CENTRE FOR
ORGANISMAL STUDIES

UNIVERSITÄT
HEIDELBERG
ZUKUNFT
SEIT 1386

DBG Section Meeting

Biodiversity and Evolutionary Biology

„Frontiers in Plant Systematics and Evolution“

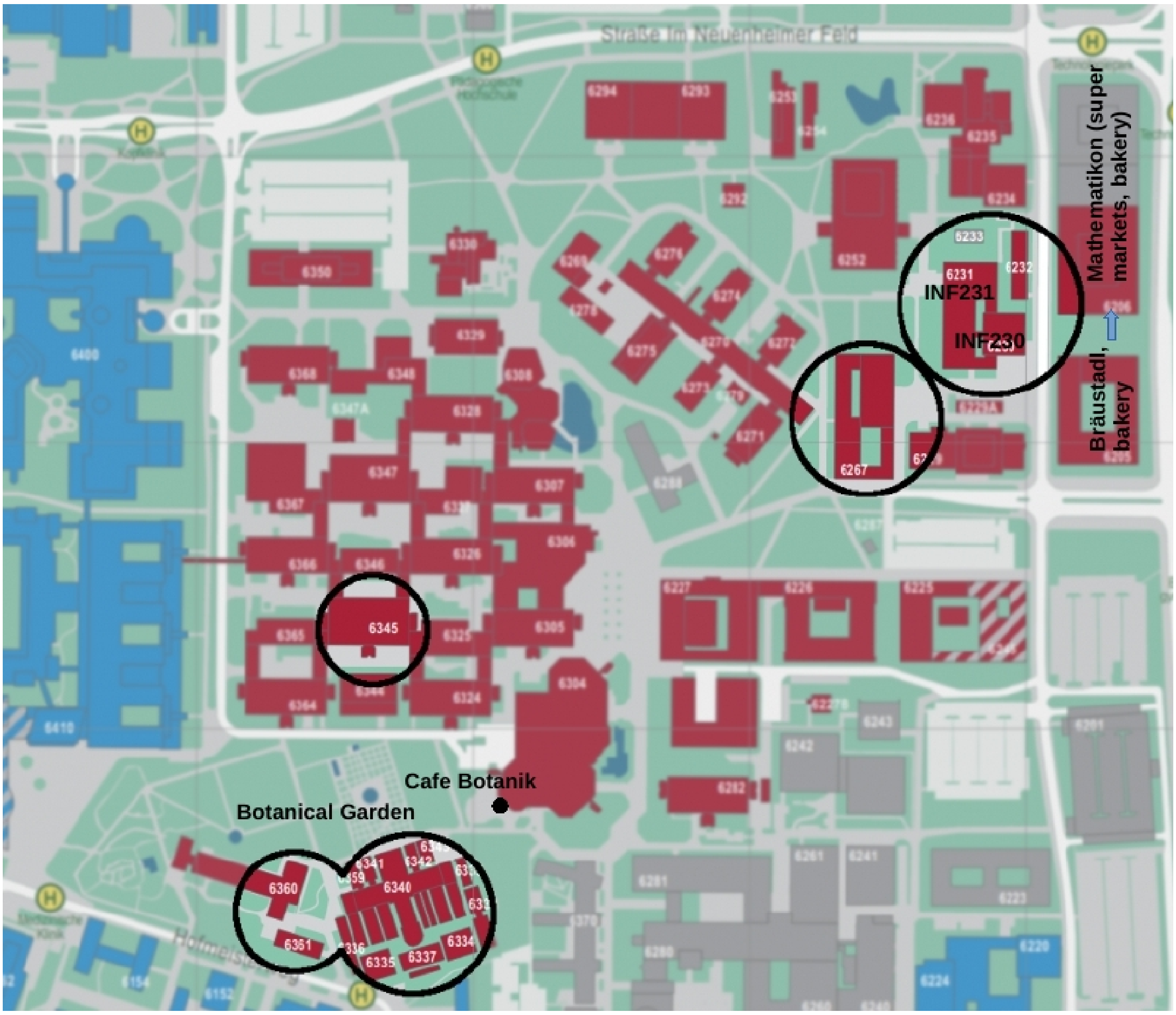
Heidelberg

27.08.-30.08.2025

Venue and directions

Im Neuenheimer Feld 230, 69120 Heidelberg, Germany

Geo coordinates of venue: 49.4179 / 8.6747, ///mangels.ungestüm.haie



Directions and parking

Turn left from Berliner Straße into the second street after Ernst-Walz-Brücke ("Im Neuenheimer Feld"), turn right, parking is possible in the "Mathematikon" basement parking garage (parking fees), across the street from building INF 230.

Public transportation

Use bus line 31 or 29 (from old town), tram lines 21 or 24 (from main station) to stop "Bunsengymnasium" or bus line 32 to "Jahnstraße". The building is in easy walking distance from there (approx. 3 resp. 10 min).

Programm

Wednesday	Thursday	Friday	Saturday
9:00-12:00 Boraginales Workshop (Max Weigend)	8:45 Welcome Note 9:00-9:45 Plenary Talk Coffee Break 10:15-12:30 SYMPOSIUM I (chair: E. Hörandl/B. Gemeinholzer)	9:00-9:45 Plenary Talk Coffee Break 10:15-12:30 SYMPOSIUM III (chair: G. Kadereit/A. Zerdoner Calasan)	9:00-11:00 SYMPOSIUM V (chair: C. Kiefer/N. Walden) Award Ceremony Concluding Remarks 12:00 End of Symposium
	Lunchbreak and Guided Tours	Lunchbreak and Guided Tours	
17:00-19:00 Registration and Icebreaker 19:15-20:15 Welcome Lecture	14:15-16:30 SYMPOSIUM II (chair: C. Oberprieler, N. Wagner) Coffee Break Poster Session I 19:00-20:00 Annual Section Meeting 20:00 Student Get-together	14:15-16:30 SYMPOSIUM IV (chair: M.A. Koch/J. Bechteler) Coffee Break Poster Session II 19:00-22:00 Get-together	

Details

Welcome Lecture

Prof. Dr. Herbert Hurka, Osnabrück, “Florogenesis of the Eurasian steppe belt – a comprehensive interpretation”

Plenary Talk Thursday

Kirsten Bomblies, Zurich, “Adaptation to cellular challenges in polyploid Arabidopsis arenosa”

Plenary Talk Friday

Yvonne Willi, Basel, “Elevational range limits and the role of trait integration”

Symposia

Symposium I	From populations to species (Hörandl/Gemeinholzer)
Symposium II	Plant reticulate evolution at different evolutionary scales (Oberprieler/Wagner)
Symposium III	Progress in plant systematics and taxonomy (Kadereit/Zerdoner Calasan)
Symposium IV	Plant life at its environmental limits (Koch/Bechteler)
Symposium V	Omic´s in systematics and evolution (Kiefer/Walden)

What and Where

Symposia, Lectures and Talks: Lecture Hall

Please upload your talks on the laptops on either Wednesday evening at the registration desk or on Thursday, Friday and Saturday on the laptop in the lecture hall BEFORE the symposia start. You cannot connect your own laptop to the beamer in the lecture hall!

Coffee Breaks: In front of Lecture Hall

Everyone will receive a conference mug at registration. Please use your mug which you have been issued at registration during the coffee breaks. Pens for labeling can be used at the registration desk. Do not bring any filled mugs into the lecture hall!

Lunch Breaks

There are several options for lunch around the venue:

Cafe Botanik (fries, salad, pizza, vegan pasta, cakes, drinks), in the same building as the Mensa near the Botanical Garden

In Mathematikon (opposite to the left from the venue towards Berliner Strasse):
    Bakeries with cafes or sitting areas
    food stores (Rewe, Aldi)

Bräustadl restaurant (also in Mathematikon)

The Mensa only accepts the Campus card, so this is not an option!

Poster Session: Room 00.004/00.005

Session I: Posters can be mounted during registration on Wednesday, August 27th or the coffee breaks on Thursday, August 28th

Session 2: Posters can be mounted during the coffee breaks on Friday, August 29th

Section Meeting: Lecture Hall

Get-together: In front of lecture hall and building.

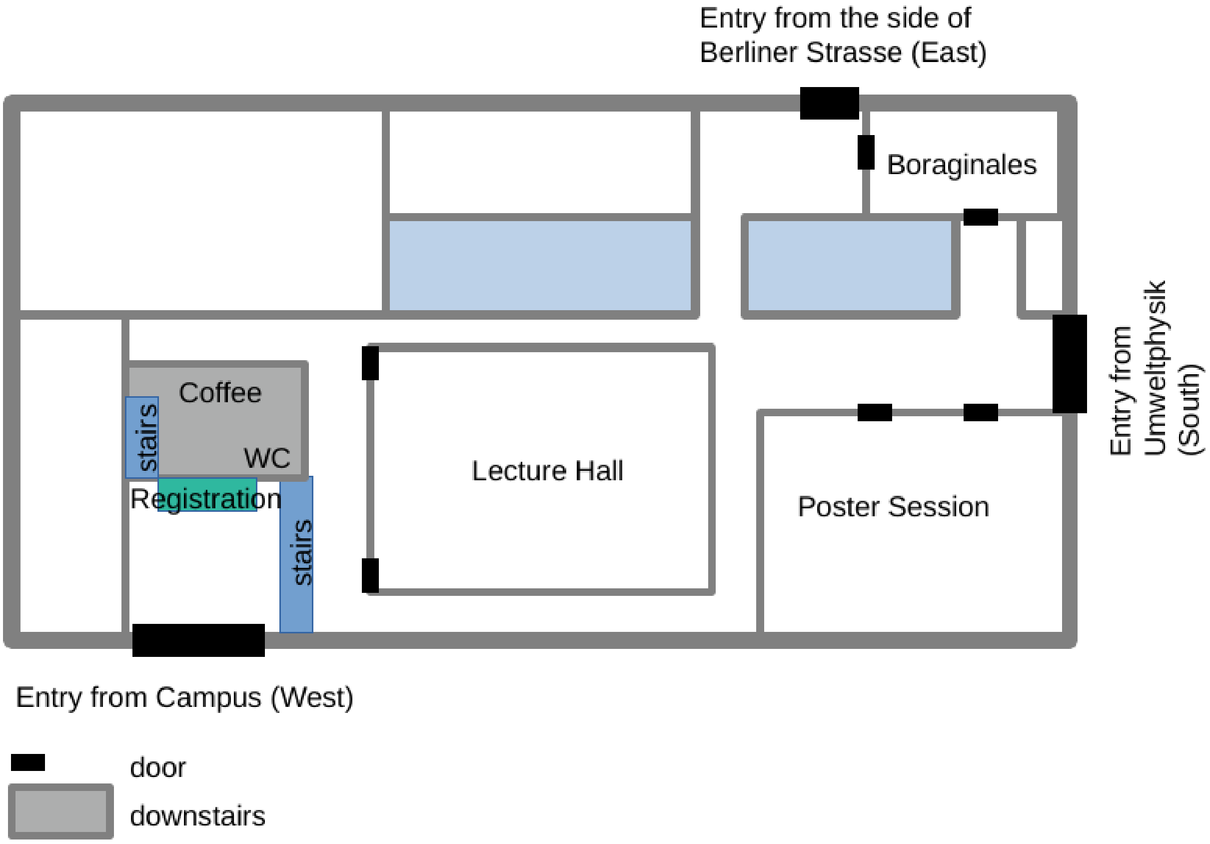
Food is served downstairs. Vegan an vegetarian options are available.

Student Get-together: Meeting in front of lecture hall

We go out for Falafel and a nice view of the Heidelberg Castle in the old town. It‘s informal and I hope we as (bachelor, Master PhD students) can get to know each other and connect.

Boraginales Workshop: Seminarraum 1

Floorplan



Guided Tours

Please collect a ticket (coloured label) at the registration desk if you want to participate.

THURSDAY, 28th August

12:45 Botanic Garden – Plant Collections (**red label**)

12:45 Botanic Garden – Current General Refurbishment (**purple label**)

13:30 Exhibition “Timeline of Evolution“ (**white label**)

Meeting point: Conference office desk

FRIDAY, 29th August

12:45 Botanic Garden – Plant Collections (**blue label**)

12:45 Botanic Garden – Current General Refurbishment (**yellow label**)

13:30 Exhibition “Timeline of Evolution“ (**orange label**)

Meeting point: Conference office desk

Abstracts

SYMPOSIUM I (chair: E. Hörandl/B. Gemeinholzer)

Introductory Talk

From populations to species

Elvira Hörandl

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Affiliation: Dept. Systematics, Biodiversity and Evolution of Plants (with Herbarium), University of Göttingen

Populations are the starting point of all evolutionary processes. Population genomic methods have revolutionized this research field, and specifically the combination with ecological, biogeographical, and reproductive data have been fruitful to understand the complexity of processes between population and species level. I will review case studies on e.g. (1) polyploid complexes combining genomic, cytological, reproductive and ecological data, (2) phylogeographical analyses on alpine hybrid zones connecting population genetics, morphology and ecology, and (3) biogeography and conservation status of endangered species. This symposium will provide further case studies testing evolutionary and biogeographical hypotheses at lower taxonomic levels.

Talks

Demographic history sheds light on biogeographic distribution of alpine willow species (Salix L.)

Pittet Loïc, Wagner D. Natascha, Hörandl Elvira

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Affiliation: University of Göttingen

The relative importance of evolutionary history and ecological niche for the biogeographical distribution of alpine plant species is still unclear. We investigated ecological niche, genetic structure and demographic history in ten willow species in the Alps. Our results show that niche breadth and optimum is insufficient to explain species' distribution. Glacial refugia have a major role, as reflected by the Western/Eastern species' genetic clusters. Demographic models best explained different species' distribution and revealed two main scenarios: (1) Divergence in isolation and recent secondary contact for widespread species. (2) Divergence with ancient gene flow but recent isolation for restricted species.

Population genetics and phylogeography of the endangered steppe plant Oxytropis pilosa

Regina Schimpf, Daniela Guicking, Birgit Gemeinholzer

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Affiliation: Universität Kassel

The migration history of continental steppe plants and the development of steppe grasslands in Europe remain poorly understood. The number of publications on this topic has increased since the early 2000s. For a long time, phylogeographic research focused primarily on Eastern European regions, and the continental steppes of Central Europe received little attention. However, in recent years, increasing attention has been given to the fragmented western outposts of these steppe ecosystems. Nevertheless, significant knowledge gaps remain, particularly concerning the historical dynamics and genetic distinctiveness of Central European steppe habitats.

In Europe, continental steppes occur at the periphery of their natural distribution range and are restricted to specific ecological niches. They are highly fragmented, confined to a few, ecologically unique locations, and rely on continuous human management. Without regular disturbance such as grazing or mowing, they would become overgrown and be displaced by surrounding deciduous forests. Their long-term persistence is therefore closely tied to both ecological conditions and sustained conservation efforts.

Effective protection requires an understanding of the current genetic status of these plant populations and the historical processes that shaped them. Population genetic analyses provide insights into genetic diversity, structure, and connectivity, while biogeographic approaches help reconstruct migration routes and detect relict populations.

To explore the development of these steppes and evaluate the conservation value of their plant populations in Central Europe, this study investigates the phylogeography and population genetics of *Oxytropis pilosa* (Woolly Milkvetch). This species is widely distributed throughout the Eurasian steppe belt, but limited to isolated populations in Europe, where it is considered endangered.

To analyse phylogeographic patterns and population genetic structure simultaneously in both fresh and historical material, 21 nuclear markers were developed using the Angiosperms353 target enrichment approach. The dataset includes 198 individuals from 18 populations in Germany, the Czech Republic, and Estonia, and 44 herbarium specimens covering a broader range. DNA was extracted and sequenced using Illumina short-read technology.

