding towards the banks we introduced *Iris pseudacorus*, *Lytrum salicaria*, *Carex* sp.pl. and *Thypha latifolia*. Many common meadow species have been sown to facilitate the colonization of soil near the wetland and some woody trees, *Alnus glutinosa* and *Salix alba*, to consolidate the banks. Only native species have been chosen in order to increase plant biodiversity. The realization of this experimental wetland is furthermore aimed to observe how the different species are able to cope with water level fluctuations and in general with the environmental conditions of the site of introduction.

S.259.5 The use of floating beds with native halophytes in restoration of coastal saltmarshes in the Mediterranean area

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Saltmarshes support a variety of important ecosystem functions. Unfortunately, they have been drastically reduced in the last centuries, especially in the Mediterranean area: most of them were "reclaimed" or otherwise transformed, and the remaining ones are still threatened. Our project's aim is to investigate the possibility to use floating beds with native halophytes to remove nutrients from eutrophicated waters in artificial saline basins or degraded saltmarshes and at the same time to contribute to the restoration and renaturalization of the sites, offering habitats to several organisms. The use of floating islands with these aims has already been tested, but usually in freshwater basins. Here we present our preliminary results regarding the cultivation of annual and perennial halophytes on floating beds in effluent basins of a marine fish hatchery, in western Sicily (Italy). The following species were tested: *Arthrocnemum meridionale* (Ramírez et al.) Fuente et al. (Am), *Salicornia alpini* Lag. (Sa), *Salicornia emerici* Duval-Jouve (Se), *Salsola soda* L. (Ss). Cuttings of the perennial species (Am, Sa) and plantlets of the annual ones (Ss, Se), collected from nearby wild habitats, have been used. Best results, in terms of growth, were obtained with the perennial and the annual *Salicornia. Arthrocnemum* and *Salsola* grew slower respect to wild plants nearby. Our preliminary results confirm the possibility to cultivate the Mediterranean native species *Salicornia alpini* and *Salicornia emerici* on floating beds on marine waters. The next step is the application of these results to saltmarsh restoration projects, including the removal of nutrients and metals from degraded ponds, the improvement of halophytic vegetation cover and the consequent improvement of the whole ecosystem.

S.259.6 Facing the ecological complexity of Mediterranean temporary ponds for tailor-made restoration, conservation and management action

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Mediterranean temporary ponds (3170*) are peculiar habitat types particularly rich in plant species but regularly reported in Europe with an "unfavourable" conservation status. They are usually heterogeneous, shallow, and small water bodies which dry entirely in summer. Alternation of the flooding period strongly influences the floristic composition, mainly belonging to the plant community *Isoeto-Nanojuncetea* (=*Isoeto durieui-Juncetea bufonii*). Besides climate alteration, inappropriate water and landscape management, pollution and trampling, habitat misinterpretation represents another threatening issue for the habitat, often underestimated. An interdisciplinary study has investigated two clusters of Mediterranean temporary ponds embedded in the Natura 2000 sites of Bosco di Palo Laziale and Bosco di Foglino (Lazio Region, Italy). Field data collection on plant communities, geo-chemical soil properties, micro-topographic characteristics and climate proxies was implemented to identify the habitat's ecological patterns, processes and interdependencies. Clustering analysis and data post-processing allowed to discriminate vegetation types and sub-types of surveyed coenoses as well as to determine the most significant ecological predictors of the habitat. This study has proved to be valid in addressing plant assemblage complexity. Its cost-effective and easy-to-use approaches can be successfully applied elsewhere to facilitate the restoration, conservation and management of this and similar ecosystems.

S.260 PERSPECTIVES ON PLANT BIOME TURNOVER IN AN ERA OF MASSIVE DATA AND NEW METHODOLOGICAL DEVELOPMENTS

S.260.1 The lability factor: biome shifts may predict diversification dynamics in flowering plants more than the biomes themselves

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The remarkable diversity of angiosperm species have prompted a search for universal drivers that modulate rates of speciation and extinction across this clade. To date, most attempts to define differences in diversification have correlated diversification rates with the presence or absence of a discrete trait. However, an often overlooked explanation is that the evolutionary lability, here defined as the rates of trait change, is a better predictor of the diversification dynamics than the observed traits themselves. This hypothesis, first proposed half a century ago in the context of biome shifts, is based on the idea that the capacity to adapt to environmental changes is the key element defining angiosperm diversification dynamics. Thus, rather than relying on single phenotypic descriptors, we test whether the propensity of change between biomes is significantly correlated with lineage speciation and extinction rates. We test this hypothesis using a phylogenetic dataset of 51 angiosperm clades including 10,636 species in closed-canopy, 4,818 in open-canopy and 3,921 widespread across both biomes. We find that trait lability is frequently associated with higher rates of both speciation and extinction. Additionally, we find that transition rates tend to be faster from open to closed-canopy biomes, contrary to prevailing ideas in the field that lineages occurring in open-canopy biomes tend to emerge from closed-canopy ones. We propose that looking at lability rather than single traits, in angiosperms and other organisms, may provide a more comprehensive and dynamic understanding of biodiversity patterns. This shift in focus from static traits to dynamic evolutionary processes offers new insights into how biodiversity is generated and maintained.

S.261.2 Assessing the power of artificial intelligence approaches for birth-death model classification

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Birth-death (BD) models applied to dated phylogenies, are a useful tool to study past diversification dynamics in the absence of complete fossil record. Parameters in these stochastic models are typically inferred using likelihood-based methods such as Maximum Likelihood or Bayesian Inference. However, these methods require the formulation of a new likelihood algorithm each time a new model is proposed, and some of the most complex models are also computationally intractable, or mathematically non-identifiable, with two models generating identical probability distributions. The last years have witnessed a revolution, with artificial intelligence (AI) methods applied to phylogenetic inference, species delimitation, or phylodynamics. However, the power of these approaches in birth-death modeling is almost unexplored. Here, we tackle a classification problem, the power of AI algorithms to discriminate among six different diversification scenarios: constant birth–death (BD), high extinction (HE), mass extinction (ME), stasis and radiate (SR), diversity dependent (DD), and waxing and waning (WW). We simulated 10,000 trees under each diversification scenario and encoded the phylogenies using two different representation techniques: a set of summary statistics and the compact bijective ladderized vector encoding. These simulations were used to train and validate two different AI methods: convolutional neural networks (CNN) and random forests (RF), and the trained AI algorithm was used to predict the most probable model of diversification for selected empirical phylogenies. Finally, we compared the performance of AI methods with previous likelihood-based approaches. The cross-validation approach showed that the percentage of correct assignment for the simulated scenarios was high for the two DL algorithms, except for BD and SR models. The most accurate strategy was the combination of RF algorithms with summary statistics as the tree representation. We hypothesize the hierarchical structure of phylogenetic trees it is more difficult to capture using CNN designed for image-based encoding.

S.260.3 Asymmetric biome lability across lineages underlies the evolution of miombo woodland savannas in Africa during the early Miocene

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Previous research has highlighted the frequency of niche conservatism during the radiation of plant lineages at regional and global scales. These studies indicate that niche conservatism played a major role in the current distribution of biodiversity. A recent analysis in tropical Africa also found high prevalence of niche conservatism at the genus level in biomes (forest and savanna), indicating that niche lability (as evidenced by the presence of a genus in two biomes) is uncommon and unevenly distributed among forest tree species in Africa. Current limitations to infer the fine-scale distribution of this trait among lineages of tropical trees is the low resolution of current phylogenetic trees and a limited sampling at the species level of the analyzed taxa. Here we explored the distribution of niche lability within an endemic African lineage of tropical trees that contains 16 genera (including three genera that are key components of miombo savannas): the Berlinia clade. Our results indicate an asymmetric distribution of the capacity to shift and diversify into these biomes in Africa. Only five genera shifted between forest and savanna during the evolutionary history of the group, and only the first transitions in the early-middle Miocene in *Julbernardia*, *Brachystegia*, and *Isoberlinia* led to an increase in the number of species. This asymmetry is also evident from the distribution of species-rich lineages that exploited both biomes identified in this study (forest and savanna), as well as from the presence of five paleoendemic (mostly monotypic) genera that have persisted solely in the forest biome since the Eocene.

S. 260.4 Reconstructing paleo-environments and paleo-diversity using Bayesian deep learning

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Throughout the long evolutionary history of life, species of all kingdoms have diversified through countless environmental changes and extinction events. Since most species that lived on Earth have gone extinct, it is difficult to infer how the evolution of biodiversity and ecosystems unfolded over millions of years. Here I present a suite of new methods to infer the spatial and temporal evolutionary dynamics across major clades in the tree of life. Analyzing the fossil record through supervised and unsupervised neural networks we infer species richness dynamics in deep time, and test hypotheses on past speciation and extinction, while correcting for the gaps and biases that characterize the preservation and sampling processes. With the integration of geological and paleontological data through Bayesian deep learning models we generate reconstructions of paleovegetation and paleotemperatures through time and space providing a more accurate environmental context around macroevolutionary hypotheses. Our results show that coupling deep learning models with evolutionary models can improve our understanding of biodiversity and its evolution across time scales.

S.260.5 The use of phylogenetic tree shape and habitat reconstructions to reveal regional environment history and flora assembly

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Phylogenetic trees are routinely used to examine the evolution of single biological lineages. Where phylogenetic data are available for multiple lineages, however, congruent macroevolutionary pattern can additionally be used to gain insights into regional environment history and flora assembly. In this talk I show how reconstructions of habitat variables across multiple phylogenies reveal the timing of key environmental transitions, while the shapes of phylogenetic trees, and their correlation with habitat variables, can offer insights into past environmental stability. A comparison of such patterns across 14 plant lineages native to the South African Cape reveals that mountain fynbos heathlands are older and have evolved under conditions of greater environmental stability than the semi-arid renosterveld and succulent karoo shrublands that dominate the low elevation zone of the Cape.

