1.1 From overlooked agrobacterial diversity to breakthrough plant transformation

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Abstract text

Agrobacteria-mediated transformation is a foundational technology in plant biology and biotechnology, enabling transgene delivery, genome engineering, and functional genomics across diverse plant species. Despite the extensive natural diversity within the agrobacteria species complex, modern transformation systems rely predominantly on a small number of laboratory-adapted strains. The potential of naturally occurring agrobacterial diversity to improve plant transformation efficiency remains largely unexplored. We investigated a diverse collection of agrobacterial strains representing distinct evolutionary lineages to assess their transient transformation capabilities in *Nicotiana benthamiana*. Comparative analyses revealed substantial variation in transient transformation efficiency among strains, with *Rhizobium rhizogenes* A4 as being one of the most effective strains. Leveraging this, we developed AS109, a disarmed derivative of A4, which displayed markedly enhanced transient expression in solanaceous species, including tomato, eggplant, and pepper, compared with commonly used laboratory strains. Furthermore, AS109 enabled efficient transient gene expression in several non-solanaceous crops, including sweetpotato, faba bean, and lettuce, indicating a broader host range than existing transformation strains. These findings demonstrate that natural agrobacterial diversity represents an underexploited resource for plant biotechnology and provide a framework for expanding the plant transformation toolbox through the exploration and deployment of diverse agrobacterial lineages.

1.2 Parallel evolution of alkaloid biosynthesis from bacterial-like decarboxylases: new enzymes from new resources

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Abstract text
Fresh insights emerge when new molecular resources are built for underexplored species. Alkaloids are a chemically diverse class of bioactive specialised metabolites, many of which have significant pharmaceutical value, yet the enzymatic origins of their biosynthetic scaffolds remain incompletely understood. To investigate the longstanding problem of nonsymmetric precursor formation of lysine- and ornithine-derived alkaloids, we generated a transcriptomic resource for the non-model plant Flueggea suffruticosa across 15 tissues and developmental stages. Biochemical characterisation, isotope labelling, mutagenesis, and phylogenetic analysis led to the discovery of ornithine/lysine/arginine decarboxy-oxidases (OLADOs): a new class of plant enzymes catalysing decarboxylative oxidative deamination of basic amino acids, resolving a biosynthetic question first posed over 50 years ago. OLADOs belong to a family of decarboxylase-like enzymes (OLADLs) previously thought to be exclusively prokaryotic, which entered plant genomes via the cyanobacterial endosymbiosis event. Using active site signatures and phylogenetics, we show that OLADO activity has evolved repeatedly and independently from OLADLs across distantly related lineages, including Solanaceae and Asteraceae: a striking case of parallel evolution. Our study demonstrates how targeted resource generation in non-model species, interpreted alongside the growing wealth of publicly available databases, can provide a general strategy for gene discovery across plant diversity.
Wood, C.X., et al., New Phytol, 249: 2954-2973. https://doi.org/10.1111/nph.70884

1.3
Harnessing plant-to-plant signalling via common mycorrhizal networks for enhanced community-level resistance in crops.

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Abstract text

Biological collections are becoming indispensable for advancing research on plant–microbe interactions, yet their value for studying common mycorrhizal network (CMN)-mediated inter-plant signalling remains underexplored. I highlight how living collections of arbuscular mycorrhizal fungi (AMF), host plant germplasm, tree genotypes, and associated metabolomic and transcriptomic datasets can be integrated to uncover the mechanisms and ecological significance of mycorrhiza-mediated plant communication. Building on published perspectives on inter-plant signalling through CMNs, I present experimental evidence showing that CMN integrity strongly influences inter-plant defence responses. In systems including Medicago truncatula, Daucus carota, hybrid aspen, and silver birch interconnected by Rhizophagus irregularis, intact CMNs altered defence-related transcripts, leaf metabolites and emitted volatiles. Importantly, these responses translate into neighbour modulated susceptibility to pathogens with contrasting species-specific disease outcomes. I argue that regionally sourced AMF collections and experiments with evolutionary diverse plant species together provide a critical foundation for testing the generality, specificity, and application potential of CMN-mediated signalling. Furthermore, linking multi-omics data from diverse plants is key to identify evolutionary conserved responses to inter-plant stress signals. Such advances will help transform inter-plant communication research from proof-of-concept studies to predictive, collection-enabled strategies for crop and forest resilience.