Preliminary results provide insights into regional genetic differentiation, within-population diversity, and the biogeographic history of Central European populations. This unified analytical approach enables the simultaneous investigation of phylogeographic patterns and population structure using both fresh and herbarium material. The results provide a foundation for assessing the genetic value of isolated populations and support long-term conservation strategies for *Oxytropis pilosa* and similar steppe relicts.

Phylogenomics unravels the complex relationships of autumn-flowering Iberian crocuses

Ruifang An, Frank R. Blattner, Nomar Espinosa Waminal, Doerte Harpke

Email: **an@ipk-gatersleben.de**

Affiliation: Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

The Iberian autumn-flowering *Crocus serotinus* group complex encompasses five recognized species (*C. clusii*, *C. cobbii*, *C. nudiflorus*, *C. salzmannii*, and *C. serotinus*) with numerous populations of uncertain taxonomic status. Variable genome sizes and chromosome numbers indicate extensive hybridization and dysploidy events, while the group's recent origin (~3.5 Mya) suggests rapid evolutionary diversification. These factors have created significant challenges for species delimitation and contributed to ongoing taxonomic confusion.

We employed an integrative taxonomic approach combining molecular phylogenetics, population genomics, and cytogenetic analyses to resolve these complexities. Our comprehensive sampling included 110 populations across the Iberian Peninsula, with genotyping-by-sequencing (GBS) of 282 individuals and whole-genome sequencing of 26 representative samples. We conducted repeatome analysis using RepeatExplorer2, estimated genome sizes via flow cytometry, performed chromosome counts, and analyzed karyotypes using fluorescent in situ hybridization (FISH).

Our analyses revealed 13 previously unrecognized diploid species within the complex. Diploid taxa exhibited genome sizes of 2C = 3.3–4.6 pg, with the notable exception of *C. salzmannii*, which showed significantly larger genomes (2C = 5.9–7.2 pg), likely resulting from ancient polyploidization followed by rapid diploidization. Polyploid lineages displayed genome sizes of 2C = 6.7–9.2 pg with chromosome numbers of 2n = 36, 44, and 48, indicating multiple independent polyploidy events and subsequent chromosomal rearrangements.

This study demonstrates that polyploidization, hybridization, genome size variation, and chromosomal restructuring have been key drivers in the rapid diversification of autumn-flowering *Crocus* species across the Iberian Peninsula.

Hidden Diversity in North American Rhododendrons: Phylogenomics and Taxonomic Resurrection of Rhododendron Subsect. Caroliniana (Hutch.) Sleumer

Dirk Albach, Ralf Bauer, Charles Horn, Gulzar Khan

Email: **dirk.albach@uol.de**

Affiliation: Carl von Ossietzky-Universität Oldenburg

Rhododendron (Ericaceae), the largest genus of woody plants with approximately 1,400 species, is well known for its complex and often ambiguous taxonomy. Although nearly 98% of *Rhododendron* species are native to the Old World, North America harbors several notable exceptions, including both deciduous azaleas and a subset of non-deciduous *Rhododendron* species. Among the latter, *Rhododendron* subsect. *Caroliniana* exhibits particularly unresolved taxonomic relationships and distinctive ecological traits. Until recently, disputes were around the question whether the subsection contains, one, two or three species. In 2021, we (Albach & Bauer, 2021) demonstrated that the subsection should be expanded to four following the discovery of *R. smokianum* in the Great Smoky Mountains. However, that study could not clearly distinguish *R. carolinianum* from *R. minus* based on ITS sequencing. Ongoing work aims to refine the taxonomy of this group and clarify its evolutionary and biogeographic history.

In this study, we employed genome-wide SNP data generated via genotyping-by-sequencing (GBS) to investigate genetic diversity and cohesion within this species complex across its full southeastern U.S. range. Special emphasis was placed on morphologically variable populations, particularly *R. minus* and *R. carolinianum*, including the type localities. Using both population genomic and phylogenomic approaches, we identified at least eight genetically distinct clusters, partly matching clear geographic groupings, partly known morphological variants. These findings fundamentally challenge traditional morphology- and marker-based classifications and highlight the limitations of existing taxonomic frameworks. Our results underscore the need for integrative approaches that combine genomic, morphological, and geographic data to more accurately define species boundaries within non-deciduous *Rhododendron* in North America.

Genetic information for the conservation of segetal plants

Tran, P., Herklotz, V., S. Ritz, C.M., Usadel, B., Schmied, H., Fortmann, L., Meyer, S., Harpke, D, Wesche, K.

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Arable land is undoubtedly the most important cultural landscape with a landcover >1/3 in Central Europe. Segetal plants, which are adapted to these habitats, contribute substantially to biodiversity and provide food sources e.g. for insect pollinators or herbivores. However, agricultural intensification has driven massive decline on phytodiversity over the last decades. In contrast to for example meadows and forests, conservation efforts are scarce for arable land. In Germany restauration action is dictated legislatively by seed transfer zones (STZs) that ensure plant regionality. These STZs are based on (bio)geographical parameters and do not capture interspecific genetic variation. Understanding population genomics is critical in restauration efforts but such data is limited for segetal species. Our project aims to investigate population genomics of seven common, nine moderately and five critically endangered segetal species across Germany using the throughput sequencing technique: ddRADseq. Our analyses revealed strong genetic fragmentation and low genetic diversity within populations of critically endangered segetal species such as *Bupleurum rotundifolium*, *Euphorbia falcata* and *Stachys annua*. In moderately endangered species (e.g. *Valerianella dentata*, *Odontites vernus* and

Agrostemma githago), geographical structures were present and not captured by the current STZs. Common species (e,g. *Anagallis arvensis* and *Thlaspi arvense*) lacked any genetic structure and showed high gene flow between populations.

The interplay between selection and the genomic landscape during the domestication of grain amaranth

Corbinian Graf, Tom Winkler, Peter J Maughan, Markus Stetter

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Affiliation: University of Cologne

The process of adaptation is vital for populations facing changing environments. Several potentially adaptive traits have been studied intensively, but intrinsic traits like the genomic landscape i.e., the composition and structure of the genome, have received less attention. Multiple features of the genomic landscape influence the molecular outcome of adaptation and recent evidence indicates that some features might be under selection themselves. However, the interplay between the genomic landscape and adaptation remains unclear. To study the impact of selection on the genomic landscape, we study the repeated domestication of grain amaranth. We assess open chromatin, methylation and recombination maps of two wild and three domesticated amaranth species. We find that more chromatin opened than closed during domestication, but that most chromatin changes are species-specific, in line with the previously reported independent domestication. We find specific regions in the genome that are differentially open between wild and domesticated amaranth, suggesting their involvement in the domestication process. A significant overlap between chromatin selection signals and genomic signals of selection indicates the interplay between the genome sequence and its folding during adaptive processes. The combination of chromatin structure and recombination landscapes along the selection gradient from wild to domesticated amaranth will give further insights into the interaction between the genomic landscape and plant adaptation. Our model of repeated adaptation to human environments provides the opportunity to understand if and how the physical genome properties are shaped by selection.

SYMPOSIUM II (chair: C. Oberprieler, N. Wagner)

Talks

Unravelling the evolutionary history of the Cystopteris fragilis complex in Europe

Dieder de Frens, Chinedum Anajemba, Daniella Ivanova, Andrei Popa, Evelin Krol, Libor Ekrt, Carl Rothfels, Michael Kessler

Email: diederdefrens@gmail.com

Affiliation: University of Zürich

The *Cystopteris fragilis* complex represents one of the most taxonomically challenging groups among ferns. It is characterized by high morphological variability, broad ecological tolerance, extensive allopolyploidisation, and a cosmopolitan distribution, all of which have historically complicated systematic efforts. Globally, the complex includes cytotypes ranging from diploid to octoploid. However, diploids are rare, and none are currently known from Europe, making it particularly difficult to reconstruct the group’s evolutionary history. This diversity in ploidy levels, likely arising through recurrent allopolyploidisation, has obscured lineage boundaries. Despite repeated attempts to delimit taxa and unravel the evolutionary processes at play using various approaches, a coherent picture of the complex's reticulate evolution and resulting diversity in Europe remains elusive, and competing species concepts persist.

To address this deficit, we are applying a phylogenetic approach that combines long-read sequencing with analytical tools tailored for polyploid-rich groups. We are analysing samples collected from across Europe, with an emphasis on regions featuring unusual substrates and potential glacial refugia, such as the Alps, the Pyrenees, and the Carpathians. Targeted sequencing of single-copy nuclear loci will be conducted using PacBio long-read sequencing, which enables the recovery of complete amplicons from all copies (homeologs) present in polyploid individuals.

Reads are clustered by locus using the PURC v2.0 pipeline, which then infers the underlying biological sequences present in each sample. These are then phased into subgenomes using *homologizer*, allowing us to reconstruct the evolutionary history of independent subgenomes without relying on known diploid progenitors. This approach is particularly well-suited to detecting signatures of allopolyploidy and hybridisation in groups with cryptic or extinct diploid ancestors.

This study combines dense geographic sampling with flow cytometry and with long-read sequencing of single-copy nuclear markers, to clarify the evolutionary structure of the *Cystopteris fragilis* complex in Europe. More broadly, the study contributes to understanding how hybridisation and polyploidisation shape plant diversity and demonstrates how appropriate methodological frameworks can address evolutionary complexity in taxonomically challenging groups.

Untangling Reticulate Evolution in the Dryopteris carthusiana Group (Dryopteridaceae) Using Target Enrichment Sequencing

Evelin Krol, Jens Freigang, Stefan Jeßen, Dieder de Frens, Emily B. Sessa, Weston Testo, Michael Kessler

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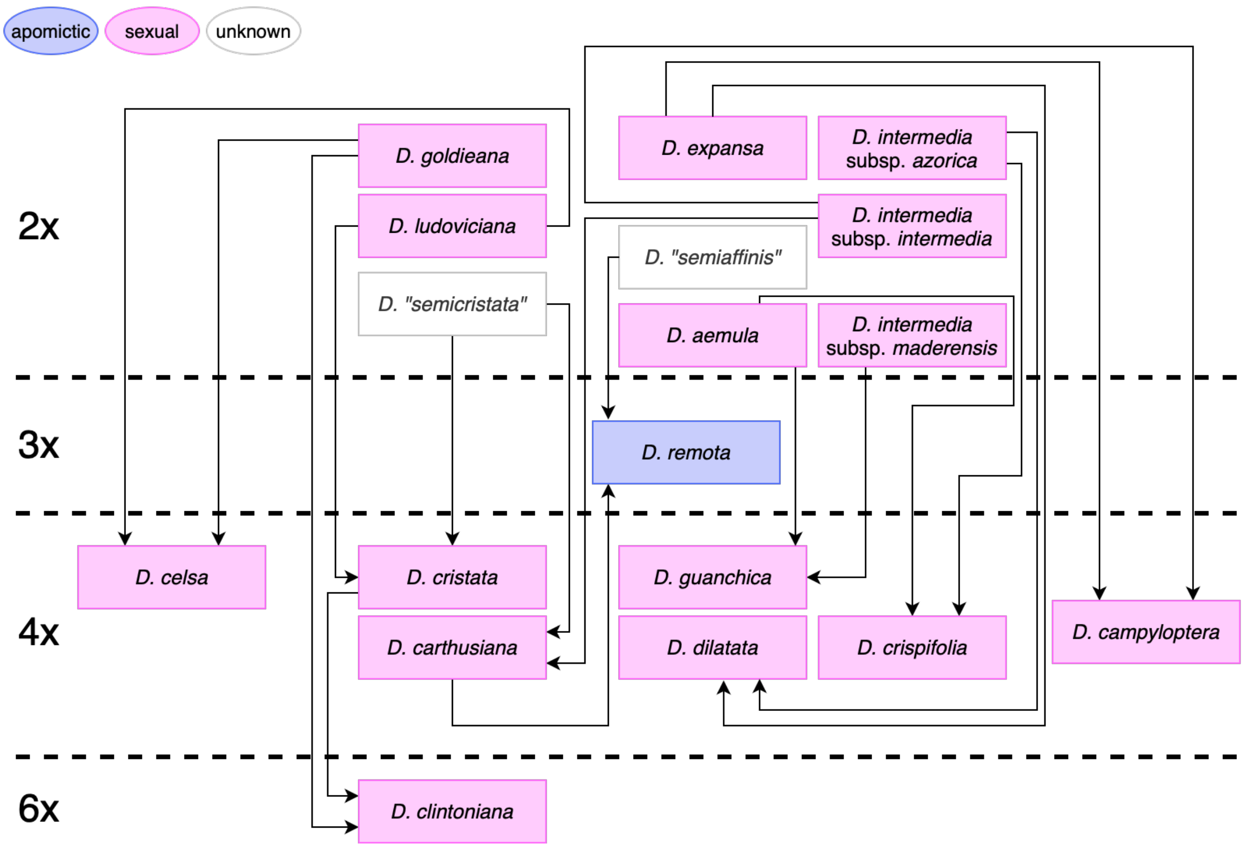
Affiliation: University of Zürich

With approximately 400 species, *Dryopteris* is the third-largest genus in Dryopteridaceae, the most species-rich fern family. Characterized by a base chromosome number of 41, *Dryopteris* frequently exhibits polyploidy and apomixis, with hybridization occurring even across distinct sections. Consequently, the evolutionary relationships within many species complexes remain poorly understood. Among them, the *Dryopteris carthusiana* group presents a particularly intriguing case, as its members exhibit extensive reticulate evolution.

Reticulation Pattern of *Dryopteris carthusiana* Group



The *D. carthusiana* group comprises diploid, tetraploid, and hexaploid species, primarily distributed in North America, with some also occurring in Europe. These taxa reproduce sexually and form complex hybrid networks, involving multiple allopolyploids, their parental species, and triploid and pentaploid hybrids and apomicts. Additionally, an unknown and likely extinct ancestor, *D. “semicristata”*, is hypothesized to have contributed to the ancestry of certain taxa. Despite previous studies based on morphology, ploidy, genome size, and a limited number of molecular markers, key aspects of the evolutionary relationships within this complex remain unresolved.

To address these gaps, we are employing target enrichment sequencing using the GoFlag408 probe set, which targets 408 exons representing 248 nuclear genes across flagellate plant lineages. By phasing hybrid subgenomes, we have determined the parental contributions of hybrid species, reconstructed the evolutionary history of this group, and identified the genetic signature of the *D. "semicristata"* subgenome. Additionally, by assembling chloroplast markers from off-target reads, we provide insights into the maternal lineages involved in hybridization events.

Multiple hybrid zones involving four Cardamine species and their triploid progeny: another nascent neopolyploidS in action?