S.260.6 Unraveling the evolutionary history of tropical rainforest plant diversity using an all evidence approach

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The latitudinal diversity gradient is one of the most pervasive patterns in biogeography and the astonishing diversity of tropical rainforests contributes disproportionately to this pattern. Macroevolutionary processes such as speciation, extinction and migration are the key mechanisms underlying the current diversity of tropical rainforests. Yet, evaluating the relative importance of each of these processes on this diversity faces challenges such as under sampling of species, difficulties in defining biome borders and the sheer scale of data needed to elucidate patterns at a global scale. We aim to solve these problems and determine the relative importance of these processes on the diversity of tropical rainforest seed plants. We estimate the biome associations of seed plants using occurrence data and the World Checklist of Vascular Plants. We then use these biome associations to investigate the effect of speciation, extinction, migration and age on the diversity of tropical rainforest seed plants. This is done by utilizing the current largest phylogeny of seed plants along with a recently developed state dependent model of speciation and extinction which can account for paleoenvironmental variations. This enables us to see how these macroevolutionary processes have varied in space and time and allows us to determine if the diversity of tropical rainforests is best explained by higher speciation rates, lower extinction rates or increased immigration. Additionally, we investigate if the number of tropical rainforest lineages has increased more steadily compared to elsewhere. Our investigation utilizes the ever-increasing amounts of data from herbaria, online biodiversity databases and DNA sequence repositories to reveal the intricate interplay of macroevolutionary processes on present day tropical rainforest biodiversity.

S.261 ACROSS LAND AND WATER: UNDERSTANDING PLANT GENE FLOW AT A LANDSCAPE SCALE. SESSION 2

S.261.1 Dispersal distance and modes of spread in a range of maritime sedge species

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Salt Marsh plants are specialists in a highly stressful, spatially restricted, though predictable environment. Dispersal, through pollen, seed or vegetative fragments will need to be efficient and possibly specialised to reach suitable habitats. *Carex* section *Phacocystis* (Cyperaceae) incorporates a group of wind pollinated long lived clonal species with an Amphi-Atlantic distribution which inhabit salt marshes. They thus present a suitable suite of species to investigate maritime dispersal methods. On the Norwegian coast three of the section; *C. paleacea, C. salina* and *C. subspathacea* occupy different niches on the salt marsh characterised by different distance from the low tide. *C. subspathacea* occupies the lowest position on the saltmarsh and is infrequently free of saltwater immersion while *C. paleacea* is only submerged at very high tides. *C. salina* is intermediate between the two. These species thus provide an opportunity to assess transport distances at small and medium scale along the Norwegian coast while the differing extent of offers an additional, potentially influencing, factor. The discovery of a *C. salina* population in Scotland in 2004, a species previously unknown in the UK, with other Scottish populations subsequently discovered, reveals that longer distance dispersal across the North Sea is also occurring. The recent spread of the species into the UK highlights the dynamic nature of the salt marshes, especially under climate change. Using genetic data obtained from microsatellite variation, patterns of dispersal and connectivity are assessed in this group. The effects of latitude and position in the salt marsh are considered alongside the possible source and pattern of long-distance dispersal. Spread via sexual or vegetative route is also assessed.

S.261.2 Is the population genetics of the invasive species Cotula coronopifolia in Europe more consistent with human vectors, migratory wa

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There is increasing evidence that migratory waterbirds act as important long-distance vectors of plants lacking a fleshy fruit. Seeds of many plants have been extracted from faeces and shown to have high germinability. However, there are almost no genetic studies addressing the influence of waterbird endozoochory on gene flow. Waterbirds can provide a means of spread across landscapes for alien species that were originally moved between continents by other means. We selected the buttonweed Cotula coronopifolia, native to South Africa, as our alien model species. This species was originally introduced to Europe more than two centuries ago, and has an extensive range. Faecal analysis confirmed endozoochory of this plant by migratory shorebirds such as Limosa limosa. Cotula coronopifolia is mainly distributed in coastal areas and is currently expanding along the Baltic coast. It is also spreading to inland wetlands with waterbirds, especially in Sweden and the UK. We are therefore studying the population structure and gene flow of 32 different populations of Cotula coronopifolia sampled in 6 European countries (UK, Germany, Netherlands, Spain, Sweden and Portugal), plus 5 populations in the native South Africa. We are using SNPs (Single Nucleotide Polimorfism) obtained from 282 individuals of Cotula coronopifolia by GBS (Genotyping by Sequencing). Questions we address include: 1) Are patterns across Europe consistent with the position of waterbird flyways? 2) Are patterns within a given landscape more consistent with dispersal by waterbirds, hydrochory, or human vectors? (i.e., are genetic distances more related to connectivity by birds, by water, or by human activities?). 3) within populations, are genetic distances determined by physical distances between plants? 4) are populations in the introduced range less diverse that those in the native range? Or has high propagule pressure (e.g. from multiple introductions via ballast from ships coming from South Africa) created the opposite effect?

S.261.3 Genetic diversity and clonal structure in wild populations of Vanilla pompona (Orchidaceae) in Costa Rica

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In Costa Rica, around a dozen species of wild *Vanilla*, including commercially significant ones such as *Vanilla planifolia* Andrews, *V. odorata* C. Presl, and *V. pompona* Schiede, are present, yet information regarding their population genetics is limited. It is suggested that genetic diversity in *Vanilla* populations may be low due to their potential formation by a few individuals with clonal reproduction. Nevertheless, wild populations may harbor genetic variants important for genetic crop improvement or conservation efforts. Despite *Vanilla pompona* is listed as endangered by the IUCN, the lack of studies on genetic diversity and population structure hinders its management and conservation. As other *Vanilla* species, *V. pompona* depends on pollinators for sexual reproduction, and the interactions among the plant, its pollinators, and dispersers shape the genetic diversity of this *Vanilla* species. To assess the genetic diversity and structure of wild *V. pompona* populations, 117 individuals from 8 populations along the Pacific region of Costa Rica were sampled. Microsatellites (SSRs) previously proposed in the literature for different *Vanilla* species were used; of the 28 SSRs tested, 18 proved transferable, and 12 were polymorphic. High genetic diversity was observed in wild *V. pompona* populations (HT = 0.588) with moderate genetic structure (FST = 0.194), and populations in the central and northern Pacific showed the least genetic distance. As suggested earlier, greater genetic diversity was evident among populations rather than within, mainly due to their high degree of clonal propagation. The high genetic diversity could be explained by their presence in extensively preserved forests, favoring large effective population sizes over extended periods, thereby mitigating the reducing effects of genetic drift. This study is essential to guide *ex situ* and *in vitro* preservation strategies by providing a clear description of genetic diversity in wild *Vanilla* populations.

S.261.4 Population genomics of the unisexual moss Pseudoscleropodium purum: from reproductive to genetic patterns

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Reproductive mode, sexual vs. asexual, determines the capacity of plants to disperse, shaping both their geographic distribution patterns and their population genetic makeup. All bryophytes have a high capacity to reproduce asexually which contributes to population maintenance, expansion at relatively short spatial scales, and retains extant genetic variation. The capacity to reproduce sexually, however, strongly depends on the sexual system. Sexual reproduction is common in bisexual species, but far less so in unisexual species. Thus, unisexual bryophytes are expected to show limited long-distance dispersal capacities and lower population genetic variation than bisexual species. Still, many unisexual bryophytes show remarkably wide distribution ranges. To date, we know little about the processes underlying such wide distribution ranges and the levels of population genetic variation and genetic structure at these spatial scales in unisexual bryophytes. Here, we study population genomics and its relation to reproductive patterns in the cosmopolitan, unisexual moss *Pseudoscleropodium purum* to contribute to filling this knowledge gap. We performed whole genome sequencing on 500 individual plants from 37 mainland and island populations across its native distribution range in Europe. With this unprecedented dataset (currently being generated), we characterize the species' large-scale spatial genetic structure and levels of genetic variation. Also, we reconstruct its biogeographic history to infer the relative contribution of sexual and asexual reproduction to colonization processes in this species. Provided that *P. purum* predominantly reproduces asexually through fragmentation and clonal growth, we hypothesize that its populations will exhibit low levels of genetic variation and that genetic differentiation will increase with increasing geographic distance between populations, following an isolation-by-distance model. We further predict that the biogeographic history of *P. purum* will conform to a stepping-stone colonization model where the geographic range expansion was dominated by numerous short-distance dispersion events.

S.261.5 Ecogeography of wild tomatoes (Solanum Sect. Lycopersicon) and closely related species, strategies for conservation and uses

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Ecogeographic analysis allows identifying species adaptive ranges and most relevant variables explaining their patterns of distribution. Additionally, it is possible to predict environmental conditions, using ecological descriptors derived from the geographical location of collected germplasm and variables obtained through Geographical Information Systems (GIS). Wild tomato species are distributed in Colombia, Ecuador, the Galapagos Islands, Peru, Bolivia and Chile, in various ecosystems from sea level to approximately 3995 m. In Central America *S. lycopersicum* L. is expanded and naturalized in different regions. A predictive classification of tomatoes and closely related groups were considered as a framework for ecogeographic characterization. The objectives were to determine ecological descriptors and edaphoclimatic diversity along the distribution range of 12 species of wild tomatoes (*Solanum* sect. Lycopersicon) and four wild species of phylogenetically related groups (*Solanum* sect. Juglandifolia and sect. Lycopersicoides), using 4228 wild tomato accessions in South America, and 1296 accessions of *S. lycopersicum* in México. An environmental information system was created with 34 edaphoclimatic variables with 1 km² resolution. Multivariate techniques (Principal Component Analysis, PCA; Cluster Analysis, CA) and GIS tools, established most relevant variables for accession distribution, as well as the groups formed according to their environmental similarity. Three Principal Components (PCs) of PCA explained more than 75% of total variation for all species. The most relevant related to seasonal variables of temperature and precipitation. CA revealed five statistically significant clusters for Mexican species and six for wild South American species. Potential distribution analysis with Maxent model (10 replicates by cross-validation) determined areas with higher probability of tomato species occurrence. This approach reveals phylogenetic patterns of adaptation, allowing promissory strategies to test predictive models involving identification of abiotic and biotic resistances in populations, associating functional traits and species diversification towards the conservation and uses of valuable genetic resources.

