

Abstract Booklet



38th Annual Conference
on Plant Population Biology

Marburg University, May 7th – 9th 2026

Dear **PopBio** participants,

We are pleased to welcome you to the annual conference of the specialist group “Plant Population Biology” (PopBio) of the Ecological Society of Germany, Austria, and Switzerland, hosted by Philipps-Universität Marburg, Germany.

This annual meeting with a long tradition brings together 86 researchers this year to share recent work and discuss advances in plant population biology, intraspecific variability, plant adaptation, plant biotic interactions and broadly related disciplines.

We look forward to a productive and inspiring conference.



Organizing Committee:

Anna Bucharova

Lea Klepka

Christian Lampei

Lena Lerbs

Sascha Liepelt

Helene Villhauer

Franziska Willems

**Marburg University, Conservation Biology Group,
Karl-von-Frisch-Straße 8, 35043 Marburg**



**Marburg
University**



Table of contents

- Conference program 3**
 - Wednesday, 06th May 2026 3*
 - Thursday, 07th May 2026 3*
 - Friday, 08th May 2026 4*
 - Saturday, 09th May 2026 5*
- Keynotes..... 6**
- Talks..... 11**
- Posters..... 45**

Conference program

38th Conference of the Plant Population Biology Section of the Ecological Society of Germany, Austria and Switzerland



Date: Wednesday, 06th May 2026 - Musician's Parlor, Old Botanical Garden

6:00pm - 10:00pm	Welcome Reception and Ice Breaker Location: Musician's Parlor, Old Botanical Garden
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Date: Thursday, 07th May 2026 - Center for Synthetic Microbiology

8:30am - 9:30am	Registration
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9:30am - 9:45am	Opening words
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9:45am - 11:00am	Session 1
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11:00am - 11:30am	Coffee Break
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11:30am - 12:30pm	Session 1 continued
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12:30pm - 2:00pm	Lunch Location: University restaurant
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2:00pm - 3:30pm	Session 2
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3:30pm - 4:00pm	Coffee Break
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4:00pm - 5:00pm	Session 2 cont.
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5:00pm - 6:45pm	Poster Session
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Date: Friday, 08th May 2026 - Center for Synthetic Microbiology

**9:00am -
10:30am**

Session 3

**10:30am -
11:15am**

Group photo and Coffee Break

**11:15am -
12:30pm**

Session 3 cont.

**12:30pm -
2:00pm**

**Lunch
Location: University restaurant**

**2:00pm -
3:30pm**

Session 4

**3:30pm -
4:00pm**

Coffee Break

**4:00pm -
5:00pm**

Session 4 cont.

**5:00pm -
6:45pm**

Poster Session

**7:00pm -
10:00pm**

**Conference Dinner
Location: Botanical Garden**

Date: Saturday, 09th May 2026 - Center for Synthetic Microbiology

9:00am - 10:30am	Session 5
10:30am - 11:15am	Coffee Break
11:15am - 11:45am	Session 5 cont.
11:45am - 12:15pm	Student awards
12:15pm - 12:30pm	Closing words
12:30pm - 1:00pm	Lunchpack distribution (Excursion)
1:00pm - 7:00pm	Excursion Location: Burgwald Forest

Keynotes

Keynote 1 Thursday, 7th May 9:45 am

Towards understanding the pangenomic basis of environmental adaptation in European beech using common gardens

Desanka Lazić, Cornelia Geßner, Katharina J. Liepe, Malte Mader, Niels A. Müller

Thünen Institute of Forest Genetics, Grosshansdorf, Germany

Understanding the genetic basis of environmental adaptation is key to predicting species future maladaptation and ecosystem stability in the face of climate change. This is especially important for long-lived organisms like trees, which may struggle to keep pace with rapid shifts in environmental conditions. Here, we resequenced 2100 individuals from 100 range-wide populations in European beech (*Fagus sylvatica* L.), a wide-spread forest tree species in Europe. We found that genetic variation closely mirrors geography, with clear isolation-by-distance patterns. Genotype-environment association (GEA) analyses identified a limited number of robust adaptive signals after accounting for extensive number of false positives. We found a high-confidence locus potentially linked to winter temperature adaptation through modulation of spring phenology. However, reciprocal transplant experiments of trees supposedly adapted to two contrasting climates suggest that phenotypic plasticity plays a major role. Additionally, genome-wide association studies (GWAS) indicate high missing heritability. To better resolve the complexity of adaptive variation and address the missing heritability, we built a European beech pangenome from 132 haplotype-resolved assemblies using PacBio HiFi long-read sequencing. The pangenome reveals substantial structural variation not captured by a single reference, offering new opportunities to link genomic diversity to adaptation. Together, these approaches illustrate how combined genomic resources can advance our understanding of forest tree adaptation under climate change.

How biotic and abiotic factors impact rapid adaptive evolution in plants

Florian P. Schiestl

*Department Systematic and Evolutionary Botany, University of Zürich,
Zollikerstrasse 107, CH-8008 Zürich, Switzerland*

Both biotic (e.g. pollinators, herbivores) and abiotic ecological factors (e.g. soil, temperature) cause selection and thus impact adaptive evolution in plants. Nevertheless, we know little about the impact of individual factors and their interactions, as well as the speed of evolutionary adaptation, because of the paucity of controlled experimental studies addressing these questions in plants and insects. Since several years my group has been using experimental evolution in semi-natural conditions in the greenhouse, to study real-time plant evolution driven by different ecological factors. In my talk I will give an overview of some of the evolutionary effects that we have demonstrated, with particular focus on floral attractiveness- and defense traits. We have found that efficient generalist bee pollinators like bumblebees select for taller plants and more attractive flowers, including higher scent emission and UV reflection. Low efficient pollinators on the other hand select for more selfing. Bumblebees also select against defense compounds, whereas herbivores select for more defense, leading to a reduction in the attractiveness of flowers. For the abiotic factors, soil enables or disables evolutionary responses to selection, through the availability of nutrients. Increased temperature leads to reduction in floral volatiles, and more but smaller flowers. Biotic and abiotic factors also show strong interactive effects, for example, bumblebee pollination leads to phenotypic divergence in response to soil type, and elevated temperature leads to more UV-reflection with bumblebee pollination. Overall, experimental evolution shows how plants can rapidly adapt to environmental factors, explaining the geographic variability in plant traits in nature. Our experiments also show how environmental change may impact evolutionary trajectories of plants in the future.

Genome editing for climate change adaptation: challenges, benefits and limitations

Maria von Korff

Heinrich Heine University Düsseldorf, Cluster of Excellence on Plant Sciences

Climate change and anthropogenic pressures threaten global crop production and the resilience of ecosystems. Advances in genome engineering offer innovative approaches to preserving and restoring biodiversity, enhancing crop resilience, and reducing the environmental impact of agricultural production.

I examine genome editing relative to other breeding methods, such as mutagenesis and conventional transgenic approaches based on foreign DNA transfer. I will then present examples of our own research to demonstrate how genome editing can leverage genetic diversity from gene banks to improve crop resilience. In this context, I discuss how wild crop relatives can be exploited to transfer novel traits into crops, with the aim of informing the development of perennial crops as a sustainable alternative to high-yielding annual systems.

Finally, I discuss the key limitations and challenges associated with genome editing for crop improvement and biodiversity conservation.

Causes and consequences of skewed sex ratios in dioecious plants

Sophie Karrenberg

Uppsala University, Ecology and Genetics, Norbyvägen 18D, 752 36 Uppsala, Sweden

Sons and daughters are expected to be produced in equal numbers, and this also applies to dioecious plants. However, deviations from equal sex ratios are common in reproductive plants in natural populations, either due to ecological differences between sexes, or genetic mechanisms.

Implications of skewed sex ratios are many: On the one hand, the evolution of dimorphisms between sexes can promote the divergence of sex chromosomes from each other. On the other hand, selfish genetic elements ("drive") may hijack the sex determining system leading to both skewed sex ratios and the evolution of sex ratio restorers.

In my talk, I will present work on sex ratio bias and sex chromosome evolution in willows (*Salix*). Populations of the dwarf willow *Salix herbacea* were highly female biased, on average, both in natural populations and under controlled conditions and we did not detect ecological differences between sexes. Individual full-sib families, however, varied largely in sex ratio. These results are hallmark signs of drive-restorer dynamics. Allele transmission analyses further support this interpretation. Our work also shows that sex is determined by segregation of Z and W chromosomes during ovule production in the females in *S. herbacea* (ZW sex determination).

Overall, our data thus suggests a rare putative case of female sex chromosome drive. According to theory, the evolution of female bias can be associated with colonizing life histories where high seed output is particularly advantageous—this scenario fits particularly well to willows.

Keynote 5 Friday, 9th May 9:00 am

Microbial contributions to within-species and -individual variability of plants under global change

Robert Junker

Philipps-Universität Marburg, Germany

Global change dimensions restructure communities, are major drivers of biodiversity decline, and thus destabilize ecosystems. Nonetheless, some individuals, species, and communities better tolerate environmental stresses than others suggesting specific mechanisms increasing their resilience and resistance. In my talk I will explore how rapid natural modulations of the plant microbiome within or across plant individuals affect plant phenotype and performance and thus increase plant tolerance to environmental stresses.

Talks

Talk 1 Thursday, 7th May 10:30 am

Loss of genetic diversity and signs of selection in Common Ash (*Fraxinus excelsior*) caused by ash dieback

Katharina Budde¹, James Doonan², Tom Hanika³, Myriam Heuertz⁴, Bartocz Ulaszewski⁵, Rita Verbylaite⁶, Erik D. Kjaer², Lene R. Nielsen²

¹Northwest German Forest Research Institute, Department of Forest Genetic Resources, Professor-Oelkers-Strasse 6, 34346 Hann. Münden, Germany

²Department of Geosciences and Natural Resource Management, University of Copenhagen, Rolighedsvej 23, 1958 Frederiksberg C, Denmark

³University of Hildesheim, Intelligent Information Systems, Universitätsplatz 1, 31141 Hildesheim, Germany

⁴INRAE, BIOGECO, 69 Route d'Arcachon, 33610 Cestas, France

⁵Department of Genetics, Kazimierz Wielki University in Bydgoszcz, Poland

⁶Institute of Forestry, Lithuanian Research Centre for Agriculture and Forestry, Department of Forest Tree Breeding and Genetics, Kaunas, Lithuania

Common ash (*Fraxinus excelsior* L.) was considered a species with high adaptive potential to climate change due to its broad ecological tolerance. However, ash dieback caused by an invasive pathogen, *Hymenoscyphus fraxineus*, has led to a severe decline of ash populations across Europe. Common garden experiments revealed that susceptibility to ash dieback is heritable. However, only a small proportion of individuals survive the disease.

Here, we investigated whether ash dieback has caused a loss of genetic diversity and detectable signals of selection in natural populations. In 2019, leaves were randomly sampled from ash saplings that had survived several years of pathogen exposure. For comparison, we used samples from adult trees collected in 2001, before the appearance of severe disease symptoms, representing the pre-epidemic generation. Mortality due to ash dieback was strong between 2001 and 2019.

Low-coverage whole-genome sequencing was performed on all samples. Genome-wide markers revealed a loss of genetic diversity in most populations. Moreover, applying a genomic prediction model based on loci significantly associated with crown health, identified through a genome-wide association study, indicated a slight shift toward lower susceptibility within a single generation—particularly in eastern European populations.

Drivers of phenological diversity among the clonal oak DF159 progenies

Monica B. Berdugo^{1,2}, Julia Baumeister¹, Maren Schmidt¹, Noemi Zainab Mbutcho¹, Katrin Heer², Lars Opgenoorth¹

¹*Plant Ecology and Geobotany, Department of Biology, Marburg University, Germany*

²*Forest Genetics, Department of Natural Resources, Albert-Ludwigs-University Freiburg, Germany*

Phenotypic variability, common in plants with broad geographical distributions, influences the way in which dominant tree species cope with ongoing climate change. In addition to climate constraints and genetic diversity, maternal effects may also contribute to driving this variability. Aiming to assess the relative importance of paternal genotype and maternal effects on the phenology of young seedlings, we targeted the open pollinated progenies of the clonal *Quercus robur* DF159 produced along a European transect. This Transect includes five locations, Bordeaux and Fontain in France, Greifenhagen and Bad Lauchstädt in Germany, and Lapinjärvi in Finland. It embodies a range of climate regimes, ranging from warm and humid to cold and dry. Acorns produced in 2024 (n=515) were sown in a common garden experiment monitored to record their germination, establishment, and phenology between 2025 and 2026. Generalized mixed effects models indicate that the germination rate and seedling establishment of acorns produced in 2014 differed among transect locations (climate), after controlling for the variability among outplanted clonal trees (maternal effects), with higher success among those progenies produced in Bordeaux and Greifenhagen. In addition, microsatellite analysis discriminating full- from half-siblings will allow us to assess the relative importance of seedling relatedness on autumn and spring phenology. Our variance partitioning approach in a clonal system indicates that maternal effects alone are able to modulate the driving role of climate on phenotypic variability of the next generation of *Q. robur*.

Satellite data show trees delay budburst across landscapes to escape herbivores

Soumen Mallick

*Würzburg University, Chair of Conservation Biology and Forest Ecology,
Glashüttenstraße 5, Field Station Fabrikschleichach, 96181 Rauhenebrach, Germany*

In recent years, budburst, the timing of leaf emergence, has advanced less than expected despite continued spring warming, suggesting counteracting ecological forces. One of these forces might be increased and earlier herbivory on young leaves under climate warming. Here, using five years of satellite radar data from 27,500 pixels (10 x 10 m) across 60 temperate oak forest sites under experimental manipulation of insect herbivore loads in Central Europe, we show that prior-year leaf herbivory delayed budburst by 3 days, cancelling the phenological advance observed during a decade of warming. This delay reduced subsequent herbivory by 55%, exceeding the effects of parasitoids or pathogens, and persisted even during pest outbreaks. Across landscapes, the delay was strongest where it likely provided the highest benefit, that is, where a given amount of delay most effectively reduced following herbivory, which suggests an adaptive tree defence. Ultimately, trees may be trapped between responding to two opposing consequences of global change: warming selects for earlier budburst, while herbivory selects for delay. Our results underscore the need to consider not only climate, but also plant-herbivore interactions and adaptive evolution to predict tree responses to a changing world.

Environmental context shapes the costs of drought escape in Californian field mustard

Katharina Hold, Elena Hamann

Institute of Plant Ecology and Evolution, Heinrich-Heine-Universität Düsseldorf, Germany

Contemporary climate change, particularly severe droughts, can drive rapid evolutionary responses in plant populations. Using a resurrection approach with *Brassica rapa* collected before and after consecutive California droughts, we previously showed that populations rapidly evolved drought escape through accelerated growth and flowering. However, these studies focused on drought in isolation, leaving open whether rapid drought adaptation incurs fitness costs under more realistic conditions where multiple stresses interact.

