New Phytologist
next generation scientists

New Phytologist next generation scientists 2025

4 – 7 August 2025
University of Birmingham

New Phytologist Foundation

UNIVERSITY OF BIRMINGHAM

WILEY

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The majority of sessions will be streamed live on Zoom webinar.
The link will be the same for all sessions:
https://us02web.zoom.us/webinar/register/4517532555829/WN_AEYu_Oh6Qlqxit1vFJxEHw

You will need to sign in to Zoom to access the sessions.
Once you've signed in/registered on Zoom, you will receive a reminder 1 hour before the live stream starts each day.

The webinar ID is: 813 1436 1347
Passcode 187020

You can view the full programme timetable online at:
https://www.newphytologist.org/nextgeneventpages/index/42

During the live event, you can use Slido to ask questions to the speakers.
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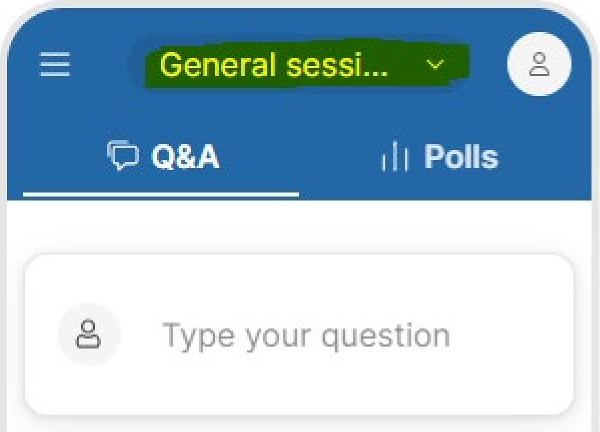
Please ensure you are in the "General sessions" room for questions to individual speakers
For Panel discussions, please switch to the room for that particular session using the drop down menu at the top.

You can start to submit questions for the Panel discussions now, and attendees can up-vote questions they want to hear asked.
Questions are moderated, therefore there may be a delay before your question appears, and we may edit your questions for clarity.



During the live stream, if you have any technical issues, please use the chat in zoom, or you can submit a question in Slido, which the moderators can respond to privately.

We hope you will enjoy tuning in to the live stream of New Phytologist Next Generation scientists!

Programme

Day 1	**Monday 4 August**
13:30 – 14:00	**Welcome to NGS** • Welcome from Keith Lindsey, Chair of the New Phytologist Foundation • Welcome from the University of Birmingham by Sami Ullah and Richard Norby • Introduction to the local organising committee • Introduction to Editors and mentors
	Session 1 Chairs: Rosa Sanchez-Lucas and Katie Field
14:00	**Keynote speaker** **Understanding arbuscular mycorrhizal fungi: from natural biodiversity patterns to land management and societal needs and expectations** 1.1 Maarja Öpik, University of Tartu, Estonia
14:30	**Decoding Synergy: How *Enterobacter* sp. SA187 enhances plant growth under low nitrogen through ethylene signaling and nitrate transporters** 1.2 Amina Ilyas, Université Paris-Saclay, France
14:45	**Arbuscular mycorrhizal fungi foraging strategies, decision making and interactions in soil chips.** 1.3 Ayla Mongès, Lund University, Sweden
15:00	**Seed dispersers help plants keep up with climate change on mountains** 1.4 Sara Mendes, University of Coimbra, Portugal
15:15	**Genetic and ecological determinants of bacterial pathogen success during plant infection** 1.5 Julien Luneau, University of Lausanne, Switzerland
15:30	Refreshment break
16:00	**Panel discussion 1 – Publishing** **Chair: Holly Slater** • Katie Field, Deputy Editor-in-Chief, *Plants, People, Planet* • Christine Foyer, Editor-in-Chief, *Plant, Cell and Environment* • Jonathan Ingram, Editor in Chief, *Plant-Environment Interactions* and *Food and Energy Security* • Anne Knowlton, Senior Scientific Editor, *Current Biology* • Maarja Öpik, Editor-in-Chief, *New Phytologist* • Catherine Walker, Associate Editor, *Nature Plants*
17:00	Flash talks part 1 – odd-numbered poster presenters **This session will not be recorded, but will be streamed live**
17:30	Close of day 1

Day 2	**Tuesday 5 August**
08:55	Morning announcements
	Session 2 **Chairs: Grace Handy and Amy Austin**
09:00	**Keynote speaker** ***Plus ça change …*** **responses of a very long-established oak forest to elevated CO_2** 2.1 Rob Mackenzie, University of Birmingham, United Kingdom
09:30	**Drought-induced photosynthetic decline and increased heat dissipation complicate SIF-based analysis of ecosystem responses to climate** 2.2 Leonardo Ziccardi, Michigan State University, United States
09:45	**An ecophysiological basis for the assembly of Australian rainforest tree communities** 2.3 Julian Radford-Smith, The University of Queensland, Australia
10:00	**Elevated CO_2 gives mature *Eucalyptus* trees additional resistance and resilience to waterlogging** 2.4 Min Zhao, Western Sydney University, Australia
10:15	**Linking above- and below-ground trait coordination at community-level to ecosystem & microbial functions under climate change** 2.5 Billur Bektas, ETH Zürich, Switzerland
10:30	**Plant science to save the world – setting the scene** **Chairs: Diego Márquez and Anna Gardner** Panellists: • Yoselin Benitez-Alfonso, University of Leeds, United Kingdom • Julie Gray, University of Shefield • Rosa Sanchez-Lucas, University of Birmingham, United Kingdom
10:50	Grab a drink and fruit pot on the way to your discussion group
11:00	**Discussion groups** Group allocations are displayed on name badges **This session will not be available on Zoom or recorded**
12:10	**Plant science to save the world – delegate presentations** **This session will not be recorded, but will be streamed live**
13:00	Lunch
	Session 3 **Chairs: Carlos Ballaré and Yoselin Benitez-Alfonso**
14:00	**Keynote speaker** **Plants of South Africa for human health: successes, prospects and challenges** 3.1 Nox Makunga, Stellenbosch University, South Africa
14:30	**Decoding the RNA language with AI-driven Foundation Model** 3.2 Haopeng Yu, John Innes Centre, United Kingdom
14:45	**Bridging innovation and adoption: understanding farmers' preferences for Agrobacterium-mediated transformation in gene-edited tomato cultivars in Nigeria**

	3.3 Seyi Adeboye, University of Abuja, Nigeria
15:00	**How spatial and temporal climate changes over deep time have influenced global plant diversity** 3.4 Jiaze Li, Imperial College London, United Kingdom
15:15	**Enhancing African ecosystem representation in land surface models: a focus on plant functional types in JULES.** 3.5 Enimhien Akhabue, University of Exeter, United Kingdom
15:30	Refreshment break
16:00	Flash talks part 2 – even-numbered poster presenters **This session will not be recorded, but will be streamed live**
16:30	**Publishing ethics workshop** Delegates will be presented with various scenarios from publishing to discuss as a group to explore the various ethical decisions facing journals/editors and reviewers. Each of the cases is based on real examples submitted to the COPE forum. **This session will not be available on Zoom or recorded**
17:30	Poster session 2 – even-numbered poster presenters
18:30	**Chairs: Keith Lindsey & Daniel Gibbs** **Special evening keynote lecture** **A research career focused on investigating how self-incompatibility works** Noni Franklin-Tong, University of Birmingham, United Kingdom
19:30	Close of day

Day 3	**Wednesday 6 August**
08:55	Morning announcements
	Session 4 **Chairs: Diego Márquez and Julie Gray**
09:00	**Keynote speaker** **Enhancing C_4 photosynthesis for carbon capture and food security** 4.1 Maria Ermakova, Monash University, Australia
09:30	**Cytochrome P450 enzyme CYP716A catalyzes the biosynthesis of bitter and hemolytic oleanolic acid in the superfood *Chenopodium quinoa*** 4.2 Pravesh Kundu, CSIR- Institute of Himalayan Bioresource Technology, India
09:45	**Beyond the DNA: an epigenetic mechanism for self incompatibility in *Arabidopsis thaliana*** 4.3 Robyn Emmerson, University of Birmingham, United Kingdom
10:00	**Linking mitochondrial dynamics with mtDNA exchange- expanding the 'social network'** 4.4 Joanna Chustecki, University of Oxford, United Kingdom
10:15	**Unique structural attributes of the PSI-NDH supercomplex in *Physcomitrium patens*** 4.5 Monika Opatíková, Palacký University Olomouc, Czech Republic
10:30	Refreshment break
11:00	**Panel discussion – Careers** **Chairs: Grace Handy and Daniel Gibbs** **With Slido support from: Andrew Placket, Lisa Lamberte and Andrea Vadillo Dieguez** Panellists • Adesola Bello, University of Birmingham Research Strategy and Services Division • Philippa Borrill, John Innes Centre • Costas Garagounis, PCR Biosystems Ltd • Claire Litchfield, University of Birmingham Enterprise • Marjorie Lundgren, Lancaster University • Matthew Naish, University of Cambridge • Carl Ng, University College Dublin • Mariana Vale, Fed. Univ. Rio de Janeiro
12:00	Lunch break
	Session 5 **Chairs: Andrea Vadillo Dieguez and Lisa Lamberte**
13:30	**Keynote speaker** **Plants as models, plants as food: what we're learning from the phyllosphere microbiome and why it matters** 5.1 Britt Koskella, University of California, Berkeley, USA
14:00	**Regulatory features determine the evolutionary fate of laterally acquired genes in plants** 5.2 Catherine Collins, The University of Sheffield, United Kingdom

14:15	**The ecology and evolution of *Nicotiana* section *Suaveolentes*** 5. 3 Charlotte Phillips, University of Portsmouth & Royal Botanic Gardens, Kew, United Kingdom
14:30	**Evolving with stress: the crucial role of natural antisense transcripts in plant resilience** 5.4 Jeky Chanwala, Umeå Plant Science Centre, Sweden
14:45	Group photo
15:00	Refreshment break
15:30	**Breakout session on careers** Group allocations are displayed on name badges **This session will not be available on Zoom or recorded**
16:30	**Science communication session** • Samantha Dobbie, BIFoR Learning and Engagement Lead, University of Birmingham • Caroline Durbin**,** Research Communications Manager, University of Birmingham • Anna Gardner, University of Birmingham
17:00	Close of day

Day 4	**Thursday 7 August**
08:55	Morning announcements
	Session 6 **Chairs: Rory Osborne and Alistair Hetherington**
09:00	**Keynote speaker** **Understanding the biosynthesis of starch granules using insights from natural variation** 6.1 David Seung, John Innes Centre, UK
09:30	**An isoaspartate-induced impairment of OsHSFC1b transactivation negatively impacts seed vigour, seed weight and size in rice** 6.2 Rakesh Kumar Achary, National Institute of Plant Genome Research, India
09:45	**Sweet shaping of root system architecture under water deficit** 6.3 Dhriti Singh, Umeå Plant Science Centre, Sweden
10:00	**The pace of life: effects of circadian clock speed on plant growth and development** 6.4 Danny Ginzburg, University of Cambridge, United Kingdom
10:15	**Effects of m6A loss on immunity and polyadenylation in *Arabidopsis thaliana*** 6.5 Carey Metheringham, University of Dundee, United Kingdom
10:30	Refreshment break Note: final poster votes are due by the end of this break
	Session 6 continued **Chairs: Anna Gardner and Ralph Panstruga**

11:15	**Photosynthetic and antioxidant responses to phosphorus fertilization in drought-stressed common beech and sessile oak from different provenances** 6.6 Antonia Vukmirović, University of Zagreb, Croatia
11:30	**A trait spectrum for ectomycorrhizal fungi – how could it improve understanding of plant–soil interactions in forests?** 6.7 Karolina Jörgensen, Swedish University of Agricultural Sciences, Sweden
11:45	**How plastic is the seed microbiome?** 6.8 Expedito Olimi, Southampton University, United Kingdom
12:00	**Panel discussion – Model-data integration** Chair: Richard Norby, *New Phytologist* Editor • Enimhien Akhabue, University of Exeter • Richard Betts, University of Exeter and Met Office • Anna Gardner, University of Birmingham • Shomari Healy, University of Birmingham • Maxim Kapralov, Newcastle University • Keith Lindsey, Durham University • Anja Rammig, Technical University of Munich
13:00	Closing and prizes: • Announcing the winners of the poster prizes • Announcement of the location of New Phytologist next generation scientists 2026
14:00	Close of Symposium and lunch

Speaker abstracts

1.1 Understanding arbuscular mycorrhizal fungi: from natural biodiversity patterns to land management and societal needs and expectations

Maarja Öpik
University of Tartu, Tartu, Estonia.

Biodiversity patterns of arbuscular mycorrhizal (AM) fungi are increasingly well understood at local, regional and global scales, in different natural ecosystems and in response to various disturbances. The major drivers of community assembly include edaphic and climatic variables as well as host plant diversity and abundance. A major role of biomes is recognised: natural grasslands are a habitat of high biodiversity of AM fungi in various climatic zones.

Farmland management constitutes a major disturbance on AM fungal diversity, yet different agricultural practices apparently preserve AM fungal diversity and functioning differently. Soil-friendly management of agricultural lands holds the potential to promote ecosystem functioning and decrease environmental load of food production.

We are conducting a country-level survey of AM fungal diversity in Estonian agricultural fields. The first results demonstrate how various management practices differently impact AM fungi, and saprotrophic, and pathogenic fungi in the fields. One of the main drivers is frequency of use of plant protection products. We also conducted a survey of farmers' opinions on soil biodiversity and related issues and learned that farmers relate to "soil", but less so to "soil biodiversity".

On the farmers' side there are strong expectations for research to provide solutions to new challenges, such as new pests, shifting climate such as more variable precipitation patterns etc. Therefore, we are working together with farmers to develop deeper understanding of soil biodiversity in the society, including farmers, various land managers, policy makers and general public. The basic research approaches and accumulated understanding on AM fungal diversity now allows us to develop applications such as biodiversity-considerate soil management guidelines for farmers, and contribute to fungal, environmental, ecological literacy in the society.

1.2 Decoding Synergy: How *Enterobacter* sp. SA187 enhances plant growth under low nitrogen through ethylene signaling and nitrate transporters

Amina Ilyas ORCID iD
Institute of Plant Sciences Paris-Saclay, Gif-Sur-Yvette, France. Université Paris-Saclay, Gif-Sur-Yvette, France

Nitrogen (N) is an essential macronutrient for plant growth and development, yet N availability often limits agricultural productivity. The excessive use of synthetic N fertilizers has resulted in significant environmental problems including greenhouse gas emissions & water pollution, highlighting the urgent need for sustainable alternatives. Beneficial plant-associated microbes present a promising solution to enhance nutrient use efficiency and promote plant growth under N-limited conditions.

In this study, we explore how *Enterobacter sp.* SA187 (SA187), a bacterium known for promoting abiotic stress tolerance, supports the growth of *Arabidopsis thaliana* under low N conditions. Through physiological and molecular analyses, we demonstrate that SA187 enhances plant biomass and improves plant N content in N-deficient environments. Our results show that SA187 regulates the expression of key high-affinity nitrate transporter genes, *NRT2.5* and *NRT2.6*. Notably, *NRT2.5* is regulated downstream of ethylene signaling pathways activated by SA187, whereas *NRT2.6* is regulated independently of ethylene. Mutant analyses confirm the distinct roles of these pathways in mediating the growth-promoting effects of SA187.

These findings highlight the potential of SA187 as a microbial solution for improving plant growth under limited N conditions. Leveraging such beneficial microbes could reduce the dependence on synthetic N-fertilizers, paving the way for environmentally sustainable strategies to enhance crop productivity.

1.3 Arbuscular mycorrhizal fungi foraging strategies, decision making and interactions in soil chips.

Ayla Mongès
Lund University, Lund, Sweden

The objective of this project is to determine how fungi can make decisions across scales that benefit the whole mycelial body and whether symbiotic interactions with plants can modify fungal decision making.

To answer these questions, we are using microfluidic chips, also called soil chips, to design physical and chemical challenges for the mycelium. The hyphal behavior is examined in diverse nutritional and symbiotic contexts by using different culture and plant-host systems such as inoculated carrot root organ culture, inoculated *Marchantia paleacea*, or without a host, grown in a myristate medium. The micrometer scale of the chip enables us to observe the growth patterns of individual hyphae as well as subcellular processes, providing insights into how fungal hyphae respond to various environmental cues. This experimental configuration is also used to examine the mycorrhizal interaction at a larger scale by facilitating documentation of the mycelium's architectural features and allowing us to monitor resource allocation within the mycelium. Additionally, we have been able to observe and document mycelial development and anastomosis formation as well as monitor the ability of the mycelium to establish novel symbiotic interactions or maintain existing ones in diverse environments.

1.4 Seed dispersers help plants keep up with climate change on mountains

Sara Mendes ORCID iD
Centre for Functional Ecology, University of Coimbra, Coimbra, Portugal

Climate change is forcing species to shift their distributions to track suitable climates. For sessile organisms such as plants, the dispersal of their seeds is crucial, as it is their only opportunity to move. Thus, on mountains, animal seed dispersers may be important in helping plants ascend to higher altitudes. However, the role of animal dispersers remains poorly understood due to a lack of empirical datasets spanning multiple disperser guilds along elevational gradients. To address this gap, I built seed dispersal networks for the five altitudinal vegetation belts of Tenerife Island (0-3,718 m a.s.l.) to evaluate whether animal dispersers enable plants to colonise higher elevations under climate change. The overall network comprised 283 unique interactions among 73 plant and 27 animal species. Seed dispersers functionally connect vegetation belts, offering viable pathways for plants to colonise upper areas. Furthermore, 11 plant species were dispersed to higher elevations beyond their current distribution range, achieving vertical distances exceeding those required to escape rising temperatures. Nonetheless, over half of the plants reaching higher elevations were exotic. This work suggests that diverse disperser communities are key for helping plants track climate change on mountainous, yet exotic plants may also benefit from this upward lift.

1.5 Genetic and ecological determinants of bacterial pathogen success during plant infection

Julien Luneau ORCID iD
University of Lausanne, Lausanne, Switzerland

Crop pathogens significantly reduce agricultural production. Early interactions between the pathogen and its environment in the host determine whether the pathogen can establish and cause disease. Here, we used functional genomics approaches (RNAseq & RB-TnSeq) to identify *Xanthomonas campestris* genes involved in early colonization of the plant leaf. We found that metabolic capacities, transport, defense evasion, and stress tolerance functions contribute to bacterial growth in the host. Interestingly, we also found that cooperation and cheating for virulence functions occurred among TnSeq mutant strains. This prompted us to investigate how the social behaviors of pathogens could shape infection outcomes. We focused on phenotypic heterogeneity within a clonal pathogen population. We asked how local interactions between individual pathogen cells and their environment affect the co-existence of phenotypically diverse subpopulations. Using computational simulations of plant infection, we identified conditions (spatial arrangement, initial abundances, plant and microbial traits) that restrict pathogen colonization. In particular, we found that bottlenecks in the plant tissue restrict co-existence and limit bacterial spreading. On the other hand, quick restoration of phenotypic heterogeneity after bottlenecks promotes division of labor for immunosuppression and ensures tissue colonization. Altogether, this research helps elucidate the strategies of plant pathogens in their natural ecological context.

1.6 Panel discussion 1 – Publishing

Chair: Holly Slater

- Maarja Öpik, Editor-in-Chief *New Phytologist*
- Christine Foyer, Editor-in-Chief, *Plant, Cell and Environment*
- Katie Field, Deputy Editor-in-Chief, *Plants, People, Planet*
- Catherine Walker, Associate Editor, *Nature Plants*
- Anne Knowlton, Senior Scientific Editor *Current Biology*
- Jonathan Ingram, Editor in Chief, *Plant-Environment Interactions* and *Food and Energy Security*

Holly Slater, The New Phytologist Foundation, United Kingdom

Holly is the Senior Commissioning Editor *for New Phytologist*. She has overall responsibility for commissioning strategies, including the prestigious Tansley reviews series. Holly has more than twenty years' experience in scientific publishing, provides advice and support to the *New Phytologist* team and contributes regularly to Foundation events and strategic development projects. Prior to publishing, Holly was a researcher in molecular–plant–microbe–interactions. She gained her PhD from The Sainsbury Laboratory (TSL), Norwich, UK, which was followed by four years of post-doctoral experience that she carried out first in TSL and then at the University of Cambridge, UK. Holly loves working in scientific journal publishing, a process that is core to the academic process, and really enjoys supporting the plant science community.

Katie Field

Katie Field is a Professor of Plant-Soil Processes at the University of Sheffield, specializing in the interactions between plants and fungi, particularly mycorrhizal symbioses. Her research explores how these interactions influence plant physiology, ecosystem function, and responses to environmental change. She also investigates the role of symbiotic fungi in plant terrestrialization and sustainable agriculture. Katie is Deputy Editor-in-Chief of *Plants, People, Planet*.

Christine Foyer

Christine H. Foyer is Professor of Plant Sciences at the University of Birmingham. She is also an Adjunct Professor at the University of Delhi, India and an Extraordinary Professor in Genetics, University of Stellenbosch, South Africa. She recently received the Sustained Excellence Award from the Biochemical Society (UK). She is a Member of the Annals of Botany Company, the Editor in Chief of *Plant, Cell and Environment* and the Publications Officer for the Association of Applied Biologists. She is a Highly Cited Researcher (2024), ranking in the top 1% by citations for the field. In the Category of Plant Science and Agronomy she is ranked #8 in the world ranking and #1 in United Kingdom. In the Best Female Scientist category she is ranked 224th in the world, 15th in the UK: https://research.com/u/christine-h-foyer. Christine is an expert in plant biochemistry and metabolism. With a strong focus on reduction/oxidation (redox) processes and signals that regulate plant growth and stress tolerance, her lab studies how primary processes such as photosynthesis regulate plant, growth development and defence, particularly through effects on the redox status of cells and cell signalling under optimal and stress conditions. Using model (Arabidopsis), crop plants and trees, her lab investigates the responses of photosynthesis and associated processes to abiotic stresses including elevated carbon dioxide.

Jonathan Ingram

Jonathan works at Wiley as Editor in Chief for the journals *Plant-Environment Interactions* and *Food and Energy Security* (both gold OA); he is also a Senior Editor for *Ecology and Evolution*. This means handling manuscripts and working with editors across a wide subject range, and developing these journals through outreach and commissioning. Previously he managed an evolving portfolio of titles at Wiley, including on behalf of external societies, focused on plant and environmental sciences. Jonathan started his publishing career with Elsevier at *Trends in Plant Science*, before moving to *New Phytologist* as managing editor and, later, *Journal of Experimental Botany* with a focus on commissioning and development. His research background is drought tolerance, focusing on CAM in his DPhil at Oxford and resurrection plants (sugar metabolism) in postdoctoral work at the Max Planck Institute in Cologne.

Anne Knowlton
Anne is a senior scientific editor at the journal *Current Biology*, which is part of the Cell Press family of journals. She comes from South Carolina, USA, where she studied biology at Clemson University for her bachelor's degree. She completed her PhD at the University of Virginia studying the assembly of the mitotic spindle. From there, she did her postdoctoral work at the University of Washington in Seattle. She has been working as an editor at *Current Biology* since 2011, and handles the plant biology papers for the journal. She is based in Baden-Württemberg, Germany.

Maarja Öpik
Maarja joined *New Phytologist* as an Advisor in 2011 and as an Editor in 2013 and became Editor-in-Chief in 2025. She is a Professor of Molecular Ecology and Director of the Institute of Ecology and Earth Sciences at the Faculty of Science and Technology at the University of Tartu, Estonia. Maarja is currently an Editor *in Fungal Ecology*, *MycoKeys* and *IMA Fungus*, and has been in the same role for *PLoS ONE* and *Plant and Soil*. She is editorial board member for *ISME Journal*.

Catherine Walker
Catherine is an associate editor at *Nature Plants* where she handles manuscripts in ecology, agriculture, forestry and plant-microbe interactions. Catherine obtained her PhD from Rothamsted Research in 2019 where her research focused on understanding the role of effectors in the establishment of Fusarium Head Blight infection in wheat. She then went on to carry out postdoctoral research with the Plasmodesmata research group at the John Innes Centre, moving from wheat to Arabidopsis, and working to uncover the contribution of symplastic connectivity and cell communication to immune signalling. In 2022, Catherine officially left the bench and took on a new role in the Biotechnology and Biological Sciences Research Council (BBSRC) where she worked in the funding delivery team responsible for oversight of peer review for varied funding calls. She joined *Nature Plants* in 2023 and is based in the London, UK office.

2.1 *Plus ça change*… responses of a very long-established oak forest to elevated CO_2

Rob Mackenzie
University of Birmingham, Birmingham, United Kingdom

“The more things change, the more they stay the same…” is attributed to French writer Jean-Baptiste Alphonse Karr, and is usually considered a pessimistic condemnation of moral and social stasis. But in an ecological context and a rapidly changing world, coping (‘staying the same’) relates to resistance, recovery and resilience, and may be a hopeful sign, especially for ecosystems with long-lived plants at their core, like the oak woodland that is the site of the University of Birmingham’s Institute for Forest Research (BIFoR) Free-Air CO_2 Enrichment (FACE) facility.

BIFoR FACE is set in UK broadleaf forest dominated by 175-year-old and 25 m tall oak trees interspersed with sycamore, hazel, hawthorn, and holly. CO_2-enrichment, scheduled to run until 2031, commenced in spring 2017. The whole canopy volume of three 30m-diameter plots is immersed in air containing 150 ppm CO_2 above current atmospheric levels throughout growing season daylight hours. Three neighbouring plots act as controls. Effects of elevated CO_2 found in BIFoR FACE include: (i) 20% greater season-average photosynthesis; (ii) 10% greater woody dry mass increment; and (iii) a faster, more conservative nitrogen cycle with 74% reduction in N_2O emissions. This ‘faster-tighter’ N-cycling in the forest allows leaf quality (C:N) to be maintained even as more carbon is assimilated.

Accompanying this forest productivity response is evidence of nascent ecosystem fragility. Susceptibility to powdery mildew and insect herbivory is unchanged in the mature trees but increased in seedlings. Pollen and flower mineral contents are significantly reduced under eCO2, and acorns contain significantly less protein but more phytic acid. These more ecologically problematic findings imply a carbon-rich, nutrient-poor, future diet for animals and insects in temperate forest ecosystems.

2.2 Drought-induced photosynthetic decline and increased heat dissipation complicate SIF-based analysis of ecosystem responses to climate

Leonardo Ziccardi ORCID iD
Michigan State University, East Lansing, USA

Amazonian forests have faced extreme droughts in recent decades often linked to El Niño events, leading to increased tree mortality, reduced carbon sequestration, and sharp rises in global atmospheric CO_2 levels. The extent to which photosynthetic drought sensitivity varies across the vertical canopy profile in Amazonian forests remains poorly quantified, despite its potential importance for these forest-wide responses. Here, we show that photosynthetic capacity and photoprotective responses vary significantly across canopy strata during drought events. Using vertical canopy sampling of chlorophyll fluorescence in mature leaves, we analyzed seasonal and drought-induced changes during the 2023-2024 El Niño Southern Oscillation (ENSO) drought. Reductions in photosynthetic electron flow occurred in mid (20–40 m) and upper (>40 m) canopy layers, alongside changes in photochemical efficiency (ΦPSII), non-photochemical quenching (ΦNPQ), and steady-state leaf fluorescence (ΦNO). The ΦNPQ/ΦNO ratio increased across all strata under drought stress, indicating enhanced photoprotection. However, photosynthesis relative to fluorescence declined, indicating a shifting SIF-GPP relationship during extreme drought that must be accounted for when using SIF remote sensing to assess canopy responses to climate extremes.