1.4
Have global environmental changes led to a reshaping of microbial soil biodiversity?

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Abstract text
Beyond their role as plant archives, herbaria can also serve as repositories of soil and the microorganisms associated with plant root systems. We characterized for the first time "ancient" soil microbiomes preserved in herbarium samples associated with cereal crops, comparing them to modern-day soil microbial communities collected from the same plant species in the same geographical area. Our dataset comprises 60 historical (from 1820 to 1970) and 35 modern samples, allowing us to assess the ecological impacts of intensive farming practices. Sequence data were obtained through a paleogenomic approach combining ancient DNA extraction in a dedicated laboratory, and shotgun metagenomic sequencing. Authenticity of the recovered ancient sequences was verified by looking for signs of post-mortem damages (cytosine deamination and fragmentation) in the most abundant taxa identified in historical samples. Both taxonomic and functional analyses (focusing on nutrient cycling pathways, antibiotic resistance genes, and carbohydrate-active enzymes) revealed significant differences between historical and modern communities, suggesting that agricultural intensification over the past two centuries has probably reshaped soil microbiome composition and functional potential. This work provides novel insights into microbial community responses to agricultural intensification and opens new perspectives for soil restoration within an agroecological framework.

2.1

Bringing new tools to historical collections: insights into the fossil record of early microorganisms

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Abstract text
Extensive palaeobotanical collections were amassed throughout the nineteenth and early twentieth centuries with the primary aim of documenting and describing fossil plants. Housed in museums and universities across the globe, these collections now represent an invaluable scientific legacy. Beyond their original purpose, they provide exceptional opportunities to investigate fossil microorganisms and their associations with plants, shedding new light on the structure, function, and evolution of ancient terrestrial ecosystems.
Collections comprise a wide range of materials, including thin sections — paper-thin slices of rock glued to microscope slides — and larger rock blocks. Thin sections have traditionally been investigated using brightfield microscopy, which provides detailed anatomical information and reveals the spatial relationships among distinct fossil organisms. Because many fossils are preserved in three dimensions, emerging non-destructive imaging approaches, such as scanning laser confocal microscopy (CSLM), offer opportunities for enhancing their characterization. Rock blocks, also represent valuable resources for the preparation of new thin sections. Recent advances in in situ molecular and geochemistry applied to these samples provide high spatial-resolution biogeochemical complements to morphological research.
Drawing on specimens preserved in these historical collections I will present results obtained on cherts formed around hot springs and in volcanogenic settings to describe fungi and other microorganisms. In particular, the Devonian Rhynie cherts (Scotland, UK) preserve a uniquely informative record of early terrestrial ecosystems. Also, the Carboniferous Esnost and Grand'Croix cherts (Massif Central, France), of volcanic origin, provide insights into early forests. These deposits all offer a record of early interactions between plants and microorganisms and how these organisms adapted to the changing face of terrestrial habitats.

2.2

Exploring archaeobotanical collections: from plant remains to past foodways

Kristiina Johanson ORCID iD
University of Tartu, Estonia, Estonia

Abstract text

This presentation explores the formation and research potential of archaeobotanical collections, focusing on the preservation, variability, and interpretation of plant-related material in archaeological contexts. Special attention is given to the different categories of archaeobotanical evidence, including plant macroremains, microremains, and biomolecular data, as well as the specific preservation conditions that shape their survival and analytical value.

The presentation introduces several case studies that demonstrate how botanical remains can be used in archaeological research. Macrobotanical remains from medieval cesspits, and charred cereal assemblages provide highly informative evidence for past foodways and agricultural practices. Plant microremains, such as phytoliths and starch grains, from dental calculus and pottery food crust, have been studied in combination with biomolecular data from potsherds and human skeletal remains. These multiproxy studies have proven particularly useful in detecting the nuances of consumption practices of selected archaeological communities and illustrate the broad interpretative potential of archaeobotanical collections in archaeological research.

2.3
A tookit for digitisation of resource-constrained herbaria: Lessons from a North-South partnership to digitise the Zimbabwe national herbarium

Patience Chatukuta ORCID iD[1], Langalenkosi Gatula[2], Christopher Chapano[3], Clemence Zimudzi[2]
[1]Max Planck Institute for Biology Tübingen, Germany. [2]University of Zimbabwe, Zimbabwe. [3]National Herbarium and Botanic Garden, Zimbabwe