Here, we grew ancestral and descendant lines in a multifactorial common garden manipulating resource availability and intraspecific competition. Resource availability was varied using soil mixtures of 20% or 80% sand, the latter reducing water and nutrient retention, and plants were grown with or without competitors. We measured functional traits related to growth and resource use to assess phenotypic variation, plasticity, and fitness differences between generations.

Environmental stress strongly shaped phenotypic expression, with soil conditions emerging as the dominant driver of trait variation and soil × competition interactions further intensifying stress across multiple traits. Reaction norms revealed substantial within-population variation in plasticity, indicating strong genotype-by-environment interactions. Selection gradients also varied across treatments, populations, and generations, suggesting that the adaptive value of key traits shifts across environmental contexts.

Together, these results suggest that evolutionary responses to drought may carry context-dependent fitness costs when plants face multiple simultaneous stresses, highlighting the importance of evaluating rapid adaptation under ecologically realistic conditions.

Genetic diversity of common grassland forb species in the Czech Republic: a guide for developing regionalized seed mixtures?

Tomáš Fér¹, Hana Skálová², Kateřina Iberl¹, Jindřich Chrtěk^{1,2}, Martin Prach¹, Tomáš Herben^{1,2}

¹Charles University, Prague, Czech Republic

²Institute of Botany, Czech Academy of Science, Průhonice, Czech Republic

We present preliminary results from an ongoing project investigating the genetic diversity of selected grassland dicotyledons in the Czech Republic. The study aims to delineate genetic patterns to guide the development of regionalized seed mixtures and determine appropriate seed transfer zone scales. Utilizing non-regional seeds poses risks such as maladaptation to local conditions, genetic erosion of wild populations, and overall genetic depauperation. We selected 14 common, non-cultivated species that represent significant proportions of meadow communities, namely *Achillea millefolium* agg., *Campanula patula*, *Campanula rotundifolia* agg., *Centaurea jacea*, *Galium mollugo* agg., *Knautia arvensis* agg., *Lathyrus pratensis*, *Leontodon hispidus*, *Leucanthemum vulgare* agg., *Lychnis flos-cuculi*, *Prunella vulgaris*, *Ranunculus acris*, *Sanguisorba officinalis*, and *Vicia cracca*. Sampling was conducted at approximately 80 localities per species (at a density of ~10 x 10 km). Methodology included flow cytometry for ploidy level identification and ddRAD sequencing to determine genetic structure, following the same protocol used in the recently completed project in Germany (RegioDiv). Preliminary findings reveal a general east-west gradient in genetic structure, with the Carpathian-related regions showing the most distinct divergence. These results will facilitate the design of evidence-based seed transfer zones within the Czech Republic and provide a framework for future research on additional grassland taxa. Ultimately, this work contributes to a broader understanding of European genetic variation patterns resulting from post-glacial migration and anthropogenic influence. In the future, we will collaborate with researchers in neighboring countries to get a larger picture of genetic variation of a large set of grassland species.

Is once enough? Seed collection timing matters for capturing trait variation and genetic diversity

Franziska Willems, Roman Dörr, Sascha Liepelt, Anna Bucharova

Marburg University, Conservation Biology, Karl-von-Frisch-Str. 8, 35043 Marburg, Germany

Seeds in natural populations are collected for many reasons including research, ex-situ conservation, species reintroductions or as a source for propagation for ecosystem restoration. For practical reasons, seed collection is often limited to a single annual harvest to reduce work load and due to logistical challenges. However, this approach may be problematic if seed collection timing influences plant traits through maternal effects, or if different genotypes in the sampled population provide seeds at different times. To examine these effects, we collected *Stellaria media* seeds over an 11-month period in an agricultural landscape and grew the offspring in a common garden experiment. In the wild collected seeds, seed weight varied across collection months. In plants that grew directly from these wild-collected seeds, collection timing influenced key traits such as germination rate, flowering time, and even the weight of the seed produced by common garden plants. To assess whether these differences are caused by maternal effects or are heritable, we grew a second generation from the seeds collected in the common garden. The results show that some of the differences detected in the first generation persist in the second one, for example germination rate and the timing of flowering and seed production. These findings suggest that restricting seed collection to a single time point may introduce selection biases and limit the capture of genetic and phenotypic variation, with potential implication for using these seeds in research, conservation or restoration.

Variation in *Trifolium repens*' floral traits along an urbanization gradient during the flowering season

Noemie Bourgoin, Juliette Dubois, Lea Mercier, Bojana Stojanova

University of Rennes, France

In the context of increasing urbanization, it is important to assess how biodiversity—and consequently, plant communities—respond to this disturbance. Although the effect of urbanization on plant traits has already been evaluated, gaps remain regarding the potential impact of seasonality on the expression of these traits. In this study, we focused on white clover (*Trifolium repens*) to assess whether seasonality (early or late flowering stage) influenced the effect of urbanization on the floral traits of *T. repens*.

A significant variation in certain floral traits of *T. repens* between natural and urban environments was identified during the early flowering period, with an increase in inflorescence height, inflorescence diameter, and petal length in urban environments. However, no significant variation was identified at the peak of *T. repens* flowering. Interestingly, the seasonal effects were more pronounced in urban than in natural populations, suggesting that the effects of urbanization are not homogenizing.

Data from pollinator observations will be additionally analyzed with in floral traits to assess whether with variation in pollinator community diversity, abundance, and activity is related to floral traits variation.

Our results show that the effects of urbanization can vary across the flowering period, likely affecting plant-pollinator interactions. Thus In the context of urban adaptation studies, reliable conclusion can only be obtained from sampling at different time points during the flowering season.

Does pollen form follow function? Effects of stigma type, pollination mode and habitat on pollen morphological traits

Sergey Rosbakh¹, Massimo Nepi², Maximilian Pichler³

¹*Leibnitz University Hannover, Germany*

²*University of Siena, Italy*

³*University of Regensburg, Germany*

1. Pollen grains display striking morphological diversity, yet the ecological drivers underlying this variation remain poorly understood.
2. We tested whether pollen morphology reflects adaptation to pollination mode, habitat moisture, and stigma type, three ecological factors that impose selective pressures on pollen dispersal, desiccation tolerance, and hydration dynamics.
3. We analysed 13 morphological traits for 1,151 Central European angiosperm species using phylogenetic regression models. Traits included pollen size and dispersal units, number and type of apertures, coatings and both external and internal features of the exine.
4. Insect-pollinated species produced larger, coated grains with thicker exine layers and more reticulate ornamentation, while wind-pollinated species had smaller, smoother grains with thinner walls and more frequent Utricle bodies. Species from wetter habitats were more likely to disperse pollen in clumps and showed distinct ornamentation patterns, but several traits hypothesised to reflect hermaphroditic responses (e.g., aperture number, furrows, opercula) showed no moisture dependence. Stigma type also influenced pollen form: dry-stigma species had more coatings, thicker exine, and more frequent opercula, while wet-stigma species had larger, thinner-walled grains with non-perforate ornamentation.
5. Our results support the idea that pollen morphology is functionally adaptive and shaped by distinct phases of pollen performance: dispersal, environmental exposure, and stigma interaction. These findings highlight the potential of trait-based approaches for understanding reproductive strategies in angiosperms.

Defence Trait Variation in Native and Invasive Garlic Mustard Populations

Corinna Schönberger¹, Luzia Hamma¹, Caroline Müller², Robert Colautti³, Oliver Bossdorf¹

¹University of Tübingen, Institute of Evolution and Ecology, Tübingen, Germany

²University of Bielefeld, Department of Chemical Ecology, Bielefeld, Germany

³Queen's University, Department of Evolutionary Ecology and Ecological Genetics, Kingston, Ontario, Canada

Plant invasions are a key driver of global biodiversity loss and ecosystem change. Plant defence traits can strongly influence invasion success by mediating interactions with herbivores. Yet, most studies on invasion success are geographically restricted or overlook among-population variability in defence traits. To address this, we quantified variation in mechanical and chemical defences across a broad geographic range of populations of the global invader garlic mustard (*Alliaria petiolata*) using a common garden experiment including plants from both native and invasive ranges. We measured leaf toughness and trichome density to test for divergence between ranges and assessed trait variability among populations. We also quantified the concentration and composition of glucosinolates, which are key chemical defence metabolites, to assess variation between and within native and invasive ranges. Here, I present the experimental framework and results of our ongoing analyses, highlighting how mechanical and chemical defence trait variation may contribute to invasion success.

Landscape opening and redistribution of floral resources facilitate gene flow among spatially isolated forest herb populations

Tobias Naaf, Jannis Till Feigs, Siyu Huang

Leibniz-Centre for Agricultural Landscape Research (ZALF), Germany

Land-use changes remain the most important driver of biodiversity loss worldwide. In Central Europe, the most evident land-use change was the clearing of the forest, which started in the Neolithic and continued until the 19th or 20th century. Also, land-use patterns in-between remaining forest fragments have been changing over the last two centuries, driven by the first and second agricultural revolution. There is growing evidence that these changes in landscape composition affect the viability of plant populations in spatially isolated habitat patches by changing their size and gene flow patterns. However, there were so far few attempts to quantify change in gene flow over time and to relate this change to landscape change. Here, we quantified gene flow changes among nine spatially isolated populations of the bumblebee-pollinated forest specialist herb *Polygonatum multiflorum* in an agricultural landscape in NE Germany based on coalescent theory and multi-generational sampling. Simultaneously, we quantified landscape compositional changes over the last 240 years.

Contemporary FST among pollen pools was generally lower than historical FST among adult populations. Gene migration had been nearly absent in the past but was now occurring among 12 out of the 36 population pairs. We interpret this general increase in gene flow as a result of the opening of the landscape before 1880 which allowed bumblebee pollinators to accomplish long-distance pollen-mediated gene flow among forest fragments. Variation in gene flow change across population pairs could be attributed to the redistribution of (a) vertical obstacles to bumblebee flights (hedgerows, forests); and (b) floral resources in form of traditional orchards and oilseed rape fields. Our spatiotemporal analysis indicates that rather than through new forest patches, the functional connectivity among existing forest herb populations can be enhanced through increased landscape permeability and a high relative importance of forest herb populations for bumblebee foraging.

Long-term CO₂ enrichment alters functional traits and stress response of a grassland perennial

Tobias M. Sandner, Gerald Moser, Christoph Müller

Justus Liebig University Gießen, Germany

Elevated atmospheric CO₂ is the principal driver of anthropogenic climate change. In addition to its indirect warming effect, higher CO₂ directly influences plant performance, often increasing productivity (“CO₂ fertilization”), raising C:N ratios and altering stomatal traits. However, it is still poorly understood if CO₂ induced trait changes are purely plastic or if selection leads to heritable adaptations to altered atmospheric compositions. Here, we present results of an experiment testing for evolutionary responses of grassland plants to elevated CO₂. In the Giessen free air CO₂ enrichment (FACE) experiment, a temperate grassland has been exposed to ambient and moderately elevated CO₂ concentrations (+20%) for > 25 years. We cultivated clonal cuttings of *Glechoma hederacea* (Lamiaceae) from both treatments in a greenhouse to study functional traits in a common environment. Moreover, we grew a second clonal generation in a competition experiment in which plants from both CO₂ origin competed against each other and a commercial grass competitor. Here we expected better performance of plants from elevated CO₂, as these were used to higher levels of productivity in the FACE experiment. Under greenhouse conditions, plants from the two CO₂ origins did not generally differ in biomass. However, plants of elevated CO₂ origin produced more shoots, whereas ambient-CO₂ plants had higher leaf mass fractions and specific leaf areas. In the competition experiment, plants from ambient CO₂ conditions outperformed plants from elevated CO₂, producing more and longer shoots, larger leaves and higher biomasses. The results suggest that even modest, sustained increases in CO₂ can trigger rapid evolutionary change in grassland species. Trait changes related to elevated CO₂ can lead to altered plant responses to different environmental factors, like reduced shade tolerance, which has the potential to reshape competitive dynamics under future environmental conditions.

TERRA: Terrestrial Geo-Biosphere Interactions in a Changing World. Tübingen's new Cluster of Excellence from an ecologist's point of view

Katja Tielbörger¹, Michaela Dippold¹, Kira Rehfeld¹, Olaf Cirpka¹, Oliver Bossdorf¹, Yvonne Oelmann¹, Andreas Schweiger², Sara Tomiolo¹

¹*University of Tübingen, Germany*

²*University of Hohenheim*

Interactions between the geosphere (rocks, soil, water, and atmosphere) and the biosphere (microorganisms, fungi, plants, and animals) determine how the Earth System responds to change. However, past research has largely considered geosphere and biosphere responses to Earth-System change separately. TERRA fills this gap by developing an integrated understanding of how geo-biosphere interactions in terrestrial systems induce and respond to environmental changes, using evidence from both the geological past and present-day to improve predictions of future global change impacts.

TERRA integrates observational, experimental, and modeling approaches spanning different periods of Earth history, in four Themes. Past geo-biosphere interactions (Theme 1) represent a pre-human 'control' state, tested against concurrent large-scale geo-bio interactions under major anthropogenic impact (Theme 2). Smaller-scale field, common garden, and greenhouse experiments take a mechanistic look at interactions between diversity and stability in the geo- and the biosphere (Theme 3). A next generation of machine-learning and process-based models integrates across scales and tests mitigation and adaptation measures to cope with global change (Theme 4).

TERRA capitalizes on understanding possible feedbacks between diversity and stability in the geosphere and the biosphere. We hypothesize that biodiversity has a stabilizing effect on the geosphere, and vice-versa, geodiversity may stabilize the biosphere. An example for this core hypothesis are invasions of non-native species along riverbanks. This system serves as ideal case study for positive geo-bio feedback loops that amplify invasion and riverbank erosion simultaneously.

An exciting new infrastructure within TERRA is the Diversitorium. It is planned as a globally unique experimental platform manipulating spatio-temporal geodiversity and monitoring the effects on biodiversity across scales. This platform is a long-term ecological experiment welcoming external contributions around geo-bio interactions.

Overall, TERRA shall inspire new avenues in (plant) ecological research and generate opportunities for international and interdisciplinary collaborations way beyond the initial core team.

The value of student theses in ecology

Finn Rehling¹, Lea Heidrich², Alexandra-Maria Klein¹, Nina Kranke¹

¹University of Freiburg, Germany

²University of Marburg, Germany

Each year, students in ecology produce hundreds of theses filled with unique data and new findings. Yet, even though universities are meant to lead the way in open science, more than 90% of institutions across Central Europe have no consistent system for sharing student theses publicly. Since only a small number of student theses ever make it into scientific journals, most remain unnoticed and unused. In this talk, I will explore the potential of student research in ecology and the barriers that prevent its visibility and reuse. Drawing on a regional survey of universities and interviews with academic staff, I will discuss some of the problems arising from the inaccessibility of student theses, common misconceptions about their scientific value, and how this lack of access ultimately limits our way of doing science. In the end, I will provide examples of good practice and propose practical recommendations for universities, supervisors, and students to make ecological knowledge more accessible, transparent, and impactful.