2.3 An ecophysiological basis for the assembly of Australian rainforest tree communities

Julian Radford-Smith ORCID iD
The University of Queensland, Brisbane, Australia

Understanding the role of climate in the assembly of rainforest tree communities is informative for predicting how future climates will impact species and communities. We surveyed rainforest tree communities across the Australian subtropics (spanning 600 to 2500 mm rainfall year^{-1}) and measured functional traits on 285 (91%) of all recorded species. We used principal component analysis to create axes approximating species' hydraulic strategies, leaf economics and stature and included these as predictors in joint species distribution models, along with traits describing dispersal ability and leaf phenology. Hydraulic strategy and leaf phenology strongly modulated species' occurrence trends along the moisture availability gradient, while stature and leaf economics modulated species' responses to minimum temperature and soil variables, respectively. Overall, we quantify the occurrence trends of almost half of Australia's subtropical rainforest tree species based on their functional traits, providing a general foundation for prediction under ongoing climate change.

2.4 Elevated CO_2 gives mature *Eucalyptus* trees additional resistance and resilience to waterlogging

Min Zhao ORCID iD
Western Sydney University, Sydney, Australia

Elevated atmospheric CO_2 concentration (eC_a), by increasing plant carbon uptake, is thought to ameliorate the negative impacts of stresses on trees. Waterlogging is a severe stress that is potentially harmful to trees, but whether eC_a offers trees extra resistance, resilience or both against waterlogging remains unclear. We examined the potential ameliorative effect of eC_a against waterlogging at the *Eucalyptus* Free-Air CO_2 Enrichment (EucFACE) facility, which experienced a 11-month waterlogging. We hypothesised that eC_a would reduce the impact of waterlogging on trees by increasing the availability of non-structural carbohydrates (NSC). We tracked the response of trees to waterlogging by measuring tree health, litterfall, photosynthesis, leaf area index (LAI), and NSC. We found that during waterlogging, eC_a plots showed higher resistance by having healthier canopies and lower twig litterfall rates. Concurrently, eC_a plots had higher LAI and healthy trees in eC_a plots had higher sugar fractions in sapwood. We inferred that eC_a provided trees with more NSC to resist waterlogging. After the waterlogging event, eC_a plots exhibited a faster recovery by having higher leaf production. The higher leaf production was associated with a higher remobilisation of NSC in live bark. In summary, our findings suggest that eC_a can ameliorate the negative impact of waterlogging and give trees additional resistance and resilience.

2.5 Linking above- and below-ground trait coordination at community-level to ecosystem & microbial functions under climate change

Billur Bektas ORCID iD
ETH Zürich, Zürich, Switzerland

Increasing temperatures and droughts are known to affect mountain plant communities, their functional trait,s and life strategies. However, little is known about how communities acclimate to climate change, and how tightly plant responses are linked to responses of ecosystem and microbial functions.

With a whole-community transplantation experiment, we compared warmed and dried communities transplanted from alpine to subalpine conditions to alpine and subalpine control communities. Five years after transplantation, we found slower growth (e.g. lower leaf nitrogen) and more outsourcing strategies (e.g. lower specific root length) in the warmed alpine communities, probably due to drought stress. While below-ground traits fully acclimated to new subalpine conditions, above-ground traits did not.

Changes in functional traits cascaded to changes in the ecosystem and microbial functions (eg. productivity, decomposition rates, arbuscular colonization, and bacterial biomass). Most of the variance in ecosystem and microbial functions was explained by the above-ground traits and links between traits and ecosystem and microbial functions did not change under treatment. In contrast, the links between below-ground traits and ecosystem and microbial functions were disrupted under climate change. This might challenge our capacity to predict the trajectories of plant and soil communities and their associated ecosystem functions under climate change.

2.6 Plant science to save the world

Chairs: Diego Márquez and Anna Gardner

Panellists:

- Yoselin Benitez-Alfonso, University of Leeds, United Kingdom
- Julie Gray, University of Shefield
- Rosa Sanchez-Lucas, University of Birmingham, United Kingdom

Yoselin Benitez-Alfonso

Dr. Yoselin Benitez-Alfonso is Professor in Interdisciplinary Plant Sciences at the University of Leeds (UK). She was born in Cuba and graduated in Chemistry at the University of Cordoba, Spain. Yoselin did her PhD in plant biochemistry and molecular biology followed by postdoctoral research at Cold Spring Harbor Laboratory in New York (USA) and at the John Innes Centre (Norwich, UK). In 2017, she was appointed Lecturer at the University of Leeds, where she secured multiple funding including a UKRI Future Leaders Fellowship. Yoselin research group focuses on cell walls properties surrounding plant intercellular channels (named plasmodesmata) with the goal to unlock knowledge for the development of new strategies for crop improvement and biomaterial development. Yoselin's interdisciplinary research is supported by several networks and virtual centers including the NSF- funded 'Plant Cell Atlas network', the Astbury Centre for Structural Biology and the Bragg Centre for Material Research. She advocates for equity, diversity and inclusion and last year, co-founded the Black in Plant Science Network (https://blackinplantscience.org/) dedicated to connect, celebrate and cultivate the next generation of plant scientists in UK. Yoselin was promoted to full Professor last year, becoming the 66th Black Female Professor in the UK. She received the 'Education and Academic Leader of the Year' Forward Ladies award and the UKRI Impact Award for 'Advancing Research Culture'. For more details on Yoselin's research and the team, visit https://benitezalfonsolab.leeds.ac.uk/ or https://astbury.leeds.ac.uk/people/yoselin-benitez-alfonso/. You can contact Yoselin at Y.Benitez-Alfonso@leeds.ac.uk or in social media at Twitter/X @YoselinBenAlf bluesky and LinkedIn. Yoselin is an incoming member of The New Phytologist Foundation's board of Trustees.

Julie Gray

Julie Gray is interested in plant responses to climate stress, and how to alleviate future heat and drought stress in crops. Her research group in Sheffield have manipulated the expression of genes to create barley, wheat and rice varieties with fewer stomata that have improved drought tolerance and reduced water requirements. Their work on wheat is included in the UK Science Museum's Future of Food exhibition, and their rice findings featured in a BBC World documentary. Julie studied Biochemistry at Liverpool University and was a PhD student at Nottingham University where she researched genes that control fruit ripening. These findings contributed to the development of the first genetically modified and gene edited foods to be commercialised.

Rosa Sanchez-Lucas, University of Birmingham, United Kingdom

Dr. Rosa Sanchez-Lucas finished a higher engineering degree in Agronomy with a project about holm oak seedlings response to drought at the University of Cordoba. After that, she completed a master's degree on Plant Protection, Production and Breeding with the project about nitrogen fertilization effects to frost response in olive tree. Her PhD in Agricultural, Food, Forestry and Sustainable Rural Development Engineering studied warming temperature effects on olive tree. Currently, she works as a postdoctoral researcher at the department of Plant Sciences at the University of Birmingham, studying the induced resistance of oak against powdery mildew.

During all her professional career, she has studied the effect of stress on trees: and how they respond through physiological and biomolecular approaches: 1) abiotic stress as drought (undergraduate), temperatures (master and PhD) and elevated CO 2 concentration (current postdoc). 2) Biotic stress as oak powdery mildew, oak acutate decline and ash dieback (current postdoc). 3)Epigenetics changes caused by plant (a)biotic stresses. 4) Transgenerational inheritance of epigenetics in forest trees.

3.1 Plants of South Africa for human health: successes, prospects and challenges

Nokwanda Makung
Department of Botany and Zoology, Stellenbosch University, South Africa

Indigenous plants play a significant role as medicines for a large fraction of the South African population and this is linked to a strong sociocultural tradition of using plants for medical purposes. A wide range of ‘omics tools has been useful in studying different taxa in our environment. Species such as *Mesembryanthemum* syn. *Sceletium tortuosum* (Aizoaceae); *Lessertia* syn. *Sutherlandia frutescens* (Fabaceae) and *Dodonaea viscosa* (Sapindaceae) have been central to our research activities where we use both non-targeted and targeted metabolomics to understand the influence of different environments on plant metabolism. Proteomic analyses under stressed conditions provided new insights into the impacts of salinity and drought stress with respect to both central and specialized metabolism. The medicinal flora of South Africa still largely remains poorly characterized despite its potential in drug discovery pipelines. The nexus of plant biodiversity and the South African bioeconomy is governed by legislation that aims to ensure fair and equitable beneficiation of the indigenous knowledge holders. Partnerships that have been established to meet current policy are also discussed as part of this presentation.

3.2 Decoding the RNA language with AI-driven Foundation Model

Haopeng Yu ORCID iD
John Innes Centre, Norwich, United Kingdom

Understanding the intricate language of plant RNA is essential for uncovering key regulatory elements driving growth, adaptation, and defense. Here, we present PlantRNA-FM, a pioneering AI-driven foundation model that integrates both RNA sequence and structure information from over 1,000 plant species. By training on 54 billion RNA elements, PlantRNA-FM accurately decodes functional motifs and structural patterns, enabling highly precise predictions of gene regulatory functions. In benchmark evaluations, the model outperformed existing approaches, successfully identifying crucial structural features such as those associated with translation efficiency. Experimental validations confirmed that certain RNA structures predicted by PlantRNA-FM promote efficient protein production in plants. Furthermore, our interpretability framework clarifies how the position and nature of these RNA motifs influence gene function, offering a comprehensive view of sequence–structure interplay. This capability not only accelerates the discovery of functional regulatory elements but also opens avenues for engineering RNA-based traits in crops. We anticipate that PlantRNA-FM will catalyze future breakthroughs in plant science, complementing traditional biology to rapidly advance our understanding and design of plant genetic systems.

3.3 Bridging innovation and adoption: understanding farmers' preferences for *Agrobacterium*-mediated transformation in gene-edited tomato cultivars in Nigeria

Seyi Adeboye ORCID iD

National Biotechnology Development Agency, Abuja, Nigeria. University of Abuja, Abujua, Nigeria

Advancements in plant biotechnology, including *Agrobacterium*-mediated transformation and gene editing, offer immense potential to enhance food security and agricultural sustainability in developing regions. This research leverages CRISPR-Cas9 gene editing to address challenges in tomato (*Solanum lycopersicum*) production in Nigeria, including low productivity, high post-harvest losses, and limited adoption of advanced technologies. Tomatoes are crucial for nutrition and livelihoods, but their short shelf life exacerbates food insecurity and financial instability for farmers. This study focused on designing and implementing CRISPR-Cas9 constructs to target the *Shelf-Life Food Regulator* (*SlFSR*) gene in two tomato varieties, Pusa Ruby and UC82, to extend post-harvest shelf life. Precise editing involved selecting optimal target sites within the *SlFSR* gene and optimizing guide RNA sequences. CRISPR-Cas9 cassettes were PCR-amplified, cloned, ligated, and introduced into tomato varieties via *Agrobacterium*-mediated transformation protocols, achieving high efficiency (~85%). Field surveys across three Nigerian states revealed socio-economic factors influencing technology adoption, such as gender disparities and reliance on rain-fed agriculture. This research demonstrates the potential of integrating socio-economic insights with precision genetic tools to enhance shelf life, stress tolerance, and fruit quality contributing to sustainable agriculture and food security.

3.4 How spatial and temporal climate changes over deep time have influenced global plant diversity

Jiaze Li ORCID iD
Imperial College London, Ascot, United Kingdom

Biodiversity loss and climate change are interlinked global challenges. Climate impacts on biodiversity are often explained through spatial factors such as climatic area or isolation, or temporal factors such as climatic antiquity and stability. However, the combined influence of spatial and temporal climatic dynamics remains unknown. Here, we integrate both dimensions to assess how the long-term geographic extent and shift of climates have shaped global plant diversity. By compiling occurrence records for 350,864 vascular plant species, we produce the most comprehensive and precise global plant diversity map to date. We identify climatic analogues spanning tens of millions of years and quantify their geographic dynamics over deep time. Incorporating spatio-temporal climate changes into statistical models explains up to 92% of the deviance in present-day global plant diversity. Our findings extend previous hypotheses by showing that plant diversity is higher in climatic conditions that have stayed widespread over deep time. We also reveal a novel mechanism: climates that have expanded and shifted moderately in space over deep time foster higher diversity by balancing persistence with diversification. By revealing spatio-temporal climate influences on biodiversity, our study informs conservation strategies that conserve ancient biodiversity in stable climates while supporting ongoing diversification under climate change.

3.5 Enhancing African ecosystem representation in land surface models: a focus on plant functional types in JULES.

Enimhien Akhabue ORCID iD
University of Exeter, Exeter, United Kingdom

The accurate representation of African ecosystems in most of the global land surface models (LSMs) remains a critical challenge, limiting our understanding of the dynamics of carbon, water, and energy across this diverse region. This study addresses these gaps by refining the Joint UK Land Environment Simulator (JULES) through improved parameterization of plant functional types (PFTs). A key foundation of this work involved the systematic classification of plant species observed in Africa, using data from the TRY plant trait database. This process identified key traits and grouped species into appropriate PFTs represented in JULES, providing region-specific parameters for JULES LSM. The ongoing project involves validating the model against flux data from 16 African sites, spanning diverse biomes such as savannas, grasslands, and tropical forests. By integrating these refined PFTs and site-specific environmental conditions, this research aims to improve model accuracy and advance our understanding of ecosystem responses to climate change. These efforts highlight the importance of regional data in enhancing the global applicability of LSMs.

Special evening lecture

3.7 A research career focused on investigating how self-incompatibility works

Noni Franklin-Tong
University of Birmingham, United Kingdom

Vernonica (Noni) Franklin-Tong is emeritus Professor at the University of Birmingham. She was educated in Suffolk and then at the University of Birmingham. Most of her career has been based at Birmingham. She is recognized at an international level for her work on self-incompatibility, cell-cell signalling and programmed cell death. In 2021 she was elected a Fellow of the Royal Society.Noni is renowned for her studies on self-incompatibility (SI). She has devoted her career to investigating cellular mechanisms involved in the regulation of the cell-cell recognition system of SI in *Papaver rhoeas* (the Field Poppy). Sexual reproduction in higher plants involves pollination, involving specific interactions between pollen and pistil. A key mechanism to prevent inbreeding is self-incompatibility (SI), which is a controlled by a single, multi-allelic *S*-locus. Incompatible ("self") pollen is rejected, and compatible ("non-self") pollen is allowed to fertilize the plant. SI plays a decisive role in determining plant reproductive success by preventing inbreeding. Regulation of pollination has high importance in relation to its impact on food security.Noni initiated pioneering cell and molecular research of *Papaver* SI. Her development of an *in vitro* bioassay allowed investigation of the cell biology of SI for the first time. This outstanding model system enabled elucidation of mechanisms responsible for rejection of incompatible pollen. Her studies have uncovered an intricate intracellular signalling network and revolutionized our understanding of the signals, downstream targets and key cellular processes that regulate SI, revealing new phenomena critical to this process, culminating in programmed cell death. Her lab achieved the first functional trans-genera transfer of a SI system using the *Papaver S*-determinants. This has implications for translational work; longer-term this may aid the quest to make F1 hybrids in some crops more easily.

Noni will talk about her research career over the years. This will be a story about her personal journey and as her career has spanned ~40 years, it will also provide a bit of a historical perspective, as when she started her PhD, plant molecular biology did not exist! Although she will touch on some of her research findings along the way, showing how the research developed, her focus will be on illustrating some of the challenges that ECRs and researchers face, in the context of her career. This will include examples of attempts to obtain funding and problems to get manuscripts published, as well as personal challenges.

4.1 Enhancing C_4 photosynthesis for carbon capture and food security

Maria Ermakova
Monash University, Australia

C_4 plants, which perform C_4 photosynthesis, often dominate hot and arid regions around the world, and C_4 crops are becoming increasingly important for global food and bioenergy security. This is due to the presence of a specialized C_4 metabolic cycle that functions as a biochemical carbon-concentrating mechanism, enabling Rubisco, the primary carbon-fixing enzyme, to operate near its maximum efficiency. Although C_4 plants already exhibit high rates of carbon fixation, further improvements in C_4 photosynthesis could further enhance carbon capture and increase crop yields. Using the model species *Setaria viridis* and the multipurpose crop *Sorghum bicolor*, we have tested multiple strategies to enhance carbon fixation under various environmental conditions. Our findings demonstrate that improving C_4 photosynthesis is a tractable strategy for increasing crop productivity, supporting rising food and energy demands, and contributing to climate change mitigation through enhanced carbon capture.

4.2 Cytochrome P450 enzyme CYP716A catalyzes the biosynthesis of bitter and hemolytic oleanolic acid in the superfood *Chenopodium quinoa*

Pravesh Kundu ORCID iD
CSIR- Institute of Himalayan Bioresource Technology, Palampur, India. Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, India

Chenopodium quinoa, a nutritionally rich pseudocereal, is gaining global attention due to its gluten-free, protein-rich seeds. However, the seeds contain bitter-tasting oleanane-type triterpenoid saponins, such as oleanolic acid, which contributes to their bitterness and hemolytic activity. Oleanolic acid is synthesized through the cyclization of 2,3-oxidosqualene by beta-amyrin synthase, followed by oxidation of beta-amyrin, a process catalyzed by cytochrome P450 (CYP) enzymes. While plant genomes contain CYP families involved in sapogenin biosynthesis, the specific enzyme responsible for oleanolic acid synthesis in quinoa was previously unidentified. In this study, we identified the CYP716A enzyme in C. quinoa, which converts beta-amyrin into oleanolic acid. Functional validation through transient overexpression and virus-induced gene silencing (VIGS) in quinoa leaves, along with UPLC-MS analysis, confirmed the role of CYP716A in oleanolic acid biosynthesis. Heterologous expression in tobacco and Arabidopsis further demonstrated CYP716A's involvement in growth and stress responses. These findings identify a novel beta-amyrin 28-oxidase enzyme and provide insights into triterpenoid saponin biosynthesis in quinoa. This research lays the groundwork for developing saponin-free quinoa varieties, which would improve the crop's palatability and health benefits.

4.3 Beyond the DNA: an epigenetic mechanism for self incompatibility in *Arabidopsis thaliana*

Robyn Emmerson ORCID iD
University of Birmingham, Birmingham, United Kingdom

DNA hypomethylation in plants is associated with enhanced stress responses, making it a desirable trait. However, methylation mutants often experience a transgenerational decline in fitness, limiting their potential for crop improvement.

We studied *Arabidopsis* epigenetic recombinant inbred lines (epiRILs), created by crossing *met1-3*, which lacks CG methylation, with Col-0, resulting in a 'mosaic pattern' of DNA methylation. A specific region on chromosome 3, inherited solely from Col-0, drew our attention. This region contains the gene *IBM1*, known to be linked to transgenerational fitness decline due to reduced intronic methylation, causing alternative splicing of the IBM1 transcript and extensive gene body hypermethylation.

Additionally, we identified *VHA* in the same region, sharing a similar methylation profile to *IBM1* and complementary floral tissue expression. We hypothesized that the interaction between IBM1 and VHA contributes to the reduced fitness in *met1-3* plants. To explore this, we performed RNA-seq on pollen and carpels, revealing interactions that may impair fertility. Genetic approaches, including crossing IBM1 and VHA knockout mutants and using CRISPR-Cas9 to generate double mutants, were also employed.

Our findings indicate an incompatibility between pollen and carpels in methylation mutants, resulting in reduced fitness and providing new insights into the role of DNA methylation in plant reproduction.

4.4 Linking mitochondrial dynamics with mtDNA exchange- expanding the ‘social network’

Joanna Chustecki ORCID iD
University of Oxford, Oxford, United Kingdom

Plant cell mitochondria exhibit collective behaviours, with individuals moving rapidly and interacting. Mitochondrial populations are evenly spread across cellular space while forming efficient networks with high potential for exchanging contents. A framework of single-cell confocal microscopy, physical modelling and graph theory quantified behaviour and connectivity of the intracellular social network. This analysis can now include functional information on genetic contents and exchange across the population.

Exogenous nucleotide staining and live imaging of *Arabidopsis* hypocotyl cells quantified mitochondrial subpopulations and potential mtDNA exchange events. By tracking individual organelles and their contents a detailed, quantitative, single-cell view can be taken. 3D image analysis counted individual mitochondria per cell, and those with/without mtDNA. We also introduced a genetically encoded photoconvertible fluorescent marker for mtDNA based on the bacterial H-NS binding protein.

Plant mtDNA exhibits high rates of recombination. It is hypothesised that plant mitochondria retain individual, non-reticulated shapes partly to segregate genomic material. My previous work shows that genetic perturbation leads to altered physical dynamics, and live imaging with photoconversion of mtDNA allows direct testing of physical control over the genome. Using these tools will allow us to probe the link between physical control of colocalisation, positioning and genetic dynamics- particularly in relation to plant development and mtDNA inheritance to the next generation.

4.5 Unique structural attributes of the PSI-NDH supercomplex in *Physcomitrium patens*

Monika Opatíková ORCID iD
Palacký University Olomouc, Olomouc, Czech Republic

Photosystem I (PSI) is a pigment-binding protein complex involved in the first phase of photosynthesis. PSI is responsible for light harvesting and represents a critical component of electron transport within thylakoid membrane, which can be realised by either linear or cyclic flow. Cyclic electron transport around PSI is primarily mediated by Proton Gradient Regulation 5 protein/Proton Gradient Regulation 5-like photosynthetic phenotype 1 protein and NADH dehydrogenase-like complex (NDH). In vascular plants, single copy of NDH binds two PSIs at characteristic positions via the light-harvesting antennae LHCA5 and LHCA6. However, this structure provides only limited information about the evolution of PSI-NDH interaction, unlike the moss *Physcomitrium patens* (*Pp*), which represents the evolutionary ancestor of vascular plants lacking the *lhca6* gene but retaining *lhca5*.

By single-particle electron microscopy, we revealed the structure of PSI-NDH supercomplex in *Pp*, which binds only one PSI to NDH and expresses a unique ability to bind PSI in two different configurations. One configuration closely resembles the angiosperms model, the other exhibits a novel, clockwise orientation of PSI. This unique flexibility indicates greater diversity at the PSI-NDH interface in evolutionary older organisms that has been lost in vascular plants, most likely due to increase in PSI-NDH complexity.

4.6 Panel Discussion – Careers

Chairs: Grace Handy and Daniel Gibbs

With Slido support from: Andrew Placket, Lisa Lamberte and Andrea Vadillo Dieguez

Panellists

- Adesola Bello, University of Birmingham Research Strategy and Services Division
- Philippa Borrill, John Innes Centre
- Constantine (Costas) Garagounis, PCR Biosystems Ltd.
- Claire Litchfield, University of Birmingham Enterprise
- Marjorie Lundgren, Lancaster University
- Matthew Naish, University of Cambridge
- Carl Ng, University College Dublin
- Mariana Vale, Fed. Univ. Rio de Janeiro

Adesola Bello

Dr Adesola Bello is a Research Development Officer within the Research Strategy and Services Division (RSSD) at the University of Birmingham. In her role, she provides specialist advice and tailored support to academics/researchers at all career stages to help secure external funding for their research projects. She works with internal and external researchers planning to undertake their research in the School of Biosciences through the pre-award process and helps them to develop their idea into a proposal, identify suitable funding for their projects, prepare their funding applications ensuring compliance with funder requirements, determine what their budgetary/costing needs are, conduct due diligence checks on potential collaborations, facilitate timely and quality bid submissions to funders, negotiate research agreements and set up successful awards before handing over to the post-award teams who help manage the live grants. Prior to joining RSSD, Adesola was a postdoctoral researcher at Imperial College London where she specialised in using metabolomics-based approaches to investigate the interplay between host metabolism, nutrition, and the gut microbiota.

Philippa Borrill

Dr Philippa Borrill is a Group Leader in the Department of Crop Genetics at the John Innes Centre. Her research investigates the mechanisms controlling functional redundancy between gene copies in polyploid wheat. She seeks to apply this knowledge in crop improvement, particularly to enhance grain nutrient content. Philippa studied Natural Sciences at the University of Cambridge and obtained her PhD from the John Innes Centre in 2014. From 2015 she held a BBSRC Anniversary Future Leader Fellowship at the John Innes Centre and developed a series of key resources for wheat genomics including a gene expression atlas (www.wheat-expression.com) which been used by over 45,000 people globally. In 2018 Philippa joined the University of Birmingham as a Lecturer (Assistant Professor) in Plant Biology. She returned to the John Innes Centre as a Group Leader in 2021. Philippa's work on wheat genetics and genomics has been recognised by awards such as the *New Phytologist* 2019 Tansley Medal for Excellence in Plant Science and the Society for Experimental Biology 2022 Plant President's Medal. Philippa is committed to making wheat research accessible to other scientists, industry and the general public. She has organised multiple training workshops in wheat bioinformatics and co-developed a wheat training website (www.wheat-training.com). Philippa was elected to Chair the Monogram (UK small grain cereals) network from 2021-2023 and collaborates with several wheat breeding companies.

Constantine Garagounis, PCR Biosystems Ltd., United Kingdom

Dr. Constantine Garagounis studied Biochemistry and Biotechnology and has a DPhil in Plant Sciences from the University of Oxford. He worked as a post-doctoral researcher and contract lecturer on plant secondary metabolism and how it affects plant microbe interactions. He has conducted various research projects in plant synthetic biology and engineering plant metabolic pathways and lectured in corresponding courses. He is currently working as a Product Manager for PCR Biosystems Ltd

Claire Litchfield

As Senior Laboratory Manager at University of Birmingham Enterprise Claire leads the team that runs the incubator laboratories for life science tenant companies at the BioHub Birmingham and Unit 9 MedTech Incubator. She provides specialist support and services enabling companies to get their products and services to market faster and more sustainably than they would do unsupported. The BioHub has recently been awarded Green Impact Laboratory Accreditation (GILA; from SOS-UK). She originally undertook her undergraduate degree in Biological Sciences (Microbiology) at the University of Birmingham (UoB) followed by a PhD in Bacterial Genetics at the University of Leicester during which she demonstrated that Campylobacter jejuni can utilise transferrins as a source of iron. Postdoctoral research followed, including projects at UoB, firstly working on plasmid displacing technology during which she developed a second generation pCURE plasmid to displace antibiotic resistance plasmids from enteric bacteria under the supervision of Prof. Chris Thomas, Scientific Director of UoB spin-out company Plasgene Ltd. Subsequently, Claire was Principal Scientist and Work Package Lead on consultancy, synthetic biology (IUK-funded) and industrial biotechnology (IUK-funded) joint projects between UoB and GSK, before moving full-time into laboratory management. Claire has knowledge of legislation applicable to companies working in the life sciences field, with specific expertise in compliance for work with hazardous micro-organisms and genetically modified organisms. Claire holds an IOSH Managing Safely qualification and a Level 3 Certificate in Leadership and Management from the Institute of Leadership and Management (ILM). For more information about the BioHub Birmingham, University of Birmingham Enterprise and the team, please visit:
https://www.birmingham.ac.uk/collaborate/enterprise/birmingham-research-park/biohub-birmingham

Marjorie Lundgren

Marjorie is a UKRI Future Leaders Fellow and Senior Research Fellow at Lancaster University. After working in environmental consulting (Tetra Tech, Lafayette, California) and plant biotechnology (Mendel Biotechnology, Hayward, California), she earned her PhD in 2015 from the University of Sheffield and gained post-doctorate experience from the University of Sheffield, Massachusetts Institute of Technology, and the Arnold Arboretum of Harvard University. Marjorie applies plant ecophysiology and phylogeographic methods to understand how diverse photosynthetic systems evolve. She is particularly interested in C3-C4 intermediate phenotypes and C2 photosynthesis and leads a C2 photosynthesis crop engineering programme.

