



Royal Botanic Gardens  
**Kew**

**State of the  
World's Plants and  
Fungi Symposium**

**Poster abstracts**

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# Poster abstracts

## **P1 Plant and macrofungi conservation in Azerbaijan and assessed species**

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Plants and fungi perform many vital functions in various ecosystems. Nowadays, the problem of conservation, maintenance and sustainable use of biodiversity in the world is more acute than ever. Plants and fungi are exposed to similar threats as other organisms in the ecosystem, which leads to the reduction and gradual extinction of their natural populations. Work on compiling a list of endangered plant species began in the 1960s, and on fungi much later. As it is well known, direct monitoring of fungi is not feasible.

Azerbaijan, as part of the Caucasus, is one of 36 biologically rich but endangered hotspots of the world. The first assessment of threatened species in Azerbaijan was performed in 1989, and the first edition of the Red Book was published, which included 140 plant and 108 animal species. Much later, in 2013 the next assessment was conducted according to the IUCN Red List categories. In total, 286 plant, 14 fungi and 223 animal species were selected for the second edition.

Specialist-verified data was collected over the past eight years reflected in the third edition this year, that includes 423, 15 non-flowering plants, 6 mosses, 14 lichens, 5 algae and 37 mushroom species. Plant and fungi were assessed based on the following categories: CR (108 species), EN (138), VU (127), NT (64), LC (9), DD (12), NE (2). Renewed data greatly improves and reflects the current situation and is the main document for setting national targets for protection and conservation strategies in the country.

## **P2 Oman Botanic Garden**

Al Harthy, L., Al Hatmi, S., Al Hinai, A.

Oman Botanic Garden, Sultanate of Oman

The Oman Botanic Garden (OBG), currently under construction in Muscat, Sultanate of Oman, is an exceptional endeavor established by a Royal Decree in 2006. It stands as a unique and ambitious project dedicated to the conservation of native flora and the preservation of plant-related cultural heritage. The primary objective of the Oman Botanic Garden is to collect, propagate, conserve and showcase the complete indigenous flora of Oman. The garden boasts the world's largest documented collection of Arabian plants, making it a crucial player in addressing the pressing need for biodiversity conservation solutions.

Notably, the diligent field work and herbarium research carried out under the OBG's assistances have resulted in hundreds of new or updated plant species records from the Sultanate of Oman. These remarkable findings predominantly originate from mountainous regions in both the southern and northern territories, areas that were previously characterized by limited botanical knowledge and exploration. The establishment of the Oman Botanic Garden heralds a significant step forward in the promotion of scientific research and conservation efforts to safeguard Oman's invaluable botanical heritage.

### **P3 Evolution of pollen in the Adesmia clade (Leguminosae, Dalbergieae): Novel morphological data support a new classification**

Antonio-Domingues, H.<sup>1,2</sup>, Fortuna-Perez, A.P.<sup>3</sup>, Rossi, M.L.<sup>4</sup>, de Almeida, R.F.<sup>1</sup>, Martinelli, A.P.<sup>4</sup>, Lewis, G.<sup>1</sup>, Luz, C.F.P.<sup>2</sup>

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Legumes comprise different pollen morphological types due to Leguminosae being one of the most diverse families of flowering plants. Representatives of the Adesmia clade (Papilionoideae, Dalbergieae) have been extensively palynologically studied in the last few years, evidencing pollen morphology's taxonomic relevance in this group. Building on these studies, we scored, coded, and mapped 16 pollen characters related to general morphology, ultrasculpture and ultrastructure into the most recent molecular phylogeny of the Adesmia clade. Quantitative and qualitative palynological data were also scored from our results for the ingroup (*Adesmia*, *Amicia*, *Poiretia*, *Nissolia* and *Zornia*) and outgroup (*Tipuana* and *Pterocarpus*) genera. All lineages of the Adesmia clade were recovered with at least one or more pollen homoplasies/apomorphies, except for *Adesmia*. The Adesmia clade was morphologically supported by colporus length, operculum ultrasculpture and nexine thickness. The Adesmia + ZAP clade (*Zornia* + *Amicia* + *Poiretia*) was supported by endoaperture length and the latter by features of the polar and equatorial axes. The remaining genera are characterised by nexine thickness (*Poiretia*), endoaperture type (*Amicia*), P/E, endoaperture type, and operculum ultrasculpture (*Zornia*). Morphological synapomorphies for *Adesmia* were unclear due to the reduced sampling in a genus with 206 accepted species. Even though most characters were found to be homoplastic across the Adesmia clade, they helped characterise all clades and most genera of this informal group. Future pollen studies on the Adesmia clade will enable the scoring and coding of additional characters and the proposition of a new classification system (subtribal) for this group.

## **P4 Filling in the gaps: Advancing botanical record-keeping and living collection management at Species360**

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The critical role of accurate and up-to-date plant records in preserving biodiversity cannot be overstated. However, the current landscape reveals a concerning situation, as less than 20% of the world's 3,765 botanic gardens have a computerised plant record system (according to BGCI's GardenSearch). The majority of gardens rely on basic solutions that prove inadequate for contemporary demands in record-keeping and hinder the efficient management of their collections.

Here, we identify key obstacles faced in maintaining accurate and up-to-date plant records, and highlight the consequences of this information gap for global biodiversity conservation. There are many cases of botanic gardens having diverse and rare holdings, whose records remain patchy and inaccessible to the broader community.

We also showcase successful case studies and initiatives where Hortis, a cloud-based plant record-keeping platform, has been used to enhance collection management. The Hortis team at Species360 are "rethinking plant records" through contemporary software design, to reduce friction and cost for adopting efficient workflows at botanic gardens. By prioritising user-friendly interfaces, enabling accessibility, and ensuring optimal user satisfaction, we see the critical role plant records can play in the face of conservation challenges and the ever-increasing need for accurate and comprehensive data.

Leveraging collections and plant records forms a crucial foundation for research and conservation efforts aiming to safeguard global plant biodiversity. By facilitating data capture, harnessing the power of data-driven insights, and fostering collaborative data management practices, our aim is to strengthen the collective knowledge and conservation work of botanical institutions worldwide.

## P5 On the rocks: Biogeography and floristic identity of rocky ecosystems in Eastern South

Azevedo, L.<sup>1</sup>, Zappi, D.<sup>2</sup>, Oliveira, D.M.G.<sup>1</sup>, Meyer, L.<sup>1</sup>, Lughadha, E.N.<sup>3</sup>, Clegg, R.<sup>3,4</sup>, Meireles, L.D.<sup>5</sup>, Melo, P.H.A.<sup>6</sup>, Pennington, T.<sup>7</sup>, Neves, D.N.<sup>1</sup>

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The geodiversity of rocky ecosystems includes diverse plant communities with specific names, but their continental-scale floristic identity and the knowledge on the role of macroclimate remains patchy. Here we assessed the identity of plant communities across multiple types of rocky landscapes and evaluated the relative importance of climatic variables in constraining floristic differentiation. We provided lists of diagnostic species and an assessment of the conservation status of the floristic groups. We compiled a dataset of 151 sites (4,498 species) from Eastern South American rocky ecosystems, including *campos rupestres*, *campos de altitude*, granitic-gneiss lowland inselbergs and limestone outcrops. We used unsupervised clustering analysis followed by ANOSIM to assess floristic groups among sites. We performed a random forest variable selection to test whether the identified floristic groups occupy distinct climatic spaces. Six groups (lithobiomes) segregated floristically according to lithology and climate. Alongside *campos de altitude* and limestone outcrops, inselbergs were divided according to the biome in which they occur (Atlantic Forest or Caatinga) and *campos rupestres* were largely segregated according to their lithological matrix (ironstone or quartzitic). Plant communities of Caatinga inselbergs were more like those of limestone outcrops, while Atlantic Forest inselbergs communities resembled *campos de altitude*. The composition of plant communities on outcrops seems to be largely constrained by lithology, but climatic factors are also meaningful for sites with similar lithology. The current network of protected areas does not cover these unique ecosystems and their floristic heterogeneity, with protection least adequate for Caatinga inselbergs, ironstone *campos rupestres* and limestone outcrops.