S.260.6 Down River? Gene flow within and between UK riparian systems

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The UK is a densely populated, industrialised and intensively farmed country. Areas of high plant biodiversity are largely restricted to nature reserves. A UK government report in 2010 called for more reserves, which were larger and linked. Interconnected sites will allow movement of advantageous genes between populations permitting adaptation to new selective pressures brought about by climate change. The aspiration of connectedness has informed UK conservation practice within the NGO sector. However, beyond a few bird species, there is little understanding of how much gene flow occurs in the UK landscape. This study fills some of this knowledge gap by assessing the extent of gene flow between plant populations growing on river margins. Such riparian systems have long been viewed as significant corridors for plant and animal movement. Taking three different species (*Carex aquatilis, Carex tomentosa* and *Geranium pratense*) across various different geographically separate river systems the work identifies patterns of variation within and between such systems. Within a river system an assessment of the strength of Ritland’s Unidirectional Flow Hypothesis can be made, while between river systems that share a common source gene flow either side of the watershed can be assessed. Finally, populations growing on completely separated river systems can be utilised to understand gene flow at the national scale. Taken together these results provide a picture of gene flow within riparian systems which will inform conservation understanding and action.

S.262 DYSPLOIDY, DIPLOIDISATION AND DIVERSIFICATION: IMPACT OF POST-POLYPLOID GENOME RESTRUCTURING ON SPECIES AND TRAIT DIVERSITY. SESSION 2

S.262.1 Descending dysploidy and repeat expansion drive the evolution of Crocus series Verni

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Spring crocuses, which comprise ten diploid and two polyploid species, as well as a polyploid complex, show diverse chromosome numbers ($2n = 2x = 8, 10, 12, 14, 16, 28$; $2n = 4x = 16, 18, 20, 22$). Phylogenomic data revealed a high rate of dysploid karyotype changes among the diploid taxa, reducing the chromosome number from $2n = 28$ to $2n = 8$ while increasing genome size within a few million years. To infer the role of repeat expansion and chromosomal rearrangements in descending dysploidy, we characterized the types and abundances of repetitive genomic elements from each taxon and performed a comparative karyotype analysis in a phylogenomic context. FISH analysis of six repeat families and chromosome painting suggest a concerted action of descending dysploidy and a burst of repetitive DNA elements as drivers to the reduction of chromosome number while increasing genome size in more recently evolved taxa. This work provides insights into dysploidy in ser. *Verni* and an opportunity to develop approaches to study other dysploid-rich clades in plants.

S.262.2 Genome evolution in the neopolyploid heterosporous fern Salvinia molesta

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Among the ferns, a group rife with exceptionally large genome sizes and high chromosome numbers, the heterosporous water ferns are distinct for their small genomes. It has been posited that hetersporous ferns, as well as heterosporous lycophytes and seed plants, have more "dynamic" genome evolution following whole genome duplication than homoploid lineages, often leading to rapid downsizing and diploidization. As a first attempt to assess genome evolution in neopolyploid heterosporous ferns, we present a draft haplotype-resolved genome assembly for the natural allopentaploid *Salvinia molesta* (1C=2.28Gb). By comparing genic content, synteny, and repetitive element composition to the previously published *Salvinia cucullata* (1C=0.25Gb) and *Azolla filiculoides* genomes (1C=0.75Gb), we assess genomic and subgenomic changes in this recently formed polyploid fern. Additionally, we discuss our findings relative to comparable studies of other heterosporous polyploid seed plants and lycophytes, as well as homosporous ferns, providing phylogenetic context for understanding post-WGD genomic changes.

S.262.3 Genomics of Engelhardia, a characteristic taxon of Southeast Asia

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Engelhardia is a characteristic flora of subtropical and tropical forests in South-eastern Asia, which is of great ecological and economic values. Due to its large latitude span of geographical distribution, insufficient research materials, and different names used for the same species in different regions, the species definition of *Engelhardia* is complicated. The classification and phylogeny of *Engelhardia* has always fascinated ecologists and biologists in recent decades, but there are still debatable. Even with the combined analysis of morphological and molecular data, the phylogeny and interspecific relationships of the genus were not clarified. Here, we are based on extensive resource investigation and sampling, integrating phylogenetic genomics and comparative genomics analysis methods, reconstructing the phylogenetic relationship of *Engelhardia* through chromosome-level genomes for the first time, and comprehensively explored the genome evolution, genetic diversity and genome structural changes of *Engelhardia*. Our study used genomics to advance our understanding of the evolution of characteristic taxa in biodiversity hotspots and solve the complex species delimitation. It also provides an insight of a comprehensive understanding of the causes of biodiversity in tropical and subtropical regions, the protection of the uniqueness of these regions, and the promotion of the conservation, restoration and sustainable use of global plant resources.

S.262.4 An optimized CRISPR system in Tragopogon (Asteraceae) facilitates functional studies of genome evolution following polyploidy

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Dynamic genomic changes following polyploidy (i.e., whole-genome duplication; WGD) may contribute to the success of polyploids. At the gene level in allopolyploids, changes include retention of both parental gene copies, function/expression divergence between the two parental copies, and loss/silencing of one parental copy. However, the rules governing these processes remain unclear, limited largely by the absence of study in organisms that best exemplify the earliest stages of WGD. Diploid and polyploid *Tragopogon* (Asteraceae) represent an excellent natural system to study the immediate consequences following polyploidy. Allotetraploid *T. miscellus* and *T. mirus* are 90-100 years old. Functional studies of genes with different retention patterns in young *Tragopogon* polyploids can be used to elucidate the genetic factors underlying the success of WGD. To accomplish this, we report here on our development and optimization of tissue culture, *Agrobacterium*-mediated transformation, and a genome editing system in *Tragopogon*. Using CRISPR/Cas9, we successfully knocked out *PDS* (encoding phytoene desaturase in carotenoid synthesis) and also *DFR* (encoding dihydroflavonol 4-reductase in anthocyanin production) in diploid and polyploid *Tragopogon*. The experiments produced mutants with the expected phenotypes, i.e., albino plants and plants without anthocyanins, respectively. In addition, the CRISPR-mediated genome editing system exhibited high efficiency: in the tetraploid mutants, modifications of all four alleles of the target gene were identified in the T_0 generation. With this exceptional toolkit in place, we have proposed functional studies of 12 *Tragopogon* genes controlling pivotal traits and having specific retention patterns following polyploidy. By following CRISPR-mediated changes in gene retention following WGD, we examine genes and complex phenotypes associated with meiosis, flower/inflorescence development, and stress response. This established genome editing platform permits functional studies in the evolutionary model system *Tragopogon*, contributing to a better understanding of the genetic consequences following WGD and the success of polyploids.

S.262.5 A Reference Quality Genome Assembly and Investigation of Whole Genome Duplication in the Mimosoid Legume Leucaena trichandra

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Previous phylogenetic and evolutionary work on the mimosoid legume genus *Leucaena* has inferred a complex history that included an ancient whole genome duplication (WGD) prior to the diversification of 19 diploidized divergently related species. Inter subclade hybridization events among a subset of these 19 species resulted in the formation of five independent allotetraploid species, some of which are important multipurpose trees in tropical agroforestry systems. Here we use whole genome sequencing from long- and short-read data to assemble a reference genome for the putatively diploidized species *L. trichandra,* the putative parent of four of the five *Leucaena* allotetraploids. The genome is used 1) in comparative genomic analyses to investigate the relative quality of the genome and the associated annotations, 2) to clarify WGD relevant events and the diploid, tetraploid, and/or octoploid nature of *Leucaena* species, and 3) to investigate the role of methylation and chromatin structure on gene expression following an ancient WGD. The comparative genomic analyses show that the chromosome-scale assembly captures contiguous gene space well and that the annotation file is comprehensive. Despite the modest genome sizes observed in *Leucaena*, our results conflict with the prior conclusion of extensive genic diploidization following a stem lineage WGD. This lack of diploidization suggests that *Leucaena* comprises 19 tetraploid species and five allooctoploid species as well as several other putatively hybrid lineages. The inferred combination of ancestral subgenomes contributing to the stem lineage WGD is also apparently complex, with three potentially distinct subgenomes representing the observed genomic diversity. Lastly, we discuss the impact of cytosine methylation and chromatin structure on the fate of duplicated genes and their expression following the ancient WGD.

S.263 BIOLOGICAL INVASIONS

S.263.1 Highly Hazardous Pesticides: The impact of their use in the fynbos biome

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Highly hazardous pesticides (HHP's) are used widely in South Africa, including the fynbos biome. There has been a global move through the Strategic Approach to International Chemicals Management (SAICM) programme of the United Nations Environment Programme (UNEP) 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 criterion deals with Multilateral Environmental Agreements (MEA's), criterion 2 deals with acute toxicity to mammals and birds and the next 4 are chronic health exposure criteria, hazard groups 7 and 8 deal with environmental exposure criteria and the criteria 9 is dioxins and 10 heavy metals. The identification and classification of HHP's are done using the 8 criteria developed by the Joint Meeting on Pesticide Management (JMPM) of the Food and Agriculture Organization and World Health Organization (FAO/WHO). The hazard criteria (HC) that will be concentrated on are HC 7 and HC 8 which deal with environmental toxicity and their impacts on fauna, flora, and ecosystem services. HHP's currently being used in the fynbos biome will be discussed together with their impacts on the ecosystem functioning in the fynbos biome. 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 (HOC) and Precautionary Principles, and mitigation measures on how to ensure compliance to the Paris Agreement targets with regards to temperatures and HHP's.