Matthew Naish

Matthew Naish is a Broodbank Senior Research Fellow in the Department of Plant Sciences at the University of Cambridge, UK, with research interests in plant genetics and epigenetics. His work focuses on understanding the regulation of centromeres - specialised chromosomal regions essential for accurate chromosome segregation during cell division. After completing a Bachelor's in Natural Sciences at Cambridge, Matthew earned a Master's in Sustainable Agriculture and Food Security from Lancaster University, UK. He completed his PhD at the University of Warwick, UK, under the supervision of Prof. José Gutierrez-Marcos, investigating the epigenetic regulation of developmental reprogramming in plant regeneration. As a postdoctoral Fellow in Prof Ian Henderson's lab at Cambridge, Matthew applied advanced long-read sequencing technologies to study centromere structure and function, including generating the first-ever gapless genome assembly for the model plant Arabidopsis thaliana. In recognition of his contributions to plant science, he was awarded the 2024 *New Phytologist* Tansley Medal for Excellence in Plant Science. He also served as a Scientific Fellow (2020-2022) to the World Economic Forum's Global Futures Council on Nature-based Solutions, contributing to international dialogue on sustainability and the role of natural systems in addressing environmental challenges. In October 2025, he will join the University of Warwick as an Assistant Professor in the School of Life Sciences, where he will establish an independent research group exploring the establishment and regulation of centromeres.

Carl Ng

I completed my BSc (Hons) in Botany, followed by a MSc in Plant Physiology at the National University of Singapore. My PhD research, supervised by Profs. Alistair Hetherington and Martin McAinsh at Lancaster University in the UK, was on calcium signalling in stomatal guard cells, where we were the first to discover sphingosine-1-phosphate in plants, and that it is calcium mobilising second messenger in the ABA signalling pathway in stomatal guard cells. This was followed by a Postdoctoral Fellowship with Prof. Sally Assman on the topic of RNA processing in ABA signalling in stomatal guard cells at Pennsylvania State University, USA. I then answered Ireland's call and started a lectureship at University College Dublin (Ireland's largest public university) where I run my own independent research group. My research interests are pretty broad, ranging from basic to applied, lab-based clean work involving plant cell cultures to getting mucky on farms. My research revolves around (i) plant and crop abiotic stress responses, (ii) sustainable agriculture with a particular focus on nitrogen use efficiency, and (iii) plant secondary metabolism and metabolic engineering. In addition to research, I am also actively involved in teaching (both undergraduates and postgraduates) and university administration (where I was Associate Dean of Science, and also Head of Plant Biology, and Cell and Molecular Biology). I joined the *New Phytologist* family first as an Editorial Advisor, before becoming an Associate Editor, and more recently, an Editor. In 2019, I hosted the New Phytologist Next Generation Scientists Symposium in Dublin, and I have been a mentor for subsequent editions of the Next Generation Symposium.

Mariana Vale

Dr. Mariana M. Vale is a Brazilian ecologist specializing in biodiversity conservation, with a focus on tropical biodiversity, climate change, ecosystem services, and pandemic prevention. She holds a degree in Biology from the Federal University of Rio de Janeiro (UFRJ) and completed her graduate studies in the United States, earning an M.Sc. in Conservation Biology from Columbia University and a Ph.D. in Ecology from Duke University. Since 2010, she has served as an Associate Professor in the Department of Ecology at UFRJ, where she leads a dynamic research group comprising approximately 20 members, including undergraduate and graduate students, as well as postdoctoral researchers. She has contributed to several prominent international scientific initiatives, including the Intergovernmental Panel on Climate Change (IPCC), the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), and the Lancet/PPATS Report on Preventing Viral Spillover. In Brazil, she serves as a scientific advisor to the federal government on climate-related matters, supporting the development of the National Adaptation Plan and the country's official communications to the Climate Convention. At the local level, she plays an active role in environmental governance, participating in protected area councils and serving on the State Environmental Council.

5.1 Plants as models, plants as food: what we’re learning from the phyllosphere microbiome and why it matters

Britt Koskella
University of California, Berkeley, USA

The plant phyllosphere (above ground) microbiome is proving an excellent system in which to probe processes of microbiome assembly, microbial interactions, and host-mediated filtering effects. More recently, it is also becoming clear that these microbial communities serve multiple important functions for their plant hosts. In this talk, I will highlight recent research from the phyllosphere that offers insight to microbiome form and function, and also discuss the importance of thinking beyond one's system and to making sure research makes it beyond the silo in which it might occur.

5.2 Regulatory features determine the evolutionary fate of laterally acquired genes in plants

Catherine Collins
The University of Sheffield, Sheffield, United Kingdom

Lateral gene transfer (LGT) is widespread in eukaryotes, including in animals and plants where it can fuel adaptive evolution and innovation. However, the factors that influence the integration and long-term retention of transferred genes remain poorly understood. The pangenome of the grass *Alloteropsis* has a high turnover of laterally acquired genes, and here we combine expression, methylation and genomic data to identify factors promoting their long-term persistence. Most transferred genes appear to be degenerating, showing lower expression levels and/or greater truncation compared to vertically inherited homologs. These degenerating genes also show significantly higher levels of DNA methylation, potentially indicating transcriptional silencing. The likelihood of a transferred gene being retained will be influenced by how easily it can be expressed in the recipient genome. In *Alloteropsis*, putatively functional laterally acquired genes had expression levels significantly more similar to their donor xenolog than to their vertically inherited homolog. This pattern suggests that transferred genes may carry cis-regulatory elements encoded on the fragment of DNA that moves between species, facilitating their expression in the new genomic context. Evolutionary novelty may also increase the likelihood that selection retains a transferred gene. However, we only found a significant difference in expression level, not sequence divergence, between donor and recipient orthologs associated with successful lateral gene transfers. Overall, our results show that most transferred genes degrade over time. However, those capable of regulating their own expression are more likely to persist and contribute to long-term evolutionary innovation.

5.3 The ecology and evolution of *Nicotiana* section *Suaveolentes*

Charlotte Phillips ORCID iD
University of Portsmouth, Portsmouth, United Kingdom. Royal Botanic Gardens, Kew, London, United Kingdom

Nicotiana section *Suaveolentes* (Solanaceae) contains approximately 80 wild tobacco species, originating in South America 5-6 million years ago. Today, species are found in Australia, some Pacific Islands, and Namibia. This monophyletic group diversified rapidly across Australia in the last 1-2 million years, despite the region's relatively stable climate with some ephemeral, xerophytic species, while others are less arid-adapted perennials. The drivers of this diversification remain unclear.

We hypothesise that closely related taxa occupy similar environmental niches, while distantly related species may occupy divergent ones. However, ecological factors like pollinators or microhabitat differentiation could also influence speciation, leading to divergent niches even among closely related taxa. The group has an allotetraploid origin ($n=24$), with species displaying varying chromosome numbers (reducing to $n=14$), offering a unique system to study the role of chromosomal rearrangement in niche divergence. Concurrently, the insular distributions of some taxa offer insights into gene flow and isolation, plus the section's disjunct distribution.

Using spatial analysis, we quantify environmental niches and investigate divergence versus conservatism in recent speciation. Phylogenetic and population genomic tools illuminate species relationships, species delimitation, gene flow, and distribution patterns, especially in island populations. Our findings contribute to understanding the evolution and ecology of *Suaveolentes,* which may reveal broad macroevolutionary patterns common to other angiosperm groups.

5.4 Evolving with stress: the crucial role of natural antisense transcripts in plant resilience

Jeky Chanwala ORCID iD

Department of Forest Genetics and Plant Physiology, Umeå Plant Science Centre, Swedish University of Agricultural Sciences, Umeå, Sweden

Noncoding DNA regions constitute a substantial portion of eukaryotic genomes, with their transcription playing critical roles in regulating biological processes. Among these, natural antisense transcripts (NATs)—RNA molecules transcribed from the non-template strand of coding DNA—represent an integral yet largely unexplored component of plant genomes. Despite their demonstrated importance, significant knowledge gaps remain in understanding the origins, evolutionary progression, and functional dynamics of NATs. Using interdisciplinary approaches such as molecular phylogenomics and synteny analysis, we uncovered unique genomic distributions of NATs compared to coding genes across various gene families. Notably, transcription factor families exhibited significant variation in NAT abundance, particularly among recently evolved subgroups. Furthermore, differential expression analysis during cold stress underscores the intricate regulatory role of NATs in facilitating environmental adaptation. Moreover, we aim to investigate the promoter regulatory regions to understand the regulatory role of NATs and their contribution to stress adaptation. The findings will redefine the role of noncoding regions in plant genomes, offering novel insights into genome evolution, regulatory networks, and plant resilience. These insights can enable innovative crop engineering strategies to enhance plant resilience, supporting sustainable agriculture and climate change adaptation.

5.6 Science communication session

Chairs: Anna Gardner and Sami Ullah

- Samantha Dobbie, BIFoR Learning and Engagement Lead, University of Birmingham
- Caroline Durbin**,** Research Communications Manager, University of Birmingham
- Anna Gardner, University of Birmingham

Samantha Dobbie

Dr Sam Dobbie is a Learning and Engagement Lead at Birmingham Institute of Forest Research (BIFoR). She is a qualified secondary science teacher with a strong academic background in plant sciences and global challenges. She has experience in translating research outputs into a range of engaging initiatives to widen participation. These include outreach activities, teacher CPD sessions and innovative educational resources for pupils in KS2 to KS5 that are rooted in best practice.

Caroline Durbin

Caroline Durbin is a communications professional with over two decades of experience delivering innovative and impactful campaigns across education, research, publishing, and the arts. As Research Communications Manager at the University of Birmingham's College of Life and Environmental Sciences, she leads strategic efforts to amplify the visibility, reach, and impact of academic research among diverse audiences including policymakers, funders, and the public. Caroline's career has spanned in-house, agency, and consultancy roles, equipping her with a versatile and strategic approach to stakeholder engagement, media relations, and digital communications. Her work focuses on building research reputations, supporting funding bids through targeted communication strategies, and empowering researchers to become confident science communicators. She has held leadership roles in both crisis and campaign communications, and her recent secondment as Head of Communications and Engagement saw her manage high-profile university initiatives around sustainability and infrastructure. Caroline brings a deep understanding of how to translate complex ideas into accessible narratives - making her a passionate advocate for effective and inclusive science communication.

Anna Gardner, University of Birmingham, United Kingdom

Dr Anna Gardner is a tree ecophysiologist with a focus on the effects of elevated atmospheric CO_2 (eCO_2) on plant physiological processes including photosynthesis, respiration, and water-use efficiency. Her research spans both temperate and tropical forests, investigating how climate change alters tree function, particularly in relation to carbon and nitrogen cycling, structural and morphological traits, and ecosystem-level responses. She is particularly interested in synthesising experimental data to inform terrestrial biosphere models and improve projections of forest responses to climate change. Dr Gardner completed her PhD in tree physiology at the University of Birmingham. She went on to a postdoctoral position at the University of Exeter, which took her to Colombia to study the effects of climate warming on tropical montane forests. In 2024, she returned to Birmingham as a research fellow, leading data synthesis for the BIFoR FACE experiment. She has also collaborated closely with EucFACE and AmazonFACE. She is a working member of the CLEANFOREST initiative and academic lead for data management at BIFoR FACE. You can get in touch with Anna at a.gardner.3@bham.ac.uk.

She is part of the local organising committee for New Phytologist next generation scientists 2025.

6.1 Understanding the biosynthesis of starch granules using insights from natural variation

David Seung
John Innes Centre, Norwich, United Kingdom

Despite the fundamental importance of starch to humankind as a major source of calories in our diets, we still do not fully understand how plants make starch. Starch is unique among carbohydrate polymers in that it forms insoluble, semi-crystalline structures called starch granules. While the synthesis of the starch polymers is relatively well understood, we are only beginning to understand how starch granule formation is initiated, and how granule size and shape are determined. Cereal grains such as wheat, rice, and maize contain starch granules with remarkably different morphologies. We have discovered two major factors that underpin this variation. Firstly, we discovered specific proteins that control the initiation of starch granules, which are distinct from the proteins that synthesise the starch polymers. This includes the enzymes starch synthase 4 and plastidial glucan phosphorylase, and their numerous non-catalytic protein interaction partners. Differences in the expression patterns of granule initiation proteins and their protein interactions between species lead to distinct spatio-temporal patterns of granule initiation, which in turn lead to distinct granule morphologies. Secondly, interspecies variation in the morphology, structure and dynamics of the amyloplast, the organelles in which starch granules are produced, plays a major role in creating distinct granule shapes. Disruption of amyloplast structure by mutating components of plastid division can greatly alter the size and shape of starch granules. Our findings advance the understanding of starch granule formation in plants, and using this knowledge, we can now manipulate granule size and shape in wheat to resemble the morphologies found in other crops. This has major implications for improving the nutritional and functional qualities of starch.

6.2 An isoaspartate-induced impairment of OsHSFC1b transactivation negatively impacts seed vigour, seed weight and size in rice

Rakesh Kumar Achary ORCID iD
National Institute of Plant Genome Research, New Delhi, India

Plants optimize seed size, weight, vigour, and various other features during seed development, which are important for successful propagation and establishment for human use. However, how plants achieve and maintain these seed traits is still elusive. Our study reveals that the rice Heat Shock Transcription Factor OsHSFC1b is highly expressed in the embryo and during the later stage of seed development. Through overexpression and gene editing approach, we found that *OsHSFC1b* not only plays a significant role in preserving seed vigour and longevity by activating various genes participating in protection mechanisms but also regulates seed size and weight by modulating auxin biosynthesis, endosperm development, and seed filling. Furthermore, the function of OsHSFC1b is compromised due to isoaspartyl modification in seeds particularly during seed storage and upon aging. Our MS/MS analyses confirm isoaspartyl modification in the asparagine residues near the DNA-binding domain and nuclear localization sequence of OsHSFC1b, which adversely affects OsHSFC1b's transactivation activity. However, PROTEIN L-ISOASPARTYL METHYLTRANSFERASE, interacts and repairs this isoaspartyl-mediated damage and facilitates the function of OsHSFC1b. Taken together, our study uncovers how isoaspartyl damage dampens the transactivation prowess of OsHSFC1b, yet the intervention of PIMT not only repairs but also elevates agronomically important seed traits.

6.3 Sweet shaping of root system architecture under water deficit

Dhriti Singh ORCID iD
Umeå Plant Science Centre, Umeå, Sweden

Root growth direction under water-deficit conditions is critical for plant survival. We used increased agar concentration in the growth medium to simulate stress conditions, limiting water availability. Our study highlights the role of glucose (Glc) in orchestrating the root growth deviation under stress conditions. We demonstrate that Glc-TOR signaling plays a central role in modulating root growth direction under stress conditions. Furthermore, our findings reveal that cytokinin signaling is instrumental in promoting root straightening during dehydration stress. The interplay between Glc-TOR and cytokinin signaling pathways fine-tunes root orientation by modulating auxin transport and signaling. Experiments with the horizontal growth conditions with Arabidopsis further support the role of Glc-TOR signaling in the regulation of root system architecture in stress conditions. Collectively, our findings reveal that Glc-induced changes in root architecture are mediated by downstream cytokinin and auxin pathways, contributing to enhanced root plasticity and improved adaptation to water-limited conditions.

6.4 The pace of life: effects of circadian clock speed on plant growth and development

Danny Ginzburg ORCID iD
University of Cambridge, Cambridge, United Kingdom

Endogenous circadian rhythms underpin plant growth and development and confer growth benefits when aligned with environmental rhythms. Despite a constant 24-hour period of daily rhythms in the environment, natural variation exists in plant circadian clock speed. Recent evidence suggests that variation in clock speed might be an adaptation to daily variations in light intensity.

We evaluated whether variation in clock speed influences relative utilization of daily light exposure by subjecting plants to time-restricted photosynthesis. By restricting photosynthetic growth to either the first or second half of the day, we observed a linear relationship between clock speed and relative utilization of daily light exposure.

These findings provide novel insights into how plant circadian oscillators regulate growth and provide opportunities for fine-tuning controlled-environment growth conditions to optimize radiation use efficiency.

6.5 Effects of m6A loss on immunity and polyadenylation in *Arabidopsis thaliana*

Carey Metheringham ORCID iD
University of Dundee, Dundee, United Kingdom

RNA modifications are critical for distinguishing self from non-self in humans, with implications for immunity and development. In humans, mRNA modifications, such as N6-methyladenosine (m6A), are essential for modulating immune responses and central to mRNA therapeutic advancements. Similarly, in *Arabidopsis*, m6A modifications mediated by the mRNA writer complex (including VIRILIZER) are vital for viability, with loss-of-function mutations causing severe and often lethal developmental defects.

We investigated the role of m6A in *Arabidopsis* and discovered that disrupting the writer complex produces a temperature-sensitive autoimmune phenotype. Mutants exhibit increased basal resistance to pathogens, heightened cell death, and immune gene dysregulation, suppressed at elevated temperatures. In contrast, the developmental defects in these mutants are not temperature-sensitive, indicating separable impacts of m6A loss on autoimmunity and development.

Alongside the autoimmune response, we observe temperature-sensitive changes to poly(A) tail length distributions in writer mutants. These changes were not restricted to genes with predicted m6A modification, suggesting global disruption in poly(A) processing which could be a result of, or lead to, the autoimmune response.

These findings highlight m6A as a critical regulator of immune homeostasis in plants, and indicate a possible connection between m6A modification, poly(A) tail length and autoimmune response.

6.6 Photosynthetic and Antioxidant Responses to Phosphorus Fertilization in Drought-Stressed Common Beech and Sessile Oak from Different Provenances

Antonia Vukmirović ORCID iD
University of Zagreb Faculty of Forestry and Wood Technology, Zagreb, Croatia

Drought stress significantly impacts forest tree physiology, disrupting photosynthesis and increasing oxidative stress. During drought, stomatal closure limits CO_2 uptake, reducing photosynthetic efficiency. This results in an accumulation of excess energy, which is redirected to produce reactive oxygen species (ROS). This study investigated the effects of drought on photosynthetic performance, chlorophyll content, and antioxidant defenses in common beech (*Fagus sylvatica* L.) and sessile oak (*Quercus petraea* (Matt.) Liebl.) saplings, and examined how phosphorus (P) fertilization affects these processes. Drought reduced chlorophyll *a*+*b* concentrations, with a more pronounced decrease in oak, indicating impaired photosynthesis. Additionally, drought-induced oxidative stress resulted in increased malondialdehyde (MDA) concentrations, indicating lipid peroxidation. Antioxidant enzymes, including superoxide dismutase (SOD), catalase (CAT), peroxidase (POD), and ascorbate peroxidase (APX), were activated to mitigate ROS damage, although phosphorus fertilization had mixed effects. While P did not significantly improve chlorophyll content, it enhanced CAT activity in oak and APX activity in both species, especially under drought conditions. Provenance differences were observed, with oak from drier habitats exhibiting better photosynthetic performance and oxidative stress management. This study highlights the interconnected roles of photosynthesis, antioxidant defenses, and phosphorus in mitigating drought stress, providing insights into improving drought tolerance in forest trees.

6.7 A trait spectrum for ectomycorrhizal fungi - how could it improve understanding of plant-soil interactions in forests?

Karolina Jörgensen ORCID iD
Swedish University of Agricultural Sciences, Uppsala, Sweden

Trait spectra have been used in various branches of ecology to explain and predict patters of species distributions. Several categorical and continuous traits have been proposed as relevant for ectomycorrhizal fungi, but a spectrum that unifies co-varying traits remains to be established and tested.

In this presentation, I propose a nutrient acquisition spectrum for ectomycorrhizal fungi, which encompasses several morphological, physiological and metabolic traits. The trait spectrum is linked to the concept of apparent carbon use efficiency and resolves the contradiction that species with high supply of host C can maintain nitrogen transfer despite building large mycelial biomass. Ectomycorrhizal fungal species would be distributed along this spectrum, with lifestyles ranging from “absorbers” with a niche in high productive forests with high availability of soluble N to “miners”, focused on exploitation of organic matter in forests with low N availability.

This spectrum highlights that ectomycorrhizal have different function, and that their relationship to their host is not simply altruistic. Instead, the outcome of the symbiotic relationship, in regards to nutrient delivery, species composition and nutrient cycling, is regulated by feedbacks between fungi and the plant.

6.8 How plastic is the seed microbiome?

Expedito Olimi ORCID iD
Southampton University, Southampton, United Kingdom

The seed microbiome was shown to have implications for plant health. Yet, there is limited knowledge regarding the factors influencing the composition and assembly of the seed microbiome, particularly in nutritionally and economically important crops like tomato (*Solanum lycopersicon*). In a large seed microbiome dataset involving 100 tomato cultivars, we examine host and environmental factors influencing the seed microbiome structure. By using predictive models, the influence on the seed microbiome of plant traits, like insect resistance, yield, seed weight, number of ovaries, berry colour, berry taste, e.tc were explored. We hypothesized that the heterogenous genetic background of tomatoes reflects on its seed microbiome, and that it is dependent on the region of production as well as certain host traits. We detected high effective bacterial diversity in the range 20 to 150 amplicon sequence variants (ASVs); with host genetics, more than geographic region of tomato production contributing towards shaping the tomato seed bacterial community (R^2=56% vs. 11%). Our study highlights the crucial role of plant genetics in shaping the seed bacterial community, uncovers the plasticity of the seed microbiome, and provides a basis for seed microbiome engineering approaches.

6.9 Panel Discussion – Model-data integration

Chair: Richard Norby, *New Phytologist* Editor

- Enimhien Akhabue, University of Exeter
- Richard Betts, University of Exeter and Met Office
- Anna Gardner, University of Birmingham
- Shomari Healy, University of Birmingham
- Maxim Kapralov, Newcastle University
- Keith Lindsey, Durham University
- Anja Rammig, Technical University of Munich

Richard Norby

Richard Norby is an ecosystem ecologist interested in the Effects of CO2 enrichment on tree growth and forest metabolism - Ecosystem responses to atmospheric and climatic change - Carbon and nitrogen cycling in diverse ecosystems - Forest tree physiology and plant physiological ecology - Synthesis of experimental results to inform models He is an Emeritus Research Fellow in the Environmental Sciences Division & Climate Change Science Institute, Oak Ridge National Laboratory; Honorary Professor at the School of Geography, Earth and Environmental Sciences University of Birmingham; and Research Professor in the Department of Ecology & Evolutionary Biology, University of Tennessee' and an Editor of *New Phytologist.*

Enimhien Akhabue

Enimhien is an Oppenheimer-Turvil Doctoral Scholar in the Department of Geography (Physical) at the University of Exeter. She is part of the Oppenheimer Programme in African Landscape Systems (OPALS). Enimhien holds a BSc in Forestry and Wildlife Management from the University of Port Harcourt, Nigeria, where she focused on forest soils and forest trees. She also earned an MSc in Silviculture and Forest Biology from the same university, with her master's thesis assessing the above-ground carbon stock and soil properties of an arboretum in Nigeria.
Her current research explores the dynamics of African landscapes through the use of the Joint UK Land Environment Simulator (JULES) Land Surface Model. She aims to improve the model's ability to simulate these landscapes more accurately, offering valuable insights for decision-makers across the continent.

Richard Betts

Professor Richard Betts MBE is Head of Climate Impacts Research at the Met Office Hadley Centre and University of Exeter. He has worked in climate modelling since 1992, specialising in the role of land ecosystems in the climate system, particularly the risk of a tipping point in the Amazon. He has been a Lead Author on three IPCC Assessment Reports and led the Technical Report for the 3rd UK Climate Change Risk Assessment. He is currently serving as Expert Advisor to the UK's Climate Change Committee for the 4th risk assessment. In 2019 he was appointed as an MBE in the Queen's Birthday Honours list, for services to understanding climate change. He is co-lead of the UK research within the AmazonFACE programme.

Anna Gardner

Dr Anna Gardner is a tree ecophysiologist with a focus on the effects of elevated atmospheric CO_2 (eCO_2) on plant physiological processes including photosynthesis, respiration, and water-use efficiency. Her research spans both temperate and tropical forests, investigating how climate change alters tree function, particularly in relation to carbon and nitrogen cycling, structural and morphological traits, and ecosystem-level responses. She is particularly interested in synthesising experimental data to inform terrestrial biosphere models and improve projections of forest responses to climate change. Dr Gardner completed her PhD in tree physiology at the University of Birmingham. She went on to a postdoctoral position at the University of Exeter, which took her to Colombia to study the effects of climate warming on tropical montane forests. In 2024, she returned to Birmingham as a research fellow, leading data synthesis for the BIFoR FACE experiment. She has also collaborated closely with EucFACE and AmazonFACE. She is a working member of the CLEANFOREST initiative and academic lead for data management at BIFoR FACE. You can get in touch with Anna at a.gardner.3@bham.ac.uk. She is part of the local organising committee for New Phytologist next generation scientists 2025.

Shomari Healy

I am currently pursuing my PhD in Environmental Science at the University of Birmingham. My thesis focuses on modelling the response of temperate forests to elevated CO2 and climate change using the BIFoR FACE experiment at the University of Birmingham (one of the largest climate change experiments in the world). I currently hold an MSc in Environmental Science and a BSc in Physical Geography from the University of Liverpool and have many broad interests and ambitions within the field of environmental science. Some of these include using drones for remote sensing and data collection within the field, understanding urban air quality and pollution, and understanding forests (tropical and temperate) under changing environmental and climatic conditions.