## **P6 Fungal conservation: Resolving gaps in the distribution of grassland fungi – where are they?**

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The grassland fungi (CHEGD) assemblage represents a functional group of soil saprotrophs dependent on long-established and undisturbed grassland. The UK is of international importance for its grassland fungi assemblages hosting 23 globally threatened taxa. These grasslands face an existential threat from changes in land-use and management.

Important grassland fungi sites can be difficult to identify and do not correspond to botanically rich sites. Many are found in the undisturbed, botanically poor, sheep grazed grasslands of the uplands and upland fringe. This makes them especially vulnerable to government-led tree-planting schemes which target such unproductive farmland. Woodland creation policy aims to avoid conflict between afforestation and other features of nature conservation value, but this is dependent on high quality data tools to inform decisions. Biological records are useful, but there are significant gaps in their distribution, suggesting that a high proportion of grassland fungi sites are unrecorded.

To address this problem, we used an individual species distribution model to create a grassland fungi predictive map for the UK. Using over 65,000 grassland fungi records from England, Scotland, and Wales, models were constructed for high priority CHEGD species. The records were assessed for recorder bias, and combined with environmental variables, to create a predictive map of the UK, highlighting locations with a high probability of supporting nationally important grassland fungi communities. On the ground validation of this model using eDNA and fruitbody surveys is planned for autumn 2023.

## **P7 Research at Oxford Botanic Garden and Arboretum**

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At Oxford Botanic Garden and Arboretum (OBGA) we run a multi-disciplinary research portfolio focused on evolution and adaptation, biomimetics and conservation. We are developing the world's most extensive parasitic plant collection for conservation and research. Linked to this work, with colleagues at the University of the Philippines, we recently carried out the country's first attempt at *ex-situ* propagation and conservation of *Rafflesia* – the genus containing the world's largest flowers; further work is examining the potential of 'desert hyacinths' (*Cistanche*) as a climate-resilient crop in China and the Middle East.

We are exploring the biomimetic potential of plants together with physicists and mathematicians, for example, the application of technological advances inspired by carnivorous plant surfaces, and offshore solar platform design inspired by giant Amazonian waterlilies. We are also exploring fundamental processes in plant reproduction and evolution using genetics and genomics in collaboration with scientists in Oxford, Napoli and Bristol; this research is exploring the adaptation of *Senecio* (ragworts) to different altitudes on their native Mount Etna.

Finally, in our commitment to global plant conservation, we are working with local partners across Southeast Asia, Ethiopia, and Japan, and identifying new approaches to engaging audiences worldwide with the scientific wonder of plants.

## **P8 Bringing plants to the table: Building a subsample of plants that represents global diversity patterns**

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Almost 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 increased at similar rates. As our understanding of plant biodiversity remains incomplete, all global studies of plant diversity patterns are based upon subset of species. Digitally available plant data suffers, however, from strong biases which severely distort our view of global diversity patterns. Our study aims to find alternatives to better estimate plant diversity patterns from incomplete data by determining the number of species needed to accurately represent different aspects of plant diversity at a global scale including species, phylogenetic, floristic, and functional diversity. The results have important implications for macroecology and conservation.

## **P9 Three in four undescribed plant species are threatened with extinction**

Brown, M.J.M., Bachman, S.P., Nic Lughadha, E.

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Many thousands of plant species remain unknown to science, most being range-restricted and/or rare – both factors that increase extinction risk. Here, we show that more than 75% of species described after 2020 would qualify as threatened if assessed for the IUCN Red List. We recommend that newly described species are assumed to be threatened and encourage taxonomists to partner with assessors at the time of description to formally evaluate the extinction risk of new species using the IUCN Red List Categories and Criteria.

## **P10 Sonoran Desert *ex-situ* conservation gap analysis: Charting the path toward conservation**

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Plant biodiversity is under threat. With two out of five plants at risk of extinction preserving taxa through *ex-situ* conservation approaches must be considered a priority. The Sonoran Desert, a highly biodiverse ecoregion spanning across Mexico and the USA, is home to at least 4,000 native taxa. In collaboration with institutions from both countries, we developed a method to determine conservation priorities. To do so, we analysed herbaria records and data from nine seed banks to identify gaps in previous conservation efforts. This study prioritises taxa based on a Final Priority Score (FPS) and models their potential distribution to identify priority hotspots. 4,029 native taxa were reported. 1,441 of them have accessions in seed banks, but only 412 have been collected inside the SD. The FPS considers potentially endemic (126) and threatened taxa (50 according to the IUCN criteria) as the most urgent to preserve. It also includes information about the storage behaviour (3,236 orthodox), useful plants (1,406), and taxa without populations in protected areas (230) to categorise the species. Although most of the SD flora is not represented in seed banks, at least 80% is predicted to produce desiccation-tolerant seeds and thus can be cost-effectively stored in seed banks. Spatial analysis shows that the central region of the Baja California peninsula stands out for its species richness and endemism. Our study presents the first *ex-situ* conservation gap analysis from the SD flora and provides a replicable methodology for identifying priority species and potential areas for *ex-situ* collection.

## **P11 Fungus-mediated plant-pollinator mutualism in *Monoon laui* (Annonaceae)**

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Floral nectar has recently been regarded as a source of new fungal species because the nectar is sugary and exposed to the air and floral visitors. Metabarcoding techniques can largely advance our knowledge on the fungal communities in the floral nectar. Here we provide evidence for a fungus-mediated plant-pollinator mutualism in a beetle-pollinated early divergent angiosperm, *Monoon laui* (Annonaceae), which has flowers that produce exudate on both the stigmas and petals. Fungi were found to develop on the site of the petal exudate and were subsequently consumed by insect larvae. Insect identification shows that the larval species are generally conspecific with the pollinators, and the fungal community comparison exhibits partial coincidence of taxonomic identities between the fungi on the bodies of pollinators and petals, which collectively indicate that the pollinators disperse fungi whilst ovipositing on the petals. The nutritional value of the two exudates reveal that the stigmatic exudate is sugar-rich, whereas the petal exudate has a greater amino acid content. Transcriptomic and proteomic comparisons between the two organs and their exudates corroborate the nutritional profiles, with a stronger immune response on stigmas. Petals with their exudate in *Monoon laui* are likely to be closely adapted to the requirements of the pollinators by providing them with brood sites and larval food (fungal hyphae), as well as assisting with maintaining their functional population size throughout the flowering season, which in turn presumably promotes pollination success.

## **P12 Adaptive genomics and phylogeography of *Guazuma ulmifolia* (Malvaceae)**

Contreras-Ortiz, N.<sup>1,2</sup>, Kidner, C.<sup>1,2</sup>, Hudson, A.<sup>1</sup>, Pennington, T.<sup>1,3</sup>, Hart, M.<sup>1</sup>, Richardson, J.<sup>4</sup>

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*Guazuma* is a genus in the Malvaceae family that also includes the cacao genus, *Theobroma*. *Guazuma ulmifolia* is a species that is widespread both geographically and ecologically in tropical America, found from Mexico to the Caribbean and right through South America, in both dry (savanna and dry forest) and wet (rain forest) biomes. This geographical and ecological amplitude is unusual and makes *G. ulmifolia* an interesting case study in both biogeography and the evolution of drought tolerance. In order to investigate both the phylogeography and nature of drought tolerance in *G. ulmifolia*, a transcriptomics approach was used to generate a coding sequence collection, using tissues from plants exposed to different drought treatments in a glasshouse experiment. The transcriptome was used to identify candidate genes that may be involved in drought response, as well as other genes useful for phylogenetic reconstruction that are likely to be selectively neutral. This information was used to identify a panel of target loci that could be used in a hybrid capture experiment to capture target sequences in 55 accessions covering the geographic and ecological range of *G. ulmifolia*. Phylogenetic trees were generated from the resulting DNA sequence data using concatenated (maximum likelihood) and multi-species coalescent (ASTRAL) approaches. The combined dataset was used to examine patterns of phylogeography within *G. ulmifolia*, which revealed that the species has achieved its wide range by multiple long distance dispersal events across the Americas (for example, two colonisations of the Antilles), and multiple shifts between wet and dry ecologies.