Abstract text
Herbaria function as critical repositories of plant diversity data, yet many institutions in resource-constrained regions remain excluded from digitisation efforts due to persistent financial and infrastructural barriers. Digitisation dramatically improves accessibility, discoverability, and preservation of plant specimen data, supporting global research on biodiversity conservation and sustainable utilisation. To respond to the need for an innovative solution for digitisation of low-budget herbaria, we present an AI-assisted modular digitisation toolkit developed specifically for the National Herbarium of Zimbabwe in partnership with the Max Planck Institute for Biology Tuebingen. Drawing on our experience digitising the herbarium's Crop Wild Relative (CWR) collection, the toolkit prioritises affordability, portability, and simplicity while maintaining high data quality standards. The system integrates three core components: (1) a low-cost, portable photostation constructed from readily available commodity hardware; (2) a streamlined cascade workflow for efficient digital imaging of specimens; and (3) an AI-assisted data management pipeline that automates key processes, including image processing, metadata extraction, and presentation with minimal technical overhead. By prioritising modular design and open-access AI tools, this toolkit empowers resource-constrained herbaria to produce standardised, high-quality digital records. Ultimately, it enables participation in global plant biodiversity initiatives, democratising access to vital botanical information for conservation, research, and utilisation.

3.1 (Unable to attend)

Decoding auxin mediated guard cell signaling mechanisms for drought tolerance in plants

Mohammad Salehin ORCID iD
North Carolina A&T State University, USA

Abstract text

The increasing frequency and severity of drought threaten global food security as the human population is reaching towards 10 billion by 2050 (Hamann et al, 2021). Stomatal guard cells (GCs) play a central role in plant water conservation, yet the molecular mechanisms that drive opening and closure of stomata remain poorly resolved. Auxin is a key regulator of drought responses, beyond its roles in growth and development (Gonzales and Kelley 2025; Salehin 2024; Waadt et al, 2024; Jing et al, 2023; Weijers & Wagner 2016). We report an integrated framework for auxin-mediated guard cell signaling that underlies drought adaptation in Arabidopsis thaliana.

We demonstrate that drought induces guard cell-specific accumulation of Aux/IAA19 and an Aux/IAA19-WRKY63-MYB28/29 transcriptional module upregulates aliphatic glucosinolates (A-GLS) biosynthesis. Genetic and physiological analyses reveals TIR1/AFB-Aux/IAA auxin co-receptors and many A-ARFs act antagonistically with abscisic acid (ABA) to fine-tune GC dynamics in a concentration- and tissue-dependent manner (Salehin et al., 2019; Takahashi et al., 2018; Shani, Salehin et al, 2017; Salehin et al., 2015). Our findings using calcium, reactive oxygen species (ROS), and auxin biosensors demonstrate rapid Ca^{2+} and ROS signatures in guard cells triggered by A-GLS, and auxin, independent of ABA to regulate stomatal dynamics.

3.2
Exploring the regulation of stomata development by abscisic acid.

Patricia Kika Obinwanne ORCID iD
University of Tartu, Estonia

Abstract text
Stomata are microscopic pores which control water loss, gas exchange, and pathogen entry. Its regulation is crucial for plant productivity and stress management. These pores, formed by pairs of specialized guard cells, predominantly occur on the abaxial surface of leaves across most plant species. However, a significant number of plant species including the model plant Arabidopsis thaliana also develop stomata in the adaxial leaf surface in a phenomenon currently understudied. The phytohormone abscisic acid is widely considered to inhibit stomatal development, though patterning also depends on cell expansion. This study examines ABA’s role in stomatal closure and development and to explore how its effect expresses in adaxial and abaxial leaf sides in Arabidopsis thaliana. Plant lines with altered stomatal densities are used to generate over expressed ABA-PYL receptor transgenic lines in varied backgrounds. Growth traits were characterised under normal and deficit conditions in overexpressed ABA receptor lines. Specific fully developed leaves were examined as against examining cotyledons. The project aims to contribute to an improved understanding of ABA's role in plant physiology, gas-exchange, growth, and yield, thus generating critical knowledge that can be applied in breeding for improved yields for optimizing plant productivity under current climate change conditions.

3.3
Higher stomatal density and glaucousness are associated with higher grain yield in winter wheat

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[1]University of Tartu, Estonia. [2]Centre of Estonian Rural Research and Knowledge, Estonia

Abstract text

As weather is changing (rising temperatures, droughts or excess rainfall), plants must adapt to survive. Stomata, through which gas exchange is regulated, open and close in response to environmental conditions. Wheat, an essential food crop, can adapt to diverse environments and protect itself against unfavorable abiotic stress conditions by accumulating epicuticular waxes - a trait called glaucousness. Here, we examined flag leaf stomatal traits and glaucousness, and their relationships with grain yield in a three-year field trial (2023-2025) with 25 winter wheat varieties. We evaluated visually glaucousness on a 1-9 scale. From each plot, we randomly selected six plants for flag leaf stomatal conductance (gs) measurements using Licor hand-held porometer and made leaf imprints for stomatal density (SD) and size. We found that SD and gs varied across years, while stomatal distribution between leaf surfaces remained stable. For 2024 and 2025, we found a significant positive relationship between abaxial SD and grain yield, and a negative relationship between adaxial stomatal size and grain yield. Glaucousness was positively correlated with grain yield across all years and with SD in the dry year 2024.