Maxim Kapralov

My fascination with plants started when I was an undergraduate student doing my first research project on evolution of C4 photosynthesis in succulent plants from deserts of the Central Asia under the supervision of Professors Vladimir Pyankov (USU) and Gerald Edwards (WSU). This work was very formative and enforced my enthusiasm for plant science and photosynthesis research. My PhD on plant genetics led to a postdoctoral research on plant molecular evolution in Prof. Dmitry Filatov’s lab (Oxford) where I began developing my independent research vision to combine evolutionary analysis with my background in photosynthesis and apply this to the evolution of Rubisco. In 2013, following presentation at 2011 Gordon conference on CO2 Assimilation in Plants, I was invited by Prof. Spencer Whitney to work in his lab at Australian National University within the Gates funded project 'RIPE: Realizing Increased Photosynthetic Efficiency for sustainable increases in crop yield'. Using chloroplast transformation in plants I showed current limitations of interspecies Rubisco translocation and how they could be overcome by co-expressing cognate Rubisco chaperones. Working with RIPE made me aware of global challenges in food security and how they could be addressed. In 2015 I returned to the UK to establish my own lab first at Liverpool John Moores University, and from 2017 at Newcastle University. Currently, we deploy classic molecular lab techniques, variety of DNA sequencing methods, and new computational tools such as machine learning to address fundamental aspects of enzyme evolution in photosynthetic organisms with the ultimate aim to improve photosynthesis and yield in crops via bioengineering solutions.

Keith Lindsey

For my first degree I read Botany at St. Catherine's College Oxford, and undertook a PhD at Edinburgh University. I carried out post-doc work in Edinburgh and then Rothamsted, before taking up a position as leader of the Plant Molecular Genetics Group at the Leicester Biocentre, and a lectureship at Leicester University (1989). I moved to a Chair in Durham in 1996. I am an Editor of the journal *New Phytologist* and Chair of the Board of Trustees for the New Phytologist Foundation. I was until recently a member of BBSRC Council, the body that determines policy, priorities and strategy for BBSRC; Chair of BBSRC Appointments Board; and a member of the Defra Advisory Committee on Releases to the Environment (ACRE), which advises Government Ministers on GM and related issues. I am former President and Chair of Council of the Society for Experimental Biology.

Anja Rammig

I am a professor for Land Surface-Atmosphere Interactions working on dynamic vegetation modelling and observational data, and I am particularly interested in model-data integration

Keynote speaker, Mentor and Organising committee bios

Amy Austin, University of Buenos Aires,
***New Phytologist* Editor, Argentina**

Amy completed her undergraduate degree in Environmental Sciences at Willamette University in 1988 and her PhD in Biological Sciences at Stanford University in 1997. Her doctoral thesis was based in Hawaii, examining controls of water availability on carbon and nutrient cycles in native forest ecosystems. A National Science Foundation (USA) postdoctoral fellowship took her to Argentina, where she began focusing on terrestrial ecosystem ecology in the Patagonian region of southern South America. She began work as a research scientist in the Scientific Research Council of Argentina (CONICET) and also joined the faculty at the College of Agronomy at the University of Buenos Aires. She is an editor at *New Phytologist* and a senior editor at the Journal of Ecology. In 2018, Amy was awarded the L'Oréal–UNESCO Award For Women in Science for Latin America.

Carlos Ballaré, Universidad de Buenos Aires and
CONICET, *New Phytologist,* Editor Argentina

Carlos L. Ballaré is professor of plant biology at the University of Buenos Aires and San Martín National University (Buenos Aires, Argentina), and a senior scientist with the National Research Council of Argentina (CONICET). He completed his MSc and PhD degrees at the University of Buenos Aires and at Oregon State University (USA), respectively, and was a postdoctoral scholar at Utah State University (USA). His laboratory has conducted pioneering research on the role of photoreceptors in regulating plant responses to the proximity of neighbors, and on the effects of ultraviolet radiation on plants and terrestrial ecosystems. The Ballaré lab uses a combination of genetic, physiological, and genomic and biochemical tools to understand the mechanisms by which photoreceptors regulate plant immunity against pathogens and herbivores. Carlos has received several awards including the recognition as one of the 50 Latin American leaders for the New Millennium by CNN and Time (1990), a Guggenheim Fellowship (2001), the Konex Merit Prize in 2013, awarded by the Konex Foundation (Argentina), and the Georg Forster Research Award from the Alexander von Humboldt Foundation (Germany) in 2017 and was elected to the National Academy of Exact, Physical and Natural Sciences of Argentina in 2021. Carlos has served on the editorial boards of several leading journals in the fields of plant biology and ecology, including Plant Physiology (2000-2005), *New Phytologist* (2017--) and Oecologia (2015--), where he is currently one of the Editors-in-Chief. As part of his outreach activity, Carlos has been a member of the

Environmental Effects Assessment Panel of the United Nations Environment Programme, between 2002 and 2019

Anjan Banerjee, IISER Pune, India

Anjan is the Rahul Bajan Chair Professor in the Biology Division of the Indian Institute of Science Education and Research (IISER Pune). He is a Fellow (FNA) of the Indian National Academy of Science, New Delhi. His research interest include Plant developmental biology, Micro RNA (miRNA) and gene regulation, Long distance signalling and plant-pathogen interaction

Adesola Bello

Dr Adesola Bello is a Research Development Officer within the Research Strategy and Services Division (RSSD) at the University of Birmingham. In her role, she provides specialist advice and tailored support to academics/researchers at all career stages to help secure external funding for their research projects. She works with internal and external researchers planning to undertake their research in the School of Biosciences through the pre-award process and helps them to develop their idea into a proposal, identify suitable funding for their projects, prepare their funding applications ensuring compliance with funder requirements, determine what their budgetary/costing needs are, conduct due diligence checks on potential collaborations, facilitate timely and quality bid submissions to funders, negotiate research agreements and set up successful awards before handing over to the post-award teams who help manage the live grants. Prior to joining RSSD, Adesola was a postdoctoral researcher at Imperial College London where she specialised in using metabolomics-based approaches to investigate the interplay between host metabolism, nutrition, and the gut microbiota.

Yoselin Benitez-Alfonso, University of Leeds, *New Phytologist* Advisor United Kingdom

Dr. Yoselin Benitez-Alfonso is Professor in Interdisciplinary Plant Sciences at the University of Leeds (UK). She was born in Cuba and graduated in Chemistry at the University of Cordoba, Spain. Yoselin did her PhD in plant biochemistry and molecular biology followed by postdoctoral research at Cold Spring Harbor Laboratory in New York (USA) and at the John Innes Centre (Norwich, UK). In 2017, she was appointed Lecturer at the University of Leeds, where she secured multiple funding including a UKRI Future Leaders *Fellowship*. Yoselin research group focuses on cell walls properties surrounding plant intercellular channels (named plasmodesmata) with the goal to unlock knowledge for the development of new strategies for crop improvement and biomaterial development. Yoselin's interdisciplinary research is supported by several networks and virtual centers including the NSF- funded 'Plant Cell Atlas network', the Astbury Centre for Structural Biology and the Bragg Centre for Material Research. She advocates for equity, diversity and inclusion and last year, co-founded the Black in Plant Science Network (https://blackinplantscience.org/) dedicated to connect, celebrate and cultivate the next generation of plant scientists in UK. Yoselin was promoted to full Professor last year, becoming the 66th Black Female Professor in the UK. She received the 'Education and Academic Leader of the Year' Forward Ladies award and the UKRI Impact Award for 'Advancing Research Culture'. For more details on Yoselin's research and the team, visit https://benitezalfonsolab.leeds.ac.uk/ or https://astbury.leeds.ac.uk/people/yoselin-benitez-alfonso/. You can contact Yoselin at Y.Benitez-Alfonso@leeds.ac.uk or in social media at Twitter/X @YoselinBenAlf bluesky and LinkedIn. Yoselin is an incoming member of The New Phytologist Foundation's board of Trustees.

Richard Betts, University of Exeter and Met Office, United Kingdom

Professor Richard Betts MBE is Head of Climate Impacts Research at the Met Office Hadley Centre and University of Exeter. He has worked in climate modelling since 1992, specialising in the role of land ecosystems in the climate system, particularly the risk of a tipping point in the Amazon. He has been a Lead Author on three IPCC Assessment Reports and led the Technical Report for the 3rd UK Climate Change Risk Assessment. He is currently serving as Expert Advisor to the UK's Climate Change Committee for the 4th risk assessment. In 2019 he was appointed as an MBE in the Queen's Birthday Honours list, for services to understanding climate change. He is co-lead of the UK research within the AmazonFACE programme.

Philippa Borrill, John Innes Centre, *New Phytologist* Advisor, United Kingdom

Dr Philippa Borrill is a Group Leader in the Department of Crop Genetics at the John Innes Centre. Her research investigates the mechanisms controlling functional redundancy between gene copies in polyploid wheat. She seeks to apply this knowledge in crop improvement, particularly to enhance grain nutrient content. Philippa studied Natural Sciences at the University of Cambridge and obtained her PhD from the John Innes Centre in 2014. From 2015 she held a BBSRC Anniversary Future Leader Fellowship at the John Innes Centre and developed a series of key resources for wheat genomics including a gene expression atlas (www.wheat-expression.com) which been used by over 45,000 people globally. In 2018 Philippa joined the University of Birmingham as a Lecturer (Assistant Professor) in Plant Biology. She returned to the John Innes Centre as a Group Leader in 2021. Philippa's work on wheat genetics and genomics has been recognised by awards such as the *New Phytologist* 2019 Tansley Medal for Excellence in Plant Science and the Society for Experimental Biology 2022 Plant President's Medal. Philippa is committed to making wheat research accessible to other scientists, industry and the general public. She has organised multiple training workshops in wheat bioinformatics and co-developed a wheat training website (www.wheat-training.com). Philippa was elected to Chair the Monogram (UK small grain cereals) network from 2021-2023 and collaborates with several wheat breeding companies.

Claire Butler, University of Birmingham, United Kingdom

Claire joined the University of Birmingham (UoB) in 2018 as a Senior Research Facilitator primarily supporting the development of research proposals in the Institutes of Immunology and Immunotherapy (III) and Microbiology and Infection (IMI) and more recently the School of Dentistry. As part of this role she worked closely with early career researchers on their first funding applications, identify suitable funding streams and develop successful applications. She now leads the research support team for the new School of Infection, Immunology and Inflammation delivering on ambitious research income targets and a complex research contract portfolio. Prior to joining UoB, Claire worked at the University of Oxford in a variety of research support roles developing research programmes locally, nationally and globally in a number of research fields including oncology, haematology, rare diseases, inflammation and the gut microbiome. Before working in research support services, Claire was a postdoctoral researcher investigating host-parasite interactions.

Samantha Dobbie, University of Birmingham, United Kingdom

Dr Sam Dobbie is a Learning and Engagement Lead at Birmingham Institute of Forest Research (BIFoR). She is a qualified secondary science teacher with a strong academic background in plant sciences and global challenges. She has experience in translating research outputs into a range of engaging initiatives to widen participation. These include outreach activities, teacher CPD sessions and innovative educational resources for pupils in KS2 to KS5 that are rooted in best practice.

Caroline Durbin, University of Birmingham, United Kingdom

Caroline Durbin is a communications professional with over two decades of experience delivering innovative and impactful campaigns across education, research, publishing, and the arts. As Research Communications Manager at the University of Birmingham's College of Life and Environmental Sciences, she leads strategic efforts to amplify the visibility, reach, and impact of academic research among diverse audiences including policymakers, funders, and the public. Caroline's career has spanned in-house, agency, and consultancy roles, equipping her with a versatile and strategic approach to stakeholder engagement, media relations, and digital communications. Her work focuses on building research reputations, supporting funding bids through targeted communication strategies, and empowering researchers to become confident science communicators. She has held leadership roles in both crisis and campaign communications, and her recent secondment as Head of Communications and Engagement saw her manage high-profile university initiatives around sustainability and infrastructure. Caroline brings a deep understanding of how to translate complex ideas into accessible narratives - making her a passionate advocate for effective and inclusive science communication.

Maria Ermakova, Monash University, Australia

Dr Maria Ermakova is a Group Leader in the School of Biological Sciences at Monash University, Australia. Maria is interested in unravelling molecular mechanisms and metabolic limitations of photosynthesis to engineer plants with enhanced photosynthesis and growth. She received a PhD from University of Turku, Finland, where she discovered novel photoprotective pathways safeguarding photosynthesis and nitrogen fixation in cyanobacteria. Following her doctoral studies, Maria conducted postdoctoral research within the Centre of Excellence for Translational Photosynthesis and the C4 Rice Project at the Australian National University. Her research has paved the way to genetically re-design plants for improved photosynthesis and productivity, and she was awarded with the Peter Goldacre medal from the Australian Society of Plant Scientists. Maria's research group at Monash University aims to genetically engineer energy-efficient crops that are better equipped to thrive in future climates using biotechnological approaches and synthetic biology tools.

Katie Field, University of Sheffield, *Plants, People Planet* Deputy Editor-in-Chief, United Kingdom

Katie Field is a Professor of Plant-Soil Processes at the University of Sheffield, specializing in the interactions between plants and fungi, particularly mycorrhizal symbioses. Her research explores how these interactions influence plant physiology, ecosystem function, and responses to environmental change. She also investigates the role of symbiotic fungi in plant terrestrialization and sustainable agriculture. Katie is Deputy Editor-in-Chief of *Plants, People, Planet*.

Christine Foyer, University of Birmingham, United Kingdom

Christine H. Foyer is Professor of Plant Sciences at the University of Birmingham. She is also an Adjunct Professor at the University of Delhi, India and an Extraordinary Professor in Genetics, University of Stellenbosch, South Africa. She recently received the Sustained Excellence Award from the Biochemical Society (UK). She is a Member of the Annals of Botany Company, the Editor in Chief of Plant, Cell and Environment and the Publications Officer for the Association of Applied Biologists. She is a Highly Cited Researcher (2024), ranking in the top 1% by citations for the field. In the Category of Plant Science and Agronomy she is ranked #8 in the world ranking and #1 in United Kingdom. In the Best Female Scientist category she is ranked 224th in the world, 15th in the UK: https://research.com/u/christine-h-foyer. Christine is an expert in plant biochemistry and metabolism. With a strong focus on reduction/oxidation (redox) processes and signals that regulate plant growth and stress tolerance, her lab studies how primary processes such as photosynthesis regulate plant, growth development and defence, particularly through effects on the redox status of cells and cell signalling under optimal and stress conditions. Using model (Arabidopsis), crop plants and trees, her lab investigates the responses of photosynthesis and associated processes to abiotic stresses including elevated carbon dioxide. She is part of the local organising committee for New Phytologist next generation scientists 2025.

Noni Franklin-Tong, University of Birmingham, United Kingdom

Vernonica (Noni) Franklin-Tong FRS is emeritus Professor at the University of Birmingham. She was educated in Suffolk and then at the University of Birmingham. Most of her career has been based at Birmingham. She is recognized at an international level for her work on self-incompatibility, cell-cell signalling and programmed cell death. In 2021 she was elected a Fellow of the Royal Society. Noni is renowned for her studies on self-incompatibility (SI). She has devoted her career to investigating cellular mechanisms involved in the regulation of the cell-cell recognition system of SI in *Papaver rhoeas* (the Field Poppy). Sexual reproduction in higher plants involves pollination, involving specific interactions between pollen and pistil. A key mechanism to prevent inbreeding is self-incompatibility (SI), which is a controlled by a single, multi-allelic S-locus. Incompatible ("self") pollen is rejected, and compatible ("non-self") pollen is allowed to fertilize the plant. SI was discovered by Darwin and plays a decisive role in determining plant reproductive success by preventing inbreeding.

Regulation of pollination has high importance in relation to its impact on food security. Noni initiated pioneering cell and molecular research of Papaver SI. Her development of an in vitro bioassay allowed investigation of the cell biology of SI for the first time. This outstanding model system enabled elucidation of mechanisms responsible for rejection of incompatible pollen. Her studies have uncovered an intricate intracellular signalling network and revolutionized our understanding of the signals, downstream targets and key cellular processes that regulate SI, revealing new phenomena critical to this process, culminating in programmed cell death. Her lab achieved the first functional trans-genera transfer of a SI system using the Papaver S-determinants. This has implications for translational work; longer-term this may aid the quest to make F1 hybrids in some crops more easily.

Constantine Garagounis, PCR Biosystems Ltd., United Kingdom

Dr. Constantine Garagounis studied Biochemistry and Biotechnology and has a DPhil in Plant Sciences from the University of Oxford. He worked as a post-doctoral researcher and contract lecturer on plant secondary metabolism and how it affects plant microbe interactions. He has conducted various research projects in plant synthetic biology and engineering plant metabolic pathways and lectured in corresponding courses. He is currently working as a Product Manager for PCR Biosystems Ltd

Anna Gardner, University of Birmingham, United Kingdom

Dr Anna Gardner is a tree ecophysiologist with a focus on the effects of elevated atmospheric CO_2 (eCO_2) on plant physiological processes including photosynthesis, respiration, and water-use efficiency. Her research spans both temperate and tropical forests, investigating how climate change alters tree function, particularly in relation to carbon and nitrogen cycling, structural and morphological traits, and ecosystem-level responses. She is particularly interested in synthesising experimental data to inform terrestrial biosphere models and improve projections of forest responses to climate change. Dr Gardner completed her PhD in tree physiology at the University of Birmingham. She went on to a postdoctoral position at the University of Exeter, which took her to Colombia to study the effects of climate warming on tropical montane forests. In 2024, she returned to Birmingham as a research fellow, leading data synthesis for the BIFoR FACE experiment. She has also collaborated closely with EucFACE and AmazonFACE. She is a working member of the CLEANFOREST initiative and academic lead for data management at BIFoR FACE. You can get in touch with Anna at a.gardner.3@bham.ac.uk. She is part of the local organising committee for New Phytologist next generation scientists 2025.

Alice Gauthey, University of Birmingham, United Kingdom

Dr. Alice Gauthey is a plant ecophysiologist at the University of Birmingham (UoB). She joined the Birmingham Institute of Forest Research at UoB as a Royal Society Newton Internation Fellow in 2024. She completed her PhD from Western Sydney University in Australia, followed by a postdoc at EPFL in Switzerland. Her research aims to investigate how climate change affect trees functioning. She is particularly interested in the complex interactions of extreme weather events, such as drought and heatwaves, and elevated carbon dioxide, and how these factors impact tree physiological responses and growth.

Sarah Gibbons, The New Phytologist Foundation, United Kingdom

Sarah joined the Foundation in 2014. She is responsible for the production of *New Phytologist* manuscripts after acceptance by Editors. She works closely with other members of the Central Office team including Helen, Lauren, Ruth and Jenny. Sarah leads on production quality control, both before and after article publication. Sarah selects images for journal front covers and devises the format/layout. Sarah also plays an active role in other Central Office activities, such as representing the Foundation at conferences and symposia.

Dan Gibbs, University of Birmingham, United Kingdom

Daniel is the Plant Science and Food Security theme lead, Deputy Head of Research in the school of Biosciences and Chair of the UoB BBSRC Strategy Group. He is the Gatsby plant science mentor at UoB, a handing editor at the Journal of Experimental Botany, and was recently appointed as a member of BBSRC Research Committee E, following a 4-year stint on Research Committee B. He is part of the Local organising committee for New Phytologist next generation scientists 2025.

Julie Gray, University of Sheffield, *New Phytologist,* Editor, United Kingdom

Julie Gray is interested in plant responses to climate stress, and how to alleviate future heat and drought stress in crops. Her research group in Sheffield have manipulated the expression of genes to create barley, wheat and rice varieties with fewer stomata that have improved drought tolerance and reduced water requirements. Their work on wheat is included in the UK Science Museum's Future of Food exhibition, and their rice findings featured in a BBC World documentary. Julie studied Biochemistry at Liverpool University and was a PhD student at Nottingham University where she researched genes that control fruit ripening. These findings contributed to the development of the first genetically modified and gene edited foods to be commercialised.

Grace Handy, University of Birmingham, United Kingdom

Grace is a final year PhD student based at the University of Birmingham. Her research interests include ecosystem responses to global change, in particular the effects of CO2 enrichment on tree growth and forest system structure and function. Her PhD research is based at the Birmingham Institute of Forest Research Free Air CO2 Enrichment experiment (BIFoR) at the University of Birmingham, where she looks at the effect of elevated CO2 on the root systems of the mature forest. Grace also has experience testing the application of AI image-processing tools for data collection in ecological studies. She is part of the local organising committee for New Phytologist next generation scientists 2025.

Alistair Hetherington, University of Bristol, *New Phytologist* Editor, United Kingdom

Alistair Hetherington is Melville Wills Professor of Botany, Emeritus at the University of Bristol where he also holds a Leverhulme Trust Emeritus Fellowship. He is a graduate of the University of St Andrews and worked at the Universities of Edinburgh and Lancaster before moving to Bristol. His research has centred on cellular and molecular aspects of stomatal function and development, with a current focus on stomatal evolution. He also has an ongoing collaboration with colleagues in Sri Lanka aimed at improving the resilience of tea to environment change. He was editor in Chief of New

Phytologist for 12 years stepping down at the end of 2024 and is now Forum Editor. He initiated the New Phytologist next generation scientist series of meetings. He is currently Chair of the UK BBSRC Fellowships Committee.

Hanna Hõrak, University of Tartu, *New Phytologist* Advisor, Estonia

Hanna Hõrak defended her PhD on the molecular mechanisms of stomatal carbon dioxide signaling in 2017 in the University of Tartu. She then completed a postdoctoral project in the lab of prof. Julie Gray in the University of Sheffield, UK on stomatal development and pathogen responses; and another in the Estonian University of Life Sciences on plant stress physiology. In 2020, Hanna started an independent research group in the Institute of Technology, University of Tartu, Estonia. Her work is focused on stomatal patterning and physiology with the aim to understand, how environmental and hormonal signals regulate stomatal development and how different stomatal patterns affect photosynthesis, plant growth, water use efficiency, and yield. Hanna's work is mostly focused on the Arabidopsis model but her interests also encompass ancient land plants and agriculturally important species such as tomato, potato, and cereal crops.

Jonathan Ingram, John Wiley & Sons Ltd, United Kingdom

Jonathan works at Wiley as Editor in Chief for the journals *Plant-Environment Interactions* and *Food and Energy Security* (both gold OA); he is also a Senior Editor for Ecology and Evolution. This means handling manuscripts and working with editors across a wide subject range, and developing these journals through outreach and commissioning. Previously he managed an evolving portfolio of titles at Wiley, including on behalf of external societies, focused on plant and environmental sciences. Jonathan started his publishing career with Elsevier at *Trends in Plant Science*, before moving to *New Phytologist* as managing editor and, later, *Journal of Experimental Botany* with a focus on commissioning and development. His research background is drought tolerance, focusing on CAM in his DPhil at Oxford and resurrection plants (sugar metabolism) in postdoctoral work at the Max Planck Institute in Cologne.

Maxim Kapralov, Newcastle University, United Kingdom

My fascination with plants started when I was an undergraduate student doing my first research project on evolution of C4 photosynthesis in succulent plants from deserts of the Central Asia under the supervision of Professors Vladimir Pyankov (USU) and Gerald Edwards (WSU). This work was very formative and enforced my enthusiasm for plant science and photosynthesis research. My PhD on plant genetics led to a postdoctoral research on plant molecular evolution in Prof. Dmitry Filatov's lab (Oxford) where I began developing my independent research vision to combine evolutionary analysis with my background in photosynthesis and apply this to the evolution of Rubisco. In 2013, following presentation at 2011 Gordon conference on CO2 Assimilation in Plants, I was invited by Prof. Spencer Whitney to work in his lab at Australian National University within the Gates funded project 'RIPE: Realizing Increased Photosynthetic Efficiency for sustainable increases in crop yield'. Using chloroplast transformation in plants I showed current limitations of interspecies Rubisco translocation and how they could be overcome by co-expressing cognate Rubisco chaperones. Working with RIPE made me aware of global challenges in food security and how they could be addressed. In 2015 I returned to the UK to establish my own lab first at Liverpool John Moores University, and from 2017 at Newcastle University. Currently, we deploy classic molecular lab techniques, variety of DNA sequencing methods, and new computational tools such as machine learning to address fundamental aspects of enzyme evolution in photosynthetic organisms with the ultimate aim to improve photosynthesis and yield in crops via bioengineering solutions.

Anne Knowlton, *Current Biology*, Germany

Anne is a senior scientific editor at the journal *Current Biology*, which is part of the Cell Press family of journals. She comes from South Carolina, USA, where she studied biology at Clemson University for her bachelor's degree. She completed her PhD at the University of Virginia studying the assembly of the mitotic spindle. From there, she did her postdoctoral work at the University of Washington in Seattle. She has been working as an editor at *Current Biology* since 2011, and handles the plant biology papers for the journal. She is based in Baden-Württemberg, Germany.

Britt Koskella, UC Berkeley, USA

Britt Koskella is an Associate Professor in the Department of Integrative Biology at the University of California, Berkeley. Her work explores the importance of the bacteria and viruses making up the microbiome in shaping plant health, ecology, and evolution. She received her BA from the University of Virginia in 2001 and her PhD from Indiana University in 2018, and subsequently held postdoctoral and independent research fellowships in both the US (funded by the NSF) and UK (funded by NERC) at Oxford University and the University of Exeter. Her work combines laboratory experimental evolution with studies of natural diversity to determine how bacteriophage viruses shape bacterial evolution, microbiome diversity, and disease. She works on the phyllosphere (above ground tissues) of both long-lived trees and short-lived, agriculturally relevant systems to better predict microbiome complexity and stability and to understand the role that microbiomes play in plant health and agricultural sustainability.

Lisa Lamberte, University of Birmingham, United Kingdom

Originally from Manila, Philippines, Dr Lisa Ellevera Lamberte is a seasoned Research Fellow with a deep interest in microbial evolution. Her expertise spans diverse research areas, particularly within human and plant-associated microbial communities, and how they shape our understanding of health and the environment. She began her research journey with a PhD at the University of Birmingham, studying bacterial gene. After completing her doctorate, she investigated the spread of antibiotic resistance within the human gut. She later transitioned into plant science, exploring the effect of tree diversity on microbial communities. Currently, she works on forward genetic screens to investigate gain of virulence in fungal-resistant wheat cultivars. Her continuity at the University of Birmingham reflects her ability to evolve across disciplines, build enduring collaborations, and contribute to a wide array of scientific domains. She is now working toward establishing an independent research program focused on microbial adaptation and resilience in agricultural ecosystems. She is part of the local organising committee for New Phytologist next generation scientists 2025.

Keith Lindsey, Durham University, *New Phytologist* Editor, United Kingdom

For my first degree I read Botany at St. Catherine's College Oxford, and undertook a PhD at Edinburgh University. I carried out post-doc work in Edinburgh and then Rothamsted, before taking up a position as leader of the Plant Molecular Genetics Group at the Leicester Biocentre, and a lectureship at Leicester University (1989). I moved to a Chair in Durham in 1996. I am an Editor of the journal *New Phytologist* and Chair of the Board of Trustees for the New Phytologist Foundation. I was until recently a member of BBSRC Council, the body that determines policy, priorities and strategy for BBSRC; Chair of BBSRC Appointments Board; and a member of the Defra Advisory Committee on Releases to the Environment (ACRE), which advises Government Ministers on GM and related issues. I am former President and Chair of Council of the Society for Experimental Biology.