## **P13 Reintroduction of rare and endangered wood-decay fungi through inoculation and translocation**

Crosier, B. J.<sup>1,2</sup>, Penttilä, R.<sup>1</sup>, Miettinen, O.<sup>2</sup>, Hamberg, L.<sup>2</sup>

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In Nordic countries, wood-inhabiting fungi are one of the most threatened species groups, and some are in danger to vanish from southern Finland and Sweden. Since the traditional methods (protection of forest areas and leaving dead wood in managed forests) do not seem to work alone, complementary methods are needed to preserve these species. Inoculation and translocation of fungi is still rare, but an interesting method to include in the conservation toolbox, especially in areas where other methods do not seem to be efficient enough.

In this project, seven species of wood-inhabiting threatened fungi will be investigated: *Amylocystis lapponica* and *Sceletocytis stellae* (spruce), *Antrodia crassa* and *A. infirma* (pine), *Perenniporia tenuis* and *Radulodon erikssonii* (aspen), and *Haploporus odoratus* (willow). We have collected 2-5 strains of each species, and cultivated them in the laboratory, while investigating optimal growing conditions (substrate, temperature). Further, we produced two different types of spawn: dowels and sawdust. The spawn was used to inoculate 1 meter log sections of both the host wood and birch wood. These logs will be translocated to protected forest sites in Finland and Sweden for further observation of colonization and fruiting bodies.

We have investigated previously inoculated pine logs and found that the mycelia of the inoculated threatened species have been able to spread to varying degrees of success. Now we will be able to monitor the success of our novel reintroduction methods and the influence of environmental factors, spawn type, and host wood-type, to determine the most effective methods of reintroduction.



## **P14 High proportion of Data Deficient taxa hinders conservation of potential fungal EDGE species**

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Fungi are severely underrepresented on the IUCN Red List of Threatened Species, with only 625 assessments of fungal species published so far. This dataset is biased, not least because priority was given to species suspected to be at risk of extinction. Thus, the current fungal assessments include a high proportion of threatened species, a proportion which should not be considered as representative of the global state of fungal biodiversity.

Here we present an initiative to help mitigate this bias, through the analysis of the assessments of 95 fungal species in monotypic families and genera, 87 assessed in this study. Through our focus on monotypic taxa, species from different geographical regions, taxonomic groups, ecological guilds and likely categories of threat were covered. The results will inform a future list of fungal species which are Evolutionarily Distinct and Globally Endangered (EDGE), species whose extinction would represent a significant loss of evolutionary history and potential.

Results show a significant prevalence of Data Deficient species, followed by Least Concern species and a small proportion of species in threatened categories – smaller than among the 625 assessments published so far. We discuss factors underlying the high proportion of Data Deficient evaluations and differences in category prevalence between global regions and ecological guilds. Challenges in fungal Red Listing will be highlighted, along with knowledge gaps that must be addressed through basic mycological and taxonomic research, especially when taking phylogenetic diversity into consideration for the establishment of conservation priorities.

## **P15 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.

## **P16 Hidden treasures: Mobilising the type collections of the Cambridge University Herbarium**

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Herbarium collections are a crucial resource for biodiversity and conservation research, as they represent an immense repository of plant material and associated data, collected over centuries. The Cambridge University Herbarium (CGE) contains approximately 1.1 million specimens, collected worldwide and dating back to the early 1700s. It is rich in historical and unique collections of plants and fungi, such as those of John Henslow (including a collection of plant disease specimens), Charles Darwin, Alfred Russel Wallace, Charles Morgan Lemann, John Lindley, John and Maria Gray, and Richard Spruce. The specimens have not yet been catalogued and only a minute fraction has been digitised (148 images on JSTOR Global Plants). At present, the CGE collections are therefore difficult to access and remain poorly known and under-used by the scientific community.

It is now crucial to mobilise the untapped taxonomic and distribution data held at CGE. Our current priority is to digitise the estimated 50,000 type specimens, of which approximately 12,000 (mostly vascular plants) have already been identified. Identifying type specimens within an uncatalogued collection is not a straightforward process, and the best approach depends on the taxonomic group and the origin of the collections of interest. In this project, I am developing a protocol to accurately identify, digitise, then upload the types to online platforms. The initial focus is on collections that are unique to CGE, spanning all taxonomic groups in the collection (algae, bryophytes, vascular plants and fungi), but collaborations and enquiries relating to specific groups or collectors are also welcome.

## P17 Angiosperms on the EDGE of existence

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With biodiversity in rapid decline, and limited resources available for conservation action, the question of which species and regions should be prioritised for conservation is both critical and urgent. Global scale analyses of biodiversity distribution and conservation prioritisation have so far generally neglected to account for plants, the structural and ecological foundation of virtually all terrestrial ecosystems. With recent estimates showing that almost two in five (39%) of the 343,000 species of vascular plants are threatened with extinction, determining which plant species are at risk and which threats they face is central to protecting not only these species, but entire ecosystems. Here, we use the Evolutionarily Distinct and Globally Endangered (EDGE) approach, a method that has not been widely used in plants, largely because few plant groups have the prerequisite data, i.e. both extinction risk assessments for all species and a densely sampled phylogeny. We implement the recently published EDGE2 protocol that include methods to account for uncertainty and the extinction risk of closely related species. We use available phylogenetic data and species imputation methods to produce a species-level tree for all angiosperms, which we combine with existing conservation assessment and machine learning extinction risk predictions to produce a first EDGE list for flowering plants. The EDGE Angiosperm Prioritisation List will facilitate the integration of flowering plants into global biodiversity analyses on an equal footing with tetrapods, thus addressing an imbalance which has undermined conservation actions for decades.

## **P18 Genetic diversity and pathogenicity of rice sheath rot disease-associated fungi in Fogera plain, Ethiopia**

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Sheath rot is a major worldwide rice disease, particularly in Ethiopia's Fogera plains, with the highest incidence and severity. Even though there have been few studies on pathogenic fungus identification, molecular-level identification of rice fungal pathogens has yet to be done in Ethiopia. This study aimed to assess the diversity of sheath rot disease-causing fungal species on rice crops grown around Fogera plains and evaluate the pathogenicity of isolates.

Samples of infected sheaths were collected from the farmlands and Fogera Rice research center, Gondar, Ethiopia. Fungal isolation was made using Potato Dextrose Agar. Identification was done by morphological appearance. Additionally, molecular identification was done using an internal transcribed spacer (ITS) of ribosomal DNA (rDNA).

A total of 16 isolates were recovered from the disease plant samples. The predominantly identified genus was *Phoma* (75%) followed by *Epicoccum* (18.75%). The pathogenicity test revealed the presence of significant difference in the mean lesion length ( $P < 0.001$ ) and percent disease severity ( $P < 0.01$ ) between isolates on rice cultivars. The result suggested that *Phoma* was the predominant isolate. The pathogenicity caused by *E. sorghinum* was very severe: producing 167 mm mean lesion length, and 55.7 % disease severity, suggesting that it is the region's most important rice pathogen.

This is the first report of ShR-causing fungi identified in rice using ITS rDNA molecular techniques in Ethiopia. Thus, this research will lay the foundation for developing management strategies for fungal diseases of rice and provide evidence to initiate a rice breeding program on ShR-resistant rice varieties.

## **P19 Digitisation of Kew Herbarium: Developing and creating new workflows for new acquisitions**

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Kew Herbarium is amid a four-year project to digitise the entire collection and is also striving for museum accreditation. Each year Kew Herbarium receives around 15-20,000 new acquisitions, which includes not only, newly collected Kew material, but also loaned material from other institutions, gifts and donations. To ensure we maintain the collections as digitised, and to meet the criteria essential for accreditation, it is essential that workflows are developed to capture our new material being processed prior to incorporation into our collections. To this end, the New Acquisitions team have reviewed historic, unstandardised workflows and have developed, trialled, and implemented agreed Collection Operation Procedures in collaboration with relevant stakeholders to manage and digitise our new acquisitions, Millenium Seed Bank and DNA voucher specimens. Our next steps focus on the adoption and incorporation of digital data records captured from the field for incoming specimens to create streamlined, effective workflows which utilize our new Integrated Collections Management System.