Genomes of *Arabidopsis lyrata* are shaped by ploidy changes and mating system shifts

Anna Glushkevich¹, Alison Scott¹, Polina Novikova^{1,2,3}

¹Max Planck Institute for Plant Breeding Research, Germany

²Department of Plant Biotechnology and Bioinformatics, Ghent University, Belgium

³VIB-UGent Center for Plant Systems Biology, Belgium

Whole-genome duplications and changes in mating type highly affect genome evolution process, however, their effect can be complex and ambivalent. For example, polyploidy can increase mutational load and reduce purifying selection. Transition to selfing, on the contrary, can increase purifying selection due to increased homozygosity. However, a decrease in effective recombination rate can negate this effect.

Here we use 30 high-quality genomes of *Arabidopsis lyrata* across the species range to study structural variation and signatures of purifying selection in diverse lineages. *A. lyrata* has undergone several independent recent transitions to selfing as well as whole-genome duplications, making it a useful model for comparing early genome evolution under these transitions.

We used the software Pannagram to characterize the whole pool of structural variants (SVs). We identified almost a million SVs across all genomes. Longer SVs, representing mostly transposable element (TE) insertions, had different frequency patterns from shorter SVs, representing random mutations. Siberian outcrossing lineages, both diploid and tetraploid, showed higher TE insertion rates. The Siberian population underwent a bottleneck, and may have partially lost the ability to control TE insertions. This resulted in higher TE insertion rates and larger genomes (about 10-20 Mb) than in the European populations. Nevertheless, the Siberian selfing population showed lower TE insertion rates and genome size. Moreover, selfing lineage showed a larger proportion of deletions compared to all other genomes. This supports previously reported model predictions of a strong drive towards genome size reduction in selfing lineages, which is, however, usually hard to show in nature.

Tetraploids from different lineages demonstrated equally enhanced both long and short SV numbers. Also, they had more structural variants inside coding sequences of the genes, suggesting relaxed purifying selection in tetraploids.

Polyploidy in Action: Disentangling the Consequences of Genome Doubling in *Arabidopsis arenosa*

Eliska Travnickova¹, Josselin Clo², Marek Brindzak¹, Denisa Nerandzicova¹, Sonia Celestini¹, Magdalena Bohutinska¹, Filip Kolar¹

¹Charles University, Czech Republic

²University of Lille, France

Whole-genome duplication (WGD) is a key evolutionary process in flowering plants, often linked to changes in phenotype, life history, and stress responses. Yet, distinguishing immediate effects of genome doubling from traits shaped by long-term evolution remains challenging. *Arabidopsis arenosa*, which occurs naturally as diploid and tetraploid lineage, offers a valuable model. By comparing natural diploids, established tetraploids, and lab-induced neo-tetraploids, we aimed to separate the direct consequences of WGD from evolved features of stabilized polyploid lineages.

Using a common garden approach, we phenotyped a range of macroscopic, life-history, fitness, and cellular traits in the ancestral diploids and both tetraploid cytotypes. Neo-tetraploids produced bigger leaves but fewer flowers and marginally fewer but heavier seeds, indicating early trade-offs of WGD. Among cellular traits, endoreduplication (DNA replication without cell division) exhibited significant variation. Its levels were similar in diploids and neo-tetraploids but significantly reduced in natural tetraploids, suggesting that the decrease in endoreduplication is not a direct effect of WGD but likely evolves over time under post-WGD selection.

To address whether WGD provides greater plasticity and evolvability, we exposed plants to drought stress in a short-term directional selection experiment. Rosette diameter and leaf area were significantly reduced across all cytotypes, while endoreduplication remained stable, reinforcing its role as a robust, non-plastic trait. To directly assess evolvability of the experimental populations, a second generation of plants is currently being grown under the same conditions, with the aim of quantifying trait shifts between generations using the breeder's equation. This approach will allow us to test whether WGD per se alters the evolutionary potential of plant populations in response to environmental stress.

Evolutionary trajectory of enhanced heavy metal hypertolerance in *Arabidopsis halleri* populations from the Central Alps

Bastiaan Tjeng, Natalia Wozniak, Vinod Kumar, Menghan Zhao, Ute Krämer

Ruhr Universität Bochum, Germany

Arabidopsis halleri is a perennial, obligately outcrossing sister species of *Arabidopsis thaliana* that is widely distributed across Europe and Asia. It inhabits soils with highly variable metallome profiles, including environments rich in heavy metals. Across Europe, multiple instances exist in which closely related populations grow on ordinary and heavy metal-rich soils, respectively, suggesting repeated local adaptation.

Recent QTL mapping experiments in accessions from contrasting soil types in the Italian Central Alps identified two cadmium tolerance candidate loci that act epistatically to confer enhanced cadmium tolerance, involving a complex interplay of non-synonymous mutations and copy number variation.

In order to examine the evolutionary trajectory of adaptation to cadmium-polluted extreme environments, we investigated the distribution of these candidate alleles across the Central Alps, their population genetic context, and local genealogies based on whole-genome re-sequencing of 100 *Arabidopsis halleri* individuals. Our results indicate that one candidate locus is confined to an entire subgroup of the Central Alps clade, whereas the putative large-effect mutation is restricted to only two populations. Our observations suggest that locally adaptive alleles may originate from both standing variation and novel mutations.

A resurrection epigenetic approach to studying rapid adaptation to climate change in *Centaureum erythraea*

Judith Haase, Niek Scheepens, Bojana Stojanova

Goethe-Universität, Germany

Plants are forced to rapidly adapt to human-induced environmental changes. Plant populations can undergo evolutionary changes within just a few generations (rapid evolution), and epigenetic variation may provide an additional mechanism of trait regulation (heritable epigenetic variation). However, phenotypic measurements from standard common garden studies do not allow us to distinguish whether phenotypic differences between populations reflect genetic evolution or heritable epigenetic variation. To address these issues, I combined the resurrection approach, a method that enables the direct comparison of past and present populations by growing ancestral and descendant seeds side by side under common conditions, with a demethylation assay, which should reduce putative epigenetic variation. I used ancestral and descendant seeds of *Centaureum erythraea* from two European populations collected decades apart. The results reveal clear phenotypic differentiation between ancestors and descendants in a common environment, with population-specific trait shifts. Comparing ancestors and descendants in the control treatment revealed that variation in physiological traits is predominantly plastic, whereas vegetative and growth-related traits show population-specific phenotypic shifts. Demethylation modestly influenced trait expression and differences between temporal origins, though not always in the expected direction and inconsistently across traits. Overall, the findings suggest that phenotypic divergence is partly mediated by heritable epigenetic variation, while its adaptive significance remains unresolved. Moreover, the study demonstrates that combining the resurrection approach with a demethylation assay is a powerful tool for testing evolutionary changes and their underlying heritable epigenetic variation.

Above- and belowground traits are linked, but do not respond equally to variations in soil nutrients, temperature and water availability

Robert Rauschkolb^{1,2,3}, Viktoria Dietrich⁴, Barbara Knickmann⁵, Birgit Nordt⁶, Martin Freiberg^{1,7}, Isabell Hensen^{1,8}, Tim Meier⁸, Ingeborg Lang⁹, Jonathan Wenk², Lucienne Krause², Christine Römermann^{1,2,3}

¹*German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany*

²*Institute of Biodiversity, Ecology and Evolution, Friedrich Schiller University Jena, Jena, Germany*

³*Senckenberg Institute for Plant Form and Function Jena (SIP), Jena, German;*

⁴*Thünen-Institute, Institute of Forest Ecosystems, Eberswalde, Germany*

⁵*Core Facility Botanical Garden, University Vienna, Vienna, Austria*

⁶*Botanic Garden Berlin, Freie Universität Berlin, Berlin, Germany*

⁷*Systematic Botany and Functional Biodiversity, Life Science, Leipzig University, Leipzig, Germany*

⁸*Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany*

⁹*Department of Functional and Evolutionary Ecology, University of Vienna, Vienna, Austria*

Plant functional traits are frequently used to compare strategies of species and to predict functions such as growth, reproduction, or phenology. While aboveground traits are well studied, comparatively little is known about belowground traits. In the context of global change, it is crucial to better understand the responses of traits, both above- and belowground, to changing abiotic factors.

In this study, we investigated the response of above- and belowground plant traits to climatic and soil parameters by cultivating five perennial herbaceous species in experimental beds at five Central European botanical gardens. After up to four growing seasons we measured above- and belowground traits, and analysed their relationships to differences in climatic conditions, soil chemistry and nutrient availability. In particular, we investigated whether above- and belowground trait pairs with similar functions respond correspondingly to environmental parameters.

We found that above- and belowground traits are tightly linked, with plant height negatively correlated with root branching and LDMC positively correlated with RDMC. Overall intraspecific variation in response to environmental factors was mainly driven by nutrient availability in terms of soil C/N ratios, while climatic differences played a less important role. Traits differed in the extent to which they were shaped by broad scale environmental conditions compared to micro-environmental conditions.

Our results emphasise that even minor differences in environmental gradients or microhabitat variations can lead to intraspecific variation in above- and belowground traits. This highlights the importance of using traits measured on sites for trait-based approaches. To some extent, easily measurable aboveground traits are linked to root traits in terms of their function and responses to environmental conditions, but we do not recommend using aboveground traits as a substitute for root traits in trait-based approaches as the correlations are very difficult to predict and may depend on the habitat.

Effects of artificial light at night and drought on plant traits across three functional groups

Maximilian Stein^{1,2}, Katharina M. Dietrich², Pia M. Eibes², Nele Meyer², J. F. Niek Scheepens¹

¹*Faculty of Biological Sciences, Goethe-University Frankfurt, Germany*

²*Faculty of Geosciences and Geography, Goethe-University Frankfurt, Germany*

Urbanization is rapidly transforming ecosystems worldwide, introducing multiple environmental stressors such as artificial light at night (ALAN) and altered water availability. While ALAN is increasingly recognized as an ecological driver, its effects on plants remain insufficiently understood, particularly in combination with drought. Plants rely on natural light–dark cycles to regulate phenological, physiological, and growth processes, and disruptions can shift ecosystem functioning. However, most studies focus on single species, limiting our understanding of responses across functional groups.

To address this gap, we conducted a controlled climate chamber experiment using plants from three functional groups (grasses, herbs, and legumes; three species per group). Plants were exposed to a full-factorial design including ALAN and a drought treatment. Phenological, physiological, and performance traits were assessed, including flowering phenology and duration, number of inflorescences, growth, biomass, specific leaf area (SLA), and leaf dry matter content (LDMC).

ALAN had strong effects across most traits, whereas drought effects were strong for some traits but negligible for others. Flowering progressed faster and occurred more often under ALAN, with variation among functional groups and a marginal three-way interaction with drought. Flowering duration was extended by ALAN but shortened by drought. Significant interactions between ALAN and drought for the duration, indicate that effects of ALAN depend on water availability. SLA increased under both ALAN and drought, whereas LDMC decreased under these treatments, with the magnitude of the effects vary among functional group. The number of inflorescences, relative growth rate and total biomass increases under ALAN, whereas the latter two traits decreased under drought. Overall, multiple two- and three-way interactions among these performance traits indicate context- and functional group-dependent responses.

Overall, plant responses to ALAN, particularly in interaction with drought, depend on species' functional identity and may reshape plant community composition under urbanization with consequences for ecosystem structure and functioning.

Functional evidence beyond correlative models: Temperature and elevation drive shifts in germination performance of an East Alpine rock crevice endemic

Katerina Iberl¹, Philipp Kirschner², Lenka Moravcova³, Camilla Wellstein⁴

¹Charles University, Czech Republic (Czechia)

²University of Innsbruck

³Institute of Botany of the Czech Academy of Sciences

⁴Free University of Bozen-Bolzano

Predicting the population dynamics of Alpine endemics under rapid climate change requires approaches that capture fine scale climatic variation beyond the limits of correlative species distribution models (SDMs). In topographically complex systems, microhabitats may not be captured by coarse macroclimatic layers, obscuring functional responses of early life-history stages. Here, we provide functional evidence that both elevation and temperature drive variation in germination performance of an East-Alpine endemic across a steep altitudinal range (200–2100 m). We quantified essential germination traits (T50, synchrony, and area under the curve) for 29 natural populations of the East-Alpine endemic *Physoplexis comosa*, measured seed traits, and assessed genetic diversity and structure. Ordination across the combined trait–environment space showed that germination responses were only weakly aligned with seed characteristics and genetic indices, whereas temperature and elevation shaped the dominant patterns of variation. Germination performance declined markedly in warmer low elevation sites, whereas high elevation populations maintained higher synchrony, shorter germination times, and overall stronger performance, likely reflecting evolutionary adaptation to the short and predictable germination windows characteristic of high elevation environments. Variation partitioning revealed that both temperature related climate variables and elevation explained substantial and largely independent portions of variation, indicating direct climatic sensitivity of germination beyond solely altitudinal patterns. Our findings show that functional germination traits provide mechanistic insight into climatic sensitivity during the most vulnerable life history stage, offering a valuable complement to SDMs and improving predictions of alpine endemic persistence under climate change.

Home-site advantage of soil seed banks across a rainfall gradient in rangelands: an experimental study in JORDAN

maid Allouzi, Katja Tielbörger, Ghadeer Omar

Tuebingen University

Soil seed banks are key drivers of vegetation reestablishment in degraded rangelands, as they contain long-lived seeds that can contribute to vegetation recovery. However, the restoration potential of seed banks may depend on their origin and the environmental conditions of the recipient area. In particular, it remains unclear whether soil seed banks exhibit a home-site advantage, resulting in higher establishment under their site of origin compared to a novel environment.

We conducted an experiment in Jordanian rangelands spanning arid, semi-arid, and relatively wetter zones that differ in precipitation and degradation levels. Soil seed bank samples were collected from experimental plots and subjected to contrasting environmental conditions representing both their origin and recipient environments. Reciprocal exposure allowed us to test the effect of soil seed bank origin across the rainfall gradient.

Seedling emergence and species composition were counted under controlled conditions to characterize the realized community, then compared to the communities derived from the translocated samples. Initial results indicate a consistent home-site advantage, with higher germination when soil seed banks were expressed under their origin conditions. This effect was particularly pronounced in arid and semi-arid zones, suggesting stronger environmental filtering and adaptation under harsher conditions.

These findings highlight the importance of soil seed bank origin and site-specific processes in determining restoration success. Translocating soil seed banks across environmental gradients may reduce establishment success, whereas incorporating home-site effects into restoration planning can enhance restoration potential and improve outcomes in degraded rangelands.