Claire Litchfield, University of Birmingham Enterprise, United Kingdom

As Senior Laboratory Manager at University of Birmingham Enterprise Claire leads the team that runs the incubator laboratories for life science tenant companies at the BioHub Birmingham and Unit 9 MedTech Incubator. She provides specialist support and services enabling companies to get their products and services to market faster and more sustainably than they would do unsupported. The BioHub has recently been awarded Green Impact Laboratory Accreditation (GILA; from SOS-UK). She originally undertook her undergraduate degree in Biological Sciences (Microbiology) at the University of Birmingham (UoB) followed by a PhD in Bacterial Genetics at the University of Leicester during which she demonstrated that Campylobacter jejuni can utilise transferrins as a source of iron. Postdoctoral research followed, including projects at UoB, firstly working on plasmid displacing technology during which she developed a second generation pCURE plasmid to displace antibiotic resistance plasmids from enteric bacteria under the supervision of Prof. Chris Thomas, Scientific Director of UoB spin-out company Plasgene Ltd. Subsequently, Claire was Principal Scientist and Work Package Lead on consultancy, synthetic biology (IUK-funded) and industrial biotechnology (IUK-funded) joint projects between UoB and GSK, before moving full-time into laboratory management. Claire has knowledge of legislation applicable to companies working in the life sciences field, with specific expertise in compliance for work with hazardous micro-organisms and genetically modified organisms. Claire holds an IOSH Managing Safely qualification and a Level 3 Certificate in Leadership and Management from the Institute of

Leadership and Management (ILM). For more information about the BioHub Birmingham, University of Birmingham Enterprise and the team, please visit: https://www.birmingham.ac.uk/collaborate/enterprise/birmingham-research-park/biohub-birmingham

Marjorie Lundgren, Lancaster University, *Plants, People Planet* Editor, United Kingdom

Marjorie is a UKRI Future Leaders Fellow and Senior Research Fellow at Lancaster University. After working in environmental consulting (Tetra Tech, Lafayette, California) and plant biotechnology (Mendel Biotechnology, Hayward, California), she earned her PhD in 2015 from the University of Sheffield and gained post-doctorate experience from the University of Sheffield, Massachusetts Institute of Technology, and the Arnold Arboretum of Harvard University. Marjorie applies plant ecophysiology and phylogeographic methods to understand how diverse photosynthetic systems evolve. She is particularly interested in C3-C4 intermediate phenotypes and C2 photosynthesis and leads a C2 photosynthesis crop engineering programme.

Rob MacKenzie, BIFoR, University of Birmingham, United Kingdom

Rob MacKenzie is Professor of Atmospheric Science at the University of Birmingham, with expertise in computer simulation of air quality at urban and regional scales, especially the effects of vegetation on atmospheric composition. In November 2013, Rob became the inaugural Director of the Birmingham Institute of Forest Research, which is an Institute reaching across the university to enable science, social science, and cultural research on forested landscapes. BIFoR hosts the only northern temperate forest Free-Air Carbon dioxide Enrichment (FACE) facility, investigating long-term (2017-2031) effects of elevated (+150 ppmv) CO_2 on mature oak woodland. Rob chairs the Trees and Woodlands Science Advisory Group of the Defra Nature for Climate Fund. He served on the NERC Strategic Programmes and Joint Capital Advisory Groups (2015-2019) and was a panel member for UK Research Excellence Framework (REF) 2021. He is part of the local organising committee for New Phytologist next generation scientists 2025.

Nokwanda (Nox), Makunga, Stellenbosch University, *Plants, People Planet* Editor South Africa

Nokwanda ‘Nox’ Makunga obtained her doctorate in 2004, joined Stellenbosch University in 2005, and is presently an associate professor at the institution. Today she is a leading researcher on South Africa’s medicinal plants. Using biotechnology, phytochemistry, and genetics, she studies the interactions between humans and plants. She couples this with investigating opportunities for socio-economic development, and has received numerous awards for her research. She is also passionate about teaching the public about science. Nox is an Editor of *Plants, People, Planet*.

Diego Márquez, University of Birmingham, United Kingdom

Diego is a plant physiologist specialising in leaf gas exchange, photosynthesis, and water use efficiency. His research combines theoretical biophysics with experimental approaches to develop mechanistic models of these key processes. His work aims to improve our understanding of plant resilience, crop productivity, and how plants respond to abiotic environmental changes over short and long timescales. He is part of the local organising committee for New Phytologist next generation scientists 2025

Matthew Naish, University of Cambridge, United Kingdom

Matthew Naish is a Broodbank Senior Research Fellow in the Department of Plant Sciences at the University of Cambridge, UK, with research interests in plant genetics and epigenetics. His work focuses on understanding the regulation of centromeres - specialised chromosomal regions essential for accurate chromosome segregation during cell division. After completing a Bachelor's in Natural Sciences at Cambridge, Matthew earned a Master's in Sustainable Agriculture and Food Security from Lancaster University, UK. He completed his PhD at the University of Warwick, UK, under the supervision of Prof. José Gutierrez-Marcos, investigating the epigenetic regulation of developmental reprogramming in plant regeneration. As a postdoctoral Fellow in Prof Ian Henderson’s lab at Cambridge, Matthew applied advanced long-read sequencing technologies to study centromere structure and function, including generating the first-ever gapless genome assembly for the model plant Arabidopsis thaliana. In recognition of his contributions to plant science, he was awarded the 2024 *New Phytologist* Tansley Medal for Excellence in Plant Science. He also served as a Scientific Fellow (2020-2022) to the World Economic Forum's Global Futures Council on Nature-based Solutions, contributing to international dialogue on sustainability and the role of natural systems in addressing environmental challenges. In October 2025, he will join the University of Warwick as an Assistant Professor in the School of Life Sciences, where he will establish an independent research group exploring the establishment and regulation of centromeres.

Carl Ng, University College Dublin, *New Phytologist* Editor, Ireland

I completed my BSc (Hons) in Botany, followed by a MSc in Plant Physiology at the National University of Singapore. My PhD research, supervised by Profs. Alistair Hetherington and Martin McAinsh at Lancaster University in the UK, was on calcium signalling in stomatal guard cells, where we were the first to discover sphingosine-1-phosphate in plants, and that it is calcium mobilising second messenger in the ABA signalling pathway in stomatal guard cells. This was followed by a Postdoctoral Fellowship with Prof. Sally Assman on the topic of RNA processing in ABA signalling in stomatal guard cells at Pennsylvania State University, USA. I then answered Ireland's call and started a lectureship at University College Dublin (Ireland's largest public university) where I run my own independent research group. My research interests are pretty broad, ranging from basic to applied, lab-based clean work involving plant cell cultures to getting mucky on farms. My research revolves around (i) plant and crop abiotic stress responses, (ii) sustainable agriculture with a particular focus on nitrogen use efficiency, and (iii) plant secondary metabolism and metabolic engineering. In addition to research, I am also actively involved in teaching (both undergraduates and postgraduates) and university administration (where I was Associate Dean of Science, and also Head of Plant Biology, and Cell and Molecular Biology). I joined the *New Phytologist* family first as an Editorial Advisor, before becoming an Associate Editor, and more recently, an Editor. In 2019, I hosted the New Phytologist next generation scientists Symposium in Dublin, and I have been a mentor for subsequent editions of the next generation Symposium.

Rich Norby, University of Birmingham, ORNL, University of Tennessee, *New Phytologist* Editor, United States

Richard Norby is an ecosystem ecologist interested in the Effects of CO2 enrichment on tree growth and forest metabolism - Ecosystem responses to atmospheric and climatic change - Carbon and nitrogen cycling in diverse ecosystems - Forest tree physiology and plant physiological ecology - Synthesis of experimental results to inform models He is an Emeritus Research Fellow in the Environmental Sciences Division & Climate Change Science Institute, Oak Ridge National Laboratory; Honorary Professor at the School of Geography, Earth and Environmental Sciences University of Birmingham; and Research Professor in the Department of Ecology & Evolutionary Biology, University of Tennessee' and an Editor of *New Phytologist*. He is part of the local organising committee for New Phytologist next generation scientists 2025.

Maarja, Öpik, University of Tartu, *New Phytologist* Editor-in-Chief, Estonia

Maarja joined *New Phytologist* as an Advisor in 2011 and as an Editor in 2013 and became Editor-in-Chief in 2025. She is a professor of Molecular Ecology and Director of the Institute of Ecology and Earth Sciences at the Faculty of Science and Technology at the University of Tartu, Estonia. Maarja is currently an Editor in *Fungal Ecology, MycoKeys* and *IMA Fungus*, and has been in the same role for *PLoS ONE* and *Plant and Soil*. She is editorial board member for *ISME Journal.*

Maarja's research addresses the interactions between plants and mycorrhizal fungi, with specific focus on arbuscular mycorrhizal fungal diversity patterns. Maarja pioneered one of the first public databases in the field, MaarjAM (Öpik *et al*., 2010), which is now widely used as a tool for arbuscular mycorrhizal fungal identification and in arbuscular mycorrhizal fungus ecological research. Maarja hosted New Phytologist next generation scientists symposium in Tartu in 2022.

Rory Osborne, University of Birmingham, United Kingdom

Rory was awarded his BSc in Biochemistry from Queen Mary, University of London in 2016. He then moved to the University of Warwick where he began his MIBTP-funded PhD in plant-microbe interactions. Under the supervision of Professor Patrick Schafer, Rory explored the role of symbiotic effector proteins in modulating host hormone signalling, and how they might contribute to mutualism. Upon earning his PhD, Rory joined the group of Professor Daniel Gibbs at the University of Birmingham to investigate how proteolysis influences plant responses to their environment, with a focus on the N-degron pathway of protein degradation. Since 2025, Rory continues to work at the University of Birmingham as an independent BBSRC Fellow. His work centres on understanding how chromatin structure influences “adaptive” immunity in plants, and how the epigenome might be engineered to develop resistance traits in crop species.

Ralph Panstruga, RWTH Aachen University, *New Phytologist* Editor, Germany

Ralph is a professor for Plant Molecular Cell Biology at RWTH Aachen University in Germany, where he also completed his PhD in the mid 1990s. He then moved as a post-doc to the Sainsbury Laboratory at the John Innes Center in Norwich (U.K.) and subsequently continued first as a post-doc, later as a research group leader, at the Max Planck Institute for Plant Breeding Research in Cologne (Germany) where he worked from 2000-2011. In 2011, he became a full professor at RWTH Aachen University. His research interest focuses on plant-microbe interactions, in particular the interaction of plants with obligate biotrophic powdery mildew fungi. He studies both fungal pathogenicity and plant defence responses at the molecular level, combining genetics, molecular biology and biochemistry. Ralph joined *New Phytologist* as an Editor in 2010 and became Head of the “Interaction” section in 2022.

Andy Plackett, University of Birmingham, United Kingdom

Andy Plackett did his PhD in the UK at Rothamsted Research, studying developmental genetics of Arabidopsis flowers. He subsequently had a long and broad-ranging postdoctoral career, with contracts at the University of Oxford (2011-2017) where he helped to establish stable genetic transformation in the fern lineage for the first time, and at the University of Cambridge (2017-2019) working as part of the Gates Foundation C4 Rice Project studying the genes underpinning chloroplast regulation inside leaf bundle sheath cells. In 2019 he joined the University of Birmingham to start a Royal Society University Research Fellowship (URF), combining his PhD and Postdoctoral research to study evolutionary changes to plant reproductive gene networks during the origin of the seed and seed-based reproduction. He is part of the local organising committee for *New Phytologist* next generation scientists 2025.

Anja Rammig, Technical University of Munich, Germany

I am a professor for Land Surface-Atmosphere Interactions working on dynamic vegetation modelling and observational data, and I am particularly interested in model-data integration

Ari Sadanandom, Durham University, *New Phytologist* Editor, United Kingdom

Biography Ari Sadanandom is the Principal Investigator of the SUMO code project. Ari Sadanandom's research group wants to understand how protein modification systems control plant growth and adaptation to their environment. Ari's laboratory has pioneered the research on SUMO, a new protein modification system that is emerging as a pivotal molecular mechanism in stress biology in plants. AS has demonstrated that SUMOylation coordinates growth control with changing environmental conditions by directly modifying the activity of major transcriptional regulators in plants. Ari Sadanandom is also director of the Durham Centre for Crop Improvement technology, a multi-disciplinary research centre that works with Agriculture industry to develop technology that is effective in field conditions. He is an Associate Editor of *New Phytologist.*

Rosa Sanchez-Lucas, University of Birmingham, United Kingdom

Dr. Rosa Sanchez-Lucas finished a higher engineering degree in Agronomy with a project about holm oak seedlings response to drought at the University of Cordoba. After that, she completed a master's degree on Plant Protection, Production and Breeding with the project about nitrogen fertilization effects to frost response in olive tree. Her PhD in Agricultural, Food, Forestry and Sustainable Rural Development Engineering studied warming temperature effects on olive tree. Currently, she works as a postdoctoral researcher at the department of Plant Sciences at the University of Birmingham, studying the induced resistance of oak against powdery mildew.
During all her professional career, she has studied the effect of stress on trees: and how they respond through physiological and biomolecular approaches: 1) abiotic stress as drought (undergraduate), temperatures (master and PhD) and elevated CO 2 concentration (current postdoc). 2) Biotic stress as oak powdery mildew, oak acutate decline and ash dieback (current postdoc). 3)Epigenetics changes caused by plant (a)biotic stresses. 4) Transgenerational inheritance of epigenetics in forest trees.

Tina Schreier, University of Oxford, United Kingdom

Tina Schreier is a BBSRC Discovery fellow in the Department of Biology at the University of Oxford. Her research focuses on the unique cellular leaf architecture of C_4 plants, which underpins their carbon-concentrating mechanism. In particular, she and her team investigate the cell biological mechanisms that control polar plasmodesmata formation and chloroplast positioning in the C_4 bundle sheath cells, and how these anatomical features contribute to enhanced photosynthetic efficiency.

Tina started working on plants and their metabolism during her PhD in the research group of Prof. Sam Zeeman at ETH Zurich. During her PhD, she discovered non-canonical roles of two chloroplast proteins that were originally thought to act as enzymes in the model plant Arabidopsis, demonstrating the important role of moonlighting proteins in plant metabolism and development. She then held a short appointment at the John Innes Centre studying carbohydrate metabolism in wheat grains with Prof. Alison M. Smith, before taking up SNSF and EMBO postdoctoral fellowships in the research group of Prof. Julian Hibberd at the University of Cambridge. There, she became intrigued by how metabolism can be facilitated by a specialised leaf anatomy in C_4 plants, and she started studying the importance of cell-to-cell connectivity in facilitating efficient photosynthesis in these plants.

David Seung, John Innes Centre, *New Phytologist* Advisor, United Kingdom

David Seung is a Group Leader at the John Innes Centre, Norwich (UK), focusing on the biology and biotechnology of starch synthesis. He received his B. Sc. degree in Plant Sciences and Agricultural Chemistry from the University of Sydney, and M. Sc. and Ph.D. degrees from ETH Zurich. David joined the John Innes Centre in 2017, initially as a BBSRC Future Leader Fellow, and then as a John Innes Foundation Chris J. Leaver Fellow. Research in his lab aims to understand starch biosynthesis at the molecular level, including the initiation process of starch granules and the control of granule size, shape and polymer composition. The lab has recently been using genetic and biochemical approaches to elucidate mechanisms that underpin the vast natural diversity in starch morphology and composition among different species and organs, including cereal endosperms and potato tubers. They have been using this knowledge to engineer starch structure to improve the functional and nutritional quality of important starch crops.

Pallavi Singh, University of Essex, United Kingdom

Pallavi is a UKRI-Future Leaders Fellow and her research employs advanced interdisciplinary technologies to drive a significant improvement in agricultural productivity and sustainability. Pallavi was awarded the SEB-President's Medal (Plants) 2024. She also received the Young Scientist Awards from the Indian National Science Academy in 2019 and from the National Academy of Sciences, India in 2017. Pallavi completed her PhD with Dr. Alok Sinha at the National Institute of Plant Genome Research (NIPGR), India, followed by a brief postdoctoral fellowship with Prof. Adam Bogdanove at Cornell University, USA. She then moved to Cambridge, UK, as a John Henry Coates Research Fellow with Prof. Julian Hibberd. In September 2022, she started her own research group at the University of Essex, focusing on various aspects of photosynthesis and using natural variation and functional genomic approaches to enhance our understanding of complex traits such as water use.

Holly Slater, The New Phytologist Foundation, United Kingdom

Holly is the Senior Commissioning Editor *for New Phytologist*. She has overall responsibility for commissioning strategies, including the prestigious Tansley reviews series. Holly has more than twenty years' experience in scientific publishing, provides advice and support to the *New Phytologist* team and contributes regularly to Foundation events and strategic development projects. Prior to publishing, Holly was a researcher in molecular–plant–microbe–interactions. She gained her PhD from The Sainsbury Laboratory (TSL), Norwich, UK, which was followed by four years of post-doctoral experience that she carried out first in TSL and then at the University of Cambridge, UK. Holly loves working in scientific journal publishing, a process that is core to the academic process, and really enjoys supporting the plant science community.

Rosie Trice, John Wiley & Sons Ltd, United Kingdom

I'm a Senior Publisher at Wiley with over 20 years experience in academic publishing. I am responsible for a portfolio of plant science journals, including New Phytologist and Plants, People, Planet. My role is to support Editors and Editorial teams on a day to day basis to help deliver high-quality, impactful research.

Prior to my career in publishing, I completed a BSc in Biology and PhD in Environmental Science. Working in publishing has been an enjoyable and rewarding experience, and I'm very pleased to be collaborating with the New Phytologist Foundation.

Sami Ullah, University of Birmingham, United Kingdom

Professor Sami Ullah is Chair in Biogeochemistry and Director of the Birmingham Institute of Forest Research (BIFoR) at the University of Birmingham UK. He is also the academic lead for the BIFoR Free Air CO_2 Enrichment (BIFoR-FACE) facility in a mature temperate forest in the UK. His research is focused on blending experimental manipulations (e.g. elevated [CO_2], atmospheric reactive nitrogen deposition, and soil management) to answer fundamental questions about changes in plant-soil-microbe interaction trajectories, plant nutrition, soil nitrogen and carbon transformations, and soil greenhouse gas fluxes. This research is underpinned by the development and application of field analytical techniques including stable isotopes tracing and high-resolution sensor technologies to explore novel relationships between ecosystem’s biogeochemical responses to environmental change. The outcome of his research is fundamental for designing soil, land use and ecosystem management strategies, and predicting the future functioning of natural ecosystems under land use and climate change scenarios. He is part of the local organising committee for New Phytologist next generation scientists 2025.

Andrea Vadillo Dieguez, University of Birmingham

Andrea is a PhD Student at the School of Biosciences and the Birmingham Institute of Forest Research. She is part of the local organising committee for New Phytologist next generation scientists 2025.

Mariana Vale, Fed. Univ. Rio de Janeiro, University of Birmingham, Brazil

Dr. Mariana M. Vale is a Brazilian ecologist specializing in biodiversity conservation, with a focus on tropical biodiversity, climate change, ecosystem services, and pandemic prevention. She holds a degree in Biology from the Federal University of Rio de Janeiro (UFRJ) and completed her graduate studies in the United States, earning an M.Sc. in Conservation Biology from Columbia University and a Ph.D. in Ecology from Duke University. Since 2010, she has served as an Associate Professor in the Department of Ecology at UFRJ, where she leads a dynamic research group comprising approximately 20 members, including undergraduate and graduate students, as well as postdoctoral researchers. She has contributed to several prominent international scientific initiatives, including the Intergovernmental Panel on Climate Change (IPCC), the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), and the Lancet/PPATS Report on Preventing Viral Spillover. In Brazil, she serves as a scientific advisor to the federal government on climate-related matters, supporting the development of the National Adaptation Plan and the country’s official communications to the Climate Convention. At the local level, she plays an active role in environmental governance, participating in protected area councils and serving on the State Environmental Council.

Catherine Walker, Nature Plants, United Kingdom

Catherine is an associate editor at *Nature Plants* where she handles manuscripts in ecology, agriculture, forestry and plant-microbe interactions. Catherine obtained her PhD from Rothamsted Research in 2019 where her research focused on understanding the role of effectors in the establishment of Fusarium Head Blight infection in wheat. She then went on to carry out postdoctoral research with the Plasmodesmata research group at the John Innes Centre, moving from wheat to Arabidopsis, and working to uncover the contribution of symplastic connectivity and cell communication to immune signalling. In 2022, Catherine officially left the bench and took on a new role in the Biotechnology and Biological Sciences Research Council (BBSRC) where she worked in the funding delivery team responsible for oversight of peer review for varied funding calls. She joined *Nature Plants* in 2023 and is based in the London, UK office.

Jo Wood, John Wiley & Sons Ltd, United Kingdom

Jo Wood is Senior Marketing Manager at Wiley and a member of the Chartered Institute of Marketing, with over 20 years' experience as a marketing professional across higher education, professional services, and the public sector. Before joining Wiley, Jo was Marketing Partner at Cranfield School of Management, where she led a team focused on MSc and PhD student recruitment marketing. Previously, she served as Development Marketing Manager at the Institute of Chartered Accountants in England and Wales (ICAEW), where she led the development and launch of new marketing initiatives, including a University Student Membership Scheme, Higher Apprenticeship programs, and a national competition. Earlier in her career, Jo gained commercial marketing experience with several SMEs across a range of industry sectors. She holds a BA (Hons) in Business Studies and has completed professional development programs in strategy and senior management with the Open University.

List of posters

Poster 1	Nabila El Arbi	Regulation of the Arabidopsis RNAPII by CDKC;2 influences temperature-dependent alternative splicing
Poster 2	Jumana Akhtar	Dissecting the role of how root hairs and secretion affect in the release of soil-binding exudates release and rhizosheath formation
Poster 3	Viraj Alimchandani	A tale of two scales: cellular and organ growth in plants, a meta-analysis
Poster 4	Caio Simões Ballarin	Exploring floral resource dimensions and their role in shaping plant-pollinator interactions.
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Poster abstracts

Poster 1

Regulation of the Arabidopsis RNAPII by CDKC;2 influences temperature-dependent alternative splicing

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Plants constantly assess environmental fluctuations and adjust their development accordingly. Varying temperatures can induce abiotic stress, and inapt responses cause severe developmental defects. Recent research efforts underline the importance of transcriptomic adjustments to coordinate appropriate abiotic stress responses. These transcriptomic adjustments are largely mediated through the regulation of RNA Polymerase II and co-transcriptional alternative splicing.

Mechanistic insights into these processes however are lacking, particularly *in plantae*. Hence, we aimed to identify additional players of the low temperature signalling in *Arabidopsis thaliana* through an EMS suppressor screen of the low-temperature sensitive splicing mutant *porcupine-1* (*pcp-1*).

We identified two alleles of the Cyclin-dependent kinase group C2 (CDKC;2), which phosphorylates the C-terminal domain of RNA polymerase II. Chemical inhibition of CDKC;2 phosphorylation phenocopied these results, confirming that decreased phosphorylation suppressed the low-temperature sensitivity of *pcp-1*. We furthermore showed that CDKC;2 is a central regulator of temperature-dependent transcription rates.

While our results highlight the crosstalk between transcriptional regulation and co-transcriptional alternative splicing, they also show that current models of RNA polymerase II phosphorylations do not fully account for the complexity of plant transcriptional regulation under abiotic stress, and thus further research is needed to understand plant specific transcriptional regulations in response to the environment.

Poster 2

Dissecting the role of how root hairs and secretion affect in the release of soil-binding exudates release and rhizosheath formation

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Rhizosheaths are specialised structures that play a crucial role in plant-soil interactions, enhancing drought tolerance and water retention capacities. Rhizosheaths are formed from root hairs and adhesive root exudates that entangle soil particles. Polysaccharides commonly found in plant cell walls and cereal root exudates, such as xyloglucan and complex gums, have soil binding properties; however, precise mechanisms governing the release of soil binding exudates remain elusive. Using *Arabidopsis* as a model and a recently developed centrifuge assay, we assess the adhesion strength of Arabidopsis roots, identifying mutants with different adhesive phenotypes. These mutants exhibit altered root hair morphologies, cell wall composition or transporter activities, all of which could influence exudate composition and release. To understand the underlying mechanisms in more detail, we are using antibodies and fluorescent protein fusions to observe cellular and sub-cellular locations of exudate components in root cells of wild type plants and previously characterised root hair, cell wall or secretion mutants. Immunohistochemical methods using monoclonal antibodies for cell wall components are enabling us to dissect molecular mechanisms affecting exudate secretion and composition further. These experiments will provide insights into the role of root hairs and root secretion in exudate release and its effects on soil aggregation.

Poster 3

A tale of two scales: cellular and organ growth in plants, a meta-analysis

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Quantifying cell growth is essential for understanding the biophysics of development and unveiling gene expression effects at the cellular level. However in plant biology, the majority of growth data is disparate and lacks a coherent framework, making it difficult to compare growth rates at different scales, between organs, and across different studies. In our meta-analysis, we have extracted and analysed growth data at the organ and cellular scale from decades of studies and proposed a mathematical framework for comparing growth between different organs across developmental stages and types of cell dynamics. Our analysis revealed that probing cellular growth during organ initiation is key to understanding later developmental stages that lead to the organ final size. By providing a map of cell and organ expansion in different organs of *Arabidopsis thaliana*, our work serves as a benchmark for experimentalists and modellers who need a reference point of organ growth in controlled conditions. We begin to bridge the gap between growth at the cellular and organ scales and expose the lack of data at the crucial early stages. Finally, the framework we established for converting and presenting growth rate data can be used in future studies to aid comparison with other works.

Poster 4

Exploring floral resource dimensions and their role in shaping plant-pollinator interactions.

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Plant-pollinator interactions are intrinsically tied to floral resources, forming the foundation upon which these ecological relationships are built. Yet, critical questions remain about how this fundamental niche dimension influences such interactions. How are floral resources distributed globally, and what drives these patterns at the biosphere scale? How do they determine the organisation of pairwise interactions among plants and pollinators at the community level? And how do floral resource functional traits shape the eco-evolutionary dynamics of interactions at the population scale? To tackle these questions, my research combines systematic reviews, biogeographical modelling, ecological network analysis, and experimental approaches in pollination biology, such as exclusion experiments. This combination of methodologies aims to clarify the role of floral resources in structuring plant-pollinator interactions across scales, advancing our understanding of their ecological and evolutionary importance within diverse interactions and floral resource landscapes.