These findings provide valuable insights for breeding climate-resilient wheat varieties that maintain high yields under unfavorable weather conditions.

3.4
A collection never studied: enigmatic Prototaxites fossils in Estonia

Oive Tinn, Rhea Kõivutalu
University of Tartu, Estonia

Abstract text

Prototaxites is an enigmatic fossil, first described in 1859 by the Canadian scientist J.D. Dawson, who mistakenly interpreted it as a fossil yew species. Since then, the identity of this peculiar fossil has been widely debated: it has been variously interpreted as algae, fungi, or even a rolled up lichen mat. A recent comprehensive study (Loron et al, 2026) concluded that Prototaxites may represent a previously unknown extinct eukaryotic lineage, distinct from plants, fungi and other major eukaryotic groups.

About a dozen species have been described worldwide. However, not a single species has ever been described from the Baltic States. Yet the presence of fragments of „petrified wood“ in the Devonian sediments of Estonia and Latvia has long been known, although generally regarded as of minor importance. They were rarely mentioned, hardly ever documented and never studied. Our study began with a mysterious object which was brought to the Department of Geology in the summer of 2026, from Tabina, a sandpit in South Estonia. The specimen looks like a lump of a tree trunk with reddish brown solid interior and light coloured crumbly „cortex“. A sample from this specimen, along with smaller pieces that had been waiting their turn in the drawer among other „perhaps sometimes later“ specimens, were examined.

3.5

Gas exchange regulation of tomato leaves and closed flower buds under changing air humidity

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Abstract text

Tomato reproductive organs may contribute to stress resilience through transpiration-driven cooling, yet stomatal regulation of flower buds remains understudied. Our ongoing study compares gas exchange and temperature regulation in tomato vegetative and reproductive organs. Gas exchange of leaves and closed flower buds was measured in the ABA-deficient mutant flacca, its wild type Ailsa Craig, and the Estonian genotype Evelle using an LI-6800 system. Stomatal conductance and net CO_2 assimilation of leaves and buds were compared under stable 70% air relative humidity (RH70). Flower-bud stomatal responses were then determined during an RH70→RH20→RH70 transition, and organ temperature was recorded. Net CO_2 assimilation and stomatal conductance were generally lower in closed flower buds than in leaves. During the humidity transition to RH20, bud gsw rapidly decreased and recovered after return to RH70 in Ailsa Craig and flacca, whereas gsw of Evelle remained comparatively stable. Higher bud gsw was associated with lower Tbud−Tair, indicating stronger bud cooling, particularly in flacca. These preliminary findings indicate dynamically regulated and genotype-specific stomatal responses in closed tomato flower buds. Ongoing measurements of flower-bud surface and internal temperatures across genotypes and greenhouse temperature regimes will clarify the role of bud cooling in reproductive heat resilience.

3.6 (Unable to attend)

Herbarium samples reveal long-term plant responses to global change in central Europe: a robust evidence across species and habitats

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[6]Department of Botany, Faculty of Science, Charles University, Czech Republic

Abstract text

Herbarium collections are more than historical archives; they offer a unique window into long-term plant responses to global change. Using specimens from ten vascular species collected in Central Europe between 1806 and 2017, we examined how rising CO_2 influences plant physiology and whether there is support for the Progressive Nitrogen Limitation hypothesis.

We analyzed foliar carbon (C), nitrogen (N), C:N ratio, stable isotope compositions ($\delta^{13}C$ and $\delta^{15}N$), and intrinsic water-use efficiency (iWUE). Findings reveal significant declines in isotopic signatures, while iWUE increased considerably. Notably, nitrogen concentrations remained stable, suggesting an alternation of N sources rather than simple limitation. These physiological responses were highly species- and site-specific.

To further decode these mechanisms, we are now incorporating oxygen isotopes ($\delta^{18}O$). Ultimately, this study demonstrates the vital role of herbarium collections in uncovering the nuanced, innovative insights necessary for accurately projecting future climate impacts on plant communities and local environments.