Genetic diversity and structure of German segetal species – results from the GISA project

Philipp Tran^{1,5}, Veit Herklotz¹, Christiane Ritz^{1,2,6}, Heiko Schmied³, Laura Fortmann³, Stefan Meyer¹, Dörte Harpke⁴, Karsten Wesche^{1,2,6}

¹Senckenberg Museum for Natural History Görlitz – Senckenberg – Leibniz Institution for Biodiversity and Earth System Research, D-02826 Görlitz, Germany

²International Institute (IHI) Zittau, Dresden University of Technology, D-02763 Zittau, Germany

³Stiftung Rheinische Naturlandschaft, D-53123 Bonn, Germany

⁴Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany

⁵Forschungszentrum Jülich GmbH, IBG-4, D-52425 Jülich, Germany

⁶German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, D-04103 Leipzig, Germany

Arable land is among the most important landcover types with ~ 12 mio. hectares in Germany. Segetal plants (so called weeds from a farming perspective), that co-occur with cultivated crops, contribute substantially to agro-biodiversity, and are associated with higher trophic levels by providing food sources for insect pollinators or herbivores. Due to agricultural intensification they have experienced a massive decline over the last decades, and most species have become endangered. In contrast to other elements of cultural landscapes (i.e. meadows, forests), restoration efforts are nearly lacking for arable land. Flower strips have been implemented as ecological restoration measure, however, employed species and seeds are often used cultivars or else come from non-local origins. In Germany, planting non-crop and non-garden species is dictated legislatively by seed transfer zones (STZs) that ensure species' regionality. In the special case of segetal plants, the almost complete lack of genetic information at spatial scales hampers the use and production of regional seeds. Moreover, Red List assessments are currently based on temporal occurrence data so far and do not include genetic information, thus invoking a risk of non-capturing genetic erosion, even for widespread species.

We applied ddRAD sequencing on 385 populations of seven common, nine rare and five threatened segetal species across Germany. We found distinct geographic structuring of genetic patterns in 14 of 21 species, legitimizing the general concept of using regional seeds for restoration measures. Some species listed as "Least concern" in relevant Red Lists showed relatively low values of genetic diversity and strong geographic structuring pointing at a non-trivial relationship between abundance of a species and potentially detrimental genetic structure.

Managing Polyploid Complexity in Grassland Restoration: Cytotype Differentiation and Implications for Seed Zones

Stefan Michalski, Walter Durka, Johannes Höfner

Helmholtz Centre for Environmental Research UFZ, Germany

Regional seed sources are widely used in ecological restoration, often including polyploid complexes—taxa with multiple ploidy levels—without distinguishing between cytotypes. Mixing ploidy levels can promote hybridization, reduce offspring fitness, and disrupt natural geographic patterns, as ploidy levels may represent distinct genetic lineages. However, detailed information on their distribution and genetic differentiation is often lacking.

We focus on six polyploid complexes commonly used for species-rich grassland restoration. We present high-resolution, national-scale maps of their ploidy levels and quantify genetic differentiation. Ploidy levels within complexes were more differentiated than seed zones within individual ploidy levels. Abundance, spatial distribution, and sympatry vs. parapatry varied widely among complexes, yet distributions consistently correlated with environmental gradients. Mixed-ploidy populations were generally rare. *Campanula rotundifolia*, *Euphorbia cyparissias*, and *Pimpinella saxifraga* exhibited regional parapatry, whereas *Achillea millefolium* agg., *Knautia arvensis*, and *Leucanthemum vulgare* agg. were more sympatric. Diploid *K. arvensis* was rare and potentially non-native to Germany.

Based on these datasets, we provide a management framework for polyploid complexes in seed zone-based restoration, requiring only cytotype distribution data obtainable at reasonable cost. The framework recommends management strategies per seed zone, depending on cytotype presence, frequency, and spatial distribution. It guides seed producers and managers in making consistent decisions to avoid fitness losses from mixing ploidy levels. Depending on abundance and distribution, either the dominant ploidy level should be prioritized, or multiple cytotypes managed independently within the seed zone.

This framework enables informed restoration practices, ensuring polyploid complexes are handled to maintain ecological integrity, genetic differentiation, and long-term viability of restored grasslands.

Plastic germination, temporal niche partitioning and emergent assortative mating in annual plants

Max Schmid¹, Katja Tielbörger¹, Amael Daval¹, Charles Mullan²

¹*Universität Tübingen, Germany*

²*University of Lausanne, Switzerland*

Temporal fluctuations in the environment can promote coexistence via the storage effect, where competing variants are buffered during unfavourable years. In annual plants, this can arise from seed dormancy: seeds remain in the seed bank across years and germinate under suitable conditions. Here, we investigate how plasticity in germination timing (where seeds use environmental cues to adjust when they germinate) affects genetic diversification and ecological speciation. Using eco-evolutionary models, we show that adaptive plasticity readily evolves via genetic associations between germination and fecundity traits, allowing seeds to germinate preferentially in years favourable for reproduction. This enhances temporal niche partitioning and promotes divergence into specialised morphs. Because these morphs germinate in different years, plasticity generates temporal assortative mating and maintains trait associations even without genetic linkage. Our results show that adaptive plasticity and genetic diversification can interact synergistically: predictive germination not only buffers fluctuations but also drives the evolution of biodiversity.

Do insular and continental populations of *Tillandsia* differ in seed dispersal traits? A test of the island syndrome on Alcatrazes Island, Brazil

Livia Garcia¹, Giovana Narezi Trotta¹, Lais Pedroso Bertaia¹, Beatriz Lucas Arida¹, Raphael da Silva¹, Juliano Sarmento Cabral², Wagner Luiz dos Santos¹, Natalia Costa Soares¹, Fábio Pinheiro¹

¹State University of Campinas (UNICAMP), Brazil

²University of Bonn, Germany

Islands are considered habitats with strong environmental filters, capable of promoting morphological modifications in species over generations, such as reductions in dispersal potential. To investigate whether populations of anemochorous species exhibit reduced dispersal in an island environment, we compared two island endemic species (*Tillandsia alcatrazensis* and *Tillandsia uiraretama*) with their phylogenetically close species occurring on the mainland (*Tillandsia geminiflora* and *Tillandsia araujei*, respectively). In addition, we analyzed a third species with populations on both mainland and insular environments (*Tillandsia gardneri*). The study was conducted on mainland populations and on Alcatrazes Island, Southeastern Brazil. Terminal velocity (TV) tests were performed under controlled conditions, along with measurements of plume length, seed width and length, and seed mass. Analyses included Wilcoxon tests to assess differences in species morphology and TV, and Spearman correlation tests to evaluate which traits influence TV. The results indicate that *T. gardneri* and *T. uiraretama* showed a significant difference in weight, being lighter than the mainland populations, contrary to expectations. Only *T. alcatrazensis* showed a difference in TV ($p < 0.001$), exhibiting a higher value. Morphological traits influence TV such that seed width shows a positive correlation ($\rho = 0.732$, $p < 0.001$), seed length a strong negative correlation ($\rho = -0.603$, $p < 0.001$), and plume length a very strong negative correlation ($\rho = -0.826$, $p < 0.001$). Seed length, and especially plume length, proved to be the traits that most strongly influence species dispersal by decreasing TV as they increase. The rupicolous and epiphytic habit appears to influence seed traits, such that epiphytic species (*T. gardneri* and *T. geminiflora*) have longer plumes than rupicolous species (*T. alcatrazensis*, *T. araujei*, and *T. uiraretama*), which results in lower TV. Therefore, the seed morphological differences of *Tillandsia* species appear to be related to habitat (rupicolous and epiphytic) rather than insularity. (FAPESP - 2025/16124-8).

Northward range expansion reduced genetic diversity and shaped population structure in tetraploid hare barley (*Hordeum murinum* L.)

Sandy Jan Labarosa¹, Helene Villhauer², Nina Döring¹, Anna Bucharova², Maria von Korff¹, Timo Hellwig¹

¹Heinrich-Heine-Universität Düsseldorf, Germany

²Conservation Biology, Department of Biology, Philipps University Marburg

Rapid environmental change is reshaping adaptive landscapes in several plant populations. Yet the genomic basis of adaptation to environmental heterogeneity remains poorly understood. Hare barley (*Hordeum murinum* L.) is a predominantly selfing winter annual species commonly associated with human disturbed habitats across Europe and the circum-Mediterranean region. It forms a polyploid complex comprising diploid, tetraploid and hexaploid cytotypes. Its broad geographic range makes it a suitable model for investigating the genomic basis of local adaptation.

In this study, we generated genotype-by-sequencing data for 932 tetraploid individuals sampled across 189 natural populations and 21 genebank accessions spanning Europe, the circum-Mediterranean, and Asia Minor. Population structure analyses resolved seven genetic clusters with substantial admixture among them. Nucleotide diversity varied significantly among genetic clusters and declined with increasing latitude. Moreover, reconstruction of historical effective population size further indicated staggered expansions, with the Balkans and Mediterranean clusters expanding earlier than Western and Central European cluster. Variation partitioning showed that space, temperature, and precipitation-related variables explained 10%, 3% and 1% of the total genetic variation, respectively. Additionally, we identified 79 single nucleotide polymorphisms (SNPs) consistently associated with climate variation at the accession's origins across two complementary genome scan approaches, suggesting putative signatures of local adaptation.

Overall, our results indicate that northward range expansion has been a major driver of population structure in tetraploid hare barley. By grouping climate-associated SNPs into 36 major loci, we identified genomic regions that may have facilitated the establishment of populations in these newly colonized areas, reflecting the polygenic nature of local adaptation.

Landscape history shapes genetic diversity in *Primula veris* populations across Europe

L. Marie Ende^{1,2}, Zuzana Münzbergová^{3,4}, Tsipe Aavik⁵, Jan Plue⁶, Hans Jacquemyn⁷, Iris Reinula⁵, Vojtěch Zeisek^{3,4}, Marianne Kivastik⁵, Tomáš Dostálek^{3,4}, Olivia Bernhardsson⁷, Epp Valdaru⁵, Sabrina Träger^{1,2}

¹*Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany*

²*German Centre for Integrative Biodiversity Research e.V. (iDiv) Halle-Jena-Leipzig, Leipzig, Germany*

³*Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic*

⁴*Institute of Botany, Czech Academy of Sciences, Průhonice, Czech Republic*

⁵*Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia*

⁶*Swedish Biodiversity Centre, Swedish Species Information Centre, Swedish University for Agricultural Sciences, Uppsala, Sweden*

⁷*Department of Biology, University of Leuven, Belgium*

Semi-natural grasslands are one of the most species-rich ecosystems of Europe but have undergone particularly strong habitat changes due to land use intensification and abandonment. Over the past decades, the area of semi-natural grasslands in Europe has been drastically reduced. With declining area, the remaining populations in these habitats became smaller, more and more distinct, and increasingly disconnected, resulting in strongly reduced or even inhibited gene flow. The consequence is genetic impoverishment leading to reduced resistance to environmental changes and diseases.

Our study species, *Primula veris* L. (cowslip, family Primulaceae), is a herbaceous plant that typically grows in nutrient-poor semi-natural grasslands and is therefore a representative for this endangered ecosystem. Our study regions span five European countries (Belgium, Germany, Czech Republic, Sweden, and Estonia) covering a broad part of the species' distribution range. We performed next-generation sequencing on 150 populations and analyzed the relationship between genetic diversity and landscape configuration of three time points over the past 100 years.

Landscape characteristics from all three time points still influence contemporary genetic diversity of the populations. This time lag in genetic response provides an opportunity to implement conservation measures preserving former genetic diversity, even in landscapes that have already undergone fragmentation and other habitat changes.

The role of local and landscape-scale factors on the genetic diversity of *Briza media* in the context of grassland abandonment

Iris Reinula¹, Walter Durka², Karin Kaljund¹, Kadri Koorem¹, Stefan Michalski², Marina Semtšenko¹, Tsipe Aavik¹

¹University of Tartu, Estonia

²UFZ Helmholtz Centre for Environmental Research, Germany

Recent changes in land use have led to drastic loss and fragmentation of semi-natural grasslands, impacting the genetic diversity of grassland plants. However, the specific effects of recent habitat shifts on the genetic diversity of wind-pollinated plants remain understudied. We assessed the relative effects of contemporary landscape composition, management and local environmental conditions on the genetic diversity and gene flow of *Briza media* in open and overgrown calcareous grasslands of Western Estonia.

We examined the genetic patterns of *B. media* across 22 populations. High-throughput sequencing (RADseq) yielded ~29,000 SNPs. We used both link- and node-based landscape genetic methods for studying the effect of landscape structure and local environmental conditions on genetic variation.

Our results revealed that *B. media* populations in managed grasslands had higher genetic diversity than those in abandoned grasslands. Higher amount of woodland in the surroundings of *B. media* populations resulted in lower genetic diversity. Additionally, the genetic diversity of *B. media* was influenced by some soil parameters. We observed increasing genetic differentiation between populations with increasing distance, but found no influence of landscape structure on the gene flow of *B. media*.

These findings suggest that shifts in grassland management and landscape change influence the genetic diversity of wind-pollinated plants, which have often been considered less sensitive to these factors. Consequently, conservation and restoration practices should also account for the potential vulnerability of wind-pollinated grasses.

How do genotypes that differently modulate the nitrogen cycle perform under distinct abiotic conditions?

Sandro Schaible¹, Leah Sinzig¹, Jonathan Gervais², Amélie Cantarel², Niek Scheepens¹, M. Stefania Przybylska¹

¹*Plant Evolutionary Ecology, Institute of Ecology, Evolution and Diversity, Goethe University Frankfurt, Max-von-Laue-Str. 13, 60438 Frankfurt am Main, Germany.*

²*Université Claude Bernard Lyon 1, Laboratoire d'Ecologie Microbienne, UMR CNRS 5557, UMR INRAE 1418, VetAgro Sup, 69622 Villeurbanne, France*

Nitrogen (N) is a key limiting nutrient for plant growth and productivity in terrestrial ecosystems. Plants can respond to N limitation in different ways. They can either adjust physiologically and morphologically to improve nutrient acquisition or they can modify nitrogen availability indirectly by influencing symbiotic and free-living soil microorganisms that drive N cycling. Although many studies have characterized how plant physiological and morphological strategies as well as plant associations with symbiotic microorganisms influence N acquisition, much less is known about plant-driven modulation of free-living soil microorganisms and how abiotic soil conditions influences these interactions. Using common garden experiments, we investigated how genotypes of *Arabidopsis thaliana* that differ in their influence on nitrification and denitrification, i.e. two key microbial N transformations in the soil, respond to variation in N availability and to soil alkalinity. We found that genotypes did not differ in aboveground biomass under low or high N availability. However, aboveground biomass in alkaline soil decreased with increasing nitrification enzyme activity, particularly in genotypes that reduce nitrification relative to denitrification. These findings suggest that soil pH may be a key driver of a plant's ability to modulate N-cycling microbial activities in the soil.