Poster 5

Ecological remediation of urban legacy pollution: Developing techniques for marginal brownfield bioremediation

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Common remediation methods (e.g. soil washing and chelate-assisted phytoextraction) are effective at removing heavy metal (HM) pollutants from soil. However, they are also costly, mobilise pollutants via leaching and oxidation and fail to address reductions in microbial biodiversity caused by HM contamination . Diverse soil microbiomes can improve plant growth, nutrient cycling, disease resistance and ecosystem multifunctionality . Thus, promoting microbial diversity in combination with phytoremediation may encourage beneficial soil processes (e.g. soil nitrification) and aid extraction efficiency of hyperaccumulators . Multi-plant systems have gained increasing interest as a potential bridge between biological and physiochemical technologies with regards to phytoremediation . This project utilises greenhouse and in-situ trials to examine the effects of multi-plant systems, as compared to monocultures, for four hyperaccumulator species. Growth of hyperaccumulators, microbial diversity of the soil and HMs in plants and soil are measured in-situ and greenhouse trials

Poster 6

Aridity modulates biomass changes following nutrient addition and extreme drought on globally distributed grasslands: the NPK-D Network first results

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Anthropogenic nutrient increases can enhance plant biomass in grasslands, while droughts tend to reduce it. Biotic factors, such as biodiversity, and abiotic factors, like aridity and soil type, influence responses to both. However, combined impact of drought and nutrient increases on grasslands remains unclear. Using a globally distributed network that simulated drought and increased nutrient availability, we sampled aboveground biomass and species composition at 26 sites across nine countries. Drought reduced biomass by 19% and nutrient addition increased it by 24%, with counteractive effects resulting in no net impact on biomass overall under drought plus nutrient addition. General responses varied with aridity, with nutrient addition alleviating drought effects best in sub-humid sites. Only graminoids responded positively to nutrients during drought. Across environmental gradients, nutrient and drought impacts on biomass diminished with higher precipitation variability. Nutrient effects were stronger in arid grasslands but weaker in humid regions and nitrogen-rich soils. At high-diversity sites, biomass increased more with increased nutrient availability and declined more with drought than at low-diversity sites. Our findings highlight the importance of local abiotic and biotic conditions in predicting grassland responses to nutrient and climate changes, offering key insights for preserving ecosystems and supporting biodiversity amid global change.

Poster 7

Understanding the genetic basis of canopy architecture and yield in tetraploid potato

Jack Bosanquet

University of Birmingham, Birmingham, United Kingdom

Potato is the sixth most important food crop by global production; however, it remains at risk from various biotic and abiotic stresses. Thus, potato breeding to maintain yields in an ever-changing environment remains a key research area. This work aims to understand the complex quantitative genetics behind tetraploid potato and how this relates to canopy architecture traits that impact stress tolerance and yield. Using GWASpoly in R to perform a GWAS with genomic (8K SNP array) and phenomic (UAV imaging) data for 282 diverse cultivars we hope to find QTL associated with yield and diverse canopy traits. Analysis using a simplex dominant model has found two SNP markers linked to yield on chromosome 6 and two linked to plant area on chromosome 1. Moreover, via discriminant analysis of principal components (DAPC) with adegenet in R and Bayesian Clustering using STRUCTURE we aim to better account for the confounding effect of population structure. DAPC revealed 4 subpopulations in the data for characterisation using STRUCTURE to allow population structure to be accounted for in the GWAS model. Ultimately, the hope is that QTL discovered in this study can inform improved marker assisted selection that speeds up the laborious process of potato breeding.

Poster 8

Fungi of Future Forests: does CO_2 enrichment affect soil fungal community composition in oak woodland?

Rachel Calder
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Soil fungal communities are crucial determinants of tree health and nutrient cycling in woodlands, yet their susceptibility to global change impacts is poorly understood. The Birmingham Institute of Forest Research Free Air Carbon Dioxide Enrichment facility (BIFoR FACE), a long-term experiment exposing sections of a mature oak woodland in England to elevated CO_2 levels, offers a unique opportunity to investigate one aspect of this. Soil DNA samples from treatment plots (+150 ppm CO_2) and control plots (ambient [CO_2]) at BIFoR FACE were subjected to DNA metabarcoding to characterise the soil fungal communities at three different time-points representing up to seven years of CO_2 enrichment. The resulting data were used to investigate fungal richness and diversity, community composition, and relative abundances of saprotrophic and symbiotrophic/ectomycorrhizal fungi. No significant differences were found between ambient and elevated [CO_2] treatments, but there was some evidence of an interaction effect between CO_2 treatment and soil horizon whereby CO_2 enrichment appeared to reduce the differences in soil fungal communities between the O (organic) and A (upper mineral) horizons. These results on soil fungal community composition will form the basis for future work looking more directly at the functioning of soil fungal communities at BIFoR FACE.

Poster 9

Can oxygen isotopes in tree rings be used to detect stomatal responses to global change?

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Stomatal conductance (g_s) is an important plant trait, regulating CO_2 and water fluxes. Although g_s decreases with elevated CO_2 in laboratory settings, it is unclear how g_s is responding *in-situ* to long-term exposure to rising CO_2 and a changing climate. Understanding how g_s will be impacted by these global changes is important for carbon and water cycles. Tree ring isotope analysis provides a unique method to assess tree ecophysiological responses to long-term exposure of slowly changing environmental variables. Changes in g_s can – in principle – be inferred from tree ring stable oxygen isotope ratios ($\delta^{18}O_{trc}$). Several studies have indeed used $\delta^{18}O_{trc}$ to conclude that g_s has not significantly changed from pre-industrial values. However, it remains unclear whether $\delta^{18}O_{trc}$ is sufficiently sensitive to detect changes in g_s as expected based on CO_2 experiments. To test this, we model the responses of g_s and $\delta^{18}O_{trc}$ to CO_2 and climate since 1900. We find that temporal g_s trends are only detectable in $\delta^{18}O_{trc}$ in dry climates and when the Péclet effect is present. In contrast to the weak effects of gs on $\delta^{18}O_{trc}$ trends, we find that temporal increases in VPD and temperature, independent of changes in gs, have far greater contributions to $\delta^{18}O_{trc}$ trends. Thus, this increasingly popular method should be used with caution, because it is highly challenging to unambiguously attribute trends in $\delta^{18}O_{trc}$ to changes in gs

Poster 10

Enhancing the Conservation and Use of Cereal, Vegetable and Forage Landraces in Great Britain to support future food security.

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University of Birmingham, Birmingham, United Kingdom

Recent agricultural intensification has led to the replacement of crop landraces with higher yielding, genetically uniform modern cultivars. Many of these lack adaptive alleles that build resilience against environmental change, posing an increasing threat to future food security. Due to continuous rounds of selecting and saving seed on farm, landraces act as a vital genetic resource to overcome this.

In Great Britain, previous attempts to document landrace diversity are outdated and incomprehensive therefore this research aims to better understand current cultivation trends and strategically determine conservation priorities. Through maintainer interviews, questionnaires and expert discussions, 196 maintainers and 564 landrace populations have been identified, with diversity hotspots in East Anglia and the Scottish Islands. The most common reasons for maintaining landraces were nutrient quality, suitability to low input systems and crop quality. Maintainer number and cultivation scale of cereal landraces has increased since 2003 however vegetable and forage landrace diversity are becoming increasingly threatened. Across all crop types, the major challenges reported by maintainers were lack of market demand, climate change and legislative restrictions. Conservation strategies must be developed to overcome these challenges, ensuring that this material still exists as a potential resource for future generations in the fight against climate change.

Poster 11

Leaf nutrient concentration is an important aspect in regulating the thermal optimum of photosynthesis

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Leaf level photosynthetic rates are directly related to the nutrient concentration, indicating a direct link between investment and return. However, the role of leaf nutrients in constraining the temperature response of photosynthetic parameters remains poorly explored. Understanding this aspect is critical for advancing our knowledge of ecological dynamics and improving predictions of the future of global vegetation under climate change. To address this gap, we tested the influence of three leaf key nutrients — nitrogen (N_{area}), phosphorus (P_{area}), and potassium (K_{area}) — over the optimum temperature of both maximum RuBP carboxylation rate (T_{OptV}) and maximum electron transport rate (T_{OptJ}). Naturally occurring trees from the Brazilian Cerrado revealed distinct nutrient-specific relationships, with T_{OptJ} being strongly related to all three nutrients while T_{OptV} only with N_{area} and P_{area}. Our findings highlight an important aspect of tropical vegetation primary productivity in the face of ongoing climate change that potentially alters nutrient biogeochemical cycles. Still, it is necessary to expand this approach to other forest ecosystems and gain a comprehensive understanding of the mechanisms behind the control of the temperature dependence of photosynthesis by foliar nutrients.

Poster 12

Circadian regulation of rhizosphere interactions

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The circadian clock underlies a suite of regulatory processes that align the timing of metabolism with 24 h cycles that occur within the environment. The circadian clock of plants influences the rhizomicrobiome, and there are circadian rhythms in certain soil bacteria (e.g. *Bacillius subtilis*). Rhizosphere interactions, such as those that influence the rhizomicrobiome composition, are mediated by exuded metabolites that include specialized metabolites. Specialized metabolites also regulate plant development and have an important application in plant biotechnology as pharmaceuticals. I am investigating the mechanisms that underlie the daily timing of communication between plant roots and the rhizosphere through specialised compounds, using *Arabidopsis thaliana* as a model. This is establishing potential regulatory pathways, in plants, for the circadian control of specialized metabolites which influence rhizomicrobiome interactions. I am focusing on roles for transcriptional regulation and chromatin remodeling in this process. My findings indicate that the circadian clock orchestrates mechanisms associated with the production of specialized metabolites. This suggests a process whereby circadian-regulated interactions could occur between plants and microorganisms, leading to timed interactions between different organisms in the ecosystem. These findings have the potential to inform on engineering useful metabolic processes.

Poster 13

Unearthing the diversity and 300-million-year evolution of phloem anatomy in ferns

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Phloem is vital for vascular plants because of its fundamental role in transporting photosynthate and comprehensive roles in signalling. Despite its importance, the evolution of phloem remains poorly understood. This is because phloem is rarely preserved in fossils and is poorly studied across vascular plant diversity including major groups such as ferns. Therefore, my research aims to uncover the diversity and evolution of the sieve elements (SEs) anatomy, the structure of conducting cells in phloem. Utilizing histology and advanced microscopy, I am examining phloem structure in extant and extinct ferns, enabling 3D visualization and quantification of SE anatomy. Intraspecific and interspecific variations are found in SE radius. A significant correlation between SE radius and stipe radius in extant ferns has been identified, despite the presence of outliers. Ancestral state reconstruction is applied to outline the evolution and to predict phloem structure in the common ancestor of ferns. By integrating fossil data, the analysis reveals a trend of decreasing SE radius over geological time. Further phylogenetic analysis shows that closely related species share similar SE radius and that the evolution of SE radius is not driven by a single external factor.

Poster 15

Auxin-triggered cAMP production induces autophagy for developmental reprogramming

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Auxin plays a vital role in regulating various biological processes, ranging from embryogenesis and organogenesis at a macroscopic level, to specific cellular activities like ion exchange, cell polarity, and endocytic trafficking (Sauer et al., 2013). Additionally, recent research has shown that auxin is possibly involved in the activation of another crucial cellular process that is macroautophagy (Rodriguez et al., 2020).
Macroautophagy (from now on referred as autophagy) is a “self-eating” catabolic mechanism for the removal of unneeded or dysfunctional cytoplasmic contents, such as protein aggregates or damaged organelles (Gou et al., 2019).
Although autophagy was initially thought of as a coping mechanism for damage and different stresses, there is now proof that this process is essential for cell homeostasis, particularly in the short-term reprogramming of somatic cells. In order to enable quick changes in cell state, autophagy thus appears to be highly controlled by a variety of pathways that are convergent on it. (Batoko et al., 2017; Rodriguez et al., 2020). Here, we will present how auxin can fine-tune autophagy to rewire the somatic cell state, through its canonical pathway, involving cAMP and transcriptional regulation, by using characterized auxin analogues, genetic methods, and proteomics approaches.

Poster 16

Osmotic changes at the crossroad of Glutamate Receptor-Like channels activation

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The perception of environmental stimuli in plants often triggers the systemic transmission of chemical and electrical signals, eliciting responses in unaffected tissues and coordinating developmental programs across various plant organs. Studies on Arabidopsis have underscored the pivotal role of Glutamate Receptor-Like channels (GLRs) in directing leaf-to-leaf electrical and calcium signals upon wounding, as well as the increase in Jasmonate levels, a key defense hormone, in undamaged systemic leaves. Whereas in response to wounding the glutamate-dependent activation of GLRs is mainly related to the apoplastic accumulation of this amino acid upon cellular disruption, it is not known if other less-invasive stresses can trigger similar effects.
Here, we report that an osmotic shock applied to the roots of Arabidopsis soil-grown plants induces in leaf tissues: (i) a change in the surface potential, (ii) an accumulation of glutamate in the apoplast, and (iii) a calcium wave that is reliant on the phloem localized AtGLR3.3 activity. Differentially from wounding, Jasmonate signalling pathway is not activated by the osmotic shock, showing that AtGLR3.3 activity is necessary but not sufficient to induce this response. Importantly, by using a tailor-made large imaging set up we show that the osmotic-induced long-distance calcium wave is conserved in Nicotiana plants.

Poster 17

(Not) Lost in Translation: Are Upstream Open Reading Frames Novel Regulators of Temperature Responses?

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The ability of plants responding dynamically to temperature fluctuations is critical for survival in our warming climate. Plants regulate their growth in response to warm temperatures, a process termed thermomorphogenesis, through the elongation of the hypocotyl and petioles, as well as hyponastic growth. These changes in growth are hypothesized to optimize cooling. Although key components of the thermomorphogenesis pathway have been identified in Arabidopsis thaliana, the pathway is not fully understood.My PhD project focuses on determining whether AUXIN RESPONSE FACTOR 2 (ARF2), a known repressor of auxin signaling, is a novel regulator of thermomorphogenesis. Preliminary findings demonstrate that arf2 knockout mutants exhibit an exaggerated growth response under elevated temperatures, implicating ARF2 in temperature-dependent growth. Furthermore, ribosome profiling (Ribo-seq) data reveal that multiple upstream open reading frames (uORFs) within the ARF2 5'-untranslated region (5'-UTR) are preferentially translated at higher temperatures, suggesting a temperature-specific translational regulation of ARF2. This project aims to determine how these uORFs influence ARF2 translation at warmer temperatures and to elucidate their functional significance in mediating ARF2's role in thermomorphogenesis. By characterizing these regulatory mechanisms both in vitro and in vivo, this research seeks to advance our understanding of temperature-responsive growth pathways in plants.

Poster 18

Modelling mature temperate forest responses to elevated CO2 and changing climatic conditions: insights from the BIFoR FACE experiment

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Climate change and elevated CO2 are greatly impacting ecosystems worldwide, resulting in more frequent and intense extreme weather events such as heat waves and drought. Understanding how ecosystems respond to elevated CO2 is critical for predicting the impacts of climate change on ecosystem processes. However, the capacity and magnitude of these ecosystems to sequester additional CO2 is uncertain when predicted using current terrestrial biosphere models (TBMs). To address this, improved mechanistic representations of ecosystem states and processes under changing climatic conditions are crucial, as well as constraining model simulations using real-world observations.

In this study, we examined the responses of mature temperate forests to rising atmospheric CO2 and changing climatic conditions using the Ecosystem Demography model. We parameterised the model with data from the Birmingham Institute of Forest Research, Free-air CO2 Enrichment (BIFoR FACE) experiment site. As the first study using a TBM at BIFoR, this study analysed the model's capacity to simulate ecosystem responses to elevated CO2 and extreme weather events. We ran two simulations and compared model outputs against field measurements of key eco-physiological measurements such as maximum rate of carboxylation and Net Primary Production (NPP). This study demonstrates the capability and limitations of the TBM to simulate mature temperate forest responses to elevated CO2 conditions.

Poster 19

Understanding the molecular determinants and spatiotemporal dynamics of auxin receptor complex assembly - a complex problem

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Auxin regulates many developmental processes in plants through ubiquitin-mediated degradation of Aux/IAA proteins and the subsequent release of transcription inhibition on auxin-regulated genes. While transcriptional effects are well understood, some auxin responses at the cell periphery, such as membrane depolarization, apoplast alkalinization, and Ca^{2+} influx, occur too quickly to be explained by transcriptional changes. AFB1, one member of the TIR1/AFB protein family of auxin co-receptors, differs from the rest of its family members in its subcellular localization and ability to trigger these rapid auxin responses.
This research uses FRET-FLIM to investigate the molecular determinants and spatiotemporal dynamics of the SCFTIR/AFB-Aux/IAA auxin receptor complex in different subcellular compartments. We have shown that despite previous reports describing a lower affinity of AFB1 to the rest of the auxin receptor complex, part of this complex is constantly assembled in the cytoplasm with AFB1. However, several questions remain: What determines the correct and functional assembly of the auxin receptor complex? Is it possible that cytoplasmic auxin perception and rapid auxin signaling happen through an SCF-independent pathway? Addressing these questions will deepen our understanding of auxin signaling dynamics and could reveal novel mechanisms of plant response to environmental cues.

Poster 20

Carnivorous Slime: changes in viscoelastic hemicellulose polymer secretion in *Nepenthes* takes pitchers from trapping-optimized to digestion-optimized, and are regulated by age and nutrient availability.

Skylar Johnson
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Carnivorous plants from the genus *Nepenthes* grow in nutrient poor soils and rely on capturing and retaining insect prey in pitfall traps to obtain nitrogen from the environment. Abundant niche specialization within the genus has resulted in a variety of trap morphologies and adaptations, including several species which use sticky viscoelastic fluids to aid in insect retention. The viscoelastic fluid of *Nepenthes rafflesiana* is composed of a hemicellulose polymer, along with enzymatic components for prey digestion. In this study, we monitored fluid physical properties and digestive abilities in wild-grown plants to gain insight into regulation of viscoelastic fluid production through the pitcher lifespan. We found that pitchers shift from a trapping-optimized to a digestion-optimized phase as they mature towards senescence, with decreasing ability to secrete viscoelastic fluids but increasing accumulation of digestive proteases. This was followed by lab-based rna-sequencing and feeding experiments to gain further insight into the synthetic and regulatory mechanisms behind viscoelasticity. It appears that the hemicellulose polymer is synthesized by standard carbohydrate processing machinery, and viscoelasticity is diminished by the addition of nitrogen to the pitchers. The convenient secretory properties of this system may represent a new model for studying synthesis of non-xylan hemicelluloses in plants.

Poster 21

How do stomata and programmed cell death contribute to anther dehiscence?

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Anther dehiscence, the process of pollen release from mature anthers, is essential for reproduction in flowering plants. In spite of its biological importance, the developmental mechanisms driving this process and the response to environmental factors remain to be resolved. Using non-invasive, controlled humidity conditions, we demonstrate that high humidity inhibits anther opening in *Arabidopsis thaliana* flowers. Our results indicate that stomatal density modulates dehiscence dynamics, implicating regulated transpiration in this process. Furthermore, subcellular marker analysis reveals that programmed cell death (PCD) occurs in specific anther tissues, the epidermis and endothecium, and is both developmentally programmed and environmentally regulated. Genetic inhibition of PCD delays dehiscence, whereas premature induction of PCD accelerates dehiscence. These results highlight a rapid, humidity-triggered PCD process as a critical factor in ensuring timely pollen release in Arabidopsis.

Poster 22

Light mediated aluminium toxicity tolerance in *Arabidopsis thaliana*

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Aluminium (Al^{3+}) ions under acid soil is a major threat to crop production. Recent studies have highlighted the role of photoreceptors and light signalling factors in nutrient acquisition (P, N, Fe) from soil. We found that darkness aggravates aluminium(Al) sensitivity whereas light, specifically blue light promotes Al tolerance by lowering internal Al accumulation in the roots. The HY5-COP1 module functions downstream to cryptochromes under Al. The *hy5* and *cop1* seedlings show a hyper and hyposensitive response to external Al respectively. Accumulation of HY5 is downregulated in the roots exposed to Al in a COP1 dependent manner. The *hy5* seedlings accumulate higher internal Al, ROS, and the *cop1* accumulate lower Al, ROS in the roots. We further observed that *cop1* could rescue the Al sensitivity in darkness as well in *stop1*. Also, HY5 transcriptionally regulates *STOP1*, *ALMT1* and *MATE* to confer aluminium tolerance. The STOP1 accumulation is higher in *cop1* in a HY5 dependent manner resulting in higher MATE levels. This is reflected in higher citrate exudation ability of *cop1* resulting in Al tolerance. Also, COP1 interacts and degrades STOP1 in darkness under Al stress. Taken together, this study suggests the role of a blue light mediated HY5-COP1 module in regulating citrate levels conferring Al tolerance.

Poster 23

Native diverse ecosystems in southern Morocco demonstrate a potential climate-resilient microbiome for sustainable agriculture

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Microbial communities play a critical role in enhancing agrosystems functioning and resilience under environmental stress. This study focuses on unraveling the dynamics, diversity and composition of microbiome across diverse arid and saline ecosystems in southern Morocco. By combining microbiome profiling with the functional characterization of culturable microbes from distinct plant-soil compartments from different ecosystems, this project aims to develop stress resilient microbial inoculants and understand the key mechanisms through which these microbes enhance plant tolerance to abiotic stresses such as salinity and drought.

Our preliminary findings revealed contrasting soil physicochemical properties, diverse vegetation profiles, and varying degrees of aridity and salinity among the ecosystems. A total of 31 bacterial isolates isolated from the three ecosystems were characterized as halotolerant (up to 100g NaCl /L) and drought tolerant (−0.30 MPa), suggesting that these bacterial isolates maintain ancestral ecological functions, making them important candidates for microbial inocula to mitigate abiotic stresses such as drought and salinity. From these isolates, various salt- and drought-tolerant consortia with additional plant-growth-promoting traits (e.g., phosphate solubilization, auxins and ammonia production) were developed and evaluated for their potential to mitigate salinity stress in wheat plants under controlled conditions. We also aim to investigate the key mechanisms by which these consortia may induce plant tolerance to salinity.

Poster 24

Seasonal Variations in Carbon and Nitrogen Exudation Rate of Young Alder and Oak

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Root exudates contribute up to 17% of the carbon fixed through photosynthesis to belowground processes, playing a crucial role in shaping rhizosphere dynamics. Despite their ecological importance, the seasonal variability in carbon and nitrogen exudation rates in young trees remains insufficiently explored, particularly in contrasting species such as alder (*Alnus glutinosa*) and oak (*Quercus robur*). This study investigates the seasonal patterns of carbon and nitrogen exudation rates in young alder and oak trees. Root exudates were collected during spring, summer, and autumn using an *in situ* method (Philip, 2008), and were quantified per root biomass. Significant variations ($p<0.01$) in carbon and nitrogen exudation were observed between species and seasons. Oak exhibited the highest exudation rates particularly in summer, releasing 111% more carbon and 98.2% more nitrogen compared to alder. Summer also marked the peak exudation rates for both species. While oak displayed higher carbon exudation rates, alder exhibited increased root respiration, particularly during summer. Furthermore, root exudate concentrations were positively and strongly correlated with specific root tips. These findings underscore species-specific exudation strategies and their implications for rhizosphere processes and nutrient cycling, in which a higher concentration of root exudate resulted in higher nitrogen cycling.

Poster 25

Assembling the puzzle: geographic isolation, biotic pressures, genome size variation and postzygotic isolation promote the rapid insurgence of a *Dianthus* ecotype on a volcanic archipelago

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The Eurasiatic clade of *Dianthus* experienced the fastest diversification ever reported in plants. However, the mechanisms underlying this radiation remain unclear and investigating the early divergence in selected case studies might significantly expand our knowledge. Here, we investigated the mechanisms underlying the origin of a *Dianthus* ecotype near-endemic to a Mediterranean volcanic archipelago. Specifically, we characterized genomic patterns and inter-ecotype postzygotic barriers, measured genome size and floral traits to test for an allometric relationship, and estimated reproductive success and biotic interactions to detect biotic drivers of divergence. The ecotype originated around 195 kya on the volcanic archipelago and a postzygotic barrier with the mainland ecotype quickly evolved. The strength of this barrier was correlated to the difference in genome size of parental plants. Also, genome size was correlated to style length which we found to be under a strong divergent selection. Our study suggests that biotic pressures can play a key role in the early divergence and documents a new postzygotic isolation mechanism between closely related lineages of *Dianthus*.

Poster 26

Interplay Between Phytohormones and Pathogen Strategies: Insights from *Leptosphaeria maculans*

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Plant defense mechanisms are governed by a complex interplay of phytohormones, which also regulate various other plant processes such as growth and development. When a plant encounters pathogens, its defense responses are activated at the expense of growth, highlighting the necessity for precise hormonal regulation. Plant pathogens have evolved strategies to circumvent these defenses, one of which involves manipulating phytohormone signaling.

The oilseed rape pathogen *Leptosphaeria maculans* can synthesize a range of phytohormones, including auxins, cytokinins, and salicylic acid (SA). The production of auxins can be stimulated by biosynthetic precursors and is linked to the induced transcription of biosynthetic genes *LmTAM1* and *LmIPDC2*. Notably, auxin excretion has been observed in *L. maculans*. The application of auxins modulates the necrotic lesion area caused by the pathogen on *Brassica napus*. Cytokinins are synthesized through the action of isopentenyl transferase and adenosine kinase. The presence of SA has been detected in the mycelium of *L. maculans*, along with the identification of orthologues of the plant biosynthetic gene *AtICS1*. Additionally, a salicylic acid-sensing mechanism, including the SA-responsive gene *LmSrg1*, has been documented. The interplay between SA and auxin signaling in *L. maculans* underscores the significance of fungal phytohormone biosynthesis in facilitating the infection process.

Poster 27

Photosynthesis in Arabidopsis Mesophyll and Guard Cell Chloroplast

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When the sun rises, plant leaves need a significant amount of energy (ATP) to keep the stomatal guard cells open, which is essential for gas exchange and photosynthesis. However, previous studies have suggested that guard cell chloroplasts (GCCs) do not engage in CO_2 fixation, leading to little or no photosynthesis occurring in these cells. This conclusion has been challenged by later research, igniting decades of discussion about whether GCC photosynthesis plays a direct role in stomatal regulation in response to CO_2. Until recently, our team introduced genetically encoded fluorescent biosensors into *Arabidopsis thaliana*, enabling us to monitor NADPH and NAD(H) in living plants without extraction or damage. With these biosensors, we were able to explore this scientific question effectively. Furthermore, we identified the source of mitochondrial reducing equivalents used for ATP generation in mesophyll cells during the daytime. In this conference, I will discuss the differences in bioenergetics between mesophyll and guard cells and how their functions are intricately coordinated in CO_2 uptake through stomata and CO_2 fixation in mesophyll cells. We had also published guidelines for utilizing in planta biosensors, and we believe these valuable transgenic lines will enhance research in plant redox biology.

Poster 28

Investigating Drivers of Variation Within Carbon and Biodiversity Co-Benefit/Trade-off Relationships in Forests To Improve Practice

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Forests play a fundamental role in mitigating climate change, absorbing around 1/3 of anthropogenic emissions, while also being home to 80% of terrestrial biodiversity. Modern forest management is mainly directed at increasing carbon stocks, often assuming biodiversity will be protected as a co-benefit. Recent studies have identified only partial overlap in high biodiversity and carbon-dense areas, suggesting that these co-benefits are not always present. Additionally, present research has mainly assessed biodiversity using trees, birds, or mammals as indicator groups. This study investigates further and attempts to identify taxa or features that reliably indicate maximised biodiversity-carbon relationships in temperate ancient woodlands and how this may impact policy and net-zero targets. Carbon data were collected at forest inventory plots in 2022 and diversity data for lichens, ground flora, mammals, and birds at the same locations during 2024. Preliminary results suggest carbon-biodiversity relationships in British ancient woodlands have no significant correlations. This highlights the need for cooperative management and planning as co-benefits cannot be assumed when protecting either carbon or biodiversity and conversely the two factors cannot be assumed to be separate. Local knowledge of both will be required to assess ancient woodlands across the UK and identify the best management practices in each case.