Judita Zozomová-Lihová, Marek Šlenker, Barbora Šingliarová, Kristína Pulišová, Terezie Mandáková, Karol Marhold

Judita Zozomová-Lihová[1], Marek Šlenker[1], Barbora Šingliarová[1], Kristína Pulišová[1], Terezie Mandáková[2,3], Karol Marhold[1,4]

[1]Institute of Botany, Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovak Republic

[2]Central European Institute of Technology, Masaryk University, Brno, Czechia

[3]Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czechia

[4]Department of Botany, Faculty of Science, Charles University, Prague, Czechia

Hybridization between species is a powerful evolutionary force that can lead to the exchange of genetic material, the formation of new species, and significant shifts in biodiversity. Hybrid zones, regions where genetically distinct populations meet and interbreed, offer unique opportunities to study these processes in real time. In particular, they provide insights into interspecific gene flow, introgression, genetic erosion, and the emergence of polyploid organisms, which have played a crucial role in plant evolution. One key mechanism of speciation in plants is allopolyploidization, where hybridization between species is followed by genome doubling, leading to the formation of new, reproductively isolated lineages. The genus *Cardamine* is an important model for this process, as it includes one of the few well-documented neo-allopolyploid species that have arisen within the last 300 years. In this study, we revealed an unprecedented case of extensive interspecific hybridization in *Cardamine*: a dynamic system of seven hybrid zones in the mountains of western Bulgaria, involving four parental species and their predominantly triploid offspring. Using a combination of flow cytometric screening, next-generation restriction site-associated DNA sequencing, and genomic *in situ* hybridization, we demonstrate the recurrent and polytopic origins of both autotriploids and allotriploids, with the latter integrating distinct parental genomes. Our findings highlight *Cardamine rivularis* as a central player in this system, likely due to its frequent production of unreduced female gametes, which drive the formation of diverse triploids. However, this species may also face the risk of genetic swamping and ecological displacement. While most triploid hybrids appear to belong to the F1 generation, their substantial genetic diversity, high frequency, and efficient clonal spread suggest significant evolutionary potential. Overall, we propose that these hybrid zones provide a rare and valuable natural laboratory for studying the emergence of neo-allopolyploid species and the broader mechanisms shaping polyploid evolution.

Molecular and ecological analyses towards an integrative taxonomic treatment of the Rhodanthemum atlanticum-group (Compositae, Anthemideae)

Pia Donhauser[1], Marco Dorfner[1], Robert Vogt[2], Christoph Oberprieler[1]

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2 Freie Universität Berlin, Berlin, Germany.

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Abstract: The genus *Rhodanthemum* B.H.Wilcox & al. (Compositae, Anthemideae) presently comprises 17 species distributed in NW Africa (mainly Morocco) and S Spain. Owing to the formation of hybrids whenever representatives of the genus share the same habitat, this syngameon is a focal study group in the Carrara project (TaxonOmics programme), which aims at the establishment of objective methods of integrative species-delimitation in intensively hybridising genera based on herbarium specimens. We have used 92 accessions of *Rhodanthemum* and three of its sister-genera *Chlamydophora, Chrysanthoglossum,* and *Leucanthemum* to infer phylogenetic relationships among all described species of the former genus based on a SNP matrix gained by AFLPseq fingerprinting. Based on a total of 43,538 SNPs, a well-supported backbone phylogeny of *Rhodanthemum* emerged that was used subsequently to further elucidate the species delimitation in the group of *Rh. atlanticum, Rh. briquetii, Rh. quezelii,* and *Rh. redieri.* After inclusion of additional 96 accessions for these four species, a data matrix of 42,240 SNPs from 3,718 loci was gained. Network analyses showed that *Rh. quezelii* subsp. *ijallabenense* from the eastern High Atlas Mts is closer related to *Rh. atlanticum* than to *Rh. quezelii* subsp. *quezelii,* and that within the former species, there is a continuous elevational transition between its typical variety *Rh. atlanticum* var. *atlanticum* and its high-elevation variety *Rh. atlanticum* var. *gelidum* in the Mt. Toubkal area in the western High Atlas Mts. Ecological data based on eco-climatological and edaphic (soil-grid) variables confirmed distinct environmental preferences of the studied taxa and may add – together with morphological variables – to an integrative taxonomy in this species group.

Unraveling Taxonomic Complexity in Northern Azaleas: A Phylogenomic Study of Rhododendron subgenus Pentanthera

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Rhododendron (Ericaceae) is one of the largest genera of woody plants, comprising approximately 1,400 species. Among its five subgenera, *R*. subg. *Pentanthera* (G. Don) represents a group of 17 morphologically and horticulturally important species, commonly known as azaleas, with a native distribution spanning North America, Japan, China, and the Caucasus. Despite their ecological and ornamental value, species boundaries within this section remain poorly resolved, partly due to overlapping morphological traits, partly due to the previously used limited genetic markers, and partly due to frequent hybridization.

Previous studies, largely based on morphology and a few molecular markers, have failed to robustly clarify phylogenetic relationships within the section. In this study, we employed Genotyping-by-Sequencing (GBS) to investigate species delimitation and evolutionary relationships within the section using population genetic and phylogenomic approaches, incorporating all taxonomic entities and morphological variability. In total, we included approximately 300 individuals representing all recognized species.

Our preliminary findings reveal extensive admixture among species, suggesting frequent hybridization and weak reproductive isolation. Furthermore, phylogenomic analyses indicate reticulate evolution within the backbone of the section's evolutionary tree. These results underscore the complexity of species boundaries in *R*. sect. *Pentanthera* and suggest that hybridization has played a substantial role in shaping current diversity. This work contributes to a deeper understanding of speciation, biogeographic history across the Eastern Asia–North America disjunction, and the evolutionary mechanisms underlying species diversification in temperate woody plants.

Unraveling the reticulated evolution in Amaranthaceae s.s. using herbariomics

Tina Kiedaisch, Anže Žerdoner Čalasan & Gudrun Kadereit

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Background

The evolutionary history of Amaranthaceae *sensu stricto* (*s.s.*) has been shaped by multiple whole genome duplications and rapid radiations, leading to an ecologically diverse group of plants that includes many widespread species with a strong potential to become weeds. Previous phylogenetic studies have struggled to resolve relationships within this

clade, primarily due to limited genomic data and inadequate taxon sampling. As a result, the current classification of this economically important plant family remains unstable and fails to accurately reflect the evolutionary history of the lineage.

Materials and methods

To address these challenges, we designed a customized bait set that targets 1,000 low-copy nuclear loci across the whole Amaranthaceae *s.s.* lineage. Leveraging the vast potential of global herbarium collections, we sampled nearly all known genera, covering 94% of genus-level diversity, including many rare or previously inaccessible taxa, some of which are included here for the first time. Phylogenetic reconstruction was conducted using both concatenation- and coalescent-based approaches. We furthermore explored gene tree discordance and alternative topologies, as well as hybridization and gene duplication events.

Results

Our study presents a globally sampled and well-resolved phylogeny of Amaranthaceae *s.s.* While most nodes in the resulting species trees were statistically maximally supported, our quartet sampling analyses revealed high levels of gene tree discordance in the backbone of one of the major clades. Phylogenetic network analyses identified two reticulation events in this region: one associated with the origin of a species-poor genus, and another connecting the Aervoids and Gomphrenoids. Furthermore, these reticulation events help explain the contrasting topology of different gene tree clusters found in the lineage. In addition to the three previously known whole genome duplication events in Amaranthaceae *s.s.*, we identified three further events: two occurring along the backbone of the phylogeny, and one specific to the Celosioid clade.

Conclusions

Our study reveals the deeply reticulate and polyploid nature of Amaranthaceae *s.s.*, shaped by at least two hybridization events and six ancient whole-genome duplications. These processes have left a strong signal of gene tree discordance, especially in the backbone of the phylogeny, and help explain long-standing difficulties in resolving relationships within the group. By using phylogenomic data from nearly complete genus-level sampling, we not only clarify previously ambiguous relationships but also uncover alternative topologies that illuminate the complex evolutionary trajectories of this lineage. This work provides a robust framework for future research into trait evolution, biogeography, and conservation priorities, and underscores the power of genome-scale data to untangle deep reticulate histories in rapidly radiating plant groups.

A phylotranscriptomics backbone of Alchemilla s.l. (Rosaceae): Exploring gene tree discordance, hybridization, and whole genome duplication.

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With at least 350 (−1100) species worldwide, *Alchemilla* in the broad sense (s.l.) has been a challenging group to study due to the presence of reticulate evolution, polyploidy, and apomixis. In a previous study using target enrichment, we identified four nodes in the backbone of *Alchemilla* s.l. with an elevated proportion of gene duplication. Furthermore, using a gene-tree reconciliation approach, it was established the polyploid origin of *Alchemilla* s.l. and the putative allopolyploid origin of the four major clades within the group. Here we revisit the backbone of Fragariineae with a focus on *Alchemilla* s.l. using a data set of 47 genomes and mainly transcriptomes (26 newly generated) to explore the patterns of WGD and reticulation in the group. We found similar patterns of WGD within *Alchemilla* s.l. that seem to have a polyploid origin along with its sister and monophyletic genus, *Farinopsis*. Furthermore, novel reticulation patterns among the major clades of *Alchemilla* s.l. are revealed based on species network analyses. We also explore the pattern of diploidization in *Aphanes*, the only annual and entirely herbaceous clade of *Alchemilla* s.l.

SYMPOSIUM III (chair: G. Kadereit/A. Zerdoner Calasan)

Introductory Talk

Resolving Cryptic Species in Cyanobacteria Through Population Genomics

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Cryptic species complicate species identification and delimitation in cyanobacteria. Here, I advocate for evolutionary species delimitation by identifying species boundaries using population genomics and by investigating the drivers of speciation. As a model, I selected the cosmopolitan cyanobacterium *Microcoleus*. Population structure inference revealed at least twelve species within *Microcoleus*. Species diverged with gene flow in the form of homologous recombination. The full continuum of divergence was observed, from incipient species to fully diverged species with ongoing gene flow. The reinforcement of species barriers was driven by both geographical and environmental factors (e.g., climate and soil properties). Highly diverged genomic regions were under selection and likely functioned in stress response. To define species within the speciation continuum, I offer a probabilistic solution to the species problem (universal probabilistic concept of evolutionary lineages), which reflects the dynamics and incomplete divergence of the species. It can be applied to all domains of life because most of the lineages seem to be maintained by the gene flow.

Talks

When Terabases are not enough: Attempting to resolve the phylogeny of Veronica subg. Pseudolysimachium (Plantaginaceae).

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Within the genus *Veronica* L. (Plantaginaceae), the subgenus *Pseudolysimachium* is well-delimited from other subgenera by morphological and molecular characters. The subgenus includes approximately 35 species that occur in natural and semi-natural grasslands throughout Eurasia and is characterized by one of the highest diversification rates within the genus, which makes it difficult to outline species boundaries. In addition, members of the subgenus are known for a high degree of phenotypic plasticity, infraspecific variation and frequent hybridization, which has resulted in the formation of at least 16 hybrids.

Veronica subg. *Pseudolysimachium* is most diverse along the northern margin of the Altai Mountains but is also relatively diverse in southeastern Europe. Whereas some species of the subgenus are widespread, others are restricted to these two areas. Due to the aforementioned characteristics, several often allopatric infraspecific taxa and even segregate species have been described.

To elucidate the phylogenetic relationships within the subgenus, we assembled three distinct high-throughput-sequencing (HTS) datasets, including hundreds of individuals. Two of these datasets were obtained from reduced representation sequencing (Genotyping-by-Sequencing and HybSeq), while the third was obtained from whole genome sequencing (Multiplexed Shotgun Genotyping), including silica-dried as well as historical herbarium specimens. Incongruencies ranging from minor to major were observed among phylogenetic trees inferred from the different sequencing datasets and analytical methods.

However, among the majority of obtained trees, the following relationships could be observed: The included specimens from Eastern Asia seem to be the earliest divergent group, branching off at the basis of all included trees. The widely distributed species *V. longifolia* and its close relatives *V. spuria* and *V. ovata* form a group obtained in most analyses. The Central Asian species *V. pinnata* appears either as sister to the Eastern Asian taxa or is nested deeply within a clade constituted by the latter. *V. gryniana* branches off at the basis of the clade including all remaining taxa, appearing as their sister. Among the remaining species, clades dominated by either *V. barrelieri* or *V. orchidea* were obtained in every analysis, appearing as sister to each other in most trees. The remaining species appear either polyphyletic (e.g. *V. incana* and *V. spicata*) or are situated in clades not obtained in every analysis. The two formerly neglected species *V. steppacea* and *V. maeotica* were identified as distinct groups in numerous obtained phylogenetic trees. However, the relationship to their respective closest relatives remains unresolved due to incongruencies among phylogenetic trees. Although we were not able to fully resolve the phylogeny of the subgenus — even with multiple high-throughput sequencing datasets — our findings have substantially advanced our understanding of its evolutionary history. In addition, our results underscore the limitations of even advanced phylogenomic methods, highlighting the impact of factors such as missing data, reference genome selection, and tree reconstruction approaches, emphasizing the need for further methodological development, particularly in the field of bioinformatics.

Blackberries of the tropical Andes: first insights on the evolutionary history of Rubus L. (Rosaceae) in South America

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Subcosmopolitan *Rubus* ranges from the subarctic to the inner tropics and is full of notorious evolutionary and taxonomic challenges. Recent research has refined the infra-generic classification and evolutionary history of *Rubus*, but the affinities of and relationships within South America and especially the numerous Andean taxa remain poorly understood. We generated a critical checklist of South American *Rubus* in order to design a sampling strategy. We then developed a novel probe set for target sequencing consisting of 1,239 orthologous genes for the genus and the family Rosaceae to improve our understanding of the historical biogeography and evolution of Andean *Rubus*. We sequenced 96 accessions, representing 32 of the 46 species accepted for South America and two species from Central America and reconstructed a phylogeny including the published data on 80 samples representing all the subgenera of *Rubus*. South American taxa are retrieved as polyphyletic and falls into three distinct clades, representing at least three colonization events. Diploid and tetraploid taxa are clearly resolved in the concatenated and multi-locus trees. However, the clarification of the origin of tetraploid and hexaploid species will require additional analyses. Additionally, the expansion of the sampling to include taxa from Central America and the Caribbean is necessary in order to fully resolve the origin and relationships of South American *Rubus*.

Untangling the hyacinth: Phylogenomic insights into the systematics and evolutionary history of Scilloideae (Asparagaceae)

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Scilloideae (Asparagaceae) are an iconic clade of ornamental geophytes predominantly found in Mediterranean ecosystems. However, genus delimitation across tribes remains contentious due to pervasive morphological conservatism. Here, we present the first densely sampled phylogeny of the subfamily based on the Angiosperms353 probe set, covering approximately 50% of all species and nearly all accepted genera. Our results confirm the polyphyly of *Scilla* and support a multigeneric framework for both Hyacinthinae and Massoniinae. Additionally, the data reinforce recent reclassification efforts in Ornithogaleae and Urgineeae, providing a robust foundation for future taxonomic revisions. A fossil-calibrated phylogeny reveals that major lineages of Scilloideae diverged prior to the onset of the Mediterranean climate regime (Late Miocene), while diversification within the most species-rich clades coincided with its establishment. This study offers

novel insights into phylogenetic relationships across the subfamily and establishes a solid framework for investigating biome-driven diversification in the context of both past and future climate change.

An updated familial classification of Boraginales based on phylogenomic and developmental data

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Boraginales is a widely accepted order with ~2700 species, but its familial classification remains in flux. We provide new phylogenetic data based on >80% of the genera with 166 newly sequenced and 88 existing samples using the Angiosperms353 probe set. The analyses largely confirm previously identified relationships with improved resolution and support. Different from previous analyses, Namaceae are identified as paraphyletic to Hydrophyllaceae and Lennoaceae are found to be nested in Ehretiaceae. Codonaceae placement remains inconclusive but it is consistently retrieved as an independent lineage. Developmental morphological analyses show that shifts in placentation and ovule number are drivers of morphological divergence, but there are some crucial gaps in our understanding. We propose the recognition of nine families in Boraginales, but emphasize the need for further morphological studies and expanded molecular sampling especially in the woody, tropical families.

Integrating comparative morphology and development into evolutionary research

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For many years, comparative morphology was the primary source of information for systematic studies. However, since the early 1990s, molecular phylogenetics and phylogenomics have revolutionised plant systematics. Technological advances and progress in our understanding of evolutionary processes have resulted in a well-resolved and stable system of plants, particularly for angiosperms. The current system of angiosperms is primarily, if not entirely, based on molecular phylogenetics.