3.7
Increased PM levels influence leaf conductance and modify transpiration dynamics, altering groundwater levels

Sombir Pannu ORCID iD[1], Prakhar Shrivastava[1], Vikram Singh ORCID iD[1], Usha Mina[2], Chandan Gupta[3], Bhupinder Singh[3], Mayank Kumar ORCID iD[1]
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Abstract text
Although atmospheric aerosols affect radiation and climate, their direct effect on plant hydraulic control is unknown. We used controlled-chamber studies with tomato plants grown under HEPA-filtered and elevated-pollution settings to determine how dust or aerosol deposition affects water use. Gas exchange was measured by LI-COR 6400XT.
Aerosol loading raised ecosystem water use by 31%, accounting for 41.6% of chamber water use and generating a cumulative excess of ~10,000 ML compared to HEPA control. Dust increases water use at every measurement and irrigation. Diurnal partitioning showed a 20% increase in water use, with 62% of surplus occurring at night. Nighttime transpiration rose 48.1% ($p = 0.0078$), while daytime changes were small (9.9%, $p = 0.25$). We found that elevated leaf temperature and poor stomatal sealing, possibly caused by mechanical blockage or hygroscopic surface activation, increase water loss.

The prevalence of nighttime excess flow supports a residual water-loss mechanism largely disconnected from daytime photosynthetic demand and a disruption of normal stomatal closure dynamics. Chronic aerosol exposure may affect stomatal control, and increasing irrigation demand in polluted areas like IGP-India. "Vegetation is widely promoted as a pollution mitigation tool—but are we overlooking the possibility that pollution indirectly accelerates groundwater depletion through plants?"

3.8

Hidden extinction debt in a tropical forest revealed by dark diversity dynamics

JING YANG ORCID iD

University of Tartu, Estonia

Abstract text

In tropical forests, where trees are long-lived, stable local richness can mask accumulating extinction debt, as individuals may persist even when local conditions no longer support their continued regeneration. We tested for such debt by asking whether observed diversity remained relatively stable despite declines in dark diversity — species suitable for a site but locally absent — and in the suitability of species still present, using long-term tree census data from Barro Colorado Island, Panama (>450,000 stems, 331 species). Local richness declined by only 3.7%, whereas dark diversity fell by 30.6%, indicating a severe erosion of community biodiversity potential. Within these seemingly stable assemblages, the suitability of present species declined by up to 8.3%, with losses disproportionately concentrated among large-statured trees. Together, these divergent trajectories reveal a tropical forest in which apparent stability in observed diversity conceals a growing extinction debt, particularly threatening the large trees that form the forest's structural core.

3.10
Cryptogam-associated microbial processes shaping N_2O and CH_4 cycling in Amazonian peat swamp forests

SI CHEN[1], Ülo Mander[1], Ramita Khanongnuch[1,2], Fahad Kazmi[1], Mohit Masta[1,3], Kaido Soosaar[1], Lizardo Fachin-Malaverri[4], Mikk Espenberg[1]
[1]University of Tartu, Estonia. [2]Natural Resources Institute Finland (Luke), Finland. [3]University of Aarhus, Denmark. [4]Instituto de Investigaciones de la Amazonia Peruana (IIAP), Peru

Abstract text
Tropical Amazonian peatlands are pivotal regulators of global carbon (C) and nitrogen (N) biogeochemical cycles and greenhouse gas (GHG) balance, sustaining massive soil organic carbon storage and mediating atmospheric gas exchange. However, the linkages between cryptogam-associated microbial processes and nitrous oxide (N_2O) and methane (CH_4) fluxes in different peat forests remain poorly understood. This study targeted intact and secondary peat swamp forests in the Peruvian Amazon, exploring seasonal variations in microbial C and N cycling functional genes of cryptogams. Results showed consistent microbial functional patterns on dominant tree species. The secondary forest harbored more abundant N cycling genes related to N_2O production, with obvious rainy-season predominance. Methane cycling genes maintained low and seasonally stable levels at both sites. Notably, C and N cycling genes peaked in rainy seasons for secondary forest but in dry seasons for intact forest. Differentially abundant core microbial taxa further mediate peatland nutrient cycling and GHG emissions, demonstrating cryptogams' indispensable role in tropical peatland ecosystem function.

3.11

Metabarcoding study of 1242 soil samples reveals global patterns in oomycete diversity and community structure

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Abstract text

Oomycetes are eukaryotic microorganisms that include important pathogens of trees, crops and aquaculture, yet the environmental drivers of their diversity and distribution remain poorly understood. In this study, we investigated global patterns of soil oomycete diversity and community composition using PacBio sequencing of the ITS region from 1,242 soil samples collected across a broad range of climatic zones and biomes.