Poster 29

Developmental Regulation and Molecular Mechanisms in the Establishment of Long-Lasting Induced Resistance

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Botrytis cinerea, the causal agent of grey-mould disease, poses a significant threat to global tomato production, with post-harvest yield losses reaching up to 50%. Our research investigates whether priming elicitors, such as β-aminobutyric acid (BABA), can enhance intrinsic plant defences and provide sustainable disease control alternatives. We have demonstrated that BABA-induced resistance (BABA-IR) is long-lasting and mediated by epigenetic mechanisms, including DNA methylation. Using whole genome bisulfite sequencing, we observed reduced DNA methylation in CHH contexts in young tomato plants compared to older plants, indicating greater epigenetic imprinting capacity at early developmental stages. Transcriptomic analysis revealed that gene expression changes associated with BABA-IR are strongly influenced by the plant's developmental stage. Specifically, we identified key genes and molecular markers linked to early developmental stages that are likely involved in establishing long-lasting resistance. Notably, BABA-IR is consistently effective in plants treated at two to three weeks of age but declines after four weeks, coinciding with flowering—a pivotal developmental transition.

Our findings provide new insights into the relationship between plant development, epigenetics, and induced resistance, offering a mechanistic understanding of how BABA establishes durable immunity in tomato. This work highlights its potential application in improving crop protection strategies in other plant systems.

Poster 30

Unfolding How Robust Shape and Surface Curvature Emerges in Plant Embryonic Leaves.

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Developmental robustness ensures consistent organ shapes and sizes despite environmental variability. In Arabidopsis, cotyledons develop through pre-germination cell proliferation and post-germination differentiation, marked by opening and surface curvature changes. Wild-type (WT) cotyledons exhibit isotropic growth post-germination, forming a flat, circular lamina with zero Gaussian curvature to maximise photosynthetic efficiency. This process relies on precise cellular and biomechanical patterns, with early stress changes guiding morphological transitions.

We investigated cotyledon development robustness in WT using live imaging and environmental variations, focusing on JAW-like TCP genes (JAW-TCPs) regulating organ morphology. Mutant cotyledons with downregulated JAW-TCPs show disrupted shapes, elliptical laminae, altered proximodistal growth, and irregular surfaces. Initial growth rates in WT and mutants are similar, with minimal curvature changes in the first 12 hours. However, mutants exhibit delayed growth and differentiation, maintaining curvature over time. Both types display a basipetal arrest front, indicating conserved growth patterns. Growth analysis reveals WT favours mediolateral growth for circular laminae, while mutants prioritise proximodistal growth, shaping curvature.

Our findings suggest that adaxial-abaxial differential growth resolves mechanical conflicts, emphasising cotyledon morphology's genetic, biomechanical, and cellular dynamics. This study highlights mechanisms underlying developmental robustness and their role in shaping leaf-like organs.

Poster 31

UV-B radiation induces jasmonate-dependent anti-herbivore defenses in Arabidopsis via UVR8 by regulating the stability of JAZ and MYC proteins

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In plants, defense responses against herbivores and necrotrophic pathogens are primarily mediated by the jasmonic acid (JA) pathway. In healthy plants, JAZ repressor proteins suppress this pathway, preventing MYC transcription factors from activating defense-related genes. Previous studies have shown that solar UV-B radiation enhances plant defenses against herbivores, but the mechanisms are not fully understood. In this study, we investigated the role of the JA pathway in mediating UV-B effects on Arabidopsis resistance to *Spodoptera frugiperda* caterpillars.

Insects grown on plants exposed to low doses of UV-B accumulated less mass compared in bioassays compared to those on control plants. This reduced growth correlated with increased bioactive jasmonates and JA response gene expression in UV-B-exposed plants. The UV-B effects were dependent on the UVR8 photoreceptor. Importantly, enhanced resistance to *S. frugiperda* by UV-B was absent in an *aos* null mutant, which is defective in a key step of JA biosynthesis. Additionally, plants exposed to UV-B radiation in the growth chamber or to natural solar UV-B in the field showed decreased stability of the JAZ10 repressor protein and increased MYC2 stability in a UVR8-dependent manner.

Our results suggest that UV-B radiation, acting through UVR8, enhances plant resistance to insect herbivory by altering the balance between repressors and activators of the jasmonate pathway.

Poster 32

Linking changes in pollinator behaviour with their effect on male fitness in buzz-pollinated flowers

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Bees play a central role in mediating patterns of pollen transfer that directly affect plant fitness. In buzz-pollinated systems, bees extract pollen by vibrating flowers and subsequently groom their bodies, removing and packing pollen grains in specialised structures. This grooming process reduces the amount of pollen available for cross-pollination and may influence male fitness. Despite the amount of pollen collected by bees not directly affecting pollen deposition, we found that the duration and frequency of buzzing and grooming behaviours significantly impact pollen deposition on stigmas. Additionally, bee body size was associated with the effectiveness of these behaviours. We used *Bombus terrestris* individuals and flowers of *Solanum sisymbriifolium* in controlled flight arena experiments to monitor bee-flower interactions and quantify both behavioural parameters and pollen transfer. Our results highlight that pollinator behaviour and morphology jointly mediate male fitness, shaping the ecological and evolutionary dynamics of buzz-pollinated plants. These findings suggest that individual-level variation in behaviour and morphology should not be overlooked when studying plant-pollinator interactions. By opening the “pollination black box,” our study provides new insights into how pollinator behaviour influences pollen dispersal and reproductive outcomes in plants.

Poster 33

A multiprotein network composed of BBX and COP1 proteins converging on HY5 fine-tunes anthocyanin synthesis in tomato fruit

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Anthocyanins, polyphenols conferring fruit coloration, are beneficial for human health. The tomato line “SunBlack” synthesizes anthocyanins in the fruit peel under light, producing purple fruits thanks to the *myb-atv* and *Aft* alleles. Light and temperature can crucially affect pigmentation in fruits. Whereas high light exposure or cool temperatures are required to allow strong purple colouration, shade or high temperatures repress anthocyanin synthesis.

To investigate this photo/thermo-dependent process, we focused on its major players: COP1, the negative regulator of photomorphogenesis which tags its targets for degradation under dark, and HY5, the master-positive regulator, which activates many processes under light, included anthocyanin biosynthesis.

We evaluated the activity of four BBX factors as HY5 cofactors under light. We analysed their expression levels, possible interactions with HY5 and other light signalling proteins and produced stable overexpression lines showing higher pigment contents.

We also evaluated COP1 and HY5 content under different conditions in the fruit, their gene expressions and molecular targets. We finally showed how COP1 levels in the nucleus increase with temperature, allowing HY5 degradation, and consequent inhibition of anthocyanin production, even under light.

Our study provides new insights into the complex network of light and temperature cross-talk regulating anthocyanin synthesis in tomato fruits.

Poster 34

Variation in the Decoupling between Photosynthesis and Stomatal Conductance under High Temperature Stress in Tropical Trees

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Global climate change is driving increases in both air temperature and atmospheric dryness, or vapour pressure deficit (VPD), significantly impacting plant and ecosystem function. An emerging phenomenon is the "decoupling" of photosynthesis and stomatal conductance (gs), where plants under heat stress exhibit declines in photosynthesis while maintaining or even increasing gs. These dynamics challenge current climate-vegetation models, which assume a tight coupling between photosynthesis and gs to optimise carbon uptake and minimise water loss.

We evaluated the prevalence of decoupling in mature individuals of 16 tropical tree species across four sites along an elevation gradient in Panama. Photosynthesis and gs were measured during temperature response curves from 22 to 48°C, with VPD maintained at 2.5 kPa. We also calculated the key model parameter g1, which is inversely related to intrinsic water use efficiency.

Both photosynthesis and gs generally declined with increasing temperature even when VPD was constant. However, we observed stomatal opening at the highest temperature in some species. Decoupling was evident through an exponential rise in g1 with temperature. The strength of decoupling varied across species and sites, suggesting differences in water use strategies. This work highlights the complexity of high-temperature gs responses in tropical trees.

Poster 35

Proximity labelling for detection of effector-receptor interactions in the Nicotiana benthamiana apoplast

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Zymoseptoria tritici causes Septoria tritici blotch (STB), a damaging disease in all wheat-producing parts of the world. Due to limited genetic diversity in elite wheat cultivars, identifying new resistance sources is critical. This study builds on the observation that several *Z. tritici* effectors are recognised in the non-host plant *Nicotiana benthamiana* but not in the natural wheat host. Our goal is to identify the recognition determinants for these *Z. tritici* effectors which could provide new sources of resistance.

Proximity labelling using TurboID has emerged as a powerful tool for studying proximal and low-affinity protein interactions. However, applying this approach in the apoplast presents significant challenges due to the unique extracellular environment. In a pilot study, we characterised the interaction between the oomycete apoplastic elicitor INF1 and the cell-surface receptor-like protein (RLP) REL to demonstrate the feasibility of proximity labelling in the apoplast. By supplying external ATP and magnesium acetate, we successfully detected biotinylation of plant proteins in the apoplast of *N. benthamiana* leaves. The next step involves confirmation that REL interacts with INF1, through mass spectrometry analysis. Simultaneously, we are extending this approach to investigate the interactomes of the *Z. tritici* effectors Zt9, Zt11, and Zt12. to understand the recognition mechanism(s) for these effectors.

Poster 36

The role of mitotic recombination in the evolution of diatoms

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Mitotic recombination, which can emerge from DNA double strand break repair, can result in significant changes to genes and genomes without sexual reproduction and has been shown to drive evolution, especially in plants. However, even though DNA repair systems are conserved throughout the tree of life, the response to DNA damage in diatoms and how it links to diatom evolution remain unknown. Polar diatoms may have evolved more effective DNA repair mechanisms to combat the greater load of DNA damage due to the extreme environments they are adapted to thrive in. Subjecting three model diatom species to the DNA damaging agent zeocin revealed significant differences between species, with the centric *Thalassiosira pseudonana* being more sensitive than two pennate diatom species. RNA sequencing is underway and may reveal differences in DNA repair pathway regulation. Furthermore, in the temperate diatom *T. pseudonana,* loss of function of the homologous recombination gene *BRCA2* led to a distinct phenotype, which includes increased sensitivity to high temperature and elongated cells. Research is ongoing to repeat experiments with the psychrophile diatom *Fragilariopsis cylindrus* and will help to compare genome evolution between temperate and polar adapted diatoms and may help elucidate adaptations to the changing oceans.

Poster 37

Image-based Genome-Wide Association Studies uncovers the Genetic Basis of GOLVEN10 peptide Control of Root Angle Traits in *Medicago truncatula*

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Root growth towards the environment with adequate supply of nutrients along the gravity vector, while avoiding the non-conducive conditions is critical for plant survival. Small signaling peptides in plants are mobile signals, upon binding with their cell-surface receptors, transmit their information systemically to start a downstream signal relay to eventually control a physiological outcome. In current study, GWAS analysis on 170 *Medicago truncatula* accessions treated with GOLVEN10 peptide was performed to understand three root traits. Association analysis identified 89 significant associations in GLV10p treated accessions. Ethylene biosynthetic pathway genes like Amino-cyclopropane carboxylate oxidase were found to be the putative causal genes involved. Based on these findings, we concluded that GLV10p is involved in regulation of ethylene signaling network in *Medicago truncatula*, leading to circling and agravitropic response of primary roots, reduced lateral root formation and changes in gravitropic-set point angle of lateral roots. To further validate the influence of GLV10p on the ethylene signaling pathway leading tortuous roots, we treated wild A17 with GLV10p,1-aminocyclopropane-1-carboxylic acid and combined application of GLV10p and ACC. Interestingly, the tortuosity was significantly reduced under ACC and combined treatment of GLV10p, and ACC and roots grew straighter towards the gravity which support the proposed hypothesis.

Poster 38

Regulation of water diffusion in non-stomatal plants

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Bryophyta are a basal group of plants that lack stomata and a hydrophobic cuticle in their haploid form. Consequently, these “cell-wall-naked” plants are classified as poikilohydric, meaning they have poor control of water loss. While this classification is widely accepted, it does not fully align with the observed strategies, which range from withstanding dehydration to long-term desiccation tolerance. We studied gas exchange under controlled dehydration conditions. Our results revealed significant variation in transpiration rates, cell wall humidity, and desiccation times across species. These differences could not be explained by tissue water storage relative to the transpiring surface area, suggesting that water loss is not entirely passive. Additionally, we found that active water loss regulation was correlated with pressure-volume derived parameters. Species with better water control also presented traits of an avoidance strategy, including elastic tissues and high capacitance, suggesting an adaptative constraint. These findings point to a basal, non-stomatal mechanism of water loss control through cell membranes and/or cell walls. Potentially, all or part of this mechanism is homologous to the non-stomatal control recently identified in angiosperms, which induces unsaturated conditions in substomatal cavities. Bryophyta present a valuable non-stomatal model for further investigating this mechanism and its evolutionary significance.

Poster 39

Abiotic stress-induced chloroplast and cytosolic Ca^{2+} dynamics in the green alga *Chlamydomonas reinhardtii*

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Calcium (Ca^{2+})-dependent signalling plays a well-characterized role in the perception and response mechanisms to environmental stimuli in plant cells. In the context of a constantly changing environment, it is fundamental to understand how crop yield and microalgal biomass productivity are affected by external factors. However, the knowledge of Ca^{2+} signalling in green algae remains limited, and even if Ca^{2+} is known to be important in different physiological processes in microalgae, many of these signal transduction pathways still need to be characterized. Here, the role of compartment specific Ca^{2+} signalling was investigated in *Chlamydomonas reinhardtii* in response to a range of environmental stressors, such as high light, nutrient availability, osmotic stress, temperature fluctuations and carbon sensing. An *in vivo* single-cell imaging approach was adopted to directly visualize signalling processes at the level of specific subcellular compartments, using *Chlamydomonas reinhardtii* lines expressing a genetically encoded ratiometric Ca^{2+} indicator. Obtained data report cytosolic and chloroplast compartment-specific [Ca^{2+}] transients, characterized by stimulus-specific kinetic parameters. Moreover, a relevant role of the chloroplast Ca^{2+} signalling was identified in response to high light, hyperosmotic shocks, heat stress and different exogenous carbon sources. Together these data will provide new understanding of the mechanisms that microalgae exploit to respond to specific natural conditions.

Poster 40

Decoding GUN1: A Master Regulator of Retrograde Signaling During Chloroplast Development

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The chloroplast is the most important organelle in plant cells, as it converts light energy into chemical energy for the plant survival. Its biogenesis involves two carefully coordinated phases: the first stage is entirely nuclear controlled, while the second relies on the retrograde signaling from plastids to the nucleus. This retrograde signaling is regulated by the pentatricopeptide-repeat-containing protein (PPR) Genomes Uncoupled 1 (GUN1), however, its mechanism remains unclear.

In our laboratory it has been demonstrated that GUN1 negatively regulates several transcription factors (TF) involved in light responses and photomorphogenesis. With the aim of elucidating the mechanism underlying these effects, we performed a proteomic analysis on *Arabidopsis thaliana* mutants lacking GUN1 (*gun1-103)* and mutants with a restored GUN1 function (*gun1-103* GUN1-YFP). In GUN1-deficient plants, two PPR proteins were absent, and these proteins were predicted to interact with GUN1 before and during the second developmental phase. Ongoing assays aim to confirm these interactions.

Altogether, these findings advance our understanding of the role of GUN1 in retrograde signaling. The elucidation of this mechanism could pave the way for innovative strategies in crop improvement.

Poster 41

Manipulation in a mutualism: exploring a role for cross-kingdom RNA interference in arbuscular mycorrhizal symbiosis

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The establishment of arbuscular mycorrhizal (AM) symbiosis is known to encompass many intricate signalling processes within the host plant and AM fungus, including signals exchanged between the two. Recently, it has been proposed that such signals may include small RNAs (sRNAs) acting in cross-kingdom RNA interference (ckRNAi). ckRNAi has most commonly been described in pathogenic interactions between plants and microbes, with inter-organismal transport of sRNAs mediated by extracellular vesicles (EVs); more recent evidence suggests its occurrence in mutualistic endosymbioses, although the mechanism of its action in AM symbiosis remains largely unexplored.

Here, we present evidence from *in silico* analyses of *M.truncatula* sRNAs that are significantly upregulated during AM symbiosis, with predicted targets in the *R.irregularis* genome. Intriguingly, these include genes involved in fatty acid metabolism, suggesting that host-mediated ckRNAi may benefit the host through modulating nutrient exchange. Gene expression analysis of candidate sRNAs and their predicted targets during AM symbiosis indicates a downregulation of predicted targets correlating with the upregulation of the corresponding sRNA; this further correlates with the presence of these candidate sRNAs in EVs as detected from sRNAseq of *M.truncatula*. Our evidence suggests that host-mediated ckRNAi may be a key layer of communication in the arbuscular mycorrhizal symbiosis.

Poster 42

Multiple Mechanisms, Convergent Control: How Neighbour Identity and Phosphorus Influence Water Directionality in the Rhizosheath

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Plants deploy multiple strategies to optimize water acquisition when competing with neighbours, particularly through root adaptations. One adaptation is the rhizosheath - soil that strongly adheres to root surfaces - which can enhance resource capture. Using water and ethanol as liquids to distinguish between physical and biochemical mechanisms, we investigated how timothy grass (*Phleum pratense*) modifies its rhizosheath properties when growing alongside chicory (*Cichorium intybus*) under contrasting soil conditions.

In a soil with naturally high phosphorus levels, timothy enhanced downward water movement in its rhizosheath by 50% when growing with chicory compared to conspecifics, regardless of additional phosphorus fertilization. This directional adaptation, achieved through changes in surface chemistry rather than structural modifications, could enhance rainfall channelling to root tips. However, in a contrasting soil type where phosphorus was limiting, timothy exhibited fundamentally different responses; structural modifications of the rhizosheath became dominant, with phosphorus availability, rather than neighbour identity, controlling water movement.

Our findings reveal that while similar functional changes may occur in the rhizosheath, plants can deploy different mechanisms depending on soil type and competitive context. This plasticity in root-level adaptation highlights how species might coexist in mixed grasslands through dynamic modifications of their resource acquisition strategies.

Poster 43

Role of TCP transcription factors in regulating stomatal development in *Arabidopsis thaliana*

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Stomatal pores of leaves facilitate gas exchange in plants and various environmental signals control their development. In this study, we focused on characterizing the role of plant-specific TCP (TEOSINTE BRANCHED1, CYCLOIDEA, PROLIFERATING CELL FACTOR) family of transcriptional factors, in stomatal development. In a yeast one-hybrid screen, we identified several TCPs as potential transcriptional regulators of *STOMAGEN,* which encodes a mesophyll-derived, secreted peptide that promotes stomatal development. Upon ectopically expressing the TCPs, we found that it dramatically promotes stomatal development in the hypocotyl but only mildly in the cotyledons. This result also correlates with the up-regulation of the *STOMAGEN* transcripts, specifically in the hypocotyl of the ectopic expression lines. Further, reporter analyses showed that both *TCPs* and *STOMAGEN* are expressed in the sub-epidermal tissues of the hypocotyl and are induced by light. Thus, we propose that TCPs function in a tissue-specific manner and up-regulate *STOMAGEN* expression in the sub-epidermal cells of the hypocotyl to promote stomatal development.

Poster 44

Transcriptome plasticity underpins host range expansion in a core member of the root mycobiota

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Plectosphaerella cucumerina, an ascomycete fungus often describe as a necrotrophic fungal pathogen, is one of the most prevalent and abundant fungal taxa that associate with roots of *Arabidopsis thaliana* in natural populations across Europe. Confocal microscopy reveals an endophytic colonization pattern of *P. cucumerina* in roots not only of *A. thaliana* but also of *Solanum Lycopersicum* and *Hordeum vulgare*. However, the mechanisms driving its broad host-range, and robust *A. thaliana* root colonization capabilities remain poorly known. This project aims at understanding host colonization strategies, genetic determinants driving adaptation to different hosts, and dominance in the root microbiome using transcriptomic and experimental evolutionary approaches. Results reveal that there is a unique fungal transcriptional response activated in response to the different plant species. Particularly, genes encoding carbohydrate active enzymes are strongly activated in response to all three plant species and large subsets display host-specific activation that reflect plant cell wall compositions of the hosts. Experimental evolution of the fungus in response to the three plant species has been performed and reciprocal inoculation revealed that the strain evolving on *H. vulgare* became less detrimental on dicot hosts. Additionally using CRISPR-mediated genome editing, we demonstrate that the glucan-degrading enzyme family GH64 connects the aggressiveness of endophytic colonization to the health of dicot plants.

Poster 45

One Leaf, Many Ages: Ontogenetic Zonation in Welwitschia mirabilis

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Welwitschia mirabilis is an iconic and evolutionarily ancient plant that has persisted for millennia in the hyper-arid deserts of southwestern Africa. While its unusual leaf morphology has long fascinated researchers, few studies have examined how internal structure changes as the leaf ages. This study investigates anatomical shifts along the length of *W. mirabilis* leaves to uncover how structural traits support long-term function in extreme environments.

Using detailed microscopy and morphometric analysis, leaf traits were quantified across zones of increasing distance from the basal meristem, corresponding to tissue age. Principal component analysis and regression models revealed coordinated increases in traits such as leaf mass per area (LMA) and tissue density with age, suggesting investment in durability over time. Meanwhile, features related to gas-exchange remained relatively stable, indicating a functional balance between persistence and photosynthetic capacity.

By analysing within-leaf trait zonation in a single, lifelong organ, this work provides rare insight into how ancient plants manage the trade-off between longevity and function. These findings echo canopy-level ageing patterns seen in modern evergreens, but within a single, continuous leaf. Understanding these relationships has broader implications for plant adaptation, climate resilience, and the evolution of leaf structural diversity under environmental stress.

Poster 46

SlMIPS2, a *myo*-inositol phosphate synthase, regulates phosphate homeostasis influencing SPX-PHR module in tomato seedlings

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Department of Plant Sciences, University of Hyderabad, Hyderabad, India

Phosphorus (P) is an essential macronutrient utilized by plants to support various metabolic processes during growth and development. Recent studies have revealed the pivotal role of inositol hexakis/pyrophosphates (InsP6–8), the derivatives of *myo*-inositol (MI), in facilitating the interaction between SYG1/PHO81/XPR1 (SPX) and phosphate starvation response (PHR) proteins. *myo*-Inositol phosphate synthase (MIPS) catalyses the first committed step in MI biosynthesis. Although the role of *MIPS* members in mediating stress responses in plants is well elucidated, their role in phosphate (Pi) deficiency remains largely unexplored. This study demonstrates *SlMIPS2* is sharply induced at an early stage of Pi starvation in tomato seedlings. Silencing of *SlMIPS2* led to improved seedling growth with enhanced soluble Pi and total P levels, and also caused a significant reduction in MI and InsP6 content in tomato seedlings under high Pi availability. These seedlings with depleted InsP6 levels accumulated lower levels of SlSPX2 protein. In contrast, stabilized SlPHL1 levels were noticed in these plants, directly implicating it in activating phosphate-starvation-inducible genes in the silenced seedlings, even under high Pi conditions. The results assign a novel role to SlMIPS2 in regulating cellular InsP6 levels and SPX–PHR interactions to control Pi homeostasis in tomato seedlings.

Poster 47

Alternative ways to deal with salinity

Jennifer Saile ORCID iD
Wageningen University & Research, Laboratory of Plant Physiology, Wageningen, Netherlands

Salt stress is a major abiotic stress that severely affects plant growth and development, causing crop losses worldwide. Therefore, it is crucial to understand the molecular mechanisms by which plants perceive and adapt to high salinity. While transcriptional responses to salt stress are well studied, the role of post-transcriptional regulation remains less explored. Alternative splicing (AS) is a post-transcriptional mechanism that generates multiple mRNA variants from a single precursor mRNA. It is increasingly recognized as critical for plant responses to salinity. However, the key regulators of salt-regulated AS, their target genes, and their roles in developmental plasticity and salt tolerance are largely unknown. Using a phospho-proteomic approach, we identified splicing regulators from the serine/arginine-rich (SR) family that are specifically phosphorylated in response to NaCl, Na^+ (NaCl and $NaNO_3$), or osmotic stress. These proteins are promising candidates for controlling salt-regulated AS. We are currently analyzing the functional significance of SR proteins and their phosphorylation state in salt-induced AS. Preliminary phenotypic analyses show that *rs* mutants are hypersensitive to salt, suggesting that RS proteins may positively regulate salt tolerance. Our findings propose that salt and osmotic stress induce phosphorylation-dependent changes in SR protein activity, which modulates AS and influences salt stress responses.

Poster 48

MAX effectors meet HMA domains: Decoding susceptibility in rice blast disease

Svenja Saile ORCID iD
INRAE, Montpellier, France

The rice blast fungus, *Magnaporthe oryzae,* causes severe yield losses in global rice production. To promote host susceptibility, it secretes effector proteins, including the sequence diverse but structurally related *Magnaporthe* AVRs and ToxB-like (MAX) effectors. Despite their importance during early infection, the virulence functions of MAX effectors and their host targets remain poorly understood.

Heavy metal-associated (HMA) domain-containing proteins have emerged as key susceptibility factors in plant-pathogen interactions. HMA domains have also been integrated into rice immune receptors, enabling direct recognition of various MAX effectors. For instance, the MAX effector AVR-Pia is detected by the RGA5 immune receptor through direct binding to its HMA domain. Recently, we found that AVR-Pia also interacts with the HMA domains of a subset of rice HMA Plant Proteins (OsHPPs), and of a related HMA Isoprenylated Plant Protein (OsHIPP). Unlike other MAX effectors, which alter HIPPs' stability and localization, AVR-Pia appears to use a distinct mechanism to manipulate these proteins.

Our ongoing research aims to unravel the molecular roles of these H(I)PPs and the mechanisms through which AVR-Pia manipulates them, providing insights into how these interactions enhance rice susceptibility to *M. oryzae*. These findings could help develop effective strategies to combat rice blast disease.

Poster 49

The above- and belowground phenology of Picea abies in response to short and long-term heat episodes

Marili Sell ORCID iD
University of Tartu, Tartu, Estonia

The air temperature in Estonia is projected to increase, affecting the growth of economically and ecologically significant tree species used for regenerating forests. Aboveground shoot growth and the development of root system do not respond the same way in response to different environmental changes.
Four-year-old Picea abies seedlings were grown separately in transparent boxes in growth chambers. We conducted two separate experiments where heat treatment were simulated by decreasing relative air humidity and soil moisture and increasing air temperature in short and long-term scales. We imaged fine roots with a smartphone, and images were analysed by the deep learning method-based program RootPainter. From that, we have data on the total fine root projection area and the area of young white root tips. Shoot growth was measured manually.
The shoot phenology followed a well-known pattern; the length of shoots increased fast at the beginning of the growing season and after stabilisation, the fine root growth proliferated. The treatments had less effect on aboveground phenology compared to belowground changes. The belowground growth dynamics was greatly affected by soil moisture changes, as predicted. After experiencing three weeks of harsh drought, the spruce seedlings showed good recovery, especially in immense pioneer root growth.