When form no longer predicts function: the role of intraspecific trait variation

Marina Semchenko¹, Anastasia Tönisson¹, Jenalle Eck^{1,2}, Yuying Jing¹, Piia Kängsep¹, Lauri Laaspere¹, Miina Oras¹, Laura Puura¹, Jianlu Wu^{1,3}, Nianxun Xi^{1,4}, Kadri Koorem¹, John Davsion¹

¹*University of Tartu, Estonia*

²*Electric Flora, Norway*

³*Northeast Normal University, China*

⁴*Hainan University, China*

Trait-based ecology offers a framework for predicting ecosystem functioning, yet it remains unclear if trait spectra identified in large-scale studies also structure variation within species. As traits can vary within species to a similar extent as across species within a given community, understanding intraspecific trait coordination and its impact on ecosystem function is important when forecasting ecosystem response to global change. Here we examined intraspecific trait and function variation in 22 populations of a common grass species *Briza media* that are experiencing a major shift in land use (long-term grazing abandonments and shrub encroachment). Plants were exposed to defoliation and shading treatments, reflecting the major environmental change factors in this system, to disentangle genetic and plastic components of trait covariation and trait impact on ecosystem functions. We found that, across environmental treatments, conservative leaf and root traits were coordinated and associated with higher multifunctionality, consistent with large-scale interspecific studies. However, under constant and undisturbed conditions (no clipping or shading), root and leaf traits became decoupled, and multiple independent trait axes enhanced different functions, revealing genetic potential for multifunctionality. Environmental constraints imposed by clipping and shading reorganised trait correlations and weakened links between traits and ecosystem functions. Our findings show that trait coordination is context dependent and largely driven by phenotypic plasticity rather than fixed genetic constraints. Predicting ecosystem responses to environmental change requires explicit consideration of intraspecific variation and genotype-by-environment interactions.

Small-scale fen restoration brings back key species and ecosystem functions

Johannes Merz, Franziska Willems, Anna Bucharova

Marburg University, Conservation Biology, Karl-von-Frisch-Str. 8, 35043 Marburg, Germany

Fen peatlands act as carbon sinks and are hotspots for specialised species, but a large proportion of fens have been drained for agricultural or forestry use, which turns them from carbon sink to carbon source, and negatively affects specialised biodiversity. Although restoration by rewetting can partially improve ecosystem functions, the successful recovery of specialised biota depends on previous land use. Rewetting agriculturally used fens often results in an ecosystem that does not resemble the original fen. The vegetation recovery of rewetted fens used for forestry is more promising, but our knowledge of vegetation development comes from boreal fens. It is unclear whether vegetation can successfully recover after the rewetting of forestry-drained fens in the temperate zone.

Our study focused on the recovery of vegetation and peat accumulation in small fens in temperate Europe that had been drained for forestry and restored by rewetting over the 38 years prior to the study. We recorded vegetation composition and measured peat depth. We demonstrate that peat layers continuously increased with time since restoration, possibly indicating peat accumulation, which is crucial for converting drained fens back into carbon sinks. The vegetation composition of the restored sites became increasingly similar to that of the near-natural sites over time, with the steepest change occurring during the first 10 years after restoration. Nevertheless, even after decades, the vegetation did not reach the quality of near-natural sites. Our results highlight that rewetting forestry-drained fens can restore ecosystem services and lead to partial vegetation recovery in temperate fens.

Allelopathy by the invasive garden lupine inhibits the germination of native herbs but promotes the growth of seedlings

Aino Kalske, Pasi Ahola, Niko Luntamo, Emilia Mäkinen, Altti Tähtinen, Satu Ramula

University of Turku, Finland

Allelopathy is the stimulatory or inhibitory effect of one plant on another plant by release of phytochemicals. It can affect the competitive interactions between plants, but the strength of the effect may depend on the tissue of the donor plant, the phylogenetic relatedness of the interacting species and the life stage of the recipient plant. Plants may also differ in allelopathy between native and invasive ranges if the trait has evolved during the invasion process. Here, we examined the allelopathic effects of the garden lupine *Lupinus polyphyllus* (Fabaceae) from native and invasive populations on six native herbs from three families (Asteraceae, Caryophyllaceae, Fabaceae). We exposed the seeds and seedlings of the test species to aqueous leachates prepared from root or shoot tissue of *L. polyphyllus* from native and invasive origins and measured germination rate, germination time and growth over the course of one growing season. Both leachates inhibited germination in all species, but shoot leachate was more allelopathic than root leachate in case of Fabaceae and Caryophyllaceae. Plants from closely related Fabaceae were least affected by *L. polyphyllus* leachates in terms of germination rate. Plants of the invasive and native origin did not differ in their allelopathic effects on germination. Leachate had the opposite effect on seedlings and resulted in higher biomass at the end of the growing season. These results demonstrate that the invasive *L. polyphyllus* can inhibit the germination of co-occurring native species and suggest that allelopathy likely contributes to its invasion success. However, the allelopathic potential has not changed over the course of the invasion and its effects are variable depending on the life stage.

Invasive *Lupinus polyphyllus* altered native species' functional traits

Marta Czarniecka-Wiera¹, Boglárka Berki², Tomasz H. Szymura³, Magdalena Szymura¹

¹*Institute of Agroecology and Plant Production, Wrocław University of Environmental and Life Sciences, Poland*

²*Centre for Ecological Research, Vácrátót, Hungary;* ³*Botanical Garden, University of Wrocław, Poland*

The defining characteristic of invasive species is their superior competitive abilities comparing to native plants, which often leads to a decline in native biodiversity within affected ecosystems. However, some native species may adapt by reallocating resources to develop traits that allow them to coexist with invaders.

In this study, we examined how the functional traits of native plants respond to the invasion of *Lupinus polyphyllus*, as well as how their CSR (competitor–stress tolerator–ruderal) strategies shift under invasion pressure. We focused on eight common grassland species (four herbs and four grasses) from the Sudety Mountains in Poland. Samples were collected from grasslands heavily dominated by *Lupinus polyphyllus* (over 50% cover) and from nearby non-invaded areas. We measured key functional traits, including plant height, leaf area (LA), specific leaf area (SLA), and leaf dry matter content (LDMC), and then evaluated each species' life strategy using the CSR framework.

Our findings show that native plants growing in invaded sites tend to be taller, have larger leaves, higher SLA, and lower LDMC compared to those in non-invaded areas. These trait shifts suggest a reduced investment in stress-tolerance strategies and a shift toward competitive and ruderal strategies. Because the studied grasslands are extensively mowed, the shading effect of *Lupinus polyphyllus* likely imposes stronger pressure than any potential benefits from plant–soil feedback mechanisms.

Posters

Thursday, 7th May 5:00 pm – 6:45 pm

Entangled Drivers: Complex Tree Diseases in Forest Ecosystems

Mona Schreiber, Marieke Lenga, Henning Otto, Christian Lampei, Lars Opgenoorth

Philipps-Universität Marburg, Germany

Forests worldwide are increasingly shaped by complex disease dynamics arising from interactions among abiotic stressors, biotic agents, and ecosystem processes. Rather than resulting from single causal agents, these syndromes emerge from interacting drivers, including environmental conditions, host susceptibility, and shifts in associated microbial communities. Climatic change further intensifies these processes by increasing the frequency and severity of droughts, heatwaves, and extreme weather events while facilitating the activity and spread of pests and pathogens.

Within this context, complex tree diseases offer a framework for understanding multifactorial decline processes and their manifestation within and among species. Using European beech (*Fagus sylvatica*) and oaks (*Quercus* spp.) as important European forest tree species, we examine how their physiological and anatomical traits shape susceptibility to decline and interact with associated pathogens, insects, and environmental stressors.

We further consider the cascading ecological consequences of tree mortality and discuss emerging approaches for monitoring and managing forest health, including remote sensing, genomics, and adaptive management strategies. Taken together, these perspectives underscore the need for integrative and cross-disciplinary approaches to understanding and responding to complex tree diseases in forests experiencing rapid environmental change.

Fruit decomposition and removal in a subtropical forest biodiversity experiment

Luisa Martha Senger¹, Nora Anderson¹, Tillmann Niedernhoefer¹, Tim Diekötter², Alexandra Erfmeier², Xiaojuan Liu³, Zhi-Shu Xiao⁴, Chao-Dong Zhu⁴, Alexandra-Maria Klein¹, Finn Rehling¹

¹University of Freiburg, Germany

²Kiel University

³Institute of Botany, Chinese Academy of Sciences, Beijing, China

⁴Institute of Zoology, Chinese Academy of Sciences, Beijing, China

Tree species richness enhances diversity at higher trophic levels and can increase ecosystem functioning. It may also shape the communities of decomposers involved in fruit decomposition and, through this, affects rates of fruit decomposition. However, such effects may be obscured by other environmental drivers, including forest structure, topography, and interactions among decomposer. To investigate these relationships, we placed ~900 plums across 96 plots along a tree diversity gradient in the world's largest forest biodiversity experiment (BEF-China) in subtropical China in autumn 2025. Fruits were exposed for four days, after which their removal and decomposition stages were assessed. Tree species richness did not influence the removal, nor the decomposition of fruits. Canopy cover decreased the removal of fruits, but increased their decomposition. Fruit turnover rates were ultimately higher in open forests. By extending previous research on other forms of necromass (carrion, deadwood, litter), this study demonstrates that tree species richness on fruit turnover rates can be weak, and improves our understanding of bottom-up effects of tree diversity on organic matter turnover.

Impact of historical climatic fluctuations on the distribution and genetic diversity of endemic feather-grass species (Poaceae: *Stipa*)

Marcin Nobis¹, Ewelina Klichowska¹, Marta Krzempek^{1,2}, Patar Sinaga^{1,2}, Afni Marpaung^{1,2}, Julia Toporek¹

¹*Jagiellonian University, Faculty of Biology, Institute of Botany, Krakow, Poland*

²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

Quaternary climatic oscillations have significantly influenced the genetic structure and distribution of high-alpine endemic plants in the Central Asian mountains. This study investigates two cold-adapted vicariant *Stipa* species, distributed in the Tian Shan and Pamiro-Alay Mts, to evaluate their evolutionary responses to past and future climatic shifts. By integrating Ecological Niche Modeling (ENM) with genome-wide SNP data (DArTseq), we reconstructed their demographic histories and predicted their vulnerability to climate warming. Our phylogeographic analysis reveals clear genetic differentiation of the studied sister species and intraspecific spatial genetic structure. Contrary to many temperate species, demographic history reconstructions indicate that both endemics maintained larger effective population sizes ("Ne") during the Last Glacial Maximum (LGM), benefiting from increased glacial connectivity that facilitated gene flow. Following the LGM, both species experienced parallel demographic declines in response to range shrinkage. While both taxa are strictly associated with calcareous rocky substrates, their current distributions are primarily constrained by specific temperature and precipitation gradients. Future projections for the late 21st century suggest that both species will face significant range contractions, as their narrow climatic niches shift toward higher elevations. However, the degree of sensitivity varies between the two vicariants due to the occurrence in climatically and topographically distinct mountainous regions. Our findings underscore that identifying historically stable habitats and understanding the genomic basis of their resilience are essential for the conservation of mountain endemics. This study provides a theoretical framework for prioritizing protection in Central Asian biodiversity hotspots where climate change poses a severe threat to "rock-associated" alpine specialists.

The research was funded by the National Science Centre, Poland, under projects 2023/51/B/NZ8/01179 and 2020/39/D/NZ8/02307.

Plant-soil feedbacks in a heathy-woodland

Hagai Shemesh¹, Tamar Orly², Rebecca Miller², Camille Truong²

¹*Tel-Hai University, Israel*

²*Royal Botanic Gardens Victoria, Melbourne, VIC, Australia*

Plant soil feedbacks (PSF) have been suggested to affect plant species diversity. Soil fungi are thought to be involved in many of these feedback mechanisms. According to the Janzen-Connell hypothesis, individuals growing in the vicinity of conspecific mature trees will display negative PSF due to host-specific soil-borne pathogens. On the other hand, compatible ectomycorrhizal fungi can favor seedling establishment near conspecifics through positive PSF. We examined PSF between *Allocasuarina paradoxa*, a dual mycorrhizal shrub and *Eucalyptus viminalis* an ectomycorrhizal tree, co-occurring in dry heathy woodland. Seeds and soil were collected in the Cranbourne bushland conservation area in SE Melbourne, Victoria. We conducted seed germination and pot trials for one month and eight months, respectively, and recorded germination success, plant growth, biomass allocation, as well as soil and root mycobiomes using ITS2 fungal metabarcoding. Germination did not vary with soil type. Both species grew larger on *E. viminalis* soil and also showed a negative correlation between arbuscular mycorrhizal fungi (AMF) richness and plant biomass. Species specific analysis revealed that the negative correlation was caused by a small number of species. Our findings support the notion that ECM fungi produce positive plant soil feedbacks while AMF plants experience negative ones. These dynamics can result in temporal and spatial changes in niche availability within the habitat, which could in turn support plant biodiversity.

Scale Dependence of Multifaceted Diversity Change Over the Last 5 Decades

Viktoria Ferenc^{1,2,3}, Friedrich Gloge^{1,2}, Mike Thiv^{1,3}, Pierre Liancourt^{1,3,4}

¹*State Museum of Natural History Stuttgart, Germany*

²*Institute of Landscape and Plant Ecology, University of Hohenheim, Stuttgart, Germany*

³*KomBioTa – Center for Biodiversity and Integrative Taxonomy, University of Hohenheim & State Museum of Natural History, Stuttgart, Germany*

⁴*Plant Ecology, University of Tübingen, Germany*

Understanding how multidimensional biodiversity change reorganizes across scales is critical for forecasting ecosystem responses to environmental change. This study investigated the scale-dependence of temporal restructuring in taxonomic, functional, and phylogenetic biodiversity facets using a comprehensive 50-year floristic dataset from Baden-Württemberg, Germany. By aggregating plant occurrence data across five nested spatial grains (approximately 6 km to 30 km), the research addressed how the dimensionality of biodiversity change shifts with scale and whether spatial organization can reliably predict temporal trajectories.

Principal Component Analysis (PCA) revealed that the internal organization of temporal biodiversity change is highly scale-dependent. At landscape scales (~6 km to ~12 km), the leading axis of biodiversity change was consistent with functional “filling” dynamics and turnover among terminal phylogenetic clades. However, at sub-regional scales (~24 km to ~30 km), patterns suggested a transition toward functional “packing” and increasing trait-space saturation, while phylogenetic restructuring appeared to involve deeper evolutionary lineages. Mixed-model analyses further revealed facet-specific scale responses: taxonomic and functional change varied primarily additively with spatial grain, whereas phylogenetic change showed scale-contingent sensitivity to warming, indicating that climate effects on lineage restructuring depend on spatial context.