## **P20 Role of microhabitats in *ex situ* conservation in the National Botanic Garden Vácrátót**

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National Botanic Garden Vácrátót (NBG) is a nearly 200-year-old romantic landscape garden. Collections represent 13,000 plant taxa on 27 hectares. Sub-spontaneous mosaic-like structure of the garden provides opportunity for a wide range of plants to grow in different microhabitats. Western part of NBG is covered with coarse alkaline sand, many endemic species of the Pannonian Biogeographic Region are living here. A clayish slope leans to the stream valley, providing a natural habitat for certain orchid species. In lowest parts, remains of an oak-ash-elm gallery forest gives habitat for several geophytes on alluvial soil.

In the end of the 19th century, large-scale landscape transformation was realized in the Garden. Thousands of rocks were transported here creating different unique rocky sights in addition suitable microhabitats for further plant taxa. Both natural stream crossing the garden and artificial ponds have significant impacts on microclimate, too.

Numerous native taxa of the Hungarian flora are grown and propagated in the NBG, due to its diverse microhabitats. Relatively high number, 124 protected and 7 strictly protected taxa are living *ex situ* in the garden currently, several populations consist of a high number of individuals. Some spontaneously appearing species complete this list, 13 protected and 1 strictly protected taxa have been found so far. Furthermore, three protected mushrooms and a moss species have been listed from NBG. Categorization and recognition further details of microhabitat types in NBG promotes enriching our *ex-situ* collection and activities on protected and endangered plant taxa of the Hungarian flora.

## **P21 Private gardens – an overlooked resource in plant conservation**

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The paper intends to discuss the possibilities of involving garden owners and users in the work of preserving plants. Most often, nature and plant conservation are discussed in a context of public regulation and initiative, while the enormous geographical area that private gardens constitute, is often overlooked. We want to discuss greater involvement of private gardens in the work of conserving species and ecosystems. At the same time, we also want to investigate whether the involvement of gardeners in this work creates an increased awareness of general climate change and the loss of biodiversity among the participants.

We have carried out a pilot project in North Zealand in Denmark regarding the preservation of old local varieties of vegetables outside of commercial trade, where the focus has been on stimulating the participants to grow these varieties. Partly to investigate whether private gardens can be used as a modular based gene bank. Partly to motivate the cultivation and use of these vegetables, which have documented health effects that are not found in similar commercial varieties.

We will report on preliminary results and experiences with scientific dissemination to gardeners, implementation of the project and the scientific quality of the gardeners' conservation work.

Finally, we want to discuss a model for an overall modular seed and plant conservation system, which is based on a citizen science model that includes training, supervision, and material support for the participants.

The project is a cooperation between RDHS, Seed Collectors Denmark and University of Aarhus and Copenhagen.

## **P22 From spatial conservation prioritisation to conservation action: Lessons from Important Plant Areas around the world**

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Area-based approaches have long dominated biodiversity conservation, reinforced by the recent Kunming-Montreal Global Biodiversity Framework. The Important Plant Area (IPA) approach is the leading global framework for spatial conservation prioritisation of plants and fungi, having been applied in over 50 countries. However, a comprehensive review of approaches and experiences is yet to be undertaken. Through a systematic literature review and semi-structured interviews, we undertook a global evaluation of IPAs to ask: 1. Where and how has the IPA framework been applied? 2. To what extent has identification led to plant conservation outcomes? and 3. How are IPAs perceived by plant conservation practitioners and researchers globally? Over 130 IPA-related sources were reviewed, spanning scientific publications, reports, websites, and databases. Meanwhile, interviews were conducted with 40 participants with direct experience of IPAs. While the vast majority of publications focused on the development of IPA guidance or the application of identification criteria, 62% of respondents were aware of IPAs which have been incorporated into conservation designations or other conservation processes in country. Despite global guidelines recommending a bottom-up approach, opinions were split on the effectiveness of IPAs in incorporating local ecological knowledge or engaging with stakeholders beyond botany. We will present key results, focusing on lessons learnt on how scientifically driven IPA identification can most effectively lead to conservation action at political and local levels. This is timely as application of IPAs continues to grow and new national programmes are launched in some of the most biodiverse tropical countries in the world.

## P23 The state of Endangered and Critically Endangered wild pear species of Central Asia

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There are three wild pears species in Central Asia classified as endangered on the IUCN Red List. Specifically, *Pyrus cajan* is listed as Endangered; both *Pyrus tadshikistanica* and *Pyrus korshinskyi* are Critically Endangered. *P. cajan* and *P. tadshikistanica* are endemic to Tajikistan, while *Pyrus korshinskyi* is distributed more widely in Kyrgyzstan, Uzbekistan, and Tajikistan. Unfortunately, these wild pears populations are declining due to multiple threats such as habitat destruction, overexploitation, hybridization, livestock grazing, pests, and diseases.

Fauna & Flora, along with its partners, have been involved in mapping wild pear trees in the region in Kyrgyzstan and Tajikistan since 2007. *P. cajan* is believed to have only two small sub-populations remaining and F&F is working with local partners to protect and restore its populations. A total of 69 wild *P. tadshikistanica* trees have been identified in three Tajik protected areas. Approximately 250 wild *P. korshinskyi* trees are known in Tajikistan. Our crucial conservation actions on these species in the nut-and-fruit forests of Tajikistan have included providing training and equipment to forest unit staff and supporting alternative livelihoods.

In Kyrgyzstan, a significant population of 489 wild *P. korshinskyi* trees have been fenced to prevent losses due to grazing. Additionally, more than 4000 saplings have been transplanted into a fenced plot in the forests of Kyrgyzstan to augment the existing populations. Alongside our partners, we are also tackling the threat of the disease fire blight in wild forests, developing an application for monitoring its spread and building local capacity for detection.



## **P24 A perspective of the future of SE Asian sedges: Opportunities in an almost unexplored field**

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Sedges (Cyperaceae) are the third most biodiverse monocot family and among the top ten in angiosperms. They are a cosmopolitan family, with high diversity in the tropics, that display a major ecological shift into temperate preferences in the genus *Carex*. The family has considerable importance in economic (strong fibres, human and cattle food source) and ecological terms (dominant vegetation elements, especially in humid or cold high latitude/altitude habitats; fast growing plants after habitat disturbance such as soil disruption or wildfires). Despite sedges' importance in tropical environments, there is still a huge gap of knowledge in Southeast Asia (SEA) and, consequently, in the conservation and genomic goals proposed during the COP15 meeting. This can be well exemplified by the recent phylogenomic classification of the family considering the newly described tribes Sumatrosirpeae and Khaosokieae that are endemic to this region. Therefore, SEA is not only among the most morphologically diverse areas for sedges, but also phylogenetically diverse. Recent studies have further revealed how little it is known about taxa inhabiting SEA countries, by low species sampling in phylogenies (e.g., ca. 1% species in *Carex* megaphylogeny), fragmentary knowledge about one of the largest diversifications (*Carex* sect. *Indicae*), or by uncertainty in the taxonomic placement based on morphology alone.

We propose the first Southeast Asian sedge project, aiming to generate taxonomic, geographical, morphological, molecular, genomic, biochemical, and ecological data to increase knowledge of the biodiversity in tropical Southeast Asia, accompanied by photographic records of taxa and sets of data that will be publicly available.