We recovered 2198 oomycete operational taxonomic units, representing 8 oomycete orders, 9 families, and 29 genera. Oomycete richness differed significantly among climatic zones and biomes, with the highest diversity observed in Mediterranean climates and temperate grassland ecosystems, while the lowest richness occurred in arid deserts, boreal forests, and subpolar environments. Overall, soil carbon and nitrogen ratio and pH were the best predictors of oomycete diversity. Notably, the set of variables associated with diversity varied markedly among dominant genera, indicating distinct ecological preferences within oomycete lineages. Oomycete community composition was also significantly associated with climatic and edaphic factors, although they explained only 8.91% of variation in the oomycete communities.

These findings provide new insights into the ecology and biogeography of oomycetes and establish a baseline for predicting potential changes in oomycete communities in response to future climate conditions.

3.12

From physical specimens to digital genomes: international legal challenges of digital sequence information in biodiversity collections

Lama Allan Abusamra ORCID iD
University of Zurich, Switzerland.

Abstract text

Botanical and fungal collections have long served as repositories of biodiversity knowledge, preserving specimens that document ecological change, species diversity, and scientific discovery across time. Advances in genomic technologies and large-scale digitization have transformed these collections into sources of digital sequence information (DSI), enabling unprecedented opportunities for international scientific collaboration and biodiversity research. However, the increasing use and global circulation of DSI have generated significant legal uncertainty within international biodiversity law.

This paper examines the evolving international legal framework governing DSI derived from biological collections. It analyzes the extent to which existing principles of access and benefit-sharing can be applied to digital genetic resources that can be accessed, shared, and utilized across borders without the transfer of physical specimens. Particular attention is given to the challenges posed by digitized historical collections, many of which originate from regions that now seek greater participation in the benefits generated from biodiversity research and innovation.

The paper evaluates recent developments in international biodiversity governance and explores the implications of emerging benefit-sharing mechanisms for museums, herbaria, research institutions, and scientific databases.

4.1

Herbarium collections reveal the adaptive significance of leaf form in Solanum

Chris Muir
University of Wisconsin-Madison, USA

Abstract text

Understanding the adaptive significance of variation in leaf form is a central goal of plant ecophysiology and evolutionary biology. Herbarium collections provide an unparalleled resource for addressing this question because they contain phenotypic data spanning broad geographic, environmental, and phylogenetic scales. Using herbarium specimens from 100 species of Solanum, I quantified variation in leaf form and combined these measurements with climatic and phylogenetic data to test hypotheses about adaptation using Bayesian phylogenetic comparative methods. The resulting analyses reveal how patterns of leaf variation are associated with environmental gradients. More broadly, this study highlights the scientific value of herbarium collections as a foundation for ecological and evolutionary research. The ability to analyze trait evolution across diverse lineages depends on generations of field collecting, specimen preservation, curation, and, increasingly, digitization. By transforming historical specimens into accessible datasets, ongoing digitization efforts are expanding the scope of questions that can be addressed and enabling new syntheses. Herbarium collections are therefore not only archives of biodiversity, but also essential infrastructure for understanding plant adaptation.

4.2 (Unable to attend)
Quantitative physiological responses of plants to 170 years of rising CO2 revealed from herbarium collections and a new isotope-based modelling framework

Ansgar Kahmen ORCID iD, Daniel B. Nelson, Jurriaan de Vos, David Basler
University of Basel, Switzerland

Abstract text

The responses of net photosynthesis (An) and stomatal conductance (gs) to elevated atmospheric CO2 (eCO2) are critical for understanding terrestrial carbon and water relations and coupled carbon-climate system dynamics. Quantifying how An and gs in plants have changed in the natural environment as atmospheric CO2 gradually increased over the past 170 years has remained challenging. Through isotopic and physiological analyses and a new modelling framework based on approximately 3000 herbaria specimens from temperate herbaceous plants we identified a profound 17.7 % increase in An, but only a small 6.6 % decline in gs as CO2 increased by 100 ppm. The responses in An and gs were remarkably consistent among different plant functional types and not related to edaphic conditions in different habitats. Furthermore, the analysis provided no indication of progressive nitrogen limitation of An and gs responses to eCO2 over time. Documented increases in An indicate that eCO2 has stimulated a general and sustained increase in photosynthetic carbon uptake by temperate herbaceous plants. Our study highlights how historic plant collections in combination with state-of-the-art analytical and innovative modelling approaches can reveal critically needed quantitative information on long-term plant physiology responses to a changing environment.