S.263.2 Soil salinity rather than nutrients decreased alien plant abundance in dune system in early succession stages: experimental evidence

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Biological invasion is now widely acknowledged as a significant threat to biodiversity, particularly within coastal dune ecosystems. While numerous studies have established connections between the invasion of dune habitats and human disturbances, less attention has been given for the understanding the influence of soil properties and plant traits on the process of plant invasion. We performed a manipulative experiment in a dune system of the Northern Adriatic Sea. We removed the spontaneous vegetation through soil tillage in the back dune system, triggering a new ecological succession to analyse alien invasion at the initial stages of plant colonization due to the present seed bank. We further altered soil properties in 8 experimental blocks by adding salt, nitrogen and organic substances (i.e., peat) and testing their effects and interactions in a full factorial design (i.e., 64 plots). We measured plant species and community traits in the experimental plots and in 8 reference plots (i.e., surrounding untouched plant community). The results showed that all the treatments decreased the species richness of alien plants, in particular where soil salt content was enhanced. Moreover, salt increased the evenness of the plant community. Interestingly, soil with increased salt content controlled the alien cover while favouring native cover, likely by reducing the initial propagule pressure and, hence, affecting the future successional stages. This study provides new information on conservation and management efforts in this ecologically sensitive habitat, giving new insight into the dynamics of biological invasion and the impacts on native ecosystems.

S.263.3 A citizen science approach for the early detection and public awareness on invasive plant species: experiences from LIFE medCLIFFS

Sònia Garcia[1], Arnau Bosch[1], Francesc Caralt[2], Carlos Gómez-Bellver[1], Neus Ibáñez[1], Jordi López-Pujol[1], Roser Melero[1], Neus Nualart[1]

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LIFE medCLIFFS, spanning from October 2021 to September 2026, is an EU-funded LIFE Nature project focused on the management of invasive alien plant species along the Costa Brava in Catalonia, specifically targeting the Cap de Creus Natural Park. The primary goal is to improve the conservation status of the habitat of community interest HCI 1240, characterized by cliffs along the Mediterranean coast with endemic *Limonium* spp., currently in an unfavorable conservation status. LIFE medCLIFFS integrates prevention, rapid detection, risk assessment, and eradication strategies. Citizen science plays a pivotal role in early detection and prevention through public awareness. Citizen science in LIFE medCLIFFS involves two networks that leverage iNaturalist. The Observers' Network gathers observations of 180 invasive or potentially invasive plant species, with 109 registered members having recorded 4345 observations until November 2023. Simultaneously, the Volunteers' Network focuses on 33 highly invasive species, with 92 trained volunteers until present, each adopting 1-kilometer transects in the study area, and providing detailed data on reproductive status and other population metrics. The project has already accumulated a substantial body of data, featuring *Opuntia ficus-indica* as the Observers' Network most observed species and *Pittosporum tobira* heading the Volunteers' Network. The initiative already offers valuable data for the further management of invasive alien plants in the targeted habitat. The detailed observations provided will feed a database to produce risk maps which will allow us to predict the risk of invasion by a given species and area. The network is also useful for the detection of new occurrences of invasives not recorded until present in the study area. Beyond the contribution to invasive species management, citizen involvement raises awareness about invasive plants through a more environmentally conscious society. It contributes to botanical knowledge, fostering a community that is sensitive to the importance of conservation and environmental management.

S.263.4 Assessing the impact of invasive annual plants on soil microbial communities in riparian habitats of Kruger National Park

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The number and magnitude of alien plant invasions in protected areas are increasing globally. In Kruger National Park (KNP), one of the world's oldest and most widely known protected areas, 146 alien plant taxa have already become naturalized or invasive. Among these, three annual plants native to the Americas – i.e., *Xanthium strumarium* L., *Datura innoxia* Mill., and *Parthenium hysterophorus* L. – form extensive dominant stands along rivers. However, their environmental impact in KNP has not yet been determined, specifically their effects on soil physicochemical attributes and microbial communities. To explore the potential impacts of these three species, we identified seven populations of each species throughout the park, and in each site, we selected a pair of invaded and uninvaded plots. Within each plot (14 plots per species, n = 42 plots), we collected five subsamples from the top 10 cm of soil and pooled them into a single replicate. Subsequently, we used these composite soil samples to analyze soil pH, humidity, nutrients (P, NO_2^-, NO_3^-, NH_4^+, and organic matter), enzymatic activities (glucosidase, urease, and phosphatase), and bacterial and fungal diversity. The findings of this research offer new insights into the impacts of annual alien plants on soil characteristics and bacterial and fungal communities in riparian habitats, thereby contributing to the strategic planning of invasive species management within an iconic protected area.

S.263.5 Baccharis halimifolia in Southern Brittany coast (France): Adaptation to salt stress and invasion dynamics

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Invasive alien species (ISA) are a serious threat to biodiversity. For several decades a plant species has been invading French Brittany coastline: *Baccharis halimifolia*. It is presently classified by the European Commission as a "Shrub, ISA of concern for the European Union". Native to North America where it grows on intertidal marshes, this species belongs to the Asteraceae family. Currently, this species has been introduced on 4 continents: Europe, Oceania, Australia and New Zealand, mainly for its ornamental value and its function as a windbreak and soil stabilizer. It is gradually invading the French coastline, where it is becoming established in a variety of coastal environments such as salt marsh, rushes, reedbeds, roadsides and wasteland. This plant is susceptible to generate ecological and landscape impacts. This species occurs preferentially in environments with low to moderate salinity. We are interested in ecophysiological responses of this species to salt stress. The ecological characteristics of several populations were studied. Plant communities were characterized, and biological traits were measured for each population in order to fully describe them. The abiotic characteristics of the soil were also reported, such as salinity and water content. In addition, Sodium and potassium leaf concentrations and osmorality were measured and the osmolytes (e.g. glycine betaïne and oses) were characterized by 1H NMR (Nuclear Magnetic Resonance) and quantified by UPLC (Ultra Performance Liquid Chromatography). Finally, the same ecophysiological parameters were studied on plants grown under controlled conditions with a salt stress gradient. In addition, seed germination ability was studied as against the gradient of salinity. This work has enabled us to understand the adaptation of *Baccharis halimifolia* to salt stress. A better understanding of these adaptive mechanisms will enable us to propose new control strategies against *Baccharis halimifolia* and anticipate its dynamic of invasion.

S.263.6 Tracking the origin and dispersal of the sycamore maple Acer pseudoplatanus, an invasive species involved in the atypical equine myopathy

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Combined with climate change and anthropogenic activities, biological invasions have rapidly become one of the world's most costly ecological problems, significantly altering ecosystems, disrupting agriculture and spreading diseases. Understanding the circumstances of invasions under changing environmental conditions and unravelling the ecological and evolutionary mechanisms underlying invasive success are major challenges for improving our ability to predict and therefore mitigate biological invasions. *Acer pseudoplatanus* is a tree species native to central and southern Europe, introduced in various parts of the world for either ornamental or timber production benefits. Its high reproductive potential and remarkable capacity for dispersal, recruitment and establishment enable it to become a redoubtable invader. Thanks to its high seed production, which can be propagated over long distances, and its rapid growth, the sycamore maple is a threat to natural forests, particularly rare for species. The study focused on the ecophysiological, genetic and biochemical variation in native (Poland, Germany, Switzerland), naturalized (north eastern France) and invasive (north western France, Ireland, United States, New Zealand) ranges of *A. pseudoplatanus*. Aims were to infer the demogenetic history and to reconstruct the routes of invasion of the species, as well as to reveal traits facilitating its invasion in response to new habitat pressures. In particular, the comparison of the profiles of the hypoglycine A metabolite involved in the etiology of atypical equine myopathy disease, of which no clinic is documented in its native range, allowed to shed light on the relationship between invasiveness and allelopathy which is the basis of the New Weapons Hypothesis (NWH).

S.264 METHODS IN INTEGRATIVE TAXONOMY: BRIDGING THE PHYLOGENY TO CLASSIFICATION GAP. SESSION 2

S.264.1 Towards reconciliation of genetic and biogeographic patterns with morphologic variation in the genus Osmunda (royal ferns)

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We present an overview of the morphology, biogeography and ecology of the fern genus *Osmunda* (i.e., without previously included taxa of *Claytosmunda, Osmundastrum,* and *Plenasium*), with a focus on the American *O. spectabilis* Willd. and Old World *O. regalis* L. While genetic data supports the separation of these taxa, commonly used morphologic characters to distinguish between *O. regalis* and *O. spectabilis* (maximum frond size; pinnae sessile vs. stalked; pinnules opposite vs. alternate; general pinnule proportions) are not infallible. We recorded morphometric differences among and between *O. regalis* and *O. spectabilis* and correlated these with spatio-environmental gradients. Our work provides an updated taxonomic overview with full synonymy and diagnostic key of *Osmunda*. We preliminarily recognize six informal subtaxa in *O. regalis* ("regalis", "abyssinica", "huegeliana", "longifolia", "transvaalensis", "obtusifolia") and three in *O. spectabilis* ("spectabilis", "palustris", "piresii") which separate in a morphological traits-based PCA. The morphotaxa appeared geographically structured and their distribution showed significant correlations with elevation, mean annual precipitation, mean annual temperature and temperature seasonality. The taxonomic rank and validity of the proposed subtaxa have to be tested through a large-scale sampling, e.g. with comparative cp/nr genomic and cytogenetic analyses. Such future analyses may help to ascertain whether the observed morphologic peculiarities are conditioned solely by abiotic factors (which would allow addressing them as forms) or are manifested in the genome.