Crucially, Procrustes comparisons showed that the congruence between spatial biodiversity structure and temporal change declined as observational grain increased. This scale-dependent divergence indicates a deviation from ergodicity at broader scales, where regional environmental drivers and landscape heterogeneity mask the local processes that shape finegrain patterns. These findings point out that biodiversity dimensionality is not a fixed property but a scale-explicit architecture. Ultimately, the results highlight that biodiversity structure in space does not uniformly represent dynamics through time, challenging the validity of space-for-time substitution across different spatial resolutions.

The effect of invasive *Lupinus polyphyllus* on the biodiversity and fodder value of semi-natural grasslands

Marta Czarniecka-Wiera¹, Antoni Szumny¹, Tomasz Szymura², Magdalena Szymura¹

¹Wrocław University of Environmental and Life Sciences

²Wrocław University, Poland

Semi-natural grasslands are essential for maintaining biodiversity in rural areas and provide a range of ecosystem services, from carbon sequestration and water retention to fodder production. Their preservation requires extensive regular mowing, which can be challenged by biological invasions. *Lupinus polyphyllus* Lindl. is one of Europe's most widespread alien invasive plant species, and its negative effect on species richness and functional diversity of native communities is especially pronounced in low-productivity environments. Less well-known is the effect of *Lupinus* on overall biomass productivity and the chemical composition of native plants, which, in turn, influences the agricultural use of the invaded but still valuable semi-natural grasslands. Here, we compared the above-ground biomass, chemical and physical properties, biodiversity indices, soil characteristics, and biomass production across 60 paired plots in semi-natural, low-productivity grasslands. The paired plots included non-invaded grassland patches and nearby invaded patches with *Lupinus* cover exceeding 50%. On the non-invaded plots, biomass productivity was almost twice as low as on invaded plots and was largely restricted by soil pH. The presence of invasive *Lupinus* had minimal impact on the productivity of native species, and *Lupinus* biomass was similar to that of the natives. Moreover, the presence of *Lupinus* in the community increased the protein content in the above-ground biomass of native species, as well as the contents of N, P, K, and Ca in the hay. The effect of *Lupinus* on biodiversity at different spatial scales (10 m² and 1 m²) was less pronounced. The results suggest that the presence of this invader shifts the productivity of the entire community and alters the chemical composition of native species, likely due to plant-soil feedback. Nonetheless, the biomass can still be utilized by farmers, decreasing the likelihood of management abandonment.

Does clonal growth reshape root system functioning?

Jana Duchoslavová, Joana Bergmann

ZALF (Leibniz-Zentrum für Agrarlandschaftsforschung), Germany

Plant roots perform the essential functions of soil resource acquisition and transport to the aboveground parts of the plant body. These two functions however form a trade-off that needs to be optimized on the level of the whole root system. Clonal growth, being common in herbs and widespread over the angiosperm phylogeny, provides plants with several specific characteristics, including formation of multiple rooting points along the plant body and the ability to transport resources between these points via clonal organs. Such architectural and physiological features can presumably have impacts on root system functioning. In comparison to non-clonal plants, the transport distance between acquisitive fine roots and leaves is shortened and transport is partly provided by clonal organs. Therefore, we hypothesize that clonal growth reduces the transport and enhances the acquisitive function of the root system. In our ongoing project HiddenFun, we test this hypothesis by comparing root functioning of phylogenetically related clonal and non-clonal species. To describe whole root system functioning, we take a multi-perspective approach and combine nitrogen uptake estimates with root morphological, architectural and anatomical traits, as well as mycorrhizal colonization rate. We here share first results of our project addressing this challenge and explore key aspects crucial for disentangling acquisitive and transport functions in roots of herbs. Understanding these basic principles hidden belowground will advance knowledge across disciplines, from agriculture to plant population and community biology.

Agroecology for Weeds. A Horizon Europe project: results on agroecological weed control in a maize Living Lab

Milan Brankov, Milena Simić, Vesna Dragičević

Maize Research Institute "Zemun Polje", Agroecology and Cropping Practices, Belgrade, Serbia

Sustainability of European farming systems is greatly compromised by the present weed management, which relies to a large extent on herbicides. The reduction of herbicide use has become major policy targets of EU Farm to Fork strategy, aiming to promote agroecology and the transition to sustainable and resilient farming systems. The project will create an Agroecological Weed Management Network, inspired by the principles of Planetary Health, inviting agroecology practitioners from all continents to an in-depth dialogue and exchange of knowledge and best practices towards agroecology-based diversified agricultural systems to shape the future of humanity and natural systems.

A maize Living Lab was established in Serbia, applying the multidisciplinary approach to create and evaluate Agroecological Weed Management (AWM) systems, and demonstrate that AWM adoption enhances sustainability and resilience of cropping systems. The Living Lab is grown under either organic or conventional system. In the first experimental year three cover crops: oat, rye, and winter vetch were sown in autumn, and terminated in spring, following by maize. The control was without CC. Weed management practices: mechanical weeding, mulching, false seedbed, bio-based herbicide, and untreated control for the organic system; and herbicide application in recommended or reduced rate, mechanical control, bio-based herbicide, and the control in conventional. The best performing CC - rye was selected for the 2nd and 3rd year. The most abundant species were *Sorghum halepense* and *Chenopodium album*. In organic system, the best weed control method was mechanical control, while in conventional, both herbicide treatments provided high efficacy (90-95% of weeds biomass reduction). As the influence of drought and weed presence in other treatments, yields were low (2-3 t/ha). These results indicate that agroecological weed management is challenging, and therefore it is necessary to subsidize farmers in order to support them to adopt agroecological strategy for weed control.

Climate change-driven cryptic divergence and adaptation to the local climate in lowland-mountain complexes of steppe species

Ewelina Klichowska¹, Patar Sinaga^{1,2}, Julia Toporek¹, Marta Krzempek^{1,2}, Afni Marpaung^{1,2}, Marcin Nobis¹

¹*Jagiellonian University, Faculty of Biology, Institute of Botany, Krakow, Poland*

²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

The Cenozoic aridification of Central Asia, driven by complex climatic and geological forcing, accelerated the evolution of steppe biodiversity. Subsequent paleoclimatic fluctuations facilitated further lineage diversification and shaped contemporary population genetic structures. Among the steppe taxa affected by this progressive desertification, the genus *Stipa* serves as a preeminent example, for which recent phylogeographic analyses increasingly highlight the crucial role of climate change in its evolutionary history. Integrating Ecological Niche Modeling (ENM) with landscape genomics (based on genome-wide DArTseq-derived SNPs), we characterized the population genetics and demographic trajectories of lowland-mountain steppe complexes within the genus *Stipa*. Our findings reveal divergent responses across lineages to paleoclimatic fluctuations, facilitating regional adaptation and cryptic speciation. Comparative analyses indicate that while altitude and temperature are the primary variables affecting ecological niches in mountain populations, lowland populations are further constrained by precipitation patterns. Local climatic adaptations have resulted in disparate habitat suitability, which in turn shapes current range limits and projected vulnerabilities to ongoing climate change.

The research was supported by the National Science Centre, Poland (2020/39/D/NZ8/02307 and 2023/51/B/NZ8/01179).

Contrasting drivers of genetic and functional variation in an Eastern Alpine endemic: Seed mass follows a longitudinal gradient rather than glacial history

Katerina Iberl¹, Philipp Kirschner², Camilla Wellstein³

¹*Charles University, Czech Republic (Czechia)*

²*University of Innsbruck*

³*Free University of Bozen-Bolzano*

Post glacial recolonization in the Eastern Alps has produced parallel gradients in genetic diversity, geography, and environment. It remains unclear whether functional traits such as seed mass carry historical signatures or primarily reflect contemporary geographic or environmental gradients. We examined whether a gradient in seed mass in an East Alpine endemic *Physoplexis comosa* is explained by (i) genetic diversity and structure, or (ii) geographic gradients, and (iii) whether proximity to glacial refugia or distance to the LGM ice margin plays any role. We combined functional traits (seed mass), genetic parameters (π , A_r , cluster membership), geographic variables (longitude, latitude, elevation), and distances to glacial refugia and the LGM ice margin. Using linear models and variation partitioning (rdacca.hp), we quantified unique and shared contributions of predictors, including sampling year as a covariate.

Genetic diversity (A_r) and genetic structure showed pronounced refugial and geographic SW–NE gradients. π reflected historical patterns but lacked a linear geographic trend. Seed mass was independent of refugial distance and elevation but showed a significant association with longitude; this longitudinal effect remained stable after accounting for sampling year, which had only a small additive influence. Reproductive output traits (seed set, % fertile capsules) showed no geographic or historical structure and may be shaped primarily by local micro site conditions and stochastic variation.

Our results reveal a clear decoupling between historical genetic patterns and functional traits. While genetic variation is strongly shaped by post glacial history and geography, seed mass follows a longitudinal SW–NE gradient and carries no historical signature. This suggests an ecological rather than historical imprint on functional traits, in contrast to genetic indices.

Mystery cases: unresolved genomic relations in widespread grassland species

Walter Durka, Stefan Michalski

Helmholtz Centre for Environmental Research-UFZ, Germany

Within the RegioDiv project, the genomic structure of >30 grassland plant species has been investigated using ddRAD SNP markers across Germany. In most cases genetic structure showed a strong spatial component, leading to spatially coherent clusters and isolation-by-distance patterns among regions. However, for a few species, strong within region genomic differentiation patterns existed across multiple regions. These inconsistencies were not driven by differentiation at taxonomic, ploidy, or plastid-nuclear levels. We present such cases, e.g. *Bistorta officinalis*, *Lychnis flos-cuculi* and *Prunella vulgaris* as an invitation to discuss potential mechanisms. The poster will work as an interactive whiteboard.

Organ plasticity and fitness in *Marchantia globosa* splash-cups

Ana-Maria Bratu¹, Valentin Laplaud¹, Mathieu Portela¹, Antoine Garcia¹, Abdillah Mohamed¹, Camille Duprat¹, Claudine Ah-Peng², Stephanie Drevensek¹, Arezki Boudaoud¹

¹LADHYX, CNRS, Ecole Polytechnique, IP Paris, Palaiseau, France

²UMR PVBMT, University of La Réunion, Réunion, France

Plants adapt their phenotypes to environmental conditions over developmental timescales through phenotypic plasticity. Considerable research has focused on how environmental cues impact plant development and phenotype, particularly in relation to crop yield [1]. However, such studies have rarely examined the plasticity of organs involved in fitness.

Here, we investigate the relationship between phenotypic plasticity and fitness using the splash-cups of the liverwort *Marchantia globosa*, a regional endemic plant present on Réunion Island known for its strong elevation gradient and diverse climatic conditions. Splash cups are specialized reproductive structures that disperse asexual propagules via raindrop impacts, making their morphology directly linked to dispersal efficiency. We examine how environmental conditions influence splash-cup morphology and assess how these morphological changes may affect dispersal performance and reproductive success.

We found that splash-cup size correlates positively with elevation. These results suggest phenotypic plasticity at the organ level. Indeed, a few meteorological variables were correlated with splash-cup morphology, with temperature showing the strongest association with splash-cup geometry.

Our results highlight the potential role of phenotypic plasticity in shaping splash-cup morphology under a major elevational gradient, with different environmental conditions, therefore influencing dispersal efficiency.

[1] Tardieu F et al. (2017) Plant Phenomics, From Sensors to Knowledge. Curr Biol 27: R770

Effects of light competition on mating strategies in a cleistogamous plant

Bojana Stojanova

University of Rennes, France

In plants, competitive environments can cause shifts in mating systems, which in turn will affect the competitive ability of the offspring. Yet empirical evidence linking competition to variation in mating strategies remains scarce, largely due to methodological constraints for the estimates of mixed-mating (i.e. selfing rates) and the challenge of isolating competition cues from correlated stresses.

Cleistogamous species provide a powerful model to address this gap. These plants produce both obligately selfing closed flowers and potentially outcrossing open flowers, with the relative proportion of each being environmentally plastic. Variation in cleistogamy therefore offers a direct proxy for changes in mating system allocation. We investigate how simulated light competition affects growth, flowering traits, and mating strategies in *Lamium amplexicaule*, an annual ruderal species with a well-characterized cleistogamous mixed-mating system.

Using a controlled environment experiment, we will investigate the effects of photoperiod and cues for light competition simulated with filters that modify the red:far red ratio. In this way, we can study plants' specific response to light competition without confounding effects of other competitive limitations (water, resources, space). The experiment is currently ongoing, with the first data on phenological, vegetative, and physiological traits available by the end of March, and floral traits by the end of April.

Based on previous observations in natural and experimental populations, we expect light competition to produce a "competitive avoidance" growth strategy (elongated internodal growth, decreased photosynthetic activity, increased specific leaf area). While competition should decrease the overall reproductive output, we expect an increase in the production of costly, open flowers, thus increasing reproduction through outcrossing.

Finally, to link phenotypic plasticity to underlying mechanisms, we will integrate transcriptomic analyses from vegetative tissues sampled prior to floral initiation, thereby targeting upstream regulatory pathways, prior to flowering, involved in environmental cue perception and mating strategy determination.

Identification of *Styppeiochloa hitchcockii* (Poaceae) using molecular markers

Tabea Giese¹, Sylvie Andriambololoner², Marina N. Rabarimanarivo², Nivo H. Rakotoarivelo², Brigitte Ramandimbisoa², Stefan Porembski¹

¹University of Rostock, Institute of Biosciences, Department of Botany, Wismarsche Str. 44-45, D-18051 Rostock, Germany

²Missouri Botanical Garden, P.O. Box 3391, Antananarivo 101, Madagascar

Styppeiochloa hitchcockii is a desiccation-tolerant, mat-forming grass on Malagasy inselbergs. Inselberg species are particularly suitable for population genetic analyses, as the island-like character of the habitat effectively separates different populations. This is advantageous for investigating questions relating to gene exchange within and between different populations. However, accurate species identification is crucial for population genetic analyses. For a long time, *S. hitchcockii* was divided into only two subspecies and different forms, as no clear differences could be determined from the existing herbarium specimens. Since then, there have been many new collections from different locations in Madagascar, what led to a revision recently. The material used in our study was collected along a north-south gradient, most of it coming from the high plateau, although there are collections from Isalo National Park, which represents a significantly different habitat. It is here that Teisher et al. 2022 have described one of the new species of *Styppeiochloa*. The new classification was made using morphological characteristics, primarily of the inflorescences. Yet the plant material used in this survey is almost entirely without inflorescences. Accordingly, another method is needed to reliably identify *S. hitchcockii* as such: molecular markers. New plastid markers were created and tested on several samples. The initial results show no clear differences between the specimens. The samples from Isalo National Park do not stand out noticeably either. The assumption that all plant material is *S. hitchcockii* can therefore be retained for now. However, these preliminary results are based on three primer pairs, and there are three more primer pairs that need to be tested. Moreover, it would be advantageous to include nuclear genome markers, as ITS, in the analysis, as plastids are usually inherited uniparental, while regions such as ITS often offer higher variability.