4.3
Leaf anatomy collections for understanding plant functional diversity

Tiina Tosens[1], Ülo Niinemets[1,2]
[1]Estonian University of Life Sciences, Estonia. [2]Eesti Teaduste Akadeemia, Estonia

Abstract text

We present a comparative leaf anatomy collection assembled through long-term research on leaf structure–function relationships across major plant forms, including algae, lichens, bryophytes, ferns, gymnosperms, cycads, and angiosperms. The collection includes original resin blocks, resin-embedded cross sections, leaf surface images, hand sections, TEM and SEM material, microscopy slides, digital anatomical images, and anatomical datasets with standardized metadata spanning broad interspecific and intraspecific variation, together with anatomical, chemical, structural, and physiological trait data. We developed a pipeline for DOI attribution to physical and digital resources using the PlutoF framework.

Rooted in characterization of leaf functional anatomy, photosynthetic limitations, resource-allocation trade-offs, and structural investments associated with secondary metabolism, these materials provide opportunities to address questions in plant ecophysiology and climate adaptation. Because visualization of internal leaf structure requires lineage-specific protocols and specialized preparation techniques, comparative anatomical datasets remain rare, making the collection a uniquely broad resource representing diverse adaptations in plant carbon assimilation and resource-use strategies. The pipeline supports long-term archival of physical and digital resources, and we encourage researchers with plant anatomy data to contribute to the PlutoF plant anatomy database.

In this talk, I describe the collection and discuss its applications across fields, from global processes to crop improvement.

5.1
Modernizing legacy AMF sequence collections for future ecological synthesis: concepts and ongoing development within MaarjAM

Bo Stevens ORCID iD, Maarja Öpik
University of Tartu, Estonia

Abstract text

Long-term biodiversity databases remain foundational resources for ecological research, but many were originally developed during earlier generations of environmental sequencing and taxonomic frameworks. The MaarjAM database has played a major role in global arbuscular mycorrhizal fungal (AMF) ecology through its virtual taxon (VT) system and extensive archive of environmental sequence records. This presentation discusses ongoing exploratory efforts and future directions for improving interoperability between legacy VT-based classifications and newer sequence-processing approaches, including ASV-based workflows, phylogenetic placement methods, and emerging taxonomic frameworks such as EUKARYOME. Current work focuses primarily on reproducible infrastructure development, database modernization concepts, and strategies for linking historical sequence resources with evolving phylogenetic and taxonomic systems while preserving continuity with existing ecological literature.

Particular emphasis will be placed on questions of provenance, versioning, confidence reporting, and long-term sustainability of microbial biodiversity databases. The presentation is intended as a discussion framework for how legacy ecological sequence collections can continue to evolve alongside rapidly changing computational and phylogenetic methodologies.

5.2

Collections Without Walls: From Fungaria and Herbaria to Global Digital Biodiversity Infrastructures.

Urmas Kõljalg
University of Tartu, Estonia

Abstract text

Natural history collections have shaped my scientific trajectory, from working with fungal specimens in fungaria and plants in herbaria to developing global digital infrastructures. These collections remain the backbone of taxonomy and biodiversity science, preserving physical evidence of life across centuries. Yet today, they are being transformed into interconnected, dynamic systems that extend far beyond institutional walls.

Through my work on the UNITE database, I have seen how DNA sequences can function as collection objects in their own right. By organising fungal sequences into species hypotheses, UNITE links molecular data—including eDNA signals—to taxonomy. At the same time, new collection types are emerging: purified DNA, sequence libraries and eDNA samples from soil, air and water. These capture otherwise hidden biodiversity and complement traditional specimens, bridging past and present observations.

With PlutoF, we aim to integrate specimens, sequences, eDNA data and metadata into a FAIR-by-design environment, maintaining essential links to voucher material. Globally, infrastructures such as INSDC, GBIF and the Catalogue of Life provide the backbone for integration, while DiSSCo ERIC offers a vision of unified digital collections across Europe.

Together, these developments are creating collections without walls—living, connected systems for understanding biodiversity change.