This well-resolved, stable system provides an ideal foundation for understanding morphological and anatomical evolution. However, it is imperative for this task that morphological and anatomical characters are clearly delineated and defined. It is important to note that the 'mature' state of characters, when considered in isolation from their development, has the potential to be misleading. This is due to the fact that it has the potential to obscure significant aspects that are necessary for a comprehensive definition.

It is therefore imperative to acknowledge the significance of development in character definition when formulating evolutionary hypotheses about character evolution in a molecular phylogenetic context.

We argue that, when combined with the latest technologies and a developmental approach, comparative morphology is an important modern scientific discipline that is essential for improving our understanding of the evolution of angiosperms and many other taxa.

Here, we present guidelines for conducting comparative morphological, anatomical and developmental studies. Examples from our current research show how this approach can be used. We want to encourage students and early-career scientists to adopt a comparative morphological approach in their plant systematics research.

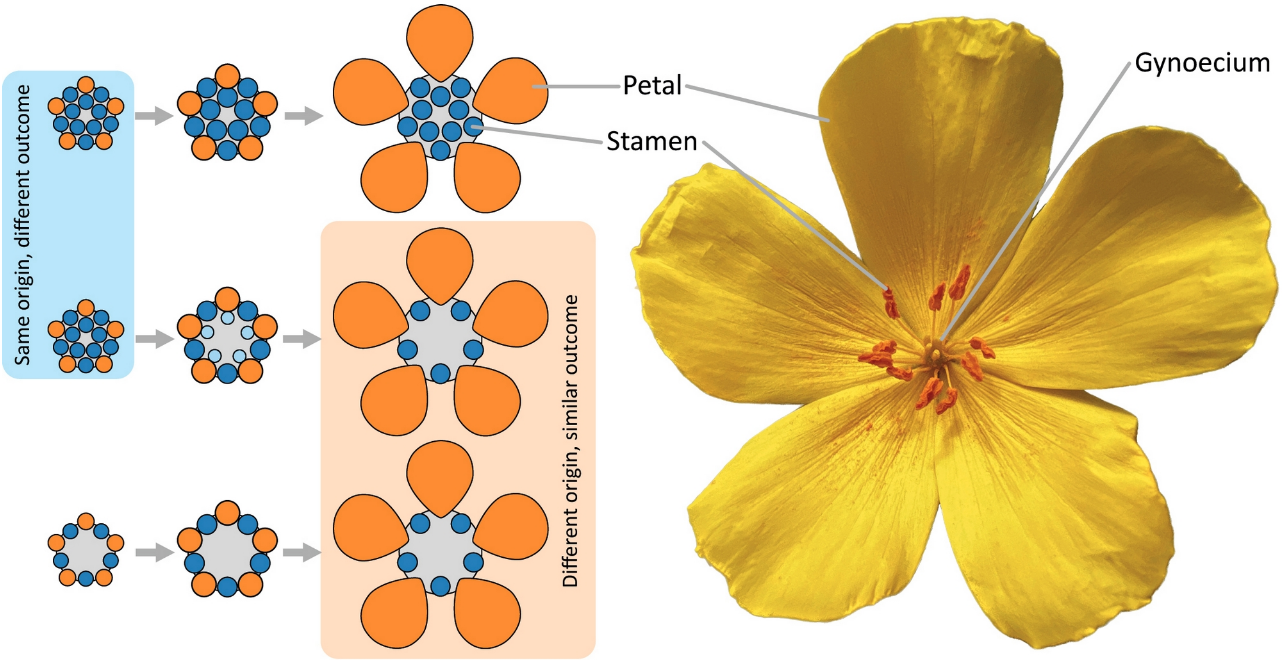

Illustration of the relationship between the early developmental stage and the mature state of flowers. The top and middle example show the development of two flowers with different androecia (i.e., the male reproductive organs) arising from the same initial developmental stage. The middle and bottom example show the development of two flowers with an identical androecium configuration arising from different initial developmental stages. These examples highlight the importance of studying flower development to fully understand the evolution of an organism or structure. The photograph of the mature flower (Balbisia weberbaueri, Vivianiaceae, Geraniales; Botanic Garden Berlin, 107-23-03-14/2) on the right illustrates the configuration of the upper schematic flower. Stamens, petals, and a small visible part of the gynoecium (i.e., female reproductive organs) are labeled. Jeiter and Smets (2024) Comparative morphology at a crossroads. American Journal of Botany e16392 https://doi.org/10.1002/ajb2.16392

Comprehensive and Sustainable Utilization of Genomic Resources: Integrating Target Enrichment, Genome Skimming, RNA-Seq, and Deep Genome Skimming for Improved Phylogenetic Resolution in Sonerileae (Melastomataceae)

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The advent of new next-generation sequencing (NGS) methods has revolutionized phylogenetics, yet challenges remain in effectively utilizing data from a wide range of sources. In this study, we combine target enrichment, genome skimming, RNA-Seq, and deep genome skimming (DGS) data to reconstruct the phylogenetic relationships within Sonerileae, the second-largest tribe in the Melastomataceae. We sampled 176 accessions representing 40 of the 46 genera in Sonerileae, including newly sequenced Hyb-Seq and DGS data along with publicly available NGS data. A newly developed reference comprising 5,626 loci was employed to integrate data from different sources. Our analyses provide a well-supported, near-comprehensive phylogeny for the tribe, outperforming previous and current studies that used only the probe set as reference. This study provides an effective and sustainable approach to integrating genomic data from multiple sequencing strategies for phylogenetic analysis and contributes a more robust phylogeny and novel insights into the evolutionary history of Sonerileae.

SYMPOSIUM IV (chair: M.A. Koch/J. Bechteler)

Talks

Growing at the dray limits of Life

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Life at the biological limits is a fascinating phenomenon that brings to mind the various aspects of the origin of life and the evolutionary dynamics and enormous adaptive capacity of biological systems. Hyperarid systems are characterized by extremely limited water availability and extreme temperature ranges which limit plant growth and survival at any spatio-temporal level from cells to populations and hours to decades. Such biological systems are found in desert habitats in polar and subtropical regions. In subtropical hyperarid desert systems, vascular plant growth is not excluded due to the presence of frozen water. These hyperarid desert systems are characterized by very little or even no rainfall, which in case is highly patchy and unevenly distributed, leading to an extreme aridity index. This heavily affects any water-dependent biological process from the cellular to the tissue and organismal levels and can also cause severe trait-offs.

The hyperarid core of the Atacama Desert in Chile is home to a unique ecosystem called Tillandsia lomas, a unique vegetation type comprised of one plant species only, Tillandsia landbeckii (Bromeliaceae). T. landbeckii forms characteristic regular and linear structured banding patterns in a sloped sand dune landscape. The species lacks a functional root system and is fully adapted to grow on sand (epiarenic growth). The source of water is coastal fog penetrating up to 25 km inland at night and fog water must be harvested at night via the shoot and leaf system and is absorbed by highly specialized trichomes. Source for nutrients are likely dust deposition but also notable bacterial communities. The few most important biotic and abiotic factors interacting with plant growth, individual fitness and vegetation integrity (sand, wind, fog, landscape parameters/slope/exposition, bacterial communities) are well aligned with each other along small and local gradients. Trait-offs are obvious on individual level, e.g. vegetation integrity depends on higher vegetation coverage and well-established linear structures, but luxurious growth may reduce individual fitness because shoot system is not stabilized sufficiently with lacking appropriate amount of sand.

T. landbeckii is an obligate CAM photosynthetic plant operating gas exchange and carbon uptake/fixation (C02 uptake) at night and keeping stomata of the leaves closed during day time while carbohydrates are built up. Water uptake is also granted by leaf cellular structures, highly specialized trichomes for fog absorbance. Considering that total leaf size and shoot dimensions as well as number of epidermal cells are limited and constraint by stable rootless plant architecture, the density of stomata and trichomes may not increase or decrease simultaneously to adapt growth to fine-scaled environmental conditions (fog supply, sand dynamics, slope and exposition) along gradients of a few hundreds of meters and show trade-offs in cell-type density and relative frequency indicating changes in cell fate. We aim to explore the principal patterns of these trade-offs in cell differentiation in epiarenic Tillandsia assuring high control of growth at the limits of plant survival. We hypothesize that alongside genotypically defined phenotypes in particular at the hyperarid core phenotypic plasticity is larger compared to the Desert´s margins.

Dodging the Drought: The Historical Biogeography of Australian Dysphania (Chenopodioideae, Amaranthaceae)

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Australian glandular goosefoot (*Dysphania*, Chenopodioideae, Amaranthaceae) is the species-richest clade of the genus, with approximately 50 currently recognised annual and short-lived perennial species that occur worldwide, primarily in open, ruderal, and seasonally arid habitats. The genus is characterised by glandular hairs containing essential oils that produce a characteristic aromatic odour that often persists in herbarium specimens for years. Australian *Dysphania* species are typically found in high numbers across a variety of habitats, ranging from deserts, semi-deserts, dried-out river and lake beds, to open or sparsely vegetated ruderal habitats across the Australian continent following a rainfall event. Despite seemingly lacking physiological mechanisms common in drought- and salt-adapted plants with whom they share their habitats, these ecologically flexible species have managed to occupy some of inland Australia’s most hostile environments, including highly specific edaphic conditions such as clay, rocky, or sandy soils with high salinity. We employed a target enrichment approach using a *Chenopodium*-specific baitset that targeted 1,721 loci to resolve the phylogeny of Australian *Dysphania* and place it within a spatio-temporal framework. We also conducted character reconstruction of several traits to investigate the potential ecological adaptations underlying their evolutionary success. Our analyses recovered highly supported topologies in both targeted nuclear and off-target plastome trees, with only moderate gene-tree discordance, and revealed a close relationship between African and Australian taxa — a biogeographic pattern observed in many other Australian chenopods as well. We found that *Dysphania* reached Australia in the Late Miocene, probably via long-distance dispersal from the north or the west, followed by a stepwise spread eastwards across the continent during the Pliocene, coinciding with the establishment of the arid zone. A tendency toward smaller seeds and straight embryos suggests adaptations for rapid germination, facilitating survival by avoiding unfavourable conditions. Moderate halophytism evolved only once in *Dysphania*, although species occurring on saline soils germinate readily only during rainfall, which reduces the soil salt concentration. Additionally, reduced floral structures observed in the entire Australian clade may reflect an adaptive trend toward conserving resources in the dry, disturbed, and nutrient-poor habitats that many Australian *Dysphania* species inhabit. Similar drought-avoidance strategies are widespread among Australia’s arid zone flora, placing *Dysphania* within a broader ecological context of ephemeral and ruderal species that capitalise on brief windows of moisture availability.

Integrating Genomics and Museomics to Uncover the Drivers of Astragalus Mega-Radiation

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Astragalus (Fabaceae, Papilionoideae), comprising over 3100 species, is widely recognized as the largest genus of flowering plants. It represents a striking case of recent and rapid evolutionary radiation, particularly in arid and semi-arid regions of the Northern Hemisphere. Despite its diversity and ecological success, our understanding of the evolutionary drivers and adaptive traits underpinning this mega-radiation remains fragmentary. This is primarily due to limited taxon sampling and poorly resolved phylogenetic relationships, which have hampered comparative analyses across the genus.

A leading hypothesis suggests that edaphic specialization and the colonization of extreme or isolated microhabitats have played a major role in the divergence and radiation of *Astragalus* lineages. We are constructing a robust phylogenomic framework for the genus using a target enrichment approach to test this and other evolutionary hypotheses. We developed a novel bait set targeting 686 orthologous genes (819 exons), specifically designed for the Astragalean clade. This tailored approach enables us to resolve deep and shallow relationships across the genus with high accuracy, even among morphologically and ecologically disparate taxa.

Our sampling strategy focuses on the main centres of *Astragalus* diversity – especially the Irano-Turanian floristic region, which hosts more than 1500 species – and is built upon the exceptional holdings of the *Astragalus* herbarium collection at the Botanical State Collection Munich (BSM-SNSB). This collection includes approximately 25000 specimens, representing global diversity and encompassing material from regions that are now difficult or impossible to access due to political conflict, particularly Afghanistan. Many of these specimens serve as invaluable historical vouchers for taxa that are otherwise underrepresented or absent from molecular studies. Remarkably, we extracted usable genomic DNA from specimens up to 115 years old.

We expanded our dataset by integrating publicly available genomic resources, including genome skimming, transcriptomes, and earlier target enrichment data. This allowed us to build the most comprehensive and robust phylogeny of Old World *Astragalus*. Our analyses recovered a well-supported tree at the subgenus level, broadly consistent with earlier studies, but also revealed notable differences in sectional delimitations and strong signals of gene tree discordance, cyto-nuclear conflict, and potential reticulate evolution. These findings point to a more complex evolutionary history than previously appreciated in the genus.

In parallel with the phylogenomic work, we developed a scalable workflow for digitizing the *Astragalus* herbarium collection at BSM-SNSB. This includes high-resolution imaging and automated extraction of text-label data. Using machine learning techniques and large language models, we retrieved occurrence data directly from specimen images, allowing us to integrate ecological and geographic information with genomic data.

Our integrative approach highlights the power of combining museomic resources with cutting-edge phylogenomics to unravel complex evolutionary radiations in hyperdiverse plant groups. By leveraging the depth and historical reach of herbarium collections alongside genomic and ecological data, we are gaining new insights into the mechanisms driving diversification in *Astragalus*, including ecological specialization, morphological evolution, and biogeographic history.

Tracing the Evolution of Bivalent and Univalent Subgenomes in Rosa Sect. Caninae

Herklotz, V., Zhang, M., Nascimento, T., Kalfusová, R., Lunerová, J., Fuchs, J., Harpke, D., Huettel, B., Pfordt, U., Wissemann, V., Kovařík, A., Marques, A., Ritz, C.M.

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Meiotic chromosome pairing and bivalent formation are essential for sexual reproduction. In polyploids, this process may be hampered by the presence of multiple homoeologous subgenomes. Odd-numbered ploidy levels often lead to sterility due to unbalanced chromosome pairing and segregation during meiosis. However, pentaploid dogroses (*Rosa* sect. *Caninae*; 2n = 5x = 35) maintain stable sexual reproduction through a unique meiotic system: 14 chromosomes form 7 bivalents and are inherited biparentally, while the remaining 21 chromosomes are maternally transmitted as univalents. The pentaploid nucleus is thus restored in the fertilised egg.
To shed light on this century-old mystery, we performed haplotype-resolved, chromosome-level genome assemblies from three pentaploid dogroses. Subgenome phasing revealed one bivalent-forming subgenome, comprising two highly homozygous chromosome sets, and three divergent subgenomes that form univalents. Comparative analyses of chromosome synteny and phylogenetic relationships, based on single-copy orthologue loci from diploid rose species, revealed that the subgenomes originated from two distinct clades within the genus *Rosa*. Analysis of pollen genomes further demonstrated that subgenomes of different evolutionary origins can form bivalents, supporting the hypothesis of multiple hybridogenic origins for dogroses and highlighting variation in subgenome contributions. Ty3/Gypsy/ATHILA retrotransposons were partially enriched in bivalent centromeres, while the satellite repeat *CANR4* was significantly more abundant in univalent centromeres, indicating a structural bimodality of dogrose centromeres—likely linked to their meiotic behaviour and meiotic drive.