## **P25 Tropical Important Plant Areas in the heart of South America: Assessing extinction risk of the endemic and rare plants in the Chiquitano dry forests and the dry Andean valleys of Bolivia**

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In Bolivia, the Tropical Important Plant Areas (TIPA) program has identified sites in the two species-rich ecoregions Chiquitano Dry Forest (BSC) and Inter-Andean Dry Valleys (VSI). gIUCN extinction risk assessments of endemic and rare species we completed, by selecting families representing species richness and level of endemism. A georeferenced occurrence database was compiled harvesting the Global Biodiversity Information Facility. This was subsequently cleaned and supplemented with occurrences from Bolivian herbaria and RBG Kew. In total, 160 BSC species and 159 VSI species met IUCN criteria for evaluation. Of the 160 BSC species, 63% are threatened with extinction (9% CR, 28% EN, 26% VU) and 14% data deficient (DD). In the VSI ecoregion, 60% of 159 species are threatened with extinction (11% CR, 29% EN, 20% VU) and 8% DD. The high percentage of DD owes to lacking data, as these species are known only from their type locality. Gap-filling field work was undertaken across the ecoregions, recording species occurrences and new species. So far, we published two new species *Astronium woodii* and *Handroanthus abayoy*, while more are in press/prep. The main threats for the BSC are rapid expansion of industrial-scale agriculture and cattle farming, while in the VSI threats are smallholder agriculture and livestock farming, and firewood collection. TIPAs designation has increased the number of extinction risk assessments for these ecoregions, improving the state of knowledge and highlighting the need for protecting the endemic plants in these two ecoregions. In turn, this is guiding identification of important areas for plant conservation.

## **P26 Using roundabouts to investigate drivers of plant and microbial community assemblage in urban spaces**

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Increased urbanisation is common across the globe. With urbanisation comes opportunity to create local habitats, though the biodiversity of such synanthropic habitats is little studied. Understanding the biodiversity potential of urban green spaces would allow for its incorporation into urban planning. We chose to investigate the potential of a common and undervalued urban space; roundabouts. These locations make for novel and interesting study sites, having a degree of isolation and human activity. As maintained environments, they undergo seasonal disturbance whilst also being left to develop for large periods of time. By considering environmental data such as soil pollutant levels with plant biodiversity information we can investigate what contributes towards healthy, diverse urban spaces.

We used six roundabouts of varying size in Skelmersdale (Northwest Lancashire) and recorded soil health, vegetation, and microbial community data to allow for a multileveled investigation into understanding levels of biodiversity in urban environments. Investigating how different plant groups (forbs/graminoids etc) communities are shaped will allow for a plant forward approach to planning, creating more healthy, diverse and functional greenspaces.

By taking a plant and microbial approach to diversity data we are also able to uncover how often underappreciated organisms such as fungi are impacted by human activity. It is this microbial data that allows us to take steps to better design urban spaces for invisible biodiversity, thus supporting global cycles and soil health.

## **P27 ParseGBIF: A tool for parsing species occurrence records into unique collections events**

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Global plans to halt biodiversity loss include the High Ambition Coalition 30x30 initiative, a commitment to conserve 30% of the terrestrial environment by 2030, and the Global Biodiversity Framework (GBF) of the Convention on Biological Diversity (CBD). Both require adequate knowledge of species and their occurrences in order to be effective. Currently, occurrence data takes the form of verifiable biological collections, plot inventories and field observations which are then digitised to make them accessible. Such knowledge is, however, lacking for most of the world's biodiversity hotspots, with much of the tropics being characterised by low numbers of observations and very biased sampling. The parseGBIF R package is designed to repackage Global Biodiversity Information Facility - GBIF species occurrence records into a more useful form for use in further analyses, spatial, or taxonomic. The parseGBIF package aims to do so by providing tools to verify and standardize species scientific names according to the World Checklist of Vascular Plants taxonomic backbone, and to parse duplicate records into unique 'collection events' or 'gatherings', in the process compiling the most informative associated taxonomic and spatial data (where more than one duplicate is available) and providing crude estimates of taxonomic and spatial data quality.

## **P28 How leaf traits impact decomposition and our understanding of the fossil record**

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Opposite to the animal kingdom, unambiguous evidence for plant mass extinction in the geologic history is lacking. This could be due to a higher resilience of plants towards rapid environmental changes or due to substantial bias in the fossil record.

To enter the fossil record, leaves must extend, or ideally avoid, decomposition since the likelihood of fast-decomposing leaves being preserved is much less than for slow-decomposing leaves. Decomposition is a highly complex process influenced by a variety of factors, including climate, decomposition community and litter quality. The latter describes the physical and chemical properties of a leaf such as leaf mass per area (LMA), %lignin and other leaf traits. Therefore, specific combinations of leaf traits may have direct impact on the plants represented in the fossil record.

A leaf litter decomposition experiment of native Irish plants in three native, undisturbed environments is in progress to test this hypothesis and identify the leaf trait combinations that have the biggest impact on decomposition. We aim to understand if leaves with these specific combinations belong to plants that share a similar ecology and/or phylogeny. This will increase our knowledge about how a suite of leaf traits influence the possibility of a plant being preserved in the fossil record. Furthermore, it will shed light on how plants respond to major events such as mass extinctions (in the geologic past) and ongoing global change.

## **P29 Fungal communities in water repellent soils in a southern Alpine valley**

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Soil water repellency (SWR) occurs when hydrophobic organic compounds accumulate at the soil surface, especially after long drought periods, an increasing phenomenon with climate change. SWR can often be detrimental, increasing surface runoff, soil erosion and land degradation, thus endangering Alpine soil landscapes, which are already exposed to extreme climatic and topographic conditions. The role and biodiversity of microorganisms, and especially of fungi, in this situation is still mostly unexplored. The aim of this work was to characterize the soil fungal communities in a sloping meadow (SM) and a forested slope (FS) both strongly acidic and with severe SWR in a Canton Ticino valley (Switzerland), sequencing the ITS1 fragment of the 18S ribosomal DNA with Illumina MiSeq System. The metabarcoding analysis detected a restricted soil fungal community in the two sites, composed only by 203 fungal taxa. In both sites, a strong presence of the saprophytic genus *Acremonium* was observed, but, in general, the composition of the two fungal communities was significantly different. In SM soils, the most abundant phylum was by far Mortierellomycota, followed by Basidiomycota and Ascomycota. On the other hand, in FS, the phyla Ascomycota and Basidiomycota were the most abundant ones, followed by Mucoromycota. The community in this site was dominated by ectomycorrhizal basidiomycetes, such as the genera *Lactifluus* and *Hydnum*. The description of these restricted fungal communities in Alpine water repellent soils is the first step towards future investigations on the role of fungi in SWR and on the best management of these sites.



### **P30 Variation in tuberisation and seed yield in African yam bean (*Sphenostylis stenocarpa* (Hochst. ex A. Rich.)**

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African Yam Bean (*Sphenostylis stenocarpa* (Hochst. ex A. Rich.) (AYB) is a legume that provides nutritional-rich seeds and tubers for human consumption. It is an underutilized crop, partly due to a paucity of investment in research on the crop and a lack of availability of improved varieties. African Yam Bean tubers are rich in protein content, ranging from 19% to 30% and higher than what is obtainable in many other legumes, including common beans and chickpeas, which contribute to the energy and nutrition requirements of more than two billion people. AYB is cultivated in West and Central Africa especially Nigeria, Ghana, and some countries of equatorial Africa. Its climate-resilient and nutritional properties give it the potential to play a very significant role in the cropping systems of sub-Saharan Africa. However, there is a lack of understanding of the cause of variation in tuberization among accessions and different environments. The main objectives of this research were to evaluate tuberization and seed yield and the factors that affect tuberization in AYB.

Twenty accessions of AYB from the Genetic Resources Centre, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria were selected for the study. From an initial study, field data were collected on the number of pods per peduncle and tuber-related traits using the AYB descriptor list. Tuberization was observed in ten accessions with considerable variation in tuber weight and size among accessions. Further experiments will explore factors that influence tuber production and the effects of interaction between genotype and environment (GxE).