S.264.2 PhyloBarcode: a novel platform for species identification with DNA sequences

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DNA barcoding, which identifies species using sequences from universal genetic markers, has become a routine method over the past two decades. As for botany, standard DNA barcodes such as *rbcL*, *matK*, *ITS*, and *trnL-F* have been established, along with some lineage-specific barcodes. Traditional identification methods primarily depend on calculating the genetic distance between the target sequence and those in a database to determine the best match. This approach often overlooks the evolutionary relationships between sequences, such as lineage-specific sequence mutation events and ignores the differential treatment of mutations in conserved versus highly variable regions. Moreover, when the genetic distance between the target sequence and multiple sequences in the database is similar, it can lead to incorrect species identification. Phylogenetic trees can make more comprehensive use of multi-sequence alignment data to construct evolutionary relationships and are theoretically applicable for more accurate species identification. However, building phylogenetic trees requires substantial computational resources, and there is a current lack of automated analysis tools, limiting its use to manual identification for a small number of species. This study has developed PhyloBarcode, a software that automates species identification by constructing and analyzing phylogenetic trees. By preprocessing common barcode sequences, building trees, and optimizing algorithms, this method not only surpasses the accuracy and utility of results compared to traditional methods using genetic distances but also does not significantly lag in running speed. For lineage-specific barcodes, we provide a quick and convenient process for importing data, building reference phylogenetic trees, and matching target sequences. To facilitate ease of use, we also offer an online platform for direct identification, thereby avoiding any technical burden. This research is poised to further enhance the accuracy of plant species identification, bringing convenience to related research and applications.

S.264.3 PlantTreeDB: a new online platform for submit, query and view of plant phylogenetic trees

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Phylogenetic trees serve as a fundamental tool for understanding plant classification and identification, providing a clear depiction of evolutionary relationships between species. The construction of precise phylogenetic trees is not only computationally intensive but also demands the dedicated effort of researchers. Despite these challenges, there is still a significant hurdle in making these resources accessible for easy retrieval, communication, and display to the public. Our research synthesized data from existing phylogenetic tree databases, academic literature, and research datasets, employing advanced methods such as Python programming and LLM models for data cleaning and integration. We meticulously identified taxonomic groups and specific species associated with each tree, culminating in a compilation of 385,143 phylogenetic trees from 10,011 phylogenetic research papers. Each entry includes detailed information and access links to the original papers, metadata of phylogenetic trees, and storage in various formats such as Newick, Nexus, and PhyloXML. Building upon this foundation, we developed the PlantTreeDB website. This platform delivers a multi-keyword, rapid, and user-friendly phylogenetic tree search service, including fuzzy searches for taxonomic groups, and supports a variety of visualization and editing methods. PlantTreeDB allows for bulk data download and submission, with specialized optimization for plant group data retrieval and submission to ensure accuracy. PlantTreeDB is set to significantly foster the sharing and exchange of plant phylogenetic data, thereby providing a substantial impetus to the advancement of research in plant evolution and systematics.

S.264.4 Systematic study of the genus Saldinia A. Rich (Rubiaceae)

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Madagascar is known for its exceptional wealth of biodiversity, particularly flora. The Rubiaceae family is one of the largest flowering plant families in Madagascar, encompassing approximately 650 described species distributed across 95 genera. Notably, 98% of these species and 30% of the genera are endemic to Madagascar, highlighting the island's significance as a hotspot for Rubiaceae endemism. Despite the numerous ongoing research projects on this family, the Malagasy Rubiaceae remain understudied and its Flora treatment for Madagascar has not been completed. *A case in point is Saldinia* (tribe Lasiantheae, subfamily Rubioideae), which is a poorly known genus mostly endemic to Madagascar, with 22 shrub species. The main objective of this study is to reconstruct the first phylogeny of the genus as a precursor to its taxonomic revision. A comprehensive morphological dataset was compiled based on more than a thousand specimens from P, TAN, and BR herbaria, including all *Saldinia* types and 125 newly collected specimens from Madagascar during spring 2023. Total DNA was extracted from silica-dried leaves and herbarium material. Four markers (nrITS and nrETS, and *matk*, *trnT-F*) from nuclear and plastid genome were sequenced. We perform the maximum likelihood and Bayesian inference analyses using outgroup taxa from the subfamily Rubioideae. The results of our analyses will be presented and discussed. This study significantly contributes to Madagascar's biodiversity knowledge and advances research on *Saldinia* and Rubiaceae. Challenges in sample collection highlight the need for further exploration in unexplored regions, especially the Comoro Islands and specific Madagascar areas.

S.264.5 Unbuttoning the button daisies: Recircumscription and classification of the cosmopolitan genus Cotula L. (Asteraceae).

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The genus *Cotula* L. (button daisies) historically comprises of ca. 50 species, distributed mostly in southern Africa with some species extending to or endemic to tropical Africa, Eurasia, the Americas, and Australia. The genus is closely related to the South American genus *Soliva* Ruiz & Pav. and the largely Australasian genus *Leptinella* Cass. The latter two genera have been revised and are morphologically well-defined, whereas *Cotula* has never been revised in its entirety and currently has no synapomorphies to define the genus. Previous phylogenetic analyses of the genus *Leptinella* included a limited sampling of *Cotula,*and recovered both genera as non-monophyletic. We here present expanded phylogenetic analyses including ±80% of the currently recognized *Cotula* species, using both nuclear (ITS) and plastid DNA regions (psbA-trnH and trnC-petN). Our analyses support the non-monophyly of *Cotula,* with *Cotula mexicana* (a South American endemic) embedded within *Soliva*, *C. alpina* (an Australian endemic) embedded within *Leptinella,* and *Cotula sensu stricto* a paraphyletic assemblage of four main clades. Together with morphological data, we here propose an expanded circumscription of *Cotula* to include *Leptinella* and *Soliva* (viz. *Cotula sensu lato*), comprising over 100 taxa with a nearly cosmopolitan distribution. Due to the size and complexity of this expanded concept, we also propose a new infrageneric classification based on both phylogenetic and morphological evidence. *Cotula sensu lato* is divided into two subgenera, *Cotula* subgenus *Soliva* (Ruiz. & Pav.) Jakoet & Magee and subgenus *Cotula,* and 21 sections. Extensive herbarium and field studies on *Cotula sensu lato* resulted in 136 taxa being recognized including four new species and seven species needing new combinations. A broad overview of the expanded phylogeny and the diversity of morphological characteristics, particularly fruit characters, within *Cotula sensu lato* is presented.

S.264.6 Morphological phylogeny of Commelinales (Commelinids, Monocots) and its congruence with molecular data

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Commelinales is a small and well-supported monocot order, sister to Zingiberales, and currently includes Commelinaceae, Haemodoraceae, Hanguanaceae, Philydraceae, and Pontederiaceae (arranged in ca. 65 genera and ca. 1,080 species). The order is Pantropical in distribution, reaching temperate areas in some parts of the world, mainly due to the wide distribution of Commelinaceae, Haemodoraceae, and Pontederiaceae. Australasia represents the diversity centres of Haemodoraceae, Hanguanaceae and Philydraceae, and Pontederiaceae has the Neotropics as its diversity centre, especially Brazil. Finally, Commelinaceae possesses two Neotropical (Mexico and Brazil) and two Paleotropical (tropical Africa and Southeast Asia) diversity centres. Despite being strongly recovered as monophyletic by molecular studies, Commelinales lacks any morphological support and circumscription. The order is probably the least studied monocot order from an evolutionary and taxonomic point of view, having suffered the most striking changes in its circumscription between different classification systems (with Commelinaceae being its only consistent member). Based on our combined efforts and extensive herbarium, field, botanical illustration, and morphological studies, we compiled an extensive 570-character morphological matrix, sampling almost a third of the species in the order. Despite the known elevated degree of morphological homoplasy in the order, the topology and relationships we recovered are remarkably congruent with the molecular phylogenetic hypotheses available to date, showing the overlooked potential of large-sized and well-curated morphological datasets. The small degree of incongruence is limited to a few intergeneric and interspecific relationships. Our dataset and analyses recover at least one synapomorphy for each of the recognised genera and families of Commelinales, aside from supporting a revisited infrafamilial classification for all families. Finally, we recover for the first time four morphological synapomorphies for Commelinales, plus a putative fifth, depending on how character states are coded for it.

S.265 FLORAS AND DIVERSITY OF EASTERN ASIA. SESSION 2

S.265.1 Taxonomic and phylogenetic studies on Costaceae from China

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Costaceae comprises seven genera and 143 species, widely distributed in tropical and subtropical regions. One genus with five species was recorded in Flora of China. Since then, there has been no comprehensive taxonomic revision on Costaceae from China. Therefore, based on extensive historical literature and herbarium studies, the relationships and classification of Costaceae from China were studied by means of field survey, morphology, and molecular phylogeny. The main results are as follows: The important characters for identification of species from China include bracts (texture and shape), bracteoles (texture and shape), buds (quantity, shape, and size), stamens (anther position and appendage shape), stigmas (shape) and its dorsal appendage (shape and color), etc. Our research supported that most of *Costus* species from China should be transferred to *Hellenia* Retz. Currently, five species of *Hellenia* recognized from China. *Hellenia deliniana* (≡ *Costus chinensis*) were recovered. Two new combinations (*Hellenia viridis* ≡ *Costus viridis*, *Hellenia oblonga* ≡ *Costus oblongus*) were proposed. Plastid phylogenomic analyses of Costaceae revealed that *Hellenia* is strongly supported as paraphyletic. Two major clades are recovered, namely the *Hellenia* s.s. subclade and the *Parahellenia* subclade. Phylogenetic analyses based on an enlarged taxon sampling of the Asian clade using a two chloroplast markers dataset (*trnK* intron and *trnL-F* spacer) confirmed the paraphyly of *Hellenia*. Meanwhile, morphological analyses suggested that members of the *Parahellenia* subclade differ from the remaining *Hellenia* species in many characters including inflorescences, bracts, stigma, axillary buds, floral tubes, and labellum. According to the present molecular and morphological evidence, the latter subclade is recognized as a new genus, *Parahellenia*. Two new species are described, four new combinations are made, and identification keys are also provided.