What evolution smells like: flower scent and phylogeny of the genus Narcissus

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Floral scent is a key trait in plant-pollinator interactions, yet broad evolutionary studies remain rare due to analytical constraints. We demonstrate the utility of GC-IMS, a novel and efficient method for floral scent analysis, in conjunction with a densely sampled phylogenomic framework for *Narcissus* (Amaryllidaceae). We resolve phylogenetic relationships based on ddRADseq, target capture, and network analyses, largely retrieving the infrageneric units that have been described based on morphology. However, the data also clearly show that reticulate evolution has played an important role in the evolution of the genus – an observation underscored by the present-day prevalence of interspecific hybrids in the wild. Integrating the phylogenetic data with GC-IMS scent profiles reveals complex patterns of conservation and divergence in scent profiles, often reflecting ancient hybridization. This study highlights the potential of generating bulk data on floral volatiles with GC-IMS and combining them with highly resolved phylogenies to improve our understanding of the evolution of floral scent as an important trait of floral function.

Born of metal: the genetic diversity and evolutionary identity of a critically endangered metallophyte violet (Viola guestphalica NAUENB.)

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The micro-endemic zinc violet (*Viola guestphalica* Nauenb.) is restricted to a single, heavy-metal-rich site in Westphalia, Germany. Despite its ecological specialization and rarity, its genetic diversity, relationship to other *Viola* taxa, and taxonomic status remain unresolved—posing challenges for conservation. We combined *de novo* genome sequencing with ddRAD-seq to investigate the genomic distinctiveness of *V. guestphalica* compared to related taxa. This approach offers new insights into patterns of gene flow, molecular extinction risks, and species delimitation. By clarifying the zinc violet‘s evolutionary identity and vulnerability, this study provides a foundation for effective conservation and meaningful preservation of this exceptional metallophyte.

SYMPOSIUM V (chair: C. Kiefer/N. Walden)

Introductory Talk

From trees to networks: Omics approaches to complex evolutionary histories

Nora Walden

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Phylogenomic and comparative genomic methods have transformed our ability to study species relationships, particularly in groups shaped by reticulate evolution. Hybridization, introgression, and polyploidy challenge traditional tree-based models and call for integrative omics approaches that leverage genome-scale data across multiple levels of complexity. I will highlight case studies on (1) the use of gene tree discordance and species network inference to detect hybridization and gene flow, (2) the reconstruction of polyploid origins through phylogenomic and synteny-based comparisons, and (3) the insights gained from comparative genomics into genome evolution and species divergence. As high-quality genomes become increasingly available across the tree of life, these approaches will become more powerful, scalable, and accessible for resolving complex evolutionary patterns.

Talks

Whole-genome reconstruction and comparative genomics of three reticulate species: Insights into genome variability of Salix section Vetrix

Ferris Heiduk, Natascha Wagner

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To date, only a few studies have analyzed the genomic composition and evolution of hybridizing non-model species. We expect to see patterns of conserved genomic regions, while other parts may be freely exchanged between species. In the case of allopolyploidization, we should be able to identify and compare the parental subgenomes. However, as hybridization continues during lineage evolution, the resulting genomic pattern becomes increasingly complex—giving rise to a genomic mosaic shaped by both retention and exchange.

The vast diversity of the genus *Salix* is shaped by hybridization, polyploidy, and introgression, especially within shrub willows (subg. *Chamaetia* & *Vetrix* clade). Within section *Vetrix*, the tetraploid species *S. cinerea* is believed to be of allopolyploid origin, with the diploids *S. aurita* and *S. caprea* as possible parents, rendering them an ideal model for gaining insights into genome evolution in *Salix*. We reconstructed the genomes of all three species utilizing PacBio HiFi sequencing and Illumina data. By phasing the subgenomes of the tetraploid species, we compared their structure to the diploid parental genomes and identified both variable and conserved genomic regions.

So far, reduced representation methods have been used to reconstruct phylogenetic relationships between shrub willow species of *Salix* sect. *Vetrix*. Ancient and recent hybridization, as well as the netlike relationships, obscure the reconstruction of a bifurcating phylogeny, leading to conflicting signals and low resolution within this clade, which was based on samples of about 14 species assigned to section *Vetrix*. To dive deeper and start untangling this possible syngameon and the interplay of evolutionary mechanisms, we will use the three genomes as references for re-sequencing the remaining species. Thus, we aim to disentangle the evolutionary patterns connected to hybridization, polyploidy, and introgression.

Diverging repeatomes in holoparasitic Hydnoraceae uncover a playground of genome evolution

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The transition from an autotrophic to a heterotrophic lifestyle is associated with numerous genomic changes. These often involve large genomic alterations, potentially driven by repetitive DNAs. Despite their recognized role in shaping plant genomes, the contribution of repetitive DNAs to parasitic plant genome evolution remains largely unexplored. This study presents the first analysis of repetitive DNAs in Hydnoraceae genomes, a plant family whose members are holoparasitic. Repetitive DNAs in the Hydnoraceae genomes were identified and annotated *de novo*. Abundant transposable elements and 35S

ribosomal DNA in the reference *H. visseri* genome were reconstructed *in silico*. Patterns of abundance and presence-absence of repetitive DNAs were individually and comparatively analyzed. Both Hydnoraceae genera, *Hydnora* and *Prosopanche*, exhibit distinct repeatome profiles which challenge our current understanding on repeatome and rDNA evolution. The *Hydnora* genomes are dominated by long terminal repeat retrotransposons, while the *Prosopanche* genomes vary greatly in their repeat composition: *P. bonacinae* with a highly abundant single DNA transposon and *P. panguanensis* with over 15% 5S rDNA, compared to ≤0.1% in the *Hydnora* genomes. The repeat profiles align with the phylogeny, geographical distribution, and host shifts of the Hydnoraceae, indicating a potential role of repetitive DNAs in shaping Hydnoraceae genomes to adapt to the parasitic lifestyle.

Flowers, fruit, and rhizome of Hydnoraceae; A. H. visseri flower; B. H. triceps flower; C. H. abyssinica flower; D. H. visseri rhizome; E. H. visseri fruit; F. H. visseri fruit section; G. P. americana flower; H. P. bonacinae flower; Photographs (A, D, E, F) by Jay Bolin, (B) by Stefan Wanke, (C) by Elijah Mbandi Mkala (G, H) by Andrea Cocucci. (G, H) were reproduced from Jost et al. (2022).

The Crocus panrepeatome reveals links between whole-genome duplications, repeat bursts, and descending dysploidy

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Dysploidy is a crucial driver of species diversification by changing karyotypes through diploidization after whole-genome duplication (WGD). WGD can trigger repeat bursts, but our knowledge of the evolutionary links between WGD, repeat bursts, and descending dysploidy is limited. Using *Crocus* as a model, we performed a panrepeatomic analysis to gain insights into the influence of WGD on repeat bursts and of repeat dynamics in descending dysploidy. We first established a phylogenetic backbone of the genus using chloroplast (cp) and 35S rDNA sequences, which we used to analyze our panrepeatome data. We identified a WGD event before the initial divergence of *Crocus* and nested WGD events before the divergence of some series coincided with repeat bursts. We demonstrated repeat-linked chromosome fusions of *C. longiflorus* chromosomes in the dysploid relative *C. vernus*. This work demonstrated the links between WGD, repeat bursts, and descending dysploidy.

Herbariomics and phyloecomorphospace exploration reveal adaptive and non-adaptive radiation events as main drivers of the evolution of Selaginella (Selaginellaceae) in the Greater Antilles.

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Selaginella in the Greater Antilles comprises 42 species, of which 88% are endemic to the archipelago and 50% are restricted to a single island. In the context of a global phylogeny, the phylogenetic position of Greater Antilles species was reconstructed by combining partial plastomes and Sanger sequencing data available from GenBank (rbcL, 5.8S, 18S, 26S, SQD1, and pgiC). A genome skimming approach and an aDNA extraction method were applied to herbarium specimens from Cuba, Jamaica, Hispaniola, and Puerto Rico in order to recover partial plastomes corresponding to 50 markers and three nuclear markers (18S, 5.8S and 26S). The sampling included 47 specimens corresponding to 38 species (90% of the native diversity). The phenotype variation (14 characters) was contrasted with the phyloecospace (altitude, substrate nature, and nine climatic variables) in the Antillean clades using a dated phylogeny as a framework. Ancestral states of morphological characters and ancestral areas were also explored. Our data support a Miocene colonization of the Greater Antilles from Continental Tropical America, in several instances with subsequent speciation events. The evolution of *Selaginella* in this region has been driven by a combination of adaptive and non-adaptive radiations following ten colonization events. Greater Antillean *Selaginella* species are predominantly prostrate plants, with rhizophores distributed along the stem. In contrast, Neotropical continental species are predominantly erect, with rhizophores located only at the base of the stem. Closely related Antillean species exhibit different strobilous phyllotaxy (quadrangular vs. bilateral), with the quadrangular phyllotaxy being the ancestral state. Moreover, these closely related taxa occupy distinct niche spaces with regard to altitude or substrate nature (e.g. serpentine vs. limestone).

Ecological Barriers and Deep-Clade Hybridization in Isoetes

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Isoetes, a globally distributed lycophyte genus with ~250 species, shows extensive polyploidy and deep genetic divergence across five major clades. While hybridization and allopolyploidy occur frequently at closely related taxonomic levels, ecological and genetic barriers appear to limit gene flow between major clades. Using PacBio HiFi multi-locus nuclear markers, we reconstructed phylogenetic relationships to assess interclade genetic exchange. Our results reveal that ecological divergence reinforces clade integrity and shapes evolutionary trajectories in *Isoetes*, up to a certain limit. This talk explore the power of genomic data to illuminate the complex interplay between hybridization, polyploidy, and ecological differentiation in a relict plant lineage.

Poster Session I

SSRseq: A future way to revisit the past?

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Posternumber: #1

Microsatellite (SSR) length polymorphism has long been a staple in the population genetic marker “kitchen”, but now successively gets displaced by various flavours of RADseq and whole genome resequencing. Still, SSR data remain important, as they are sometimes the only record of past genetic diversity.

Re-using samples from four conservation genetic studies on the declining medicinal plant *Arnica montana* (Asteraceae), we investigated the homology of SSR alleles across Europe and its impact on population genetic measures. We found considerable variation in the difference between sequence-, sequence length- and electrophoretic length-based allelic diversity across loci, impacting also other, derived genetic diversity measures.

In the light of our results, we discuss possibilities and limits of using historic SSR data for conservation genetic monitoring and evolutionary time series studies.

Elodea canadensis MICHX. and Elodea nuttallii (PLANCH.) H. ST. JOHN (Hydrochoritaceae) in Hesse – Population genetics of two often confused species

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Posternumber: #2

The Project examines the diversity of invasive and potential invasive aquatic alien species in Hesse. The first record of *E. canadensis* in Germany dates back to1854. Since then, the plant has spread quickly in large numbers and in a short period of time, hence the name “Wasserpest”. *E. nuttallii* was recorded almost exact 100 years later. Due to its later appearance and the similar morphology between both species under certain conditions has led to the underestimation of *E. nuttallii*. This species has an even further distribution as *E. canadensis* now. *E. nuttallii* also appears in habitats former overgrown by *E. canadensis*. While *E. canadensis* could be seen as an enrichment by now, *E. nuttallii* is affecting species growth and species richness by occupying resources and space in the locality and gives a significant impact on the ecology. But only little is known about the genetic composition within the populations. Our results show only a small molecular variance between populations but a high molecular variance within those populations. The populations of *Elodea* sp. have a middle to low genetic diversity.

Deciphering the taxonomic and evolutionary puzzle in Erysimum (Brassicaceae) using an integrative approach

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Posternumber: #3

We focus on clarifying the evolutionary history and speciation in *Erysimum*, a species-rich but understudied genus with recent diversification and remarkable karyological diversity. By integrating morphometric, flow cytometric, cytogenetic, and phylogenomic analyses, we elucidate evolutionary relationships in the species complex of *E. odoratum*, uncover genetic patterns inconsistent with traditional taxonomic treatments, and discover multiple cytotypes that exhibit significant differences in genome size and include both dysploidy and polyploidy. Isolation-by-distance, biogeographic barriers and chromosomal rearrangements (dysploidy) are identified as major barriers to gene flow driving diversification within this species complex, but which is also blurred by reticulate events (introgression, allopolyploidy).

Population genetics in the Hessian endangered orchid *Anacamptis morio* (L.) R. M. Bateman, Pridgeon & M. W. Chase – first results

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Posternumber: #4

Anacamptis morio is a Hessian terrestrial orchid whose populations are declining due to factors like habitat loss, fragmentation and climate change. In order to obtain an overview of the genetic structure of the populations, genetic diversity and genetic differentiation are analyzed. Two molecular methods ISSR (Inter Simple Sequence Repeats) and SCoT

(Start Codon targeted) are used for this purpose. Initial results indicate moderate genetic differentiation and for genetic diversity a range between H_e 0.212 to H_e 0.275.

The genetic diversity of *Herminium monorchis* (L.) R.Br. in Hesse and its implications for conservation.

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Posternumber: #5

The rare orchid *Herminium monorchis* faces severe threats in Hesse due to climate change, habitat fragmentation and changes in land use. This study analysed genetic diversity within and between populations using ISSR and ScoT markers. The results provide valuable insights into population structure and genetic variation, forming the basis for conservation planning. Seed material was also collected for artificial propagation. The aim is to cultivate resilient individuals for potential reintroduction into their natural habitats. These findings will inform the development of targeted strategies to support the long-term survival of *H. monorchis* in the wild.

Genome-wide SNPs developed by genotyping-by-sequencing reveals diversity and population structure of the Atacama endemic genus Eulychnia Phil. (Cactaceae).

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Posternumber: #6

Eulychnia (Cactaceae), a small neo-endemic columnar cactus genus, has an evolutionary history that remains poorly understood. Recent analyses date its diversification to the early Pleistocene, yet taxonomic boundaries are still dubious. A recent revision suggests three endemic species - *E. breviflora* and *E. acida* from the Atacama Desert´s coastal fog zones, and *E. ritteri* from southern Peru - including nine subspecies. This study aims to offer new insights into evolutionary drivers, population genetics, and genetic diversity within the genus. Genotyping-by-sequencing (GBS) data provided 2188 informative single nucleotide polymorphisms-SNPs across 54 populations (636 individuals) distributed across all the genus range. Analysis of molecular variance (AMOVA) revealed slightly higher genetic variation within *E. breviflora* ($\phi = 0.51$) compared to *E. acida* ($\phi = 0.48$). Clustering analysis, including sNMF (Sparse Non-negative Matrix Factorization), phylogenetic tree and network reconstruction, and principal component analysis (PCA), consistently separated populations by geographic distribution. The Mantel test showed stronger isolation by distance (IBD) in *E. breviflora* (r = 0.78) compared to *E. acida* (r = 0.58). Diversity indices (H_O, H_E, F_{ST}, and allelic richness) revealed moderate genetic diversity despite an inbreeding tendency detected by the inbreeding coefficient (F_{IS}). Progressive aridification has fragmented the genus´s habitat, driving its evolutionary divergence and population structure through geographic isolation. Nonetheless, genetic signatures of a historically broader distribution persist in *E. breviflora* subsp. *atacamensis* (the only inland subspecies from *E. breviflora*) and in several northern *E. breviflora* subsp *taltalensis* populations. These populations exhibited high genetic diversity (allelic richness and heterozygosity) comparable to core populations; an outcome suggesting rather a relic refuge than a more recent founding event. The f-branch statistic revealed that *E. acida* retains higher genetic connectivity via overlapping populations experiencing gene flow, whereas *E. breviflora* exhibits stronger fragmentation, restricted gene flow and intensified local adaptation producing isolated, low-diversity populations. Conservation efforts in *E. breviflora* subsp. *iquiquensis*, north of Antofagasta, should be prioritized for its critical genetic bottleneck and the Copiapó-Coquimbo hybrid zone for its enhanced diversity. These results showed that habit fragmentation, reduced gene flow and local adaptation are driving *Eulychnia* speciation. The current taxonomic concept does not reflect the genetic clusters and falls short in recognizing hybrids at contact zones.