### **P31 Preservation biases in the fossil record can be linked to modern plant extinction risk through leaf traits**

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It is widely believed that a sixth mass extinction event is imminent; however, this may be the first time that plants, particularly angiosperms, will experience a mass extinction event, making the current elevated extinction rates in the plant kingdom particularly concerning. It is thought that plants do not experience mass extinction on the same scale as animals, due to the lack of evidence across previous mass extinction boundaries. However, plant groups at greatest risk of extinction may not be preserved in the fossil record, thereby biasing our view of plant extinction. By improving our understanding of plant preservation in the fossil record and of how leaf traits may be associated with preservation potential and extinction risk, we can ascertain whether we are witnessing the beginning of a unique mass extinction in the plant kingdom. This outcome can be achieved by combining three lines of research: (1) the correlation between leaf traits and extinction risk in modern floras; (2) the preservation potential of leaf traits in the fossil record; and (3) a comparison of leaf traits seen in modern floras with those preserved in the fossil record. If specific leaf traits associated with the extinction risk of modern floras were also associated with extinction in the fossil record, then the preservability of those leaf traits in the fossil record consequently influences our view of the response of plants to previous mass extinctions.

### **P32 EDGE Zones: Spatial priorities for the conservation of plant and animal evolutionary history**

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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, areas where the greatest losses are predicted to occur must be identified. Typically, prioritisation studies have reported on vertebrate diversity but here we contrast global priorities for vertebrate and plant groups. For both clades, we reveal distributions in threatened evolutionary history along with patterns of Evolutionarily Distinct and Globally Endangered (EDGE) species. We then identify a series of spatial priorities of evolutionary history, termed EDGE Zones, and quantified the protection levels and human disturbance within each. We believe these EDGE Zones can highlight areas of utmost concern to the researchers and practitioners looking to safeguard the Tree of Life.

### **P33 Use of mycorrhiza to improve restoration success in tropical forest, Southeastern Madagascar**

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Classified as one of the thirty priority sites for Primates conservation, Kianjavato in Southeastern Madagascar is a key area for lemur conservation which is a part of the corridor Fandriana-Vondrozo. Due to slash and burn agriculture, the biodiversity richness is decreasing. For conserving the remaining forests and for connecting all forest fragments, reforestation and restoration efforts were launched to conserve this area since 2012.

To improve tree survivals, mycorrhiza was used to inoculate the seedlings. Height, basal diameter, crown diameter, number of leaves and number of branches for all seedlings were monthly measured and noted. All seedlings were classified by ages groups as: 1, 3, 6 and 12 months. Five target species, *Uapaca thouarsii*, *Uapaca ferruginea*, *Canarium planifolium*, *Noronhia introversa* and *Cryptocarya ovalifolia*, the most used species by lemurs were selected. We aimed to assess the effect of inoculation of native mycorrhiza on the five target species.

Results showed that inoculated seedlings had high survival rates ( $p < .0001$ ) compared to the control ( $n = 10,000$ ). Inoculation strengthened seedlings in their growth in height and diameter. To increase survival rate, the inoculations should be done when the seedlings are 1 month for *Uapaca ferruginea*, *Noronhia introversa*, *Cryptocarya ovalifolia*; 6 months for *Uapaca thouarsii* and 6 to 12 months and *Canarium planifolium*. Through the effects of inoculation on seedlings growth and survival, we identified that the use of mycorrhiza is beneficial for restoration and for the sustainability of the ecosystem. It will make the seedlings more resilient to variations of soils types.

### P34 Phylogeny, diversification, historical biogeography and conservation of Madagascar orchids

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Madagascar is a hotspot with c. 1,000 orchid species, of which 85% are endemic.

The Orchidaceae of Madagascar therefore represents an exciting model for studying topics such as phylogeny and phylogenetic uniqueness, diversification, and historical biogeography. Some of these topics remain poorly explored. Our study will use the Angiosperms353 target capture probe set to reconstruct the most comprehensive phylogenetic framework of Madagascan orchids at generic level. We will also target the *Calanthe* alliance (Orchidaceae, Epidendroideae, Collabieae), to clarify the phylogenetic relationships in and between the allied genera, viz. *Calanthe*, *Cephalantheropsis*, *Gastrorchis* and *Phaius* in Madagascar and Asia.

Extensive fieldwork in Madagascar, combined with samples from the Kew Herbarium, the Kew DNA Bank and Kew's Living Collection has resulted in a robust sampling set, which covers 50 genera and 173 species of Madagascar orchids and 9 genera and 56 species of Asia orchids. Our sampling includes 69 accessions of the *Calanthe* alliance. Molecular lab work is on-going to generate target capture data for the comparative phylogenetic studies.

Our results will elucidate the phylogenetic relationships, diversification patterns, and historical biogeography of the orchids of Madagascar. A better understanding of their diversity and evolution will support conservation efforts. Only 229 species are currently listed in the IUCN Red List; Preliminary data suggests that more than 70% of the orchid species native to Madagascar are threatened with extinction. Around 47% of Madagascan orchids are listed as traded in the CITES database.

### **P35 Diversity and evolution of Cyperaceae in Madagascar with focus on *Bulbostylis***

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Identified as the third largest monocot family in the world, the Cyperaceae family represent one of the most species-rich plant families in Madagascar with around 310 native species placed into 24 genera including one monotypic endemic genus *Trichoschoenus*.

Our research focusses on the genus *Bulbostylis* or hairsedges to investigate the link between sedge diversity and endemism and ecosystems in the Central Highland of Madagascar because it represents the only large endemic radiation of a sedge group using the C4 photosynthetic pathway linked with a preference for open canopy habitats. The results of our study may provide further evidence, independent from data on the Poaceae or grass family to reply to the broader question whether the grasslands of the Central Highlands of Madagascar are natural or man-made. It will also provide baseline data for species- and area-based conservation management.

To resolve relationships between the Madagascan *Bulbostylis* species, DNA sequence data from 96-192 accessions sampled during fieldwork in Madagascar and in herbaria will be generated using the Angiosperms353 targeted sequencing probes. Our results will be used to complete a taxonomic treatment of the genus *Bulbostylis* which will include an identification key, descriptions, illustrations, distributions maps and IUCN Red List assessments for each species.

Since 2019, our efforts to study the Cyperaceae in Madagascar have already resulted in the publication of a new species to science, i.e. *Bulbostylis itremoensis*. Additionally, an updated version of the Flora of Cyperaceae from Madagascar at generic level was published in English and French versions to aid identification.

### **P36 Ecological and evolutionary constraints on floral chemical defences in wild tomato**

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The shift from outcrossing to self-fertilisation is one of the most common evolutionary transitions and leads to phenotypic and genetic changes that influence plant ecological interactions. Selfing plants often have a smaller floral display than outcrossing plants, as selfing provides reproductive assurance in the absence of pollinator attraction. Additionally, there is evidence that selfing plants show greater plasticity in their damage response than outcrossing plants. We hypothesised that defence traits in selfing plants would be less constrained by pollinator attraction, and that this effect would be stronger in flowers than in leaves. This hypothesis was tested using selfing and outcrossing species of wild tomato. We investigated the influence of mating system on plant constitutive and induced defence following methyl jasmonate application to the plants. Chemical analysis of the tissues revealed differential expression of defence in leaves and flowers and showed that selfing flowers are better defended than outcrossing flowers. Feeding bioassays using the herbivore *Manduca sexta* showed a similar pattern, with flowers producing stronger constitutive defences than leaves. Leaves show greater overall plasticity in their damage response than flowers, indicating the pollinator constraint on induced defence acts more strongly in the flowers. This study is one of a relatively small number of studies that consider the multi-level interactions of plants, pollinators and herbivores from the perspective of plant mating systems, and the results of the study indicate the importance of studying the evolution of plant traits within the constraints of multiple trophic level interactions.

### **P37 Community engagement to promote *in situ* conservation of threatened trees**

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Fauna & Flora has extensive experience with the conservation and management of threatened tree species and their habitats, having taken action for almost 200 species in 24 countries. Our context-specific approach engages communities and local stakeholders as the long-term guardians of the land, building local capacity to continue management independently. We support land managers to prioritise and protect threatened tree species, including securing habitat, addressing species-specific threats, supporting natural regeneration, and boosting populations through planting if needed, to enable the development of self-sustaining populations. Our projects in Raja Ampat, Indonesia and Quan Ba, Vietnam exemplify the importance of community involvement in achieving conservation success.