List of Participants

	First name	***Last name***	***Affiliation***	***Country***
Delegate	**Tsipe**	**Aavik**	University of Tartu	Estonia
Delegate	**Kessy**	**Abarenkov**	University of Tartu	Estonia
Poster presenter	**Lama Allan**	**Abusamra**	University of Zurich	Switzerland
Delegate	**Ayesh Piyara Wipulasena**	**Aleihela Yamannalage**	University of Tartu	Estonia
Selected speaker	**Patience**	**Chatukuta**	Max Planck Institute for Biology Tübingen	Germany | Zimbabwe
Flash talk | Poster presenter	**Si**	**Chen**	University of Tartu	Estonia
Organising committee	**John**	**Davison**	University of Tartu	Estonia
Publishing panel member	**Tõnu**	**Esko**	University of Tartu	Estonia
Delegate	**Atefe**	**Farshadi**	University of Tartu	Estonia
Selected speaker	**Gianluca**	**Grasso**	Muséum National d'Histoire Naturelle	France | Italy
Delegate	**Philemon**	**Gyamfi**	University of Tartu	Estonia | Ghana
Delegate	**Aveliina**	**Helm**	University of Tartu	Estonia
Organising committee	**Hanna**	**Hõrak**	University of Tartu	Estonia
Flash talk | Poster presenter	**Elena**	**Ivandi**	University of Tartu	Estonia
Delegate	**Pirko**	**Jalakas**	University of Tartu	Estonia
Invited speaker | Publishing panel member	**Kristiina**	**Johanson**	University of Tartu	Estonia
Delegate	**Inga**	**Jüriado**	University of Tartu	Estonia
Delegate	**Sarkal**	**Jyakhwa**	University of Tartu	Estonia
Flash talk | Poster presenter	**Rhea**	**Kõivutalu**	University of Tartu	Estonia
Invited speaker | Publishing panel member	**Urmas**	**Kõljalg**	University of Tartu	Estonia

	First name	*Last name*	*Affiliation*	*Country*
Delegate	**Hannes**	**Kollist**	University of Tartu	Estonia
Delegate	**Kadri**	**Koorem**	University of Tartu	Estonia
Delegate	**Thea**	**Kull**	Estonian University of Life Sciences	Estonia
Delegate	**Lauri**	**Laanisto**	Estonian University of Life Sciences	Estonia
Delegate	**Lauri**	**Laaspere**	University of Tartu	Estonia
Delegate	**Roland**	**Lehemets**	University of Tartu	Estonia
Staff	**Sarah**	**Lennon**	The New Phytologist Foundation	UK
Delegate	**Anni**	**Lepik**	University of Tartu	Estonia
Delegate	**Elvi**	**Liiv**	University of Tartu	Estonia
Selected speaker	**Bo**	**Maxwell Stevens**	University of Tartu	Estonia| USA
Delegate	**Ebe**	**Merilo**	University of Tartu	Estonia
Invited speaker | Publishing panel member	**Chris**	**Muir**	University of Wisconsin–Madison	USA
Flash talk | Poster presenter	**Patricia**	**Obinwanne**	University of Tartu	Estonia
New Phytologist Editor-in-Chief Publishing panel member | Organising Committee	**Maarja**	**Öpik**	University of Tartu	Estonia
Organising committee | Selected speaker	**Zigmunds**	**Orlovski**	Latvian Biomedical Research and Study Centre	Latvia
Delegate	**Kadri**	**Pärtel**	Estonian University of Life Sciences	Estonia
Delegate	**Jaak**	**Pärtel**	University of Tartu	Estonia
Delegate	**Meelis**	**Pärtel**	University of Tartu	Estonia
Delegate	**Kersti**	**Püssa**	University of Tartu	Estonia
Delegate	**Laura**	**Puura**	University of Tartu	Estonia
Delegate	**Triin**	**Reitalu**	University of Tartu	Estonia
Flash talk | Poster presenter	**Taavi**	**Riit**	University of Tartu	Estonia
Flash talk | Poster presenter	**Ireene**	**Roman**	University of Tartu	Estonia

	First name	*Last name*	*Affiliation*	*Country*
Delegate	**Irja**	**Saar**	University of Tartu	Estonia
Staff	**Samantha**	**Smyth**	The New Phytologist Foundation	UK
Invited speaker | Publishing panel member	**Christine**	**Strullu-Derrien**	Muséum National d'Histoire Naturelle, Paris, France Natural History Museum, London, UK	France | UK
Delegate	**Ave**	**Suija**	University of Tartu	Estonia
Delegate	**Riin**	**Tamme**	University of Tartu	Estonia
Delegate	**Kaisa**	**Torppa**	University of Tartu	Estonia
Selected speaker	**Tiina**	**Tosens**	University of Tartu	Estonia
Delegate	**Rufus**	**Trepp**	University of Tartu	Estonia
Delegate	**Ingmar**	**Tulva**	University of Tartu	Estonia
Organising committee	**Tanel**	**Vahter**	University of Tartu	Estonia
Delegate	**Triin**	**Varvas**	Estonian University of Life Sciences	Estonia
Delegate	**Martti**	**Vasar**	University of Tartu	Estonia
Selected speaker	**Charlay**	**Wood**	University of Wisconsin–Madison	USA
Flash talk | Poster presenter	**Chih-Hang**	**Wu**	Academia Sinica	Taiwan
Flash talk | Poster presenter	**Jing**	**Yang**	University of Tartu	Estonia
Delegate	**Irma**	**Zettur**	University of Tartu	Estonia