Population genetics and phylogeography of the endangered steppe plant Oxytropis pilosa

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Posternumber: #7

The migration history of continental steppe plants and the development of steppe grasslands in Europe remain poorly understood. The number of publications on this topic has increased since the early 2000s. For a long time, phylogeographic research focused primarily on Eastern European regions, and the continental steppes of Central Europe received little attention. However, in recent years, increasing attention has been given to the fragmented western outposts of these steppe ecosystems. Nevertheless, significant knowledge gaps remain, particularly concerning the historical dynamics and genetic distinctiveness of Central European steppe habitats.

In Europe, continental steppes occur at the periphery of their natural distribution range and are restricted to specific ecological niches. They are highly fragmented, confined to a few, ecologically unique locations, and rely on continuous human management. Without regular disturbance such as grazing or mowing, they would become overgrown and be displaced by surrounding deciduous forests. Their long-term persistence is therefore closely tied to both ecological conditions and sustained conservation efforts.

Effective protection requires an understanding of the current genetic status of these plant populations and the historical processes that shaped them. Population genetic analyses provide insights into genetic diversity, structure, and connectivity, while biogeographic approaches help reconstruct migration routes and detect relict populations.

To explore the development of these steppes and evaluate the conservation value of their plant populations in Central Europe, this study investigates the phylogeography and population genetics of *Oxytropis pilosa* (Woolly Milkvetch). This species is widely distributed throughout the Eurasian steppe belt, but limited to isolated populations in Europe, where it is considered endangered.

To analyse phylogeographic patterns and population genetic structure simultaneously in both fresh and historical material, 21 nuclear markers were developed using the Angiosperms353 target enrichment approach. The dataset includes 198 individuals from 18 populations in Germany, the Czech Republic, and Estonia, and 44 herbarium specimens covering a broader range. DNA was extracted and sequenced using Illumina short-read technology.

Preliminary results provide insights into regional genetic differentiation, within-population diversity, and the biogeographic history of Central European populations. This unified analytical approach enables the simultaneous investigation of phylogeographic patterns and population structure using both fresh and herbarium material. The results provide a foundation for assessing the genetic value of isolated populations and support long-term conservation strategies for *Oxytropis pilosa* and similar steppe relicts.

Barriers to gene flow in *Platanthera* (*Orchidaceae*) hybrids and morphological “mosaic” species

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Posternumber: #8

Of the species-rich orchid genus *Platanthera*, two species, *P. bifolia* (incl. e.g. *P. fornicata*) and *P. chlorantha*, are widely distributed throughout Central Europe. We characterised a third and genetically well-separated taxon and have shown that it has a wider Central European distribution. This taxon has been described as *P. muelleri* A.Baum & H.Baum in 2017, which we consider a synonym of *P. pervia* Petermann 1846. This third species combines characters from the other two species in a mosaic pattern and is not a simple “intermediate” taxon. Hybrids between all three species occur with a low frequency and display intermediate traits in their flower morphology. Understanding the pollinator flower interaction and therefore the gene flow and reproductive barriers between the three species is crucial for further characterisation of *Platanthera* in Central Europe and local protection. We analysed the emitted volatiles of the flowers, which are used to attract pollinators, with GC-MS in genetically typified pure and mixed *Platanthera* populations. Pollinators were monitored in the same populations by continuous video capture. The measured volatiles and video-captured pollinators (moths) show the impact of plant-insect coevolution of the past on today's local gene flow.

Phylogenetic relationships among Chilean Baccharis L. (Compositae, Astereae) taxa inferred from 3RADseq and AFLPseq

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Posternumber: #9

Abstract: *Baccharis* L. (Compositae, Astereae) is a New World genus and comprises approximately 350 to 500 species (depending on the genus circumscription). In Chile, the genus in its narrow sense is represented by 16 species, most of which forming hybrids when sharing the same habitat and/or flowering time. As a syngameon the genus poses considerable taxonomic problems and, therefore, is a focal study group in the Carrara project (TaxonOmics programme), which aims at the establishment of objective methods of integrative species-delimitation in intensively hybridising genera based on herbarium specimens. As an initial step of the project, the phylogenetic relationships among the Chilean taxa of *Baccharis* were examined using the combination of the 3RADseq and AFLPseq methods to gain SNP information. Owing to the overlapping but non-identical composition of the two datasets, gene trees were constructed based on SNP matrices both from the 3RADseq (12,583 locus-wise gene trees) and the AFLPseq SNP information (2,345 locus-wise gene trees) and conjointly used for species-tree reconstructions. According to these species-tree reconstructions, the Chilean taxa of *Baccharis* are assignable to three well-supported monophyletic groups: the *B. tola*-group of section *B.* sect. *Cespitosae,* a group of six species of *B.* sect. *Cuneifoliae* around *B. rhomboidalis,* and a large group of nine species comprising members of both *B.* sect. *Cuneifoliae* and sect. *Pedicellatae.* Low support values for monophyletic groups within these three clades point towards incongruences among gene trees caused by hybridisation and/or incomplete lineage sorting. Future studies will use integrative species-delimitation approaches including genealogy, morphology, ecology, and geography to clarify the taxonomic status of the taxa within the three clades revealed by the present study.

Cryptic diversification in Crocus: Insights from phylogenomics and resolved genome duplications

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Posternumber: #10

Whole genome duplications (WGDs) play a key role in plant evolution. In *Crocus* (Iridaceae), genome size variation and frequent dysploidy have obscured signals of past WGD events. Moreover, the phylogenetic backbone of *Crocus* has remained unresolved, limiting evolutionary interpretation.

To establish a robust framework, we reconstructed the phylogeny of *Crocus* using chloroplast genomes, 35S rDNA sequences, and 14 nuclear single-copy genes. Genomic long-read sequencing was also performed for six representative species. Gene duplications were identified using BUSCO, and synonymous substitution rates (Ks) were calculated to estimate the timing of duplication events.

Our analyses revealed a WGD event (Cr-β) dated to 14.9–19.7 Mya (Ks = 0.118–0.168), preceding the diversification of all current *Crocus* lineages. The presence of shared paralogs with *Afrocrocus* and *Syringodea* suggests that Cr-β was an allopolyploidization event involving the ancestor of these genera and *Crocus*. Additionally, multiple more recent WGDs were detected in different lineages within the genus.

Identifying WGDs and particular hybridization events provides a better understanding *of* subsequent diploidization processes and a solid foundation for revising the genus and resolving long-standing taxonomic ambiguities in *Crocus*

Molecular and ecological analyses towards an integrative taxonomic treatment of the Rhodanthemum atlanticum-group (Compositae, Anthemideae)

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Posternumber: #11

Abstract: The genus *Rhodanthemum* B.H.Wilcox & al. (Compositae, Anthemideae) presently comprises 17 species distributed in NW Africa (mainly Morocco) and S Spain. Owing to the formation of hybrids whenever representatives of the genus share the same habitat, this syngameon is a focal study group in the Carrara project (TaxonOmics

programme), which aims at the establishment of objective methods of integrative species-delimitation in intensively hybridising genera based on herbarium specimens. We have used 92 accessions of *Rhodanthemum* and three of its sister-genera *Chlamydophora, Chrysanthoglossum,* and *Leucanthemum* to infer phylogenetic relationships among all described species of the former genus based on a SNP matrix gained by AFLPseq fingerprinting. Based on a total of 43,538 SNPs, a well-supported backbone phylogeny of *Rhodanthemum* emerged that was used subsequently to further elucidate the species delimitation in the group of *Rh. atlanticum, Rh. briquetii, Rh. quezelii,* and *Rh. redieri.* After inclusion of additional 96 accessions for these four species, a data matrix of 42,240 SNPs from 3,718 loci was gained. Network analyses showed that *Rh. quezelii* subsp. *ijallabenense* from the eastern High Atlas Mts is closer related to *Rh. atlanticum* than to *Rh. quezelii* subsp. *quezelii,* and that within the former species, there is a continuous elevational transition between its typical variety *Rh. atlanticum* var. *atlanticum* and its high-elevation variety *Rh. atlanticum* var. *gelidum* in the Mt. Toubkal area in the western High Atlas Mts. Ecological data based on eco-climatological and edaphic (soil-grid) variables confirmed distinct environmental preferences of the studied taxa and may add – together with morphological variables – to an integrative taxonomy in this species group.

Applied Conservation Genetics in *Nuphar pumila*: From ddRAD to CAPS Markers

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Posternumber: #12

Nuphar pumila (Timm) DC. (Nymphaeaceae), the least water lily, is a glacial relict and regionally endangered aquatic species in Central Europe, threatened by eutrophication, habitat alteration, and introgressive hybridization with *N. lutea*. Building on genome-wide SNP data from ddRAD sequencing, we developed species-diagnostic CAPS markers targeting fixed nuclear polymorphisms to enable rapid and cost-effective genotyping for conservation purposes.

We applied this marker system to over 600 samples from 52 populations across Central Europe. The results corroborated population structure and hybridization patterns previously inferred from ddRAD data and revealed a higher-than-expected number of genetically pure *N. pumila* populations. In addition, we used the CAPS markers in several targeted case studies to assess the status of relict populations in Mecklenburg-Vorpommern, reevaluate the presence/absence of hybrids in the UK, and confirm absence of hybrids an ex situ collection intended for reintroduction.

Our findings demonstrate the utility of reduced-representation genomic data to inform applied marker development and highlight the value of CAPS markers as a practical tool for conservation management in *Nuphar*.

An integrative workflow for the open and reproducible taxonomic treatment of Greece‘s largest plant genus

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Posternumber: #13

By combining big data and advanced tools, we present an efficient workflow in integrative taxonomy, illustrated through the development of the first open-access and reproducible treatment for *Centaurea* (*Asteraceae*) within the Flora of Greece project. Thousands of specimens were digitized, leveraging AI for label data, and detailed floral images were captured. Structured morphological data (100 characters/specimen) and phylogenomic data (1061 nuclear loci via HybSeq) were integrated. Using the EDIT platform for Cybertaxonomy, we automated generation of species descriptions and distribution maps, and compiled a comprehensive treatment including keys, nomenclature, photos, and more —demonstrating a scalable model for open, modern taxonomy.

The Meliaceae TEN (Taxonomic Expert Network)

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Posternumber: #14

In the context of the accelerating biodiversity crisis and growing demand for reliable, integrative taxonomic resources, the World Flora Online (WFO) initiative has emerged as a collaborative platform to compile and curate an authoritative, global plant species checklist. Central to this initiative are the Taxonomic Expert Networks (TENs), which bring together specialists on specific plant families to maintain and update taxonomic data through the Rhakhis data management system. This presentation introduces the newly established Meliaceae TEN, which aims to create a dynamic and up-to-date taxonomic backbone for this ecologically and economically important pantropical plant family.

Meliaceae, with over 750 accepted species distributed across 58 genera, is a family of mostly trees and shrubs of significant importance in (sub)tropical ecosystems. Despite its relatively moderate size, taxonomic understanding of the family is limited in some genera, with a lack of recent, integrative revisions for many genera. A 2023 assessment of expert-curated data for the family revealed a low level of agreement between global taxonomic checklists, underscoring the urgent need for harmonized and actively curated taxonomic information.

The Meliaceae TEN was formed to address this gap by assembling a network of global experts in the family's taxonomy, phylogeny, and systematics. Through the WFO's Rhakhis platform, mediated by a database expert involved in the TEN, TEN members can collaboratively edit taxonomic records, reconcile synonymies, correct bibliographic references, and incorporate phylogenetic insights in real time. This shift from static data accumulation to active, community-based curation marks a turning point in how taxonomic knowledge is maintained and disseminated. By facilitating direct involvement of taxonomists in data stewardship, the system empowers experts to respond promptly to new discoveries and taxonomic proposals, reducing the lag between publication and integration into global resources.

In addition to improving taxonomic coherence, the work of the Meliaceae TEN supports broader scientific and conservation goals. A robust and up-to-date taxonomy enables accurate species counts, informs assessments of species distributions and extinction risks, and provides a stable framework for ecological and ethnobotanical research. Moreover, by aligning with the WFO infrastructure, the outputs of the Meliaceae TEN are openly accessible and interoperable with other biodiversity databases and portals, amplifying their impact across disciplines.

This presentation will highlight the current progress and structure of the Meliaceae TEN, discuss the collaborative workflow enabled by Rhakhis, and outline taxonomic challenges specific to the family—such as poorly resolved generic boundaries and underexplored tropical floras. Lessons learned from other successful TENs will be discussed to contextualize the Meliaceae TEN's strategy and priorities. The presentation will also invite contributions from other specialists and institutions, fostering a spirit of international collaboration and long-term sustainability for this taxonomic effort.

Ultimately, the Meliaceae TEN serves as a model for how expert networks can revitalize taxonomy in the digital age, turning scattered expertise into coordinated action. As biodiversity faces mounting threats, such efforts are not just academic—they are foundational to understanding and preserving the richness of plant life on Earth.

Geographic patterns of rDNA ITS polymorphisms reveal genetic differentiation in Iranian Nerium

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Posternumber: #15

Oleander (*Nerium*; Apocynaceae) is a taxon widespread in dry areas between the Mediterranean and Central Asia. In Iran, it is traditionally assumed that two species occur: *N. oleander* and *N. indicum*, discernable by the fragrant flowers of the latter. However, most taxonomic treatments of the genus assume that it is monotypic. We investigated

Iranian *Nerium* populations with ISSR markers and by sequencing the rDNA internal transcribed spacer (ITS) region. While ISSRs resulted in geographically structured population relationships, in the ITS sequences distinct differences were detected in the number of polymorphic sites per individual. Genome skimming through whole-genome shotgun (WGS) sequences showed that the populations in the north and south of the taxon’s distribution area were characterized by single and uniform ITS sequences, whereas in the central populations individuals harbored two rather diverse ITS sequences. While this pattern resembles a hybrid zone between two taxa, sequence analysis did not support this conclusion. As we found no indication for polyploidization, our results suggest geographically structured differences in rDNA evolution, potentially driven by unequal rates of concerted evolution or independent evolution of multiple rDNA loci. We currently try to match the ITS patterns with the assumed species assignments to see if the differences might be characteristic for *N. oleander* and *N. indicum*, respectively.

Testing machine learning approaches for species delimitation in taxonomically complex groups – A case study in Toona (ENDL.) M.ROEM., Meliaceae

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Posternumber: #16

Recent advances in machine learning hold much promise for fast-tracking species delimitation and integrative taxonomic approaches yet their applicability in taxonomically complex groups remains underexplored. The small but socioeconomically important tropical timber genus *Toona* (4−6 species, Meliaceae) has thus far evaded taxonomic clarification and represents an ideal system to test these new techniques. We will compare established species delimitation approaches (e.g., Stacey, DAPC) to unsupervised machine learning (SuperSOM) and use the resulting genetic clusters as labels to train a Support Vector Machine classifier using image scans of herbarium vouchers. Ultimately, this approach promises to unlock the diverse information available from the herbarium resources and pave the way towards resolving other taxonomically complex groups.

Advancing Evolutionary Understanding of the Iconic Andean Tree Genus Polylepis (Rosaceae)

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Posternumber: #17

The culturally and economically significant Andean tree genus *Polylepis*—which forms the world's highest-elevation treelines—has long eluded a well-supported phylogenetic reconstruction, possibly due to extensive gene flow, hybridization, and polyploidization. To address this, we investigate sympatric populations of *P. neglecta* (Bolivia) and *P. incana* (Ecuador) using genomic (ddRADseq) and morphological data. Our goal is to provide empirical evidence for these evolutionary processes and to propose strategies for reconstructing the phylogeny of the genus. We hypothesize that, despite high levels of gene flow and hybridization, species boundaries remain distinct, and that ddRADseq data will provide high phylogenetic resolution.