Poster 50

The effects of drought on tropical root growth and nutrient cycling in tropical forests

Rachel Selman
The University of Edinburgh, Edinburgh, United Kingdom

Tropical forests in Amazonia are essential for the regulation of global biogeochemical cycles. Prolonged drought stress can be a significant driver of change in tropical ecosystems and there is uncertainty about how this effects soil carbon cycling and nutrient turnover. This research aims to measure the effects of drought on tropical plant fine root morphological strategies and root productivity and subsequent implications for nutrient cycling processes. The study site is ESCAFOR (Efeitos da Seca da Floresta), a throughfall exclusion (TFE) experiment in Caxiuaña National Forest, Pará State, Brazil, established in 2001. This site consists of a 1-hectare plot covered by clear polythene panels that exclude 50% of the rainfall and a replica 1-hectare natural control plot. The experiment provides a unique opportunity to study the effects of drought on forest ecosystem functioning following 23 years of drought treatment. Root biomass and morphological measurements were taken from root samples collected every 3 months from in-growth cores and compared between the drought and control plot alongside measurements of soil moisture and soil nutrient content. These comparisons will shed light on how long-term drought influences wider tropical forest carbon and nutrient cycling processes.

Poster 51

ABA-signaling differs between the extremophyte *Eutrema salsugineum* and its close glycophytic relative *Arabidopsis thaliana*

Lina Spiller ORCID iD
Julius-Maximilians-University of Wuerzburg, Wuerzburg, Germany

With abiotic stress playing a major role in agricultural crop loss, it is becoming ever more important to understand the molecular mechanisms behind stress responses in plants, to counteract the global climate change and ensure sustainable crop yields. The phytohormone abscisic acid (ABA) plays a crucial role in stress response and, though the signal pathway has been widely studied, quantitative data describing the massive protein-protein-interaction rearrangements within the core signaling complex are widely lacking. This project serves to advance the understanding of protein-protein interaction dynamics within the core ABA-signaling complex through comparative characterization of ABA receptors between the glycophyte *Arabidopsis thaliana* and its close halophytic relative plant *Eutrema salsugineum*. An optimized bimolecular luminescence complementation (BiLC) assay was established and applied to study and quantify the interactions between ABA-receptors (PYLs) and the PP2C phosphatase (ABI1). The obtained insights into the dynamics and affinities revealed a significant difference between the two model plants: the interaction of EsPYL3 with ABI1 showed a 5-fold higher ABA-affinity than the *Arabidopsis thaliana* orthologue. Accompanying structure-function research identified the structural basis of the differing ABA-affinities. To which extent the increase in ABA-affinity has contributed to the stress tolerance of *Eutrema salsugineum*, will be analyzed through following phenotyping studies.

Poster 52

Long-distance defence signalling is modulated by jasmonic acid and abscisic acid in *Arabidopsis thaliana*.

Erin Stroud ORCID iD
University of Warwick, Coventry, United Kingdom

Pathogen-induced activation of host resistance proteins (Effector Triggered Immunity, ETI) induces broad-spectrum systemic protection against subsequent infections, termed Systemic Acquired Resistance (SAR). Salicylic acid (SA) is classically associated with SAR induction almost at the exclusion of other phytohormones. We demonstrate a concerted role for jasmonic acid (JA), abscisic acid (ABA), electrical and calcium signalling in the earliest stages of SAR signal propagation and translocation. Using the *JASMONATE-INDUCED SYSTEMIC SIGNAL 1* (*JISS1*) promoter, temporal-spatial dynamics of ETI-elicited SAR signalling were monitored at the whole plant and subcellular levels using *JISS1:LUC* and *JISS1:GFP* lines, respectively. Systemic *JISS1:LUC* signalling was observed following challenge with ETI-inducing bacterial pathogen *Pseudomonas syringae* pv. *tomato* strain DC3000 (DC), and *JISS1* expression was upregulated rapidly following infection. Pre-treatment of *A. thaliana* with ABA prior to infection abolished *JISS1:LUC* induction. *JISS1:LUC* signalling was unaffected in SA pathway mutants, but was abolished in JA mutants. Systemic *JISS1:LUC* signalling was also observed in response to the fungal pathogen *Sclerotinia sclerotiorum.* Consistent with literature on JA-dependent wounding responses, ETI-activated systemic electrical potentials were dependent on both jasmonate signalling and *JISS1.* Together, these results indicate that JA, but not SA, signalling is crucial for eliciting *JISS1*-mediated systemic defence to DC in *A. thaliana.*

Poster 53

The non-linearity of tundra warming responses, their thresholds, and their mechanisms

Kohsuke Tanigawa ORCID iD
Swedish University of Agricultural Sciences, Umeå, Sweden

Cold climate ecosystems are particularly vulnerable to warming, with ongoing climate change posing high risks to their essential functions such as carbon storage. The responses of these ecosystems to warming arise from complex combinations among individual components including plants, soil microbes, and interactions between them such as plant-soil and plant-plant dynamics. Importantly, the decoupling of plant and soil responses to warming could disrupt these interactions, potentially leading to non-linear shifts in ecosystem functionality as thresholds of warming are surpassed.

With the objective to test the existence and mechanisms of these thresholds and to better understand the warming responses of the Swedish tundra, we tested the warming responses of various tundra ecosystem components: soil and its microbial communities, understory herbs and ericaceous and ectomycorrhizal shrubs, overstory ectomycorrhizal trees, and the interactions between them. These tests were conducted through controlled climate chamber experiments with multiple combinations of plants and soils, and tested in the field with field soil transplantation experiments. My presentation provides an overview of the results of the experiments I conducted, and attempts to propose a unified theoretical framework for understanding the non-linear responses and thresholds of tundra ecosystems under global warming.

Poster 54

The ecology of woody encroachers: Identifying the species and their ecological strategies driving savanna change

Elizabeth Telford ORCID iD

University of Sheffield, Sheffield, United Kingdom. Royal Botanic Gardens Edinburgh, Edinburgh, United Kingdom

The savannas are vast reservoirs of unique disturbance-adapted plant diversity with these ecosystems directly supporting the livelihoods of 15% of the global population. The near future of savannas are uncertain due to large increases in woody cover (encroachment) that negatively impact biodiversity, changing ecosystem functioning. Encroachment is an overlooked but highly pervasive global change impact on savannas affecting over 5 million km^2 with extensive regions of Africa being rapidly transformed. To date, research has focused on quantifying encroachment extent and its environmental correlates. Using invasion ecology frameworks our study makes a pivotal shift to examine the species driving encroachment. What are they? Are these species a random subset of the available species pool? We examined the species of the dominant genera of African savannas *Dichrostachys, Prosopis, Senegalia, Vachellia, Combretum*, and *Terminalia* and found that the species responsible for continental-scale vegetation change is driven by just 63 species classified as encroachers. Furthermore, encroachers differ systematically from non-encroachers, exhibiting broader environmental tolerances, larger geographic range sizes, a propensity for traits related to tall stature, and a flexible plant habit. Our findings suggest encroachers are a specific group of species with an ecology responsive to global change drivers such as rising atmospheric CO_2, altered fire and herbivory regimes.

Poster 55

Optimising strawberry propagation in TCEA systems

Keiri Winnie Swann
Reading University, Reading, United Kingdom

The UK strawberry industry produced 106,400 tonnes of fruit in 2023, worth £421M (DEFRA, 2023), yet production per hectare must increase significantly to reduce reliance on imported fruit (60,000 tonnes worth £232M in 2023). Major limitations include high labour and plant material costs, pest and disease control, unmarketable fruit, variable yields, and unfavourable weather. Improving marketable yield per plant, rather than increasing plant density or area, is key to addressing these challenges.

Variable marketable yield per plant, both in-field and under controlled conditions, often results from uneven planting material quality, much of which is imported, and latent pests and diseases that emerge post-planting. While some growers propagate their own material to overcome this, variable UK weather can limit the potential of these propagules, particularly out-of-season.

Total Controlled Environment Agriculture (TCEA) systems provide a promising solution for year-round production of high-health, high-yielding strawberry propagules. In a three-year project funded by Defra's Farming Innovation Programme, we are investigating the effectiveness and economic viability of TCEA for producing disease-free, high-cropping plants. Our research focuses on how light intensity and carbon dioxide enrichment during propagation influence plant quality and photosynthesis. Initial results will be shared to demonstrate the potential of TCEA in transforming UK strawberry propagation.

Poster 57

Can AI modelling of protein structures distinguish between sensor and helper NLR immune receptors?

AmirAli Toghani ORCID iD
The Sainsbury Laboratory, Norwich, United Kingdom

NLR immune receptors can be functionally organized in genetically linked sensor-helper pairs. However, methods to categorize paired NLRs remain limited, primarily relying on the presence of non-canonical domains in some sensor NLRs. Here, we propose that the AI system AlphaFold 3 can classify paired NLR proteins into sensor or helper categories based on predicted structural characteristics. Helper NLRs showed higher AlphaFold 3 confidence scores than sensors when modelled in oligomeric configurations. Furthermore, funnel-shaped structures—essential for activating immune responses—were reliably predicted in helpers but not in sensors. Applying this method to uncharacterized NLR pairs from rice, we found that AlphaFold 3 can differentiate between putative sensors and helpers even when both proteins lack non-canonical domain annotations. These findings suggest that AlphaFold 3 offers a new approach to categorize NLRs and enhances our understanding of plant immune systems' functional configurations, even without non-canonical domain annotations.

Poster 58

Phenotypic plasticity masks evolutionary change in grassland plant traits in response to land use abandonment.

Anastasia Tõnisson ORCID iD

University of Tartu, Tartu, Estonia

Traditionally managed grasslands are among Europe's most biodiverse habitats but are threatened by land abandonment. While the negative effects of grazing cessation on species richness are well known, its evolutionary impacts remain understudied. Intraspecific functional diversity is crucial for grassland restoration and adaptation to climate change.

We investigated trait responses in *Briza media*, a common grass, across 11 pairs of grazed and abandoned grasslands along the Baltic Sea coast. At abandoned sites, plants exhibited phenotypic plasticity, with traits like greater height and specific leaf area enhancing light competition but reducing stress tolerance (lower dry matter content). However, clonal offspring grown under common conditions showed heritable shifts toward greater tissue protection at abandoned sites, revealing countergradient variation.

Trait diversity measured in the field was higher at abandoned sites due to greater variation in light and litter conditions. Yet, heritable trait variation was greater in grazed populations, which were characterized by higher species richness and flowering densities.

Our results show that land-use change drives evolutionary shifts and reduces heritable trait variation, which phenotypic plasticity in the field can mask. Thus, field-based trait diversity assessments may not reliably capture the heritable variation critical for population adaptation.

Poster 59

Arbuscular mycorrhizal mixotrophy in green plants

Cas Verbeek ORCID iD

Naturalis Biodiversity Center, Leiden, Netherlands. University of Amsterdam, Amsterdam, Netherlands

Living in the roots of plants, arbuscular mycorrhizal fungi (AMF) aid the plant with the acquisition of otherwise inaccessible mineral nutrients. In exchange, plants supply the AMF with photosynthetic products which serve as the fungus' sole source of carbon that it uses to grow its mycelium. Having lost all chlorophyll and therefore the ability to photosynthesize, rare mycoheterotrophic plants cheat this symbiosis and rely on AMF supplied carbon instead, thus acting as indirect parasites on the surrounding vegetation. However, recent evidence using stable isotopes of carbon and nitrogen (^{13}C and ^{15}N) has shown that many green plants may also tap into this carbon source, indicating that the partial mycoheterotrophic (or arbuscular mycorrhizal mixotrophic) mode of life might be present in up to 40% of all land plants. Therefore, the goal of my PhD project is to determine (i) how common AM partial mycoheterotrophy is and in which environments it occurs, (ii) which fungi are involved and (iii) how these plants and fungi are linked through mutualistic interaction networks. Mixotrophy is expected in plants with the *Paris* symbiotic morphotype in the shaded understory of (tropical) forests and these plants are expected to preferentially interact with well-connected generalist AMF, similar to mycoheterotrophs.

Poster 60

Root nitrogen uptake extends beyond leaf and root growing seasons in wetland monocots

Ziqi Ye ORCID iD
Laurentian University, Sudbury, Canada

All plant functions vary seasonally; however, root phenology is not well understood, with research mainly focusing on root production. The question remains, how does the phenology of root senescence and nutrient uptake relate to root production phenology and species functional traits.

Using ^{15}N isotope addition and whole-plant organ harvests, we investigated root production and nitrogen uptake phenology over 18 months in Northern Ontario for four wetland monocots in a common garden experiment. These species represent distinct root overwintering strategies: overwintering roots (resource-conservative) and annual roots (acquisitive).

Production of annual roots peaked in summer and stopped by August, while overwintering root production peaked in autumn, with 50% of their annual production from August to October. However, nutrients are taken up during seasons without new root growth: Annual roots still absorbed added 15N to rhizomes in October, and overwintering roots absorbed 15N early in spring and even in winter (soil temperature 0–5°C). Seasonal variation in the N concentration indicates a storage function for overwintering roots, similar to that of rhizomes.

Shoulder seasons fall and spring can be crucial for below-ground processes, particularly nutrient uptake and accumulation, with this importance varying by species and potentially linked to their economic strategies.

Poster 61

Role of flavonols in petal pigmentation and morphogenesis in a small group of Hibiscus

Selin Zeyrek ORCID iD
Sainsbury Laboratory, University of Cambridge, Cambridge, United Kingdom

Angiosperm co-evolution with pollinators has resulted in the explosion of petal patterns we see today. Colourful patterns displayed on the petal epidermis play crucial roles in attracting, selecting and guiding pollinators thus affecting reproductive fitness and speciation. However, how plants create those motifs is unclear.

The petals of Hibiscus trionum, a new model organism, sport a striking bullseye with a purple centre and cream surround separated by a narrow boundary region. Epidermis cells in the different bullseye domains have distinct identities, exhibiting specific colour, shape and texture. Flavonols give the distal region its distinctive cream colour; transcriptome and LC-MS analyses indicate they may also regulate cell shape and texture.

Modifying expression of the three H. trionum FLAVONOL SYNTHASE (FLS) genes directly or through their putative regulators results in plants with striking floral developmental defects, including: arrested cell development, irregular cell shape and aberrant organ development. I am now investigating the as-yet unknown mechanism by which flavonols contribute not only to pigmentation but also to cell shape and size specification during bullseye formation. Ultimately, my results should provide us with an understanding of the morphogenic action of flavonols and their contribution to the production of diverse bullseye morphologies during evolution.

Poster 62

Coordinated plant-nematode ecological trait dimensions shape soil carbon pools and fluxes

Chongzhe Zhang ORCID iD
Nanjing Agricultural University, Nanjing, China

An important aim of ecology is to understand the ecological strategies of organisms, how strategies relate to species traits, how traits and strategies of species affect ecosystem functions, and how these effects may be mediated by, or affect, other species. As for many aspects of ecology, far less is known about the world belowground than aboveground. For the plant roots there seems agreement about two main trait-strategy dimensions. But what about the soil fauna? For example, what are the ecological strategies of soil nematodes, a group that plays key roles in ecosystem carbon cycles? From sampling grasslands, shrublands and forests forming a natural restoration chronosequence, we first identified the primary trait-strategy dimensions of nematodes and quantified their relationships with plant trait-strategy dimensions. For nematodes, one major dimension concerned reproduction, with species varying from low to high fecundity. This dimension aligned with the root collaboration dimension. The other represents a “nematode economics spectrum”, or NES, that represents strategies from rapid growth potential to longevity. Variation along the NES is coordinated with the root economics spectrum. We then assessed how these coordinated trait-strategy dimensions contributed to soil carbon dynamics. The collaboration–reproduction dimension is related to carbon fluxes while the fast–slow continuum is associated with carbon pool size.

Poster 63

Limonene emission in transgenic tobacco downregulates APX activity under drought

Hao Zhou ORCID iD
Lancaster University, Lancaster, United Kingdom

Drought stress affects the production of volatile organic compounds such as monoterpenes, but their role in regulating plant stress responses is unclear. Wild-type tobacco plants that do not naturally produce monoterpenes, and transgenic plants with upregulated monoterpene production, particularly (−)-limonene (LG12), myrcene (MG1), and (−)-α/β-pinene (PG11), were allowed to dry the soil in different compartments to avoid non-target effects of monoterpene compounds. Drought initially increased monoterpene emissions, which subsequently declined as stress intensified. Transgenic plants exhibited reduced biomass and leaf area, and despite maintaining higher leaf water potential and turgor than wildtype plants, transgenic plants had slightly more sensitive stomatal conductance under drought stress. Although drought-enhanced foliar hydrogen peroxide (H_2O_2) content and superoxide dismutase (SOD) activity did not significantly differ between genotypes, (–)-limonene production downregulated ascorbate peroxidase (APX) activity and increasing malondialdehyde (MDA) content under drought conditions compared to wildtype plants. However, re-watering restored APX activity and decreased oxidative damage, and seed production did not differ between genotypes. Thus, monoterpene biosynthesis and production modulate drought tolerance by affecting leaf water status and oxidative status but doesn’t interfere with photosynthetic processes under drought stress. Future research should explore the regulatory mechanisms linking monoterpene biosynthesis and emission to hormonal and antioxidant processes, as well as their interaction with native signalling pathways.

Poster 64

Uncovering mechanisms and pathways underlying root growth angle regulation in response to drought stress

Sibongile Zimba ORCID iD
University of Bristol, Bristol, United Kingdom. University of Leeds, Leeds, United Kingdom

Optimising root phenotypes for improved resource capture under drought, is an unexploited opportunity for sustainable agriculture in the context of climate change and global warming. Root system architecture (RSA) is potentially programmable component for crop improvement due to its plasticity. Knowledge of the molecular mechanisms underlying the effect of drought on root growth angle (RGA) during drought remains limited. Here, we investigate mechanistic pathways underlying sorghum RGA regulation under drought conditions. We screened sorghum RSA using high-throughput phenotyping protocols in varying drought stress and control conditions followed by high-throughput transcriptomic analyses. Our results reveal that RSA vary dramatically across genotypes with differing drought adaptability. Further analyses shows that the nodal RGA is a significant component of this variation. This study demonstrated that the RGA of seedlings can support later field performance predictions, and therefore, a potential target for breeding. It further shows that drought influences steeper, deeper rooting in water-stress-tolerant varieties. The study further identified drought-dependent regulation of auxin-responsive genes not yet characterised in sorghum, which may play a crucial role in regulating RSA in response to drought. Our data provide a practical framework for the targeted selection of germplasm as valuable pre-breeding material of high-yielding varieties that are robust to climate change and have optimized growth in low-input conditions.

The following posters presenters are members of the organising committee, and are not eligible for the poster prize.

Poster A

Investigating early stages of infection in bacterial cherry canker disease using a metabolomics approach

Andrea Vadillo Dieguez ORCID iD
School of Biosciences and the Birmingham Institute of Forest Research, University of Birmingham, United Kingdom

Bacterial cherry canker poses a significant threat to *Prunus avium*, resulting in leaf spots, cherry fruit necrosis or water soaking, and wood necrotic cankers, negatively impacting crop production and plant health across horticultural, ornamental, and wild settings. This disease is caused by strains within the *Pseudomonas syringae* species complex (Ps). Virulence factors, such as type III effector proteins and phytotoxins, enable bacterial proliferation and disease manifestation. There has not yet been any detection of a resistant cultivar of *P. Avium* to this disease, highlighting the importance of studying molecular plant-pathogen interactions to understand the disease process and to improve breeding lines. This study investigated the disease progression dynamics and metabolic plant responses during early infection stages. Artificial inoculation of plants utilising *Pseudomonas syringae pv. syringae (Pss)* 9644 and *Pss* effector and toxin deletion mutants was conducted on susceptible *P. avium* cut shoots. The disease progression was monitored over four weeks post-inoculation (wpi). Results showed that deletion of a majority of, or all, virulence factors significantly impeded growth and lesion development. However, deletion of toxins allowed the bacteria to grow and show disease symptoms. Untargeted metabolomics analysis on the WT and mutant-infected woody tissue help to discover differential metabolic features that could be biomarkers of disease that belong to the carboxylic acid, organonitrogen and triterpene class compounds among others. This analysis will provide further insights into the metabolic responses of cherry plants to bacterial canker."

Poster B

Explaining the variation in mesophyll airspace resistance: A physiological basis linked to CO_2 diffusivity in the liquid phase

Diego A. Márquez ORCID iD
University of Birmingham, United Kingdom

Mesophyll conductance to CO2 (gm) often varies under different physiological conditions, even in the absence of anatomical changes. In this study, we show that this variation can be explained by changes in the diffusivity of CO2 in the liquid phase (Dliq).

Using a dual-surface gas exchange framework to estimate the CO2 concentration at the mesophyll surface (cw), we observed apparent variation in mesophyll airspace resistance (ri). However, since the structure of the intercellular airspace remained unchanged, these apparent shifts in ri must arise from downstream effects.

Specifically, increased liquid-phase diffusivity alters the distribution of fluxes across parallel gas-phase pathways, shifting the effective weighting between gas and liquid paths. This reallocation leads to measurable changes in cw, even though airspace properties remain constant.

Our results suggest that liquid-phase facilitation mechanisms—possibly involving carbonic anhydrase—underlie the observed variability in gm. These findings challenge the assumption that anatomical features alone govern gm and highlight the physiological regulation of CO2 diffusion within the leaf

Poster D

Changed fine root biomass and morphology in a mature temperate forest under elevated CO_2

Grace Handy ORCID iD
University of Birmingham, United Kingdom

Evidence suggests that forests can sequester more carbon under elevated carbon dioxide (eCO_2), yet it remains unclear where and for how long this carbon is stored. Forests' capacity to remain as carbon sinks under eCO_2 may depend on tree root systems adjusting to overcome potential nutrient and water limitation. It remains uncertain whether and how root systems can change across depth under eCO_2 in mature forests. Here we assess fine root biomass, morphology and depth distribution using 1 m deep soil cores from BIFoR FACE, an oak dominated, mature, deciduous, free-air CO_2 enrichment experiment (+150 µl/L i.e. mid-21st century projected atmospheric CO_2 concentration). We show that fine root biomass was ~40% greater under eCO_2, concentrated in the top 50 cm of soil and equivalent to ~36% more root carbon standing stock. The distribution of fine root biomass did not shift to greater depths, but changes in fine root morphology showed higher specific root length with increasing depth. Therefore, mature forest root systems can adapt under eCO_2, with greater fine root biomass and changes in morphology leading to a larger fine root surface area and greater potential for resource acquisition across the soil profile.

List of participants

Event role	First name	Last name	Affiliation	Country
Selected speaker	Rakesh	Achary	NIPGR, New Delhi	India
Selected speaker	Seyi	Adeboye	Nat. Biotechnology Research& Dev Agency	Nigeria
Selected speaker	Enimhien	Akhabue	University of Exeter	United Kingdom
Poster presenter	Jumana	Akhtar	University of Bristol	United Kingdom
Poster presenter	Viraj	Alimchandani	IRBV, Université de Montréal	Canada
Mentor	Amy	Austin	University of Buenos Aires	Argentina
Mentor	Carlos	Ballare	Universidad de Buenos Aires and CONICET	Argentina
Mentor	Anjan	Banerjee	IISER Pune	India
Poster presenter	Aakash	Basi	University Of Birmingham, CENTA	United Kingdom
Selected speaker	Billur	Bektaş	ETH Zürich	Switzerland
Mentor	Adesola	Bello	University of Birmingham	United Kingdom
Mentor	Yoselin	Benitez-Alfonso	University of Leeds	United Kingdom
Mentor	Richard	Betts	University of Exeter and Met Office	United Kingdom
Poster presenter	Viviana	Bondaruk	University of Buenos Aires	Argentina
Mentor	Philippa	Borrill	John Innes Centre	United Kingdom
Poster presenter	Jack	Bosanquet	University of Birmingham	United Kingdom
Mentor	Claire	Butler	University of Birmingham	United Kingdom
Poster presenter	Rachel	Calder	University of Birmingham	United Kingdom
Poster presenter	Imogen	Carter	University of Leeds	United Kingdom
Selected speaker	Jeky	Chanwala	Umeå Plant Science Centre	Sweden
Selected speaker	Joanna	Chustecki	The University of Oxford	United KIngdom
Poster presenter	Gabby	Clarke	University of Birmingham	United Kingdom
Selected speaker	Catherine	Collins	University of Sheffield	United Kingdom

Poster presenter	Tony	de Oliveira	Forschungszentrum Jülich GmbH	Germany
Poster presenter	Richard	Dekeya	John Innes Centre	United Kingdom
Mentor	Samantha	Dobbie	University of Birmingham	United Kingdom
Mentor	Caroline	Durbin	University of Birmingham	United Kingdom
Poster presenter	Nabila	El Arbi	The Spring Institute for Forests on the Moon	France
Selected speaker	Robyn	Emmerson	University of Birmingham	United Kingdom
Keynote	Maria	Ermakova	Monash University	Australia
Mentor	Katie	Field	University of Sheffield	United Kingdom
Local organising committee	Christine	Foyer	University of Birmingham	United Kingdom
Keynote	Noni	Franklin-Tong	University of Birmingham	United Kingdom
Poster presenter	Zishan (Sannie)	Fu	University of Edinburgh	United Kingdom
Mentor	Costa	Garagounis	PCR Biosystems Ltd.	United Kingdom
Local organising committee and poster presenter	Anna	Gardner	University of Birmingham	United Kingdom
Mentor	Alice	Gauthey	University of Birmingham	United Kingdom
Poster presenter	Caterina	Giannini	ISTA	Austria
Mentor	Sarah	Gibbons	The New Phytologist Foundation	United Kingdom
Local organising committee	Dan	Gibbs	University of Birmingham	United Kingdom
Selected speaker	Danny	Ginzburg	University of Cambridge	United Kingdom
Mentor	Julie	Gray	University of Sheffield	United Kingdom
Poster presenter	Matteo	Grenzi	University of Milan	Italy
Local organising committee and poster presenter	Grace	Handy	University of Birmingham	United Kingdom
Poster presenter	Emma	Hardy	University of Dundee	United Kingdom
Poster presenter	Shomari	Healy	University of Birmingham	United Kingdom

Mentor	Alistair	Hetherington	University of Bristol	United Kingdom
Mentor	Hanna	Hõrak	University of Tartu	Estonia
Poster presenter	Lorena	Huffer	Institute of Experimental Botany	Czechia
Selected speaker	Amina	Ilyas	Institute of Plant Science Paris-Saclay	France
Mentor	Jonathan	Ingram	John Wiley & Sons Ltd	United Kingdom
Poster presenter	Skylar	Johnson	University of Exeter	United Kingdom
Selected speaker	Karolina	Jörgensen	Swedish Uni. of Agricultural Sciences	Sweden
Poster presenter	Anna	Kampova	Charles University	Czech Republic
Mentor	Maxim	Kapralov	Newcastle University	United Kingdom
Poster presenter	Debojyoti	Kar	IISER Bhopal	India
Poster presenter	Said	KHOURCHI	Mohammed VI Polytechnic University	Morocco
Mentor	Anne	Knowlton	Current Biology	Germany
Keynote	Britt	Koskella	UC