S.265.2 Construction of China National Botanic Garden System and Plant Diversity Protection

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China is one of the countries with the richest plant diversity in the world, with more than 38,000 species of higher plants. In-situ protection and ex-situ protection are two forms of wild plant protection. The natural reserve system with national parks as the main body is the main form of in-situ protection, and the national botanical garden system is the main form of ex-situ protection. Both are indispensable, organic complementation. At present, China has established the China National Botanical Garden in Beijing and South China National Botanical Garden in Guangzhou. In the next step, we comprehensively consider factors such as China's climate zones and typical vegetation zoning characteristics, biodiversity hotspots, the stability and sustainable development of plant ex-situ conservation, and select more than 10 national botanical garden candidate gardens to be included in the spatial layout to build a The "1+N" national botanical garden system with the China National Botanic Garden as the core and regional botanical gardens as the support, and will gradually realize the full coverage of ex-situ protection for more than 85% of China's wild native plants and all key protected wild plant species, providing China plan for the protection of plant diversity. The China National Botanical Garden was officially established in December 2021. It focuses on ex-situ plant protection and has functions such as scientific research, popular science education, gardening, culture and leisure. In the future, the National Botanic Garden will collect more than 30,000 species of living plants through the construction of a specialized garden collection system, greenhouse clusters and germplasm resource banks, covering 80% of the families and 50% of the plant species in China, accounting for 10% of the world's plant species, to undertake the responsibility for ex-situ conservation of regional plants and fulfill the mission of global species protection.

S.265.3 Plant Taxonomy and Botanical Gardens in China and the world

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China is one of the richest countries in plant biodiversity in the world, not only from taxonomic view but also from horticultural point as well. However, its plant resources are still not very clear today, even Chinese flora has been studied more than 250 years. Especially In the past seventy years, Chinese taxonomists worked very hard and finally finished the first completed flora in Chinese, *Flora Reipublicase Popularis Sinicae* (FRPS, 1959-2004), with 31,180 vascular species in 300 families and 3,434 genera, documented first time in the Chinese History of botany. And among them, 233 genera (6.8%) and 16,864 (54%) are endemic. More recently, new English version of *Flora of China* (FOC, 1994-2013), cooperated with Missouri Botanical Garden, in 25 volumes in text plus additional 25 volumes in Illustration, with total 312 families 3,328 genera and 31,362 species recorded, and it all resources has been online (flora.huh.harvard.edu/china/) as well as in Chinese in China (iplant.cn). Besides above, Chinese taxonomists also finished more than seventy local floras in or above Chinese province level in the past more than half of century. So far, each province in China has its own flora, plus few major natural areas, such as Chinese Desert, Chinese Loess Plateau, and famous Tsinling mountain in central China. In this report, both current situation and future prospect of plant taxonomy and botanical gardens are fully reviewed. Particularly for the huge challenge in conservation biology of plant resources is in front of Chinese gardens, including survey, protection, conservation and utilization. And it has a long way to go for Chinese taxonomists to understand their plant resources well, to fully protect its various plant resources better, and to use them smartly and continuingly purpose. Especially, from conservation view, Chinese taxonomists should more hard work, particularly within botanical gardens both home and abroad.

S.265.4 How to understand biogeographic patterns in Southeast Asia from diversity of Engelhardia (Juglandaceae)?

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Southeast Asia is recognized as global biodiversity hotspots with conservation priority. Since the mid-19th Century, Southeast Asia has been widely considered as one of the most important cradles and frontiers of biogeography. This connection stems from the groundbreaking field works of Alfred Russel Wallace, who spent 8 years to extensively explore the regions and proposed the geographic distribution patterns of fauna in Malesia. However, many distribution patterns were from fauna or animal diversity. Thus, more plant taxa are necessary to explore the biogeographic patterns in Southeast Asia. Here, some superficial ideas and recommendations are presented to address the unresolved challenges of the field of biogeography in Southeast Asia from *Engelhardia*. The related information includes species delimitation, taxonomic revision, biogeographic patterns in the regions. The comprehensive taxonomic revision of *Engelhardia* will provide insights into Southeast Asia. As well, the results urge caution when using the concepts of subspecies and varieties in order to prevent confusion, particularly with respect to species delimitation for tropical and subtropical species. Also, biogeographic patterns of *Engelhardia* have told that the tropical elements were transformed from the tropical elements; Miocene cooling and the onset of the EASM facilitated the transformation of *Engelhardia* from the tropical Indochina Peninsula to subtropical China. The lineages around Hainan Island, China mainland and Indochina Peninsula showed that Engelhardia dispersed from Chiang-nan to Hainan Island via land bridge, so that drift of Hainan Island did not occur, which was impossible to affect the evolutionary trajectory of plants. In all, I hope the works from *Engelhardia* will serve as a link between past and future, intends to be the gain of propaganda, and facilitates the flourishing development of biogeography in Southeast Asia.

S.265.5 From α- to β-diversity: Understanding the historical, present, and future diversity patterns of Fagaceae in Southwestern China

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Macroecological research aims to understand factors influencing species composition and diversity. Understanding the distribution patterns of species is essential for prioritizing areas for conservation. This study investigates the alpha (α) and beta (β) diversity facets of Fagaceae across past (historical), present, and future timelines in Southwestern China. We used over 11,000 geographical observations to predict the spatial patterns of the α- and β-diversity of 120 species. We modeled the α-diversity via stacking prediction using an individual species distribution model at 50 km × 50 km grid cells. We used pairwise Sørensen dissimilarity to quantify total β-diversity and its components -turnover (β_{SIM}) and nestedness (β_{NES}). We integrated climate variables along with topographic and edaphic predictors to understand the species diversity. Finally, simultaneous autoregression (SAR) model was used to evaluate the effects of predictor variables on the α- and β- diversity patterns. Our results indicate a temporal decline in the α-diversity from 120 during the past to 49 in the future. However, species occurrence area has expanded, fostering an increase in the β-diversity, and it may potentially continue to increase in the future. At present, the southern region exhibits the highest α-diversity, while high β-diversity occurs in the central region. The findings underscore that the species β_{SIM} is a driving factor of differing species composition during the past and present periods, while β_{NES} will be a dominant factor in the future. During the past, climatic and topographic factors significantly influenced the α-diversity, and similar factors continue to impact the β-diversity and its components. In the future, climatic variables will play a significant role in determining the diversity patterns.

S.266 EVOLUTION OF PLANT SEXUAL REPRODUCTION. SESSION 2

S.266.1 Whole genome duplication enables rapid evolution of male, but not female, function in bisexual flowers

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Whole genome duplication (WGD) has well-known phenotypic effects at the cell and organismal level, with potential functional consequences for pollen -the haploid, single-celled male gametophyte phase of angiosperms. A review of species with diploid (2x) and autotetraploid (4x) cytotypes, showed 2x pollen from artificial and crop neo-autotetraploids was double the volume of 1x pollen from diploid progenitors (*N* = 65, 34 species, respectively). In contrast, 2x pollen of wild autotetraploid cytotypes was only 54% larger (significantly smaller-than-doubled volume; *N* = 54). These results suggest WGD doubles pollen volume, whereas post-WGD evolution is biased to pollen size reduction. To understand why, I asked if WGD disrupts sexual allocation patterns that reflect evolved size-number trade-offs in *Galax urceolata,* a species with natural diploid (2n = 2x = 12) and cryptic autotetraploid (2n = 4x = 24) populations. I measured floral organ sizes and numbers in four 2x and four 4x populations (20 plants/population), verified using flow cytometry. 2x and 4x plants had the same number of flowers and floral parts, including ovules, whereas 4x floral organs were 20-24% longer, reflecting conserved progenitor-like floral allometries. Autotetraploid anthers were 2.12 times the volume of diploid anthers, enough to accommodate doubled volume of 1x pollen numbers. Surprisingly, autotetraploid anthers produced 76% more viable pollen of 33% larger size than diploid anthers. Total per-plant sexual allocation to anther and ovule volume in 4x plants increased by 76% and 68%, respectively, but 4x plants produced 83% more male, but only 6% more female, gametes. In sum, WGD seems not to alter sexual allocation at the organ level, but instead WGD-enlarged microsporangia have enabled the rapid evolution of smaller and more neo-2x pollen, whereas WGD-enlargement of megasporangia are limited to one egg/ovule. WGD generates greater opportunity for sexual selection on male than on female gamete numbers.

S.266.2 Variation in sexual dimorphism for multiple traits among populations sampled at a continental scale for a dioecious annual plant

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Plants originating from different populations and environments often exhibit distinct trait values for life history, morphology, and physiology as a result of local adaptation. Similarly, in plants with separate sexes, males and females often have distinct phenotypes that optimise their respective sexual functions (sexual dimorphism). This phenotypic variation can be summarised in terms of a trait correlation matrix, which can limit responses to selection. There has been substantial research on trait correlation matrices within populations and their implications for constraints on adaptation, but there is still limited work on how these matrices differ among environments and between the sexes. We sowed seeds of the European ruderal plant *Mercurialis annua* L. (Euphorbiaceae) sampled from 21 populations from seven regions across Europe and the Middle East, spanning a wide range of environmental conditions, and measured a suite of life history and morphological traits associated with fitness and sexual reproduction in a large common garden. We present the results of our analyses that point to substantial variation in trait correlations among populations, regions and sexes. We discuss the results in relation to environmental variation among source sites and in terms of constraints that limit evolutionary responses to selection and phenotypic divergence between the sexes. Our study provides valuable insights into the multidimensional nature of plant adaptation across spatial scales seldom studied for wild populations, especially for species with separate sexes.

S.266.3 Stable co-existence of females, males and hermaphrodites through interactions between maternally and biparentally inherited genes

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The co-existence of females, males and hermaphrodites (trioecy) is rare in both plants and animals, and the few cases that do exist are poorly understood. Here, we provided a new model explaining the stable coexistence of these three sexual phenotypes. In contrast with previous models, which investigate the invasion of a hermaphroditic population by cytoplasmic male sterility (CMS), our model considers the invasion of CMS into a population in which males and hermaphrodites already coexist (androdioecy). We compared the invasion and fixation of CMS in androdioecious versus hermaphroditic populations and show that the existence of males prior to CMS invasion facilitates the maintenance of trioecy even in the absence of pollen limitation – though pollen limitation does also promote the maintenance of trioecy under certain conditions. We discuss these results with reference to the case of trioecy in the annual plant *Mercurialis annua* and consider trioecy as a possible evolutionary path from hermaphroditism and dioecy.