Evolution of germination traits of *Trifolium repens* along an urbanization gradient across climates

Dominic Schmidt¹, Giovanni Scopece², Lucrezia Laccetti², Niek Scheepens¹, Bojana Stojanova³

¹*Plant Evolutionary Ecology, Faculty of Biological Sciences, Goethe University Frankfurt*

²*Department of Biology, University of Naples Federico II*

³*University of Rennes*

Urbanization creates novel environmental conditions that may drive rapid evolutionary responses in plant populations. Among the most prominent urban environmental changes are increased temperatures caused by the urban heat island effect and altered water availability. These conditions can strongly influence early life-history stages such as seed germination and dormancy, which determine the subsequent plant performance. However, empirical evidence for how urbanization shapes germination traits across different climatic regions remains limited.

This study investigates the evolution of germination and mechanical dormancy traits in *Trifolium repens* along urbanization gradients across Europe, as part of the URBANPOLL project. Seeds were collected from 84 populations distributed across three biogeographic regions (Mediterranean, Continental, and Boreal) within multiple urban areas. Using a controlled environment germination experiment, seeds from urban and non-urban populations were exposed to contrasting temperature treatments representing cold, optimal and warm germination conditions. Germination percentage, germination speed (measured using the normalized Timson index), and early seedling development were quantified to assess population-specific responses to temperature extremes. In addition, the proportion of mechanical dormant seeds was determined to evaluate variation across climatic origins and urbanization gradients.

In line with previous studies on germination and dormancy, we expect Mediterranean and urban populations to germinate better at higher temperatures. We further expect higher proportion of mechanically dormant seeds in Mediterranean and urban populations, consistent with the role of warm and dry environments in promoting dormancy. Moreover, we also assess how the interaction between climatic origin and urbanization gradient shapes germination and dormancy responses, testing whether urban-natural differences vary across biogeographic regions. Furthermore, we expect populations that have the highest germination rates in extreme warm temperatures to also have high germination rates in extremely cold temperatures, but not vice versa. Data analysis is ongoing at the time of abstract registration, and results will be presented during the conference.

Trait variation in one long established and one recently introduced fleabane species along urbanization gradients

Hanja Irina Kappes, Niek Scheepens, Dávid U Nagy

Goethe University Frankfurt, Germany

Invasive species and land use change, such as urbanization, are two of the most impactful drivers of biodiversity loss worldwide. The lack of uncovered soil, combined with the urban heat island effect and a high human density, creates extreme conditions. Plants in urban habitats often grow in pavement joints with limited water availability, and are exposed to heat, continuous sunlight or deep shade, pollution, and mechanical disturbances. At the same time, urban environments can vary strongly at small scales depending on local conditions and urbanization intensity. In temperate regions, native plant diversity decreases from city edges towards the city center, whereas the proportion of neophytes increases. Two globally widespread and potentially invasive neophytes commonly occurring in urban, ruderal, and agricultural habitats are Canadian fleabane (*Erigeron canadensis*) from North America and the Tall fleabane (*Erigeron sumatrensis*) from the South American subtropics. Adaptation to urban environments may increase their persistence under climate change and potentially promote further invasion into non-urban habitats. This study aims to find out, whether intraspecific trait variation occurs along urbanization gradients in these two fleabane species, whether these variations differ between them, and whether variation is associated with environmental variables. To investigate this, phenological, morphological and functional traits were determined in 43 populations of *E. canadensis* and 34 populations of *E. sumatrensis*, as well as several environmental factors, along three transects from the completely urbanized city center to the city edges of Frankfurt (Hesse, Germany). Due to the long establishment time (approx. 350 years), *E. canadensis* is expected to be more adapted to urban conditions and therefore shows trait variations in response to small-scale environmental differences. In contrast, *E. sumatrensis* which has been present for only about 45 years, is expected to show weaker trait differentiation along the urbanization gradient due to its shorter residence time.

Hidden Sensitivity: Specialist Pollinator Networks Respond More Strongly to Latitude Than Generalist Ones

Rafael de Oliveira, Viktoria Ferenc, Pierre Liancourt

Staatliches Museum für Naturkunde Stuttgart, Germany

Latitudinal gradients strongly influence the diversity and structure of plant-pollinator networks. At higher latitudes, environmental constraints tend to reduce species richness and promote more generalized interaction patterns. However, how latitude affects different functional components of networks remains poorly understood, and signals may be obscured when analysing networks only as a whole. By using a comprehensive dataset of 924 plant-bee networks across Europe, we tested latitudinal patterns of diversity and network topology after partitioning networks by bee pollen-specialization: polylectic bees (collecting pollen from many unrelated plants) and oligolectic bees (restricted to a single plant family). Across both network types, plant and bee species richness declined with increasing latitude, with a stronger decline in oligolectic bee networks. Network specialization (H2 index) was higher in oligolectic than in polylectic networks, but did not change significantly with latitude in either type. In contrast, Connectance increased with latitude in both types of networks, and this effect was significantly stronger in oligolectic networks. Together these findings suggest that, while both oligolectic and polylectic networks simplify with increasing latitude, networks composed by oligolectic bees are particularly sensitive, exhibiting greater losses in richness and more pronounced increases in connectance. This underscores that specialist pollinator networks are especially vulnerable to the challenges posed by higher latitudes, responding more strongly than their generalist counterparts.

Genetic population structure and environmental niche models of the alpine grass *Ptilagrostis malyshevii* (Poaceae) in the Central Asian mountains

Marta Krzempek^{1,2}, Ewelina Klichowska¹, Marcin Nobis¹

¹Jagiellonian University, Poland

²Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland

The sky island topography of Central Asian mountains harbours remarkable examples of alpine endemism, yet the interactions between Pleistocene climate dynamics, genetic isolation, and interspecific gene flow in these ecosystems remain poorly understood. The strictly alpine grass genus *Ptilagrostis* occurs across Central and North-Eastern Asia, inhabiting high-elevation meadows and wet alpine grasslands. One of its representatives, *Ptilagrostis malyshevii*, is distributed across the mountainous regions of Central Asia. To investigate the evolutionary history and biogeography of *P. malyshevii*, we employed an integrative approach. We used Ecological Niche Modelling (ENM) to determine the species' current range and reconstruct its past distribution during the Last Glacial Maximum (LGM). Simultaneously, we utilized DArTseq-derived single nucleotide polymorphisms (SNPs) to assess the spatial genetic population structure, reconstruct historical changes in effective population size, and test for interspecific gene flow. ENM analyses revealed that *P. malyshevii* occupies a remarkably stable niche, restricted to high-elevation areas and strongly associated with moisture availability. Throughout the Pleistocene, the species responded to climate oscillations mainly through altitudinal shifts. Genomic analyses identified a highly pronounced spatial genetic structure, reflecting the geographic distribution of isolated populations across secluded mountain ridges. Reconstructions of effective population size indicated a dynamic demographic history with distinct past expansion. Past range dynamics provided an opportunity for secondary contact with a northern related species, *P. mongholica*. Genomic tests strongly supported a post-glacial hybridization event, with a cryptic hybrid lineage persisting in a contemporary contact zone. Our findings demonstrate that adaptation to high-altitude niches, topographic isolation, and secondary post-glacial contact influenced the genetic diversity and evolutionary trajectory of alpine plants in Central Asian mountain systems.

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Linking geodiversity and geostability to genetic diversity in South African Proteaceae

Kayleigh Mengel¹, Deborah Leigh^{2,3}, Oliver Bossdorf¹

¹Eberhard Karls Universität Tübingen, Auf der Morgenstelle, 72070 Tübingen, Germany

²Senckenberg Research Institute, Frankfurt, Germany

³Institute of Ecology, Evolution, and Diversity, Faculty of Biosciences, Goethe University Frankfurt, Frankfurt, Germany

Among global biodiversity hotspots, the Fynbos biome hosts the world's richest extratropical flora. The Fynbos exhibits high spatial turnover of plant diversity linked to strong variation in climate, topography, and geology. The region underwent significant Pleistocene climatic shifts, marked by relative stability in the west and transitions to subtropical grasslands in the east. How such geodiversity and geostability shape genetic diversity and adaptive potential, however, is not yet fully understood. The Fynbos' ~9,000 plant species largely derive from 33 clades. Among these, the Proteaceae, particularly *Protea*, exhibit remarkable variation in functional traits and dominate the Fynbos overstorey, contributing greatly to water, carbon, and nutrient cycling. Whole-genome sequencing of individuals from 810 maternal families across 18 *Protea* species will be conducted to quantify genetic diversity and its relationship to geodiversity and dispersal ability. For the first time, a multi-species map of *Protea* genetic diversity hotspots will be generated. To estimate adaptive potential, we will link trait variation to genomic relatedness and quantify additive genetic variance (VA) for populations, then model VA as a function of geosphere variables and dispersal. Finally, demographic histories will be reconstructed to connect past climatic stability with present-day genetic diversity. By linking genetic diversity, adaptive potential, and demographic history to geodiversity, this study will deliver the first multi-species genetic baseline for *Protea* in the Fynbos biome, providing vital insights for biodiversity conservation under future climate change.

Bound by ammonia: pollution constrains *Cetraria sepincola* at the margin of its Central European range

Michael Boxriker, Viktoria Ferenc, Holger Thüs

State Museum of Natural History Stuttgart, Germany

Small isolated populations of cold-adapted species at the edge of their climatic range are highly sensitive to environmental change making them powerful ecological indicators. *Cetraria sepincola* (Ehrh.) Ach. is an epiphytic lichen that exemplifies this role. While common in Nordic countries its distribution in southern Europe has become fragmented and largely restricted to cold habitats. We investigated populations in high conservation value habitats including wetlands montane stone fields and wooded meadows in south-west Germany where the species persists at the margin of its Central European range and is increasingly rare. Its dependence on specific climatic conditions and selective photobiont associations makes it particularly responsive to climate and land-use change. Using historical records recent observations nitrogen deposition data and associated species we identified key environmental factors shaping its distribution.

Our analysis confirms that the populations are at climatic margin and persist under a tight interplay of abiotic and biotic constraints. High-density occurrences coincide with low ammonia concentrations indicating sensitivity to nitrogen enrichment. The species forms specific partnerships with *Trebouxia* lineages from clade S including OTU S28 (= *T. barrenoae*) which are typical of lichens on acidic substrates. Their occurrence in the co-occurring acidophyte *Hypogymnia physodes* suggests a local reservoir of compatible photobionts, because *C. sepincola* lacks asexual propagules and relies on environmental acquisition.

However, this dependence may become increasingly unstable as environmental conditions shift. At several sites nitrophytic species of the Xanthorion community are colonizing the same substrates introducing incompatible *Trebouxia* photobionts. Such community changes likely reduce the availability of suitable photobionts and constrain establishment and persistence. Together, these findings indicate that climate change, ammonia exposure, and photobiont community shifts interact to elevate extinction risk for *C. sepincola* and other sensitive lichens at their distribution limits.

Genomic adaptation during early establishment in European beech (*Fagus sylvatica*)

Marieke Lengua¹, Christian Lampei¹, Lars Opgenoorth¹, Katrin Heer², Mona Schreiber¹

¹Philipps-University Marburg, Germany

²Albert-Ludwigs-Universität Freiburg

Trees, as long-lived organisms, rely on their capacity to adapt to changing environmental conditions. Recent hot and dry summers and rapidly shifting climates have highlighted their vulnerability to environmental stressors. High genetic diversity may buffer populations against such stress and contribute to long-term resilience. *Fagus sylvatica*, an outcrossing species with high seed production, experiences juvenile mortality and only a small fraction of seeds reaches maturity, creating high potential for natural selection during early life-stages. Under stable conditions, selection is expected to favor competitive traits such as rapid growth, whereas selection under extreme climatic events may favor traits associated with stress tolerance. Seedlings and saplings are additionally exposed to variable microclimatic conditions at the forest floor, shaped by environmental heterogeneity and forest management (e.g., canopy openings), which amplify temperature extremes and vapor pressure deficit.

Within TREEvolution, we analyze genomic diversity across life stages to assess adaptive potential. By comparing allele frequencies between seedlings and adult trees, we detect clear, genome-wide shifts in surviving seedlings, indicating strong early-life selection. These shifts are linked to enriched GO terms, pointing to functional pathways involved in stress responses. Moreover, genotype–environment associations are stronger and distinct in seedlings compared to trees, demonstrating a pronounced shift toward climate-driven selection in the youngest cohort. Building on these findings, we assess the effects of canopy openness (open vs. closed) on genomic patterns in young beech trees and focus on saplings aged 0–8 years to link genomic variation with environmental conditions during establishment. Preliminary analyses indicate greater height and stem diameter under open canopy conditions in two of the three regions.

Together, this work provides insights into how early developmental stages shape the adaptive trajectory of European beech under climate change.

Linking hybridization and climate-associated genomic variation in Central Asian *Stipa*

Patar Sinaga^{1,2}, Ewelina Klichowska¹, Marcin Nobis¹

¹*Institute of Botany, Faculty of Biology, Jagiellonian University, Gronostajowa 3, 30-387 Kraków, Poland*

²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

Climate change has the potential to shift species distributions and strengthen the roles of hybridization and introgression in plant evolutionary responses. In this context, *Stipa* (Poaceae), a genus widely distributed in Central Asia and known for frequent hybridization, is relevant for testing the relationship between species boundaries, genomic variation, and changes in habitat suitability under future climates. We analyzed specimens representing 11 *Stipa* species from Central Asia based on SNPs. The genetic structure was analyzed using fastStructure, introgression was tested with Patterson's D in Dsuite, and habitat suitability was modeled using nine selected bioclimatic variables. Future projections were conducted using two GCMs, two emission scenarios (SSP245 and SSP585) in 2041–2060 and 2081–2100. The results show seven parental–hybrid groups, five of which involve *S. richteriana* as one of the parents. FastStructure and PCA support a hybrid origin, while Patterson's D detects significant gene flow signals in six parental–hybrid groups. Distribution show varying interspecies response, but generally, suitable habitats tend to shift northward, while southern and central regions exhibit greater fragmentation and loss of suitability, especially under SSP585 and by the end of the century. RDA further separates the taxa into three main groups associated with different climate gradients: (1) *S. caucasica*, *S. karataviensis*, and *S. arabica* s.l. are associated with bio1, bio15, and bio19; (2) *S. borysthena* and *S. kirghisorum* are associated with bio8; and (3) *S. richteriana*, *S. orientalis*, *S. sareptana*, and *S. lessingiana* with bio7. Here, candidate loci are heavily dominated by bio1—Annual Mean Temperature (113 loci), while bio8—Mean Temperature of Wettest Quarter is only associated with one locus, indicating that temperature is the main climatic predictor associated with genomic variation.