All together now? A phylogenomic analysis and systematic revision of the diverse family Plantaginaceae

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Posternumber: #18

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, mainly by including parts of the Scrophulariaceae but also several other, small families. This circumscription has basically not changed in the past 20 years, since the first molecular studies targeting those families were published. Nowadays around 106 genera are part of Plantaginaceae, containing approximately 2100 species, which are representing around 1% of the eudicots.
Nevertheless, despite ongoing research, relationships among genera and tribes are still unresolved and evolutionary trends in characters unclear.
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. 134 samples could be included into further analysis, representing 88% of the genera in the family. The data was cleaned, assembled, extracted and aligned via Captus, a concatenated tree was calculated via IQ-TREE, including Ultrafast bootstrap support and Shimodaira-Hasegawa approximate likelihood ratio test (SH-alrt).

Four genera were found in the outgroup, which were thought to be part of Plantaginaceae, namely *Ildefonsia, Triaenophora, Uroskinnera* and *Trungboa*. The concatenated tree itself splits into two major sister clades, one containing the Gratioleae and Angelonieae, while all other tribes belong to the second clade. In Angelonieae, *Cheilophyllum* was included the first time in a DNA-based analysis and is found to be sister to *Scoparia*. In Antirrhineae *Maurandella* is possibly paraphyletic with respect to *Maurandya*. Twelve tribes are well supported, strengthening former decisions of placing parts of other families within Plantaginaceae. The genera-wise largest tribes Gratioleae and Antirrhineae show some smaller changes, mainly keeping their former taxa. Most of the smaller tribes hold no surprises, Hemiphragmeae still appears as a monotypic tribe, as sister to Veroniceae. The placement of some genera is still uncertain, due to low coverage or inaccessibility of material.

Our phylogenetic hypothesis shows good support values for the family backbone, clarifying members for the twelve tribes and reveal some notable changes within the tribes. This includes *Conobea* being integrated into *Bacopa*, *Neopicrorhiza* being suggested for integration into *Picrorhiza* and *Achetaria* being found to be a synonym of *Matourea*. On the other hand, two new genera were separated from *Stemodia*, *Umbraria* and *Lapaea*. *Maurandya* may be part of *Maurandella*, leaving it paraphyletic at this point. *Wulfenia* was found to be sister to the rest of the tribe of Veroniceae, and *Kashmiria* was sequenced here for the first time, and was recovered as sister to *Picrorhiza*.

Flames of the Lowlands: Fire Lilies of Northwestern Germany

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Preliminary results

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Posternumber: #19

The genus *Lilium* comprises approximately 100 species, predominantly found in the cold and temperate regions of the Northern Hemisphere. These species have gained considerable importance as ornamental plants, particularly in the global cut flower industry, in which they are highly valued for their striking appearance and diversity. The genus is taxonomically divided into seven sections: *Archelirion*, *Leucolirion*, *Lilium*, *Martagon*, *Oxypetalum*, *Pseudolirium*, and *Sinomartagon*, as originally proposed by Comber in 1949. In Germany, only two native species of *Lilium* are present: *Lilium martagon* L., classified under *L*. section *Martagon*, and *L. bulbiferum* L., which belongs to *L*. section *Sinomartagon*.

Lilium bulbiferum is notable for being the most widespread lily in nature in Europe. Its natural range extends from the Pyrenees through the Apennines to the Balkan across various mountainous regions. Interestingly, this species is found in the north-western lowlands of Germany, an area that lies well outside its typical montane distribution. In these lowland regions, especially in Lower Saxony near the Dutch border, *L. bulbiferum* historically occurred as a weed, particularly in rye fields("eternal rye fields"). Historical accounts from the 19th century recount how farmers were wary of this plant, viewing it as an undesirable weed, yet at the same time, some admired its beauty enough to transplant it from the fields into their home gardens.

Recent taxonomic work by Koch (2023) has identified three distinct taxa and one variety of *L. bulbiferum* sensu lato in Lower Saxony based on morphological characteristics. These include the presence or absence of aerial bulbils, the position of these bulbils, their development timeline, and the characteristics of the bract undersides. In western Lower Saxony, plants have been documented that lack aerial bulbils but develop subterranean bulbils on stolon-like stems. These populations are now mostly extinct due to modern agricultural practices that have altered or destroyed their habitats. However, these individuals fit very well to the morphological description of *L. (bulbiferum subsp.) croceum* Chaix in the Pyrenees and the west Alps.

With regards to the third taxon, eastern Lower Saxony is home to *L. buchenavii* Focke ex R.J. Koch that bears aerial bulbils on their inflorescences and feature smooth bract undersides. A particularly distinct variety, *Lilium buchenavii* var. *govelinense* R.J. Koch, is endemic to the Govelin area in the Göhrde region. This variety is characterized by the presence of aerial bulbils, a later flowering period, and hairy bract undersides, distinguishing it from other taxa. Additionally, the typical form, *Lilium bulbiferum* sensu stricto, is found in the Harz region. This taxon is marked by the presence of axillary bulbils both in the inflorescence and in the leaf axils of stems at various developmental stages.

The main objective of this study was to investigate the genetic diversity among these different fire lily populations in Lower Saxony and to determine their potential phylogenetic relationships with populations found in the mountainous regions of Central Europe. In pursuit of this aim, plant samples from various locations were collected. These included populations of *L. buchenavii* and *L. buchenavii* var. *govelinense* from Lower Saxony, as well as *L. bulbiferum* s. str. from the Harz (Lower Saxony), Prignitz (Brandenburg), and southern Austria.

DNA was extracted from the collected samples and analyzed using MIG-seq (Multiplexed ISSR Genotyping by Sequencing). Phylogenetic trees constructed from the DNA sequence data showed clear genetic differentiation corresponding to the taxa described by Koch (2023). Specifically, *Lilium buchenavii*, *L. buchenavii* var. *govelinense*, *L. bulbiferum*, and *L. croceum* formed distinct monophyletic groups. In particular, the “eastern clade” consists of *L. buchenavii*, *L. buchenavii* var. *govelinense* and the samples of the Harz and Prignitz region. The samples of *L. croceum* group into a “western group” and the samples from Austria group together in an “Austrian group”.

Structure analysis further revealed that the *L. buchenavii* population in Lower Saxony comprises genetically homogenous individuals, indicative of a single meta-population or the dominance of a single clone. *Lilium croceum* comprises genetically homogenous individuals, even the samples from Dutch *L. croceum* are genetically identical. Conversely, individuals from the Harz and Prignitz regions exhibited genetic variation, suggesting influences from multiple geographic origins.

To deepen the genetic comparison, the sampling area will subsequently be expanded to include populations from France, Sweden, Switzerland, and southern Germany. This additional data will help clarify the biogeographic distribution of *Lilium bulbiferum* s.l. and its closely related taxa in Europe.

Poster Session II

Phytoremediation-Oriented Evaluation of Nickel Stress Responses in Anubias nana Engl. Grown in Aquatic Systems

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Posternumber: #22

Introduction: Nickel (Ni), a heavy metal that occurs naturally and can accumulate in aquatic environments as a result of both natural and human activities. Although Ni plays a minor but essential role in plant growth, excessive levels can have adverse effects on plants physiology through the disruption of vital biological processes and functions. *Anubias nana* Engl. (Araceae) is a popular slow-growing aquatic plant, is a promising candidate for heavy metal accumulation due to its high adaptability.

Methods: This study examined the mineral nutrient profile of *A. nana* Engl. under Ni exposure and assesses its potential for sustainable heavy metal removal in aquatic ecosystems. Additionally, the genotoxic effects of Ni exposure were assessed. Genomic template stability (GTS) was calculated using ISSR markers (UBC808, UBC834, UBC841, UBC842) with a focus on detecting the appearance or disappearance of DNA bands and variations in their intensity. Plants were cultivated in tanks containing 0.2% Hoagland solution for a period of 10 days at a temperature of 28 ± 1°C, with the objective of promoting growth and acclimatizing to the aquarium environment. Thereafter, the plants were subjected to $NiCl_2.6H_20$ stress, with concentrations of 0, 10, 25, 50, and 100 µM. Leaves, stems and roots were harvested 10 days after Ni treatment (both washed and unwashed) were analyzed using a PerkinElmer Optima 7000DV ICP-OES to determine their heavy metal and mineral nutrient contents (B, Ca, Cu, Fe, K, Mg, Mn, Na, Ni, Zn). The total chlorophyll content and phytoremediation parameters, including bioaccumulation index (BAI), bioconcentration factor (BCF), translocation factor (TF), surface adsorption (SA), surface adsorption efficiency (SAE) and removal efficiency (RE), were subsequently calculated to assess the plant’s physiological responses to Ni exposure and to evaluate its phytoaccumulation potential.

Results: The findings demonstrated a concentration-dependent increase in Ni accumulation. The highest Ni accumulation, was detected at 47.310 mg kg^{-1} was detected in unwashed leaf samples at 100 µM. At the same concentration, the stem exhibited the highest BAI, reaching 16.33. The highest BCF was identified as 3.93 in the leaf at 10 µM, while the highest TF was 2.3 in the leaf/root at 10 µM. The surface adsorption value reached 4.75 at 100 µM, while the maximum adsorption efficiency in leaves was 77% at 10 µM. Additionally, the highest water removal efficiency (RE) was determined as 7.95% at

100 µM. These findings indicate that *A. nana* is a capable accumulator of Ni. Genotoxicity analysis revealed no new band formation or loss, although distinct changes in band intensity were observed. A GTS value of 100% suggests that Ni exposure did not compromise the plant’s genetic integrity. Overall, *A. nana*demonstrated strong Ni accumulation capacity alongside high genomic stability.

Not all willows bloom alike: Species-level reproductive phenology of Salix in the Swedish Arctic (2017–2024)

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Posternumber: #23

Phenological mapping provides crucial insights into how plants respond to environmental change, offering a window into ecosystem-level shifts under climatic stress. Phenological responses of arctic plants to climate change are of increasing interest due to their ecological importance and sensitivity to environmental variation. We investigated the interannual variation in reproductive phenology of eight *Salix* species - comprising five shrub and three dwarf shrub species - on Mt. Nuolja, northern Sweden, spanning the years 2017 to 2024. We focused on three phenological phases: flowering, fruiting, and seed dispersal.

We hypothesized that phase onset and duration shifted significantly between 2017 and 2024, reflecting a trend toward earlier and/or longer phenological activity. We also expected consistent interspecific differences in phenological strategies and predicted that species would cluster into functionally similar phenological groups, partly aligned with phylogenetic relationships.

To test these hypotheses, we first examined how the onset and duration of these phases varied across years, both within and between species. Using ANOVA and Tukey post-hoc comparisons, we identified consistent temporal shifts in phenological timing, with significant interspecific and interannual differences in both onset and duration. The most pronounced differences occurred between the two consecutive years 2017 and 2018, illustrating strong sensitivity of reproductive timing to annual environmental variation. To better understand potential drivers of this variation, we compared mean April-July temperatures with the timing of phases.

We further used PCA and k-means clustering to identify functional phenological groups. Species separated primarily along PC1 (timing of onset and end), with Cluster 1 (dwarf shrubs *S. herbacea, S. polaris, S. reticulata* and shrub species *S. glauca*) flowering, fruiting, and dispersing later than Cluster 2 (Shrub species *S. hastata, S. lanata, S. myrsinifolia, S. phylicifolia*). PC2 (duration) contributed to within-cluster variation but did not define cluster boundaries. These groupings were compared to phylogenetic relationships using Phylomorphospace; while some clusters aligned with taxonomic affiliations, others reflected functional convergence, indicating that ecological adaptation plays a strong role in phenological strategies.

Our findings emphasize the importance of species-specific phenological data for predicting ecological responses to climate change. Divergent reproductive strategies among closely related *Salix* species may lead to ecological shifts that are not synchronized, despite their shared subgeneric background. Given their foundational role in tundra ecosystems, such variation could reshape interactions with pollinators and herbivores. Therefore, understanding the phenological dynamics of individual arctic willows is vital for anticipating ecosystem-level responses in a rapidly warming Arctic.

Not induced but modulated: Pyrenoid density controls carbon acquisition in hornworts during submersion and hyperoxia

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<u>Posternumber: #25</u>

Hornworts are the only land plants capable of forming proteinaceous microcompartments in their plastids—pyrenoids—which enable carbon concentration at the single-cell level. By engaging de novo proteomics, ultrastructural imaging, and computational analyses, we demonstrate here that *Anthoceros agrestis*, a pyrenoid-forming species, upregulates key components of an algal-like biophysical carbon concentrating mechanism under submersion and high-oxygen conditions, leading to plastid remodeling and pyrenoids with denser matrices. In contrast, *A. fusiformis*, which lacks pyrenoids, mainly accumulates lipid droplets instead. Our findings suggest that hornworts modulate pyrenoid density—not formation per se—as a unique acclimation strategy, revealing a novel mechanism for surviving environmental fluctuations, shedding new light on land plant evolution, and also offering promising insights for crop bioengineering.

Drowning in a sandy ocean: Epiarenic growth of *Tillandsia* in the hyperarid Atacama Desert

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Posternumber: #26

The northern Chilean Atacama Desert is among those regions on Earth where life exists at its dry limits. There is almost zero rainfall in its core zone, and the only source of water is provided by a spatio-temporally complex fog system along the Pacific coast, which is far reaching into the hyperarid mainland. In these areas there is hardly any vascular plant growing, and, thus, it is intriguing to be faced with a vegetation type build up by one single and highly specialized bromeliad species, namely Tillandsia landbeckii Phil., forming regular linear structures in a sloped sand dune landscape. Rootless Tillandsia growth form is called “epiarenic”, because the plant shoot system depends on mobile sand as a stabilizing substrate, while older shoots gradually die off and are buried by sand. Sand is trapped by the branching shoot system and elongated linear leaves, and the growth rate and leaf length balance the impact of oversanding versus stabilization of aboveground biomass and functional plant architecture. Here we study three reference populations in the south, north and central of the Tillandsia landbeckii distribution range to characterize sand properties such as grain size and particle sortation required for growth and sufficient vegetation fitness. We show that there is a strong adaptation of Tillandsia landbeckii to sand properties.

Evolution of epiarenic *Tillandsia* species in the hyper-arid Atacama Desert:
A Pleistocene scenario of parallel evolution and adaptive hybridization

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Posternumber: #27

As one of the driest and oldest deserts in the world, the Atacama Desert is an extreme habitat forcing organisms to adapt. The genus *Tillandsia* includes some specialists for a life at the dry limits, which perform CAM photosynthesis, lack a functional root system and instead display specialised trichomes for absorbing water and nutrients. There are nine *Tillandsia* species in the Atacama Desert that mastered growing on bare sand (epiarenic

growth) and depend heavily on the night-time fog as the only water source. However, the mechanisms underlying the evolution of epiarenic growth and the time period during which *Tillandsia* evolved this growth form are still unknown. Therefore, a maximum-likelihood phylogenetic reconstruction based on 278 plastome sequences of Tillandsioideae and representatives of other Bromeliaceae subfamilies was performed. On this basis, divergence times of epiarenic *Tillandsia* species were estimated with BEAST. Using the nuclear encoded *Agt*1 gene, which has been introduced earlier as valuable barcoding marker, epiarenic *Tillandisa* and their closest relatives were examined for orthologous gene copy variations to uncover reticulate interspecies gene flow. The results revealed that epiarenic *Tillandsia* evolved multiple times independently during the Pleistocene. In addition, interspecies gene flow and formation of hybrid species appears to be a common phenomenon among epiarenic *Tillandsia*. These findings suggest that, although epiarenic growth has evolved in parallel multiple times, some epiarenic *Tillandsia* species may have acquired this growth via adaptive hybridization.