S.266.4 Towards characterization of the genetic self-incompatibility system in Beta vulgaris

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The majority of flowering plant individuals are co-sexual with hermaphroditic flowers, possessing the ability to self-fertilize. Self-fertilization is however an infrequent mode of reproduction and nearly half of all flowering plants strictly avoid self-fertilization through an array of physiological, temporal and genetic mechanisms. Genetic self-incompatibility (SI) systems guarantee the rejection of pollen identified as ‘self’ based on protein-protein interaction. The response is controlled by an S-locus that contains two linked protein-coding regions, one uniquely expressed in pollen or anther and the other in the pistil. While pivotal in plant reproduction, SI-systems have been characterized in only a handful of species, owing to their limited homology, high sequence diversity and intricate architecture. The *Beta vulgaris* complex (family Amaranthaceae) includes three subspecies and several cultitypes, among them commercially important crops of temperate climates such as the sugar beet. Species in the genus *Beta* exhibit complex genetic self-incompatibility that has been lost in varietal populations, and remains little understood from a physiological and genetic perspective. We present an *in silico* investigation into the genetic basis of SI in *B. vulgaris* using high-quality genomic resources. We targeted candidates for an RNAse-based SI system, which has the broadest taxonomic distribution among angiosperms and closely related taxa. Specifically, a highly contiguous long-read assembly and other data were utilized to identify SI candidate genes. We harness the unique features of the S-locus to identify candidates based on phylogenomic relationships, structural features, high heterozygosity and tissue-specific expression. We proceed to explore the highly dynamic evolution of gene structure in the putative S-loci in different beet taxa. The results will provide first hints to an RNAse-based SI system operating in *B. vulgaris* and provide a foundation for further studies on molecular mechanisms of SI.

S.266.5 A hemizygous supergene controls homomorphic and heteromorphic self-incompatibility systems in the olive family (Oleaceae)

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Self-incompatibility (SI) evolved independently multiple times and prevent self-fertilization in hermaphrodite angiosperms. Several groups of Oleaceae such as jasmines exhibit distylous flowers, with two compatibility groups each associated to a specific floral morph. Other Oleaceae species, in the olive tribe, harbor two compatibility groups without associated morphological variation. The genetic basis of both homomorphic and dimorphic SI systems of Oleaceae are unknown. By comparing genomic sequences of three olive subspecies (*Olea europaea*) belonging to the two compatibility groups, we first locate the genetic determinism for self-incompatibility within a 700-kb hemizygous region present only in one of the two types. We then demonstrate that a homologous hemizygous region is also involved in controlling distyly in jasmine. Phylogenetic analyses support a common origin of both systems following a segmental genomic duplication in their ancestor. We postulate that self-incompatibility and ditvly imply two genes in the hemizygous region that are involved in gibberellin and brassinosteroid regulation, underpinning the diversity of incompatibility systems in the group.

S.266.6 Using geometric morphometrics for the study of stylar polymorphisms: Insights into the evolution and function of mating phenotypes

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Linum was among the first examples of heterostyly reported by Darwin, and extensive research has been carried out since then in this study system. The yellow-flowered *Linum* clade (Sections Linopsis and Syllinum), mainly distributed in the Mediterranean Basin (MB) and the Cape Floristic Region (CFR) in South Africa, includes a great variation of mating phenotypes, including typical heterostyly, three-dimensional heterostyly and various types of monomorphic conditions. There is limited, mostly qualitative data about the pollination biology of the genus, but it has been suggested that pollinators may be the drivers of convergent evolution of stylar polymorphisms in the MB and CFR. In this talk, I illustrate the use of geometric morphometrics to link the study of form and function across mating phenotypes in the yellow flaxes' lineage. We use geometric morphometrics to investigate the variation of mating phenotypes in South African and Mediterranean yellow *Linum* species and their pollinators. Using phylogenetic analyses, we reconstruct the ancestral character and the evolution of the mating phenotypes and the convergent evolution of stylar polymorphisms in MTEs in relation with the pollination niche of species. We test the hypothesis that pollinators, through their morphological fit, are the evolutionary drivers of (i) the great variation of mating phenotypes in South African and Mediterranean yellow flaxes; and (ii) the convergent appearance of heterostyly in both separate regions.

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S.267 PHYLOGENETICS AND PHYLOGENOMICS. SESSION 2

S.267.1 Addressing phylogenetic incongruences in Cantharellales (Fungi, Basidiomycota) through a 526 protein-coding-gene capture kit

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The order *Cantharellales* contains economically important species because of their edibility (*Cantharellus, Hydnum*), being orchid-mycorrhizal (*Tulasnella*) or plant pathogens (*Rhizoctonia*). However, within this group nuclear ribosomal regions produce phylogenetic conflicts due to an accelerated rate of evolution and cause long-branch attraction problems, making them useless to infer phylogenetic relationships between family clades. This is why, despite 4 monophyletic lineages *Hydnaceae, Cejpomycetaceae, Tulasnellaceae, Botryobasidiaceae* are consistently retrieved in phylogenetic studies, their relationships remain unclear and are strongly dependent upon the genetic marker and taxon sampling employed. In this scenario, we designed a kit to capture 526 orthologous single-copy protein-coding genes in *Cantharellales* filtered from 10 representative genomes. Filtered genes were sequenced across a set of more than a hundred samples of *Cantharellales*, representative of its diversity and including many generic types. The analysis of the dataset containing DNA sequences of 526 genes resulted in a fully supported backbone for the *Cantharellales*, with relationships among the *Ceppomycetaceae*, *Tulasnellaceae*, *Botryobasidiaceae* and *Hydnaceae* resolved. Novel phylogenetic relationships are revealed within the *Hydnaceae*. Our results show that an updated classification at generic level needs to be proposed urgently within the *Cantharellales*. We infer from our test that *Cantharellales*-kit constitutes an excellent approach to construct a multiple-marker, fully supported phylogeny of *Cantharellales*. Our test suggests furthermore that the kit will function well in sister groups of Cantharellales, such as in *Dacrymycetales* and *Sebacinales*.

S.267.2 Reconstruction of Orchid Phylogeny

Yajun Wang[1,2,3], Dongliang Lin[1,2,3], Hanchen Wang[1,2,3], Zhiping Wang[1,2,3], Chongbo Ma[1,2,3], Shiyu Qin[4], Bingyi Shao[1,2,3], Chao Ye[1,2,3], Jianwu Li[5], Miaomiao Wang[3], Xuelian Guo[1,3], Xiaohua Jin[1,3]

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Orchidaceae is among the largest families of angiosperm distributed all over the world except Antarctica. There are more than 30,000 species in 748 genera and five subfamilies (Apostasioideae, Vanilloideae, Cypripedioideae, Orchidoideae, and Epidendroideae), interrelationships within family are not well resolved. Recent technical advances in molecular biology have provided unprecedented opportunities in resolving complex phylogenies, such as that of Orchidaceae, in a repeatable way. In order to further our understanding of the evolutionary history of orchids, we sampled a total of 163 species in this study, covering all five subfamilies and 20 of 22 tribes, and combined transcriptomic and genomic data of orchids to reconstruct a comprehensive, robust, and reliable phylogenetic framework of orchids.

S.267.3 Phylogenomic analysis of Santalaceae s.l. gives insight into the evolution of a unique respiratory pathway in mistletoes

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Parasitic plants in the family Viscaceae (mistletoes) have been shown to have highly unusual mitochondrial genes compared to other flowering plants. Genes encoding respiratory complex I are even lost. In order to investigate where in the evolutionary history of this group these bizarre changes have occurred, a solid hypothesis of their evolutionary relationships is needed. In order to reconstruct a phylogeny, we have sampled all Australian representatives of both Viscaceae and the closely related family Amphorogynaceae (both included in Santalaceae s.l.) as part of the GAP initiative. Since the families are not restricted to Australia, numerous species from other regions of the world were also sampled. Taxon sampling additionally included other representatives of the order Santalales for a total of approximately 200 samples. Using target capture sequencing with the Angiosperms353 bait set, we obtained data from over 300 nuclear loci, which were used for phylogenetic reconstruction based on both concatenation and coalescence methods. The phylogenetic trees derived from the two methods are largely congruent and confirm a sister group relationships of Viscaceae and Amphorogynaceae. Generic relationships within the families are also largely consistent with previous hypotheses, but the denser taxon sampling allows for more detailed hypotheses about species relationships within genera. The phylogeny will be used to trace the evolution of mitochondrial genes, and preliminary data suggest a deeper origin than ancestral Viscaceae for the onset of evolutionary drastic changes. It is even possible that gene loss has occurred multiple times during the evolution of mistletoes.

S.267.4 Phylogeny of Virola (Myristicaceae) and species delimitation for the Floras of Brazil and the Guianas

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The Neotropical Myristicaceae includes six genera. Virola (Myristicaceae) is the genus with the highest number of species and the broadest geographical range, occurring from Central America to South Brazil, with a peak of diversity in Amazonia. Species delimitation in Virola is mostly based on the number and the spacing of the secondary veins, the indument, inflorescence branching, length of anthers and filament column, and on fruit shape and size. Currently, around 70 species names are accepted, with a few disagreements on synonymies in the literature. During an ongoing treatment of the genus for Flora do Brasil and the Flora of the Guianas, morphological data had limited power to address the disputed synonymies and the status of the monotypic genus Bicuiba, reduced to synonymy in the Brazilian literature but still accepted elsewhere. As an attempt to add new evidence for species delimitation and to understand the evolutionary relationships among species, we generated different sets of molecular data. Plastome and ITS regions were sequenced in 86 herbarium samples of 35 species. We also carried out targeted sequencing of nuclear genes (Angiosperm 353 probe set) in part of these samples and new ones, in total 79 herbarium specimens of 36 species. Plastome and ITS data were in general not informative or incongruent. The sampling of multiple specimens per species and analysis of the different datasets have offered additional support for decisions on synonymies. The resulting phylogeny based on the targeted sequencing of nuclear genes indicated that Virola can be divided in three well supported clades; one of which formed by sub-canopy to canopy species including the widespread V. sebifera and V. calophylla, agrees with previous findings. The study of independent molecular datasets integrated to morphology is a strategy for supporting taxonomic decisions and better understanding the evolution of the genus.