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Regional species loss, local functional retention: contrasting patterns across calcareous and siliceous grasslands

Undine Schöllkopf^{1,2,3}, Viktoria Ferenc^{1,2,3}, Maria Májeková⁴, Richard Michalet⁵, Pierre Liancourt^{1,3,4}

¹*Department of Botany, State Museum of Natural History, Stuttgart, Germany*

²*Institute of Landscape and Plant Ecology, University of Hohenheim, Stuttgart, Germany*

³*KomBioTa – Center for Biodiversity and Integrative Taxonomy, University of Hohenheim & State Museum of Natural History, Stuttgart, Germany*

⁴*Plant Ecology, University of Tübingen, Germany*

⁵*University of Bordeaux, CNRS, Bordeaux INP, EPOC, UMR 5805, Pessac, France*

Calcareous and siliceous grasslands represent two of Europe's most species-rich semi-natural habitats, both declining despite legal protection. They are characterized by strongly contrasting edaphic environments, yet it remains unclear whether these differences translate into differences in functional community structures at the local scale. Preliminary analyses using over 50 years of floristic mapping data from Baden-Württemberg, Germany, showed that regional species pools declined in both grassland types but losses were significantly stronger in siliceous grasslands. The strongest losses were among moisture-demanding species with larger leaves and larger specific leaf area. Yet, whether regional species losses translate into functional impoverishment of local communities remains an open question.

To address this, we sampled 24 local grassland plots and measured five functional traits (leaf area, specific leaf area, leaf dry matter content, plant height, and leaf turgor loss point) alongside species cover. Siliceous grasslands supported significantly greater functional dispersion and Rao's quadratic entropy than calcareous grasslands, reflecting a wider range of coexisting functional strategies – despite showing no difference in community-weighted mean traits. This pattern is consistent with stronger environmental filtering in calcareous grasslands, where multiple simultaneous stressors can compress functional trait space.

Thus, despite disproportionate long-term regional species losses, siliceous grasslands currently retain greater local functional diversity. Potentially, moisture-demanding specialists have been partly replaced by drought-tolerant colonizers buffering functional diversity at the local scale. These results suggest that substrate type modulates not only the magnitude of biodiversity loss but also the functional trajectory of grassland communities under climatic drying.

TREEvolution II: Environmental drivers and the genetic basis of Beech vitality loss

Henning Otto¹, Christian Mestre-Runge¹, Kezia Goldmann², Katrin Heer³, Lars Opgenoorth¹, Christian Lampei¹

¹Philipps-University Marburg, Germany

²Albert-Ludwigs-Universität Freiburg

³Helmholtz-Zentrum für Umweltforschung - UFZ

The share of European Beech in German forest stands has been actively increased in the past decade with the goal to make forests more resistant to changing climatic conditions. However, recent hot and dry summers showed that beech forests with older trees (>60 years) are also vulnerable to drought stress resulting in thinned crowns, severe leaf browning and reduction in basal area increment. Consequently, doubts are rising, about whether European Beech is still a suitable tree for future German forests. Diverse symptoms were reported, including *Phytophthora* infections and the beech complex disease, that mostly describe infections of the main stem, or the above-described vitality loss that first manifests in the tree crown. What is missing so far is a combined assessment of these symptoms in population wide screenings, and studies testing these symptoms in an evolutionary context.

In TREEvolution II we use a combined assessment of stem and crown health status of 1500 beech trees, applying conventional assessing methods in combination with remote sensing techniques like airborne LiDar and multispectral imaging. The project is based within the Biodiversity Exploratories, with the trees distributed across 95 plots within the three regions Schorfheide-Chorin, Hainich, and Swabian Alb. This design will enable us to test for selection and symptom associated genomic loci within each region separately. We will investigate the genomic basis of the healthy phenotype in the European beech and the co-occurrence probability of various disease symptoms. Our results will provide a basis to better understand the distribution of beech disease symptoms and their interrelatedness and add an evolutionary perspective to the discussion on the future of beech as an important forest tree in Germany. On this poster we outline our project that started this spring and provide first results from the phenotyping campaign.

Land use intensification shapes plant–soil interactions and resilience to drought

Laura Puura¹, Anastasia Tõnisson¹, YuYing Jing¹, Lauri Laaspere¹, Piia Kängsep¹, Miina Oras¹, Anna Marija Firere¹, Kadri Koorem¹, Richard Bardgett², John Alexander Davison¹, Marina Semtšenko¹

¹*University of Tartu, Estonia*

²*Lancaster University*

While the negative impact of land use intensification on plant species richness is well documented, the potential for long-term intensification to shape local plant-soil adaptation and stress resilience remains unexplored.

To address this knowledge gap, we established 3- and 6-species plant communities using seeds collected from either extensively or intensively managed grasslands in the Yorkshire Dales (UK). We combined plants with soil communities from either the same or opposite management type, different levels of fertilisation, and a drought treatment. We hypothesize that plant populations from intensively managed grasslands exhibit higher productivity due to selection under fertilised conditions but demonstrate lower drought tolerance and weaker associations with soil mutualists compared with extensively managed populations. Our study will reveal how long-term land use intensification affects grassland populations and their resilience to future environmental change via altered plant-soil interactions.

To moo or to mow – disentangling the effects of management on *Gladiolus imbricatus* in coastal meadows

Xenia Uffrecht¹, Lauri Laanisto¹, Marika Kose¹, Nicola Pavanetto²

¹*Estonian University of Life Sciences, Estonia*

²*University of Göttingen*

During the twentieth century, management ceased in most semi-natural grasslands in northern Europe, followed by tall herb and shrub encroachment. For conservation it is essential to understand, what kind of extensive management is suitable to restore these species-rich habitats.

This study examines how different management regimes influence the abundance of the rare *Gladiolus imbricatus*, an indicator species for Baltic boreal coastal meadows. We investigated three restored sites that have been managed since 2001 using different approaches: mowing, crushing (mulching), and grazing. Additional adjustments to management practices in 2021, namely modified mowing dates and grazing intensities, allowed us to further assess management effects.

Population data were collected from 2021 to 2025 (ongoing) in permanent plots, recording abundance of *G. imbricatus* across three life stages: juvenile, vegetative, and generative. Population structure was characterized by the ratio of juveniles to adults (vegetative and generative), ranging from regressive (<1) to dynamic (>3).

Consistent with previous research, total abundance was closely related to population structure. Cutting regimes (mowing and crushing) were generally more favorable for this bulbous, tall perennial herb than grazing. Notably, crushing (mulching) had the strongest positive effect on species abundance. Mowing date did not influence population dynamics significantly, while high grazing intensity appeared less beneficial than moderate grazing.

To promote viable populations of *G. imbricatus* in coastal meadows, vegetation removal through crushing or mowing should be prioritized over grazing. Where grazing is applied, lower intensities are recommended. Although our results do not provide conclusive evidence for an optimal mowing date, we would advise conservation practitioners to consider variable mowing regimes that include early-season mowing, as well as seed ripening times when mowing late. This study gives further insights into the considerations necessary when selecting appropriate management regimes in coastal meadows.

The European spruce bark beetle (*Ips typographus*) – An additional opportunity for bog restoration?

Lisa Grunwald¹, Jörg Müller², Anna Bucharova¹

¹Marburg University, Conservation Biology, Karl-von-Frisch-Str. 8, 35043 Marburg, Germany

²University of Würzburg, Conservation Biology and Forest Ecology, Ecological Station Fabrikschleichach, Germany

Mires are among the world's most important carbon sinks, but they are also among the most degraded. Human land use changes converted them into carbon sources and endangered the specialised flora and fauna. Therefore, restoration is identified as a key measure to restore the ecosystem functions and biodiversity of mires. An established restoration method of forestry-degraded mires is the forest-to-bog restoration. As most forestry-degraded mires suffer from drainage and high density of spruce, the restoration includes deforestation and the closing of ditches. Due to the high costs of active restoration, passive restoration by ecosystem engineers is getting more important. An underrated ecosystem engineer is the European spruce bark beetle (*Ips typographus*). The European spruce bark beetle is the most frequent bark beetle in Europe, which can build up high population sizes and can cause spruce forests to die off across vast areas. Within this property, he is comparable to an active forest-to-bog restoration. Therefore, we want to analyse the opportunity of the European bark beetle as a passive restoration possibility. To this end, we will compare areas affected by the European spruce bark beetle and active restoration sites at various stages of recovery and elevations with intact and degraded mire areas. To assess their potential, we will focus on biodiversity and mire formation processes. In total, this project is scheduled to run for three years in cooperation with the Bavarian Forest National Park.

Testing the invisible fraction in aged seeds: Effects disappear in the second generation

Lea Klepka, Sascha Liepelt, Anna Bucharova

*Department of Biology – Conservation Biology Research Group,
Philipps-University Marburg, Karl-von-Frisch-Straße 8, 35032*

Stored seeds are crucial repositories of plant genetic diversity. However, long-term storage inevitably reduces viability. During storage, chemical processes can delay germination, impair seedling performance, and even alter adult plant traits (direct storage effects). Moreover, because seed mortality during storage is unlikely to be random, storage may act as a selective filter, causing the loss of certain genotypes and creating a so-called “invisible fraction”. This phenomenon describes the part of the original population that is lost during storage.

It remains unclear how relevant the invisible fraction is across wild species. To address this, we simulated long-term storage by exposing seeds of 6 grassland species to artificial ageing (50% relative Humidity, 45°C). We then hand-pollinated individuals within each treatment to produce a second generation free from direct storage effects. In a common garden experiment, we compared the second-generation offspring of plants grown from aged seeds to those from fresh seeds to test for evolutionary consequences of storage.

Artificial ageing strongly affected germination and adult plant traits in the first generation, confirming substantial direct storage effects. However, these effects largely disappeared in the second generation. Offspring of plants from aged seeds showed a weakly delayed germination, while all other traits remained unaffected.

We conclude that, despite direct effects of seed storage on the first generation, the loss of certain genotypes during storage seems to be of no major concern. However, subtle evolutionary consequences cannot be fully excluded. While population trait means may not shift dramatically, storage effects should still be considered when using stored seeds for ecological restorations or resurrection studies.

Parent–offspring inheritance of plant size and flower number in native species cultivated for ecological restoration

Carolina Selic, Anna Bucharova

*Marburg University, Conservation Biology, Karl-von-Frisch-Str. 8,
35043 Marburg, Germany*

For ecological restoration projects, it is essential to use seed sourced from regionally and locally adapted plant populations. To provide this seed in large quantities, these species must be cultivated and multiplied in farmers' fields. However, in agriculturally managed fields, the plants are exposed to a different selection pressure than in nature. As a result, they may develop a domestication syndrome. Over several generations, the plants become larger, the biomass increases, their flowering time shifts earlier and they produce more flowers. If larger plants with many flowers are consistently favored due to this domestication syndrome, they may produce more seeds and therefore dominate the next generations. As a result, genetic diversity can decrease within only a few generations. In natural populations, it is advantageous to have a large variation in different traits, such as height, because environmental conditions can change easily. From previous common garden experiments, we can assume that differences in height and flower number are caused by genetic variation. In this selection experiment, we aim to test whether plant size and flower number are heritable. In this study, I collected seeds from 50 individuals of each of six species from a regional seed production field. I ensured that the sample included particularly large and small plants, as well as individuals of intermediate size. I measured the height of the parent plants in the field and counted their flowers. I then establish a common garden experiment in the botanical garden by planting these seeds. Once the plants have reached seed maturity, I quantify the size and flower number of the offspring and compare these traits to the measurements obtained from the parent plants. This helps us understand the mechanism behind size inheritance. I hypothesize that the plant size and number of flowers observed in offspring plants are inherited from their parents.

Beyond the water:**How small stream restoration affects plant and bird diversity**

Lena Lerbs¹, Alina Singer¹, Anna Dotzert¹, Stefan Pinkert², Nina Farwig², Sascha Liepelt¹, Anna Bucharova¹

¹Marburg University, Conservation Biology, Karl-von-Frisch-Str. 8, 35043 Marburg, Germany

²Marburg University, Conservation Ecology, Karl-von-Frisch-Str. 8, 35043 Marburg, Germany

River restoration aims to improve water retention in the landscape and the ecological value of water bodies around the globe. In Europe, most restoration projects focus on small streams, yet their ecological benefits are poorly documented. Effects on aquatic biota are often limited, as unrestored sections hinder colonization, and short restoration stretches have little impact on water quality. We therefore investigated how small stream restoration affects terrestrial biota - in particular plants and birds - as these groups provide important ecosystem services and have a high conservation value. We surveyed 55 restored and adjacent non-restored small stream sections in Hesse, Germany, using vegetation and bird surveys. Restoration increased plant species richness, the abundance of moisture-associated plant species and the heterogeneity on a landscape level. Plant species richness strongly varied with restoration age: it was highest in young restorations, declined until year 16, and then increased again. The plant moisture index was significantly related to the channel depth. Bird diversity and abundance also increased with restoration, mainly driven by the coverage of woody plants. With our study, we actively contribute to a broader understanding of how small stream restoration supports biodiversity. By identifying ecological responses of different terrestrial taxa, we aim to inform future restoration efforts with solid scientific evidence.

Climate-driven trait variation and potential lag of adaptation in *Hordeum murinum* across Europe

Helene Villhauer¹, Sandy J. Labarosa², Timo Hellwig², Maria von Korff², Anna Bucharova¹

¹Marburg University, Conservation Biology, Karl-von-Frisch-Str. 8, 35043 Marburg, Germany

²Heinrich-Heine-Universität Düsseldorf, Institute of Plant Genetics, Germany

Hordeum murinum is a grass species native to Europe, the Mediterranean, and Western Asia. It grows in disturbed habitats, and anecdotal literature says it spreads in response to climate change. In 2023, in collaboration with 50 local researchers, we scored reproductive and growth-related traits and collected seeds of *H. murinum* in the wild across Europe and northern Africa, in total 207 populations. In 2024, to test for heritable variation among populations, we sowed the wild-collected seeds and grew the plants in two types of soil in two common gardens differing in climate.

We found significant differentiation among populations, maternal plants, and treatment in all measured traits. However, the relative contribution of the heritable and phenotypic plasticity differed between traits. For example, flowering time was predominantly heritable, with population identity explaining 82% of the variation, while biomass was highly plastic, with treatment explaining 71% of the variation. Heritable trait variation in *H. murinum* was driven primarily by broad-scale climatic gradients, particularly mean annual temperature. Trait clines along thermal gradients were consistent between in situ observations and in the common garden experiment: For example, plants were smaller and reached seed ripening earlier in warmer areas in situ. Similarly, plants originating from warmer regions grew smaller and flowered earlier under common garden conditions. However, fitness optimum peaked in populations originating from warmer climates, indicating that populations are not keeping pace with ongoing environmental changes.