To protect tree species in Raja Ampat, three community groups located on the buffer zone of conservation areas in Waigeo Island, Raja Ampat were trained to conduct biodiversity surveys and patrols. They patrol across 60km<sup>2</sup> and have developed two nurseries. Survey data on target species distribution has been used in management planning of two nature reserves on Waigeo Island. We are currently expanding this successful model to two further islands in the archipelago.

Our project in Quan Ba, Northern Vietnam aims to conserve existing populations of the critically endangered *Magnolia grandis* and co-existing threatened trees by tackling threats. Community-based teams were established to patrol and report logging incidents within project sites; 2022 saw no reports of logging of mature *M. grandis*. We engage farmers to prevent the weeding of *M. grandis* wildlings from cultivated lands. Community members operate three nurseries, caring for and transplanting seedlings, boasting a survival rate of >90% one-year post-planting.

### **P38 Priorities for advancing research on African Convolvulaceae: Diversity, endemism hotspots and knowledge gaps**

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Sweet potato and its wild relatives (*Ipomoea* s.l.) are part of an iconic pantropical plant family, Convolvulaceae, also known for the ornamental morning glories and bindweeds. Recent key advances in molecular techniques have opened new avenues in exploring systematic, evolutionary, physiological and ecological questions, such as the origin of the hexaploidy of sweet potato, or the evolution of storage roots. However, the availability of data for the sweet potato wild relatives is geographically very uneven, with recent efforts having focused more on American and Asian taxa. In a thorough review of available taxonomic, geographic and genomic data, we identify that Africa and Madagascar harbour c. 25% of the worldwide species diversity of Convolvulaceae, with Eastern Africa standing out as the most important endemism hotspot for this plant group. For 90% of species, the conservation status is yet unknown, and for 93% there is no available genomic data. A summary of the diversity and main knowledge gaps for African and Malagasy Convolvulaceae is presented, with recommendations of geographic regions, taxa and scientific areas on which future taxonomic and conservation efforts should focus.

### **P39 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.

### **P40 Genetic diversity of germplasm banks of *Hancornia speciosa*, a food resource in Brazil**

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The plant *Hancornia speciosa* is an important food resource in Brazil. Its main product is its fruits, commercialized *in natura* or as a frozen pulp or ice cream. Due to its economic relevance, this species is a priority for research. However, *H. speciosa* continues to be exploited in an extractive manner in its natural habitat and the main conservation strategy is germplasm banks. Thus, this study aimed to evaluate the genetic diversity of *H. speciosa* accessions in germplasm banks using DARTSeq SNP markers. Genotypes were sampled from three germplasm banks: Embrapa Tabuleiros Costeiros (172), Embrapa Cerrados (191), and Universidade Federal de Goiás (147), totaling 510 accessions. The data was analyzed using the *dartR* package and filtered for Call Rate ( $\geq 80\%$ ) and Minimum Allele Frequency ( $\geq 0.01$ ); 1,292 SNPs remained. Genetic diversity was estimated by observed and expected heterozygosity ( $H_o$ : 0.167 <  $H_e$ : 0.196), Shannon Index ( $I$ : 0.310), and inbreeding coefficient ( $f$ : 0.145). A Wahlund effect is attributed to the inbreeding coefficient considering the allogamous mating system of the species and the heterogenous composition of each bank; therefore,  $f$  is explained by a strong subdivision within each population. An Analysis of Molecular Variance (AMOVA) showed greater genetic variation within (91%) than among (9%) populations and a Principal Components Analysis (PCA) allowed for the separation of genotypes according to the population of origin. The knowledge of the genetic variance among germplasm banks is fundamental to creating core collections for *H. speciosa* and to determining strategies to sample genotypes within biodiversity hotspots.

## **P41 New insights into the relationships between plants and fungi in early terrestrial environments**

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The 407-million-year-old Rhynie chert is one of the Scotland's geological jewels. It is recognized not only as a chronicle of early land plant evolution, but also as a record of the adaptation of Fungi and other microorganisms to the changing face of terrestrial habitats. Remarkable fossil evidence from this geothermal site shows that Fungi were already diverse, however, evidence for the occurrence of Dikarya (the subkingdom of Fungi that includes the phyla Ascomycota and Basidiomycota) is scant.

By using white light microscopy and confocal laser scanning microscopy on historic petrographic thin sections, we described a new fungus that colonized the aerial axes and leaf-like appendages of the plant *Asteroxylon mackiei* (Lycopsida). This new fungus is characterised by conidiophores arising in clusters from a loose sporodochium-like stroma. Conidia clearly developed at the top of the filaments, arising separately, sometimes adhering in chains; the first conidia formed holoblastically.

We present evidence that the fungus burst through the cuticle and caused a reaction in the plant that gave rise to dome-shaped surface projections. This represents the earliest fossil evidence of a plant pathogenic fungus.

We attribute the fungus to an extinct lineage of Ascomycota, making it another distinctive fossil affiliated to this clade in the Rhynie chert. None of the fossils described as Ascomycota from the Rhynie chert can be placed with confidence in the crown group, but together they provide the earliest compelling fossil evidence for stem group Ascomycota.

## **P42 The case of Arctic lichens: Do lichens adapt or experience bleaching as a response to warming?**

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Lichens are recognized as extremophiles, but they also serve as sensitive climatic indicators. Previous research has indicated a decline in Arctic lichen abundance due to climate warming. However, most observational studies lack a mechanistic understanding of this decline. Moreover, despite their prominent roles in Arctic ecosystems, the extent to which lichens can acclimatise to long-term changing climates remains poorly understood. Our research focuses on investigating the physiological and morphological responses of lichens subjected to experimental warming using the open-top chamber experiment in Ny-Ålesund, Svalbard. We aim to enhance our understanding of the carbon balance of polar lichens under warming conditions and ascertain whether these lichens as a whole, or their individual symbionts, possess adaptive capabilities or experience physiological degradation. Such deterioration may manifest as bleaching, similar to that of corals, due to disruption of lichen symbiosis, potentially leading to widespread ecosystem collapse. Our results indicate that lichens subjected to warming physiologically deteriorated and did not acclimatise after experiencing warmer conditions. These findings hold significance within the context of the imminent threat posed by climate warming in the Arctic as well as the potential impact on the ecosystem services provided by lichens.

## **P43 Effect of imitated self-pollination and cross-pollination on fruit set in *Cephalanthera longifolia* and *Cephalanthera rubra* (Orchidaceae)**

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A fruit set experiment on *Cephalanthera longifolia* and *Cephalanthera rubra* was performed in southern Lithuania. At each site, 60 individuals growing under the same conditions were selected for the study. For the cross-pollination and self-pollination experiments of *Cephalanthera longifolia*, 309 and 325 flowers were used, respectively, and 325 flowers were used for the control. For *Cephalanthera rubra*, 86 flowers were used for both the cross-pollination and self-pollination experiments and 85 flowers for the control.

The pollinia used for the cross-pollination experiment were collected from individuals growing at least 100 m from the test site. For the self-pollination experiment, pollinia of the same flowers were used and the plants used for the control were not subject to any manipulation. The pollinia were transferred onto the stigma with tweezers.

We found that 69.6% and 71.6% of the flowers of *Cephalanthera longifolia* produced fruit after simulated cross-pollination and self-pollination, respectively, while 6.5% of the flowers produced fruit in the control group. The results of the experiment with *Cephalanthera rubra* showed that after simulated cross-pollination and self-pollination, 86.0% and 97.7% of the flowers produced fruit, respectively, whereas 24.7% of the flowers produced fruit in the control group.