S.267.5 A phylogenetic framework for the model genus Kalanchoe (Crassulaceae)

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Kalanchoe (Crassulaceae) is a diverse genus native to Madagascar and Africa, and to a lesser extent, the Arabian Peninsula and tropical southeast Asia. The genus is known as a model system for CAM photosynthesis and vegetative reproduction as well as for its horticultural value, invasive potential and use in traditional medicine. Surprisingly, however, *Kalanchoe* lacks a reliable phylogenetic framework. To address this issue, we inferred a phylogeny based on ddRAD-seq data representing 70% of the taxa recognised in the genus. We recovered four major clades, broadly corresponding to the current subgeneric classification, with exceptions. The recently reinstated subgenus *Calophygia* resolves as sister to the rest of the genus, and the predominantly mainland-African subgenus *Kalanchoe* forms a strongly supported monophyletic clade. However, the relationship among the remaining two clades containing species from subgenera *Bryophyllum*, *Kitchingia* and *Pubescentes*, receives less support. A Malagasy origin of the genus is confirmed, from where the African continent was colonised only once, with two subsequent dispersals each to the Arabian Peninsula and tropical southeast Asia. The production of bulbils on the leaf margin was found to be an apomorphy within the subgenus *Bryophyllum* while propagules on the inflorescence can occasionally be found in all four major clades.

S.267.6 The sexual system of the dioecious species Laurus azorica

Catarina Branco[1,2,3], Rúben Rego[1,2,4], Gabriel Marais[1,2,3], Raquel Linheiro[1,2,3], Raquel Tavares[1,2,3], Sylvain Santoni[5], Hugo Tessarotto[5], Jos Käfer[6], Alessio Iannucci[7,8], Claudio Ciofi[7], Maria A. Diroma[7], Chiara Natali[7,9], Marco Morselli[10], Guilherme Roxo[1,2,4], Roberto Resendes[1], Manuela Sim-Sim[11,12,13], Helena Trindade[11,13], Sara Vicente[11,14], João P. Marques[1,2], Vitor Sousa[11,15], José Melo-Ferreira[1,2,3], Ann Mc Cartney[16], Alice Mouton[7,17], Giulio Formenti[18], Mónica Moura[1,2,3]

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The *Laurus* genus exhibits a current distribution encompassing the southern Black Sea region, the Mediterranean Basin, Morocco, and the Macaronesian islands (i.e., the Azores, Madeira, and Canaries archipelagos). Despite numerous attempts, previous studies faced challenges in elucidating the taxonomy, ploidy, and phylogenetic relationships within this genus. Concerning the taxonomy, two species are traditionally recognized: *L. nobilis* and *L. azorica*. This study delves into *L. azorica*, a dioecious tree endemic to the Azores archipelago that falls within the European Reference Genome Atlas (ERGA) initiative to ensure high-quality reference genomes of the European biodiversity. Despite the well-established dioecy of this species, its sex-determination system remains elusive. Here, we aim (i) to obtain a chromosome-level assembly and (ii) to identify its sex determination system. Firstly, long-read sequencing data from Pacific Biosciences (PacBio) were acquired to ensure a robust genomic dataset. Additionally, chromatin conformation capture data (Hi-C) were incorporated to facilitate the construction of a chromosome-level assembly. Then, Illumina short reads for 32 individuals were obtained, ensuring an even representation of phenotypic males and females. SD_{POP} (Käfer et al. 2021) analysis will be applied to infer the genes' sex-linkage by modelling populations' allele and genotypic frequencies. This framework allows statistical testing of alternative sex-determination systems (i.e., presence or absence of sex chromosomes, distinguishing between XY and ZW systems). Our preliminary results suggest that *L. azorica* is tetraploid (n=18), consistent with prior studies on this genus. Ongoing research is expected to yield additional insights into the sex-determination system and contribute valuable information to broader studies on dioecy and sex-determination mechanisms in plant species. Moreover, this study serves as a cornerstone for further exploration into the evolutionary dynamics within the *Laurus* genus.

S.268 CONSERVATION STATUS OF MAGNOLIA IN SOUTH AMERICA

S.268.1 Conservation status of Magnolia in South America: the case of Colombia

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Magnoliaceae is a family of trees and shrubs with approximately 350 species mainly distributed in Asia and America. Having a well-known taxonomy with 33 species distributed along the whole territory, many of them endangered, Magnoliaceae was chosen as a pilot group in Colombia to implement the National Strategy for Plant Conservation in 2001. Since then, several people and organizations have performed significant efforts to look for trees and populations, increase public awareness, and identify ecological requirements for their growth and establishment. After nearly 20 years of continuous work, several new species have been discovered and formally described positioning Colombia as the country with the most *Magnolia* species (40) in South America. *Magnolia* species are characterized by a restricted geographical distribution with very small populations, even reduced to isolated trees highly affected by habitat fragmentation and overharvesting. Consequently, most species are currently considered a priority for conservation. Besides, 90% of the species are endemic to Colombia, highlighting the urgent need to keep working on public awareness and effective conservation programs in which conservation in situ by means of the constitution of reserves is a priority This presentation will show the conservation status of Colombian magnolias, the successful results achieved so far, and the conservation priorities and challenges that still need to be faced.

S.268.2 Conservation status of Magnolia in South America: Brazil

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Within the family Magnoliaceae Juss., the genus *Magnolia* L. has the largest number of species, including more than 300 species worldwide, whose number is increasing due to the recent discovery of new species, mainly in the Neotropical region. The group is mainly represented by trees that are usually represented by a few records in herbariums. Determining the conservation status of Magnolia species is a challenge, since of the 75 species in South America, 59 are threatened according to IUCN threat categories. However, as the species have been assessed for several years, there is a need to know the current conservation status, update this assessment, and provide information for those species with deficient data. The objective of this lecture is to discuss these strategies to update the conservation status of Magnolia species in South America, especially in Brazil, so that we can contribute to the effective conservation of this interesting group of plants characterized by vulnerable populations, especially in the face of climate change scenarios. There are many species of Magnolia in America that are threatened with extinction and are included in the IUCN Red Lists. However, numerous species lack information and need studies to compensate for their threatened status. The consolidation of this information in the different countries of South America provides important decisions in the field of public policies that can help in the maintenance of Magnolia species. The importance of the Global Conservation Consortium for Magnolia is highlighted, engaged in the dissemination and construction of effective collaborative work in the conservation of these plants. For Brazil, only the following species are considered: *Magnolia amazonica* (Ducke) Govaerts, *Magnolia grandiflora* L., *Magnolia ovata* (A.St.-Hil.) Spreng.

S.268.3 Conservation status of Magnolia in South America: Ecuador

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Magnolia diversity in Ecuador is high, actually 24 species are recorded, and 17 are endemic. The conservation status of these species is worrying, mainly because the number of adult-reproductive individuals is low, and their threats are latent. Currently, 80% of the species are severely threatened; six are assessed as Critically Endangered (CR) and 11 are Endangered (EN). There is an urgent need to start with *in-situ* and *ex-situ* conservation plans. Some actions have been created; for example, Jocotoco Foundation is monitoring fruits to obtain seeds for propagation in nurseries for *M. buenaventurensis*, *M. canandeana*, and *M. dixonii.* Around 1,500 seedlings are growing and being used in restoration programs in their habitats.

S.268.4 An integrative study of species distribution modelling and conservation genetics: Magnolia in Hispaniola

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On the island of Hispaniola in the Caribbean, five endemic species of *Magnolia* occur, all of which are threatened with extinction. Little is known about their distribution and genetic health, hampering targeted conservation actions. The objective of this study was to assess the potential distribution and the genetic health of the Magnolias of Hispaniola, and to formulate concrete guidelines for effective conservation management. Using species distribution modelling (SDM), we predicted habitat suitability for the Magnolias of Hispaniola. Using 17 SSR markers, we genotyped 417 individuals of the three endangered *Magnolia* species from the Dominican Republic, to test for genetic structure and degree of inbreeding. The SDM and genetic data confirm the recognition of the four studied Magnolia as species. The studied individuals of the three Dominican Magnolias are structured into five populations which show ample genetic diversity and little inbreeding overall. For conservation management, we propose, on the one hand, to focus on exploration using the SDM results. On the other hand, we propose to focus on protection and reinforcement using the genetic and occurrence data. Our study exemplifies how integrating different research techniques, as well as working closely with conservation practitioners, may lead to a better understanding regarding the requirements for an effective conservation plan.

S.268.5 Unveiling the genetic patterns of Magnolia calimaensis: Insights into local endemism and conservation

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An endemic species occurs naturally, exclusively, and is highly adapted to a specific geographic area. If this area is very small, the species is termed as local endemic and generally consists of small or a single population. The genus *Magnolia* is an interesting study model of local endemism since out of the 39 species recorded for Colombia, 80% are endemic and restricted to less than 100 km². The species of the genus are also hermaphroditic, and both entomophily and self-pollination are reported as their main reproductive syndromes. Here we study *Magnolia calimaensis* (Lozano) Goavaerts, an endemic tree species of the Bajo Calima region on the Pacific coast of Colombia, which is critically endangered with fewer than 100 individuals in the wild. To understand the origin of local endemism in *M. calimaensis*, 38 individuals were sampled from Bajo Calima and Bahía Málaga localities. Microsatellite marker analysis revealed low genetic diversity and high inbreeding coefficients for both populations (He: 0.24 / F: 0.53 for Bajo Calima, and He: 0.29 / F: 0.29 for Bahía Málaga). Significant genetic differentiation between locations suggests dissimilar population conditions. Results imply that the species' gregarious distribution and local endemism may be linked to reproductive biology, like geitonogamy, rather than landscape composition. Urgent genetic restoration strategies are needed to preserve M. calimaensis populations, highlighting the importance of further reproductive biology studies.

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