NaijaFLO: A comprehensive vascular plant database for biodiversity research, conservation, and management

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Posternumber: #28

The Database of Vascular Plants of Nigeria (NaijaFLO) is a comprehensive, expert-verified, and curated checklist of all vascular plant species reported in Nigeria. Developed at the German Centre for Integrative Biodiversity Research (iDiv), NaijaFLO is maintained by an international team of editors and contributors. For each core taxon (species, subspecies, variety, or form), the database provides the accepted scientific name, corresponding basionyms, distribution status (native, introduced, cultivated, excluded, doubtful, or absent), and growth habit within Nigeria. In addition, we aim to cite at least one vouchered herbarium specimen for each taxon. All taxa are linked to established classifications, including IPNI, POWO, WFO, LCVP, WP, and APD, with sources referenced for all taxonomic, classification, and distribution information. NaijaFLO covers 7,770 taxa (species, subspecies, varieties, or forms) across 232 families and 1,859 genera, including 6,753 species, of which 5,396 are native and 41 are endemic. All data will be released under a CC BY 4.0 license, making it publicly accessible through the iDiv PlantHub and the Global Biodiversity Information Facility (GBIF). NaijaFLO serves as a vital resource for the scientific community, policymakers, businesses, and non-governmental organisations to support research, conservation, management and use of biodiversity.

Reconstructing the domestication history of Ipheion uniflorum

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Reconstructing the domestication history of Ipheion uniflorum

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Posternumber: #29

This study reconstructs the domestication history of Spring Starflower (*Ipheion uniflorum*) using an integrated genomic-morphological approach. We analysed 50 individuals via GBS (genotyping-by-sequencing) and combined it with prior genetic data from wild populations. Phenotypic variation was quantified across 86 specimens, and DNA content was estimated for all cultivars. Results suggest multiple different geographic origins of cultivars. They are genetically differentiated from each other and morphologically divergent from natural populations. All analysed specimens are diploid except cv. 'Jessie'. Our findings are relevant for understanding domestication mechanisms and provide hints for maximising future breeding efforts. Priority locations and genotypes for conservation are identified.

Against the flow: A northward migration of Salix sitchensis along the Pacific Coast

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Posternumber: #30

As an interdisciplinary field of research, biogeography aims to understand the dispersal of species within a geographical context. Understanding the biogeographical patterns of phylogenetic clades can facilitate the understanding of species distribution and enable predictions of future distributional shifts under ongoing climate change. The genus *Salix* (Salicaceae) is a fascinating taxon, and its great variability, affinity for reticulate evolution, and predominantly northern distribution offer exciting and potentially novel insights into evolutionary and biogeographical processes. Preliminary results have indicated an origin for North American shrub willows in the circumpolar region, diversifying from the north into the south-western and eastern areas. Based on a well-resolved backbone phylogeny of shrub willows, we focused on a distinct clade comprising twelve species characterised by different ploidy levels, high phenotypic plasticity, and patterns of reticulate evolution. Fifty-seven samples representing the twelve species were used for phylogenetic reconstructions, population structure approaches, molecular dating, and ancestral range estimation to gain insights into spatio-temporal evolution. All analyses were based on RAD sequencing data. The findings revealed at least three well-separated, monophyletic species, and substantial gene flow among at least five species, suggesting ongoing or historical hybridisation. A simplified and stable phylogenetic topology including six species suggested a geographical origin for the entire clade in the Western Cordillera, with subsequent range expansions towards the coastal and Mediterranean regions of California. Notably, *Salix sitchensis*, a monophyletic species distributed along the west coast, appears to have migrated from the Puget Sound region southward to the Coast Range of California and northward towards Kodiak Island, Alaska. This remarkable species made its way back to the north, where its ancestors might have previously begun to colonise North America. Molecular dating places the divergence events within the clade before the most recent glacial fluctuations. However, glaciation likely shaped the current distribution, as glacial ice covered most of its range. The discrepancies between the molecular dating and the recent distribution underscore the need for further investigation to clarify the role of past climatic events in shaping North American shrub willow biogeography.

Cross-laboratory integration of GBS data enables phylogenetic resolution in tree taxa: a case study from Tilia

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Posternumber: #31

The integration of genotyping-by-sequencing (GBS) data generated in different laboratories is a methodological challenge in phylogenetic studies, particularly when working with taxa showing complex genetic structures and unclear species boundaries. In this study, GBS datasets produced independently using the same enzymatic protocol but sequenced on different platforms were combined and analyzed. The genus *Tilia*, known for its taxonomic complexity and broad distribution across Eurasia, was selected as a model group. The joint analysis revealed that cross-laboratory data integration retained consistent phylogenetic signals and resolved relationships at both inter- and intraspecific levels. The congruent placement of shared taxa demonstrated the reliability of this approach, even in the absence of a reference genome. These findings support the application of standardized GBS workflows in collaborative phylogenomic research and highlight the potential for expanding geographic and taxonomic coverage through data sharing and harmonization.

Did the Sunda-Sahul Biotic Exchange result in plant diversification? A case study of switching disperser communities and fruit traits in Aglaia (Meliaceae)

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Posternumber: #32

Southeast Asia is one of the most biodiverse regions on Earth, and its unique patterns of biodiversity are closely linked to its geological history. The Sunda continental shelf (Peninsular Malaysia and parts of Indonesia and the Philippines) and the Sahul continental shelf (Australia and New Guinea) collided approximately 25 Mya (Zahirovic et al., 2016; Hall, 2017). This event facilitated the meeting and exchange of Sundanian and Sahulian lineages for the first time after 150 million years of independent evolution (Kooyman et al., 2019), resulting in the so called ‘Sunda-Sahul Biotic Exchange’ (SSBE).

Recent research suggests the biotic exchange between the continental shelves was uneven, with more lineages moving eastwards from Sunda to Sahul compared to the

opposite direction (Sniderman & Jordan, 2011; Crayn, Costion, & Harrington, 2015; Joyce et al., 2021). Plants with zoochorous fruits represent a common component of the exchanged flora, even though each shelf has different faunal disperser communities. Most notably, primates are not present on Sahul but are among the most important seed dispersers in Sunda and Wallacea (Joyce et al., 2021). One of the main questions yet to be answered is whether the difference in animal and disperser communities across Southeast Asia caused a switch in dispersal syndrome in the plants of the region.

To investigate this question, we will undertake a case-study on fruit evolution and biogeography in the genus *Aglaia* (Meliaceae). *Aglaia* is the most speciose genus in the mahogany family (Meliaceae), endemic to the lowland tropics of India, SE Asia, Australia and the pacific islands. The genus is thought to have originated in Sunda, with multiple transitions between Sunda, Sahul and Wallacea since the Miocene. Fruit morphology is highly variable in *Aglaia*, with primate, bird and Cassowary dispersal syndromes common in the genus. It remains to be understood how this fruit diversity evolved in *Aglaia*, and whether the different fruit types have switched in conjunction with the biogeographic shifts (and consequential shift in disperser communities) across Sunda, Sahul and Wallacea.

We are going to reconstruct the phylogeny of all *Aglaia* species with additional representatives from highly variable species and outgroup taxa. Using target-capture, we are going to sequence the Angiosperm353 loci as well as loci in a custom bait kit especially designed for Meliaceae, in order to resolve the high levels of paralogy within the family.

We are going to characterise the fruit morphology of *Aglaia* through detailed fruit developmental and anatomical studies. To complete the identification of key fruit traits, we are going to analyse fruit volatile organic compounds (VOCs) emitted by fruits. VOCs can be indicative of dispersal syndromes linked with specific animal guilds.

After reconstructing the biogeographical history of *Aglaia* and the ancestral state of its fruits, we are going to test for correlations of biogeographic shifts with shifts in the evolution of fruit characters. Switches in fruit types or key fruit traits coincident with biogeographic shifts are likely to be driven by the selection pressure of different disperser communities across Sunda and Sahul (and not random drift).

This study aims at gaining new insights in the effects of the Sunda-Sahul Biotic Exchange on plant diversification, and more in detail, whether diversification in *Aglaia* has been driven by switching disperser communities after jumping Wallace’s Line.

Genome size variation in grasses (Poaceae)

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Posternumber: #33

Variation in genome size is known to have functional consequences and is an essential parameter for understanding evolutionary patterns of organisms. Using flow cytometry, we studied the nuclear genome sizes (2C values) in 130 genera and 305 species of the Poaceae, including most subfamilies and major evolutionary lineages. The data were analyzed together with the chromosome numbers to give information on the size of monoploid chromosome sets with the chromosome base number x (1Cx values). The findings provide new insights into the evolution of genome size in grasses, in particular the origin of the family, the pan-grass whole-genome duplication (ρ-WGD) and the rise of its major phylogenetic lineages named the BOP and PACMAD clades. Our results support the concept of an ancestral grass karyotype (AGK) with $x = 12$, conserved in some subfamilies such as the Bambusoideae, Oryzoideae, Pharoideae and parts of the Pooideae, and thus it remained almost unchanged for nearly 100 Ma. The major genome rearrangements, for example, the transition from $x = 12$ to lower monoploid chromosome numbers are lineage-specific and occurred after the separation of the BOP and the PACMAD clades, i.e. when the diversification of their subfamilies had begun.

Using RAD sequencing for species delimitation of Salix ceretana and Salix lapponum (Salicaceae)

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Posternumber: #34

Species identification and delimitation is not only a taxonomic issue but also an ecological, evolutionary and conservation-related one. How to define species is constantly under discussion and consequently, delimiting species can be difficult or at least controversial. Therefore, different approaches are required, such as the combination of morphological and molecular data. *Salix ceretena* (P. Monts.) J. Chmelař (Salicaceae) is a Pyrenean endemic whose taxonomic classification is currently under discussion. It is listed in literature as distinct species, subspecies or synonym of *Salix lapponum* L. The poster shows the results of a RAD sequencing approach with phylogenetic and population structure analyses that was used to examine genetic relationships within the *Salix*

lapponum/*ceretana*-complex. Additional morphological characteristics were observed for the four samples from the Montmalús mountain. In total seven samples from the Eastern Pyrenees were collected, and the sampling was supplemented by five samples of *S. lapponum* and four outgroup taxa. The results of both the phylogenetic and population structure analyses showed four samples from the Montmalús mountain forming a monophyletic clade and being separated from two samples from Spain that were genetically more similar to the four included *Salix lapponum* samples from Norway. Two samples from Andorra and France showed a deviating pattern. The morphological data slightly supported the observed cluster of the Montmalús mountain whose individuals shared procumbent shrub habit. The results indicate a distinct genetic pattern among the samples identified as *S. lapponum* and *S. ceretana*, which give first hints towards a taxonomic treatment as two distinct species. Further investigations including a broader sampling and a more detailed morphological analysis are necessary to investigate the species complex within the Pyrenees sufficiently.

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

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Sexual reproduction is known to drive plant diversification and adaptation. However, it is intriguing to study vegetatively reproducing systems adapting to broader environmental conditions. Here we investigate the evolutionary and spatio-temporal history of a dodecaploid Eurasian deciduous woodland species, *Cardamine bulbifera* Crantz (Brassicaceae), which reproduces and spreads via vegetative structures only.

The species has been among the most successful range-expanding understorey woodland plants in Europe, raising the question of the genetic architecture of its gene pool, since its hexaploid but putatively outcrossing closest relative, *C. quinquefolia*, displays a smaller distribution range in Eastern Europe towards the Caucasus region. *Cardamine bulbifera* is of early Pleistocene origin, with a history of past gene flow with its hexaploid sister species *C. quinquefolia*, likely during the last glacial maximum in shared refuge areas in Eastern Europe, Western Turkey and the Crimean Peninsula region. Caucasian endemic diploid *C. abchasica* is considered an ancestral species providing additional evidence for the origin of the species complex in the Caucasus region. *Cardamine bulbifera* successfully expanded its distribution range postglacially towards Central and Western Europe accompanied by a transition to exclusively vegetative propagation being the major innovation to rapidly expand the distribution range following postglacially progressing woodland vegetation throughout Europe.

In northeastern Austria we discovered a refuge population system along the very biodiversity-rich Thaya valley harboring genotypes from the ancestral but also the recently colonized areas. Plastome data and nuclear genomic ddRAD analyses of the population system indicate prevalence of five clonotype groups in particular ecological woodland niches referring to six genetic clusters in total as revealed by admixture and SplitsTree analyses including the ancestral species. All eastern plastome types co-segregate with the respective proportion of the nuclear genome indicating limited gene flow and long-term persistence of clonal variants contributing to population-level fitness and adaptive potential.

Split or spread - A spatio-temporal framework of the evolution of annual *Arabis* species in Eurasia

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Life history in plants appears to be an important determining factor for the capacity to cope with major environmental change. Consequently, the evolutionary history of life form may have constrained significantly present-day biogeographic distribution patterns of phylogenetically related species, which had either to adapt or migrate during Pleistocene climatic fluctuations. In particular in Brassicaceae the molecular basis of monocarpic and polycarpic flowering behavior is well understood, and it is thought to be a trait, which reciprocally conversed. The Brassicaceae consist in total of c. 25% of monocarpic species. However, species-rich tribes such as Arabideae consist of only 8% monocarpic species indicating evolutionary and environmental constrain towards reversals. Here we utilized whole plastid genome sequencing through next-generation sequencing (NGS) to investigate the spatio-temporal timing of the evolution of annual species in the tribe Arabideae (Brassicaceae). Based on these data, we conducted phylogenetic reconstructions, divergence time estimations, and plastid haplotype distribution analyses. Past and present ecological niche modeling was performed for monocarpic taxa from three different Arabideae clades, *Arabis auriculata*, *Arabis nova* subsp. *iberica*, and *Arabis montbretiana*. With the integration of these approaches, we test the hypothesis that the evolution of monocarpic species in tribe Arabideae at low frequency is associated with large-scale biogeographic patterns reflecting migration rather than adaptation or reversals.

Capacity building in crucifer research – from *BrassiBase* to a taxonomic expert network (*Brassi*TEN)

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Networks of scientists working in coordinated efforts to advance plant systematics and taxonomy are becoming increasingly vital. Beyond the necessity of cataloguing and naming plant diversity—which is fundamental for supporting and safeguarding threatened biodiversity—there is also a growing need for robust comparative analyses across all taxonomic levels. Such endeavours rely heavily on a dependable taxonomic framework, ideally embedded within a solid phylogenetic context. *BrassiBase*, a taxonomic knowledge platform, was launched in 2012. Since then, significant progress has been made in phylogenetic research and taxonomic revisions, leading to the availability of comprehensive evolutionary concepts. A newly developed version of *BrassiBase* is presented here, now integrated with World Flora Online (WFO) and underpinned by the most current phylogenetic analyses. This version features an updated species checklist encompassing 61 tribes, 363 accepted genera, 4,148 accepted species, 428 subspecies, 58 varieties (excluding nominotypical taxa), and a total of 10,725 synonyms. The phylogenetic placement tool (PPT), which utilises ITS sequence data, has been significantly enhanced and now incorporates off-target ITS sequences obtained through next-generation sequencing. These achievements are the result of collaborative work by a large, well-connected community of scientists dedicated to serving the broader scientific community. We advocate for interdisciplinary collaboration within coordinated networks to advance the taxonomy, systematics, and evolutionary research of crucifers, thereby laying the groundwork for future cross-disciplinary research in plant biology and beyond.