No statistically significant differences were found between the fruit set success of *Cephalanthera longifolia* and *Cephalanthera rubra* after simulated cross-pollination and self-pollination, and significantly more flowers produced fruit than in the control group. Hand pollination of flowers can be used for the restoration of very small and isolated populations of both studied *Cephalanthera* species.



#### **P44 Kew's collections go digital: Incorporating a volunteer programme into a mass digitisation project**

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We have embarked on a four-year project to mass digitise Kew's Herbarium and Fungarium collections consisting of c.8.5 million specimens, one of the largest collections of preserved plants and fungi in the world – Kew's 'Science Collections Digitisation Project'. This has been made possible by obtaining funding from the UK Department for Environment, Food and Rural Affairs. By making our collections digitally available, we will increase their accessibility, provide a digital backup of the collections providing mitigation of loss through disaster and increasing curatorial efficiency and provide a source of data. Images of specimens will be available on our new data portal, along with their accompanying label information, forming an online catalogue of plant and fungal specimens, which will be an invaluable resource available internationally for the world to use!

To this end, we have taken on a third-party contractor (Max Communications Ltd) to digitise the collections, in addition to work by our in-house Digitisation Team and the development of a Volunteer Programme, whereby we have been building a volunteer community, both remote and onsite, to support the mass digitisation of Kew's collections, which also allows us to engage with a wider audience, especially through our remote volunteer opportunities, therefore extending our reach and further increasing access to our collections. The aim is that Volunteers also benefit from taking part in the programme, gaining new skills and finding it a rewarding experience.

#### **P45 Revisiting the history of the TI herbarium to envision the future of herbaria in Japan**

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Natural History Collections (NHCs) include specimens deposited in universities and museums around the globe, and represent a huge source of biodiversity data, with still unknown potential. It is estimated that more than 3 billion specimens are deposited in NHCs around the globe, representing a dormant source of taxonomic and biogeographic information. In the case of botanical collections, specimens are deposited in herbaria, which are facilities that, due to the nature of plant collections, can store hundreds of thousands of specimens in a relatively small space. In Japan, 74 herbaria are registered to the Index Herbariorum, accounting for more than 13 million plant specimens. Herbaria in Japan date back from the XIX century, with the first herbarium to be founded in Japan in 1877: the University of Tokyo's TI Herbarium. This herbarium is the oldest in Japan and holds a collection of more than 1,800,000 specimens (including more than 20,000 type specimens), corresponding to ca. 14% of the total botanical collection of Japan. The collection at the TI herbarium includes plants from Japan, and important collections from Korean Peninsula, China, Taiwan, the Himalayan region, and many other East Asian countries. Cataloguing and making this collection available to research is of primordial importance, but the lack of resources and of investments to the museum impose great walls to the maintenance of the collection. This presentation aims to revisit the TI herbarium history, showcasing the importance of its collection, and highlighting endeavours that face the threatened preservation and future of herbaria in Japan.

## **P46 Debunking “wild”: The potential contribution of paleoecology and archaeology to ecosystem conservation**

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Restoring and rewilding environments are increasingly advocated as sustainable solutions to the threat of biodiversity loss. These approaches are based on recent ecological data and support the idea of landscapes as areas of lost wilderness spoiled by recent destructive human action. Yet, many of our ecosystems derive from millennia of human-environment interactions and their “wild” golden origins are long lost. It can however be difficult to disentangle human from natural processes which have shaped specific landscapes since prehistory.

How can we then appreciate the cultural context of our landscapes whilst protecting them from the threat of biodiversity loss? Paleoecology and archaeology provide keys to understanding landscape history and long-term human impact on ecosystems. By questioning what is “natural”, these approaches can shed light on how long-term human-environment interactions have contributed to shape modern-day ecosystems and suggest adequate ways forward for their conservation.

Through a practical case-study from the Peak District, this poster ought to outline some of the contributions that paleoecology and archaeology can make to ecosystem conservation. By providing long-term ecological data and showing how this remote landscape was heavily managed since at least the Roman period, conclusions of the study challenge the idea that halting farming and sheep grazing will allow the return of biodiverse ecosystems. Rather, this case-study is used to advocate for conservation approaches that acknowledge both the cultural character of present-day British landscapes and the need for promoting biodiverse ecosystems, for instance through methods such as conservation grazing.

## **P47 Using the Global Inventory of Floras and Traits (GIFT) for plant macroecological research**

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Answering the most pressing questions in plant macroecology requires knowledge of species distributions and plant functional characteristics. Much of this information has accumulated over centuries of botanical exploration and is contained in regional Floras and checklists, which offer curated information on the species composition, species’ biogeographic status and functional traits. Here, we outline how the Global Inventory of Floras and Traits (GIFT; <https://gift.uni-goettingen.de>), a repository of information from regional Floras and checklists, can be used for macroecological and biogeographic research. GIFT integrates plant distributions, functional traits, phylogenetic information, and region-level geographic, environmental, and socio-economic data. Version 3.0 of GIFT holds species lists for 3,485 regions with full global coverage, including ~ 367,854 taxonomically standardized plant species names and ~4 million species-by-region occurrences. GIFT also includes species-level information for 109 functional traits and more than 5.7 million trait-by-species combinations. Data from GIFT is openly available via the GIFT R-package (<https://CRAN.R-project.org/package=GIFT>). As exemplified by several studies, GIFT allows for assessing the taxonomic, functional, and phylogenetic composition of regional floras from regional to global scale. Recently, GIFT has been used to produce global predictions of taxonomic and phylogenetic diversity of vascular plants, to describe diversity patterns across life and growth forms, and to assess drivers of phylogenetic endemism in seed plants worldwide. As such, GIFT opens up new avenues for investigating regional patterns of global plant diversity and testing hypotheses related to past and present geographic and environmental drivers and anthropogenic influence.

#### **P48 Challenges of upscaling herbarium digitisation to complete the entire collection**

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Kew is a year into its largest digitisation project to date, aiming to unlock its herbarium and fungarium collections by 2026. Collectively, this is estimated to be around 8.25 million specimens. Previously, funded projects such as the Global Plants Initiative (GPI) and Re flora have enabled targeted digitisation of parts of the collections. Unlocking the full herbarium would continue to support extinction risk assessments, understanding collection bias, gaps in taxonomy, and improve the efficiency of those working with herbarium specimens (Canteiro et al., 2019).

Upscaling from projects that were limited in scope to an institution-wide effort has required utilising curatorial and research knowledge to re-work and establish new workflows to enable progress at an increased scale with time limitations. Certain families and collections require input from specialists as they differ from standard specimens which are easier to interpret and image. These include *Arecaceae* (Palms), *Orchidaceae* (Orchids) and the atypical specimen sheets that require more time and thought, for example those with more than one specimen on a sheet. As a result of this collaborative effort, by July 2023 the Digitisation Project had accomplished the digitisation of 1.4 million specimens. At the end of this ambitious four-year target, Kew will fill knowledge gaps, facilitate global research, and hopefully will have encouraged the next generation of herbarium users.

#### **P49 Poster submission withdrawn**

#### **P50 Biogeographic studies in *Zornia* J.F.Gmel. (Leguminosae: Papilionoideae): Evolutionary transitions between biomes**

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The genus *Zornia* J.F.Gmel is the second most numerous representative of the *Adesmia* clade (Leguminosae: Papilionoideae), with ca. 80 species. *Zornia* is the only genus within the clade with a pantropical 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 samples from Central America, Asia, Oceania and Africa that were not sequenced before. Therefore, this study aims to investigate evolutionary patterns of distribution in *Zornia* and answer biogeographic questions related to ancestral range estimation and evolutionary transitions between biomes. Our preliminary results suggest that *Zornia* emerged in the caatinga in Northeast Brazil. From there, the evolutionary path of the genus continued to the cerrado and thrived to the savannas of the Americas, where 40% of the present species occur. Then adapted to the high elevation grassland in South America and Central America. After the transoceanic dispersal, the genus dispersed to the African savannas and then to the savannas in India and Australia. Our study answers how the transoceanic dispersal occurred in *Zornia*, as previously it was not clear if this dispersal occurred from America to Africa or Australia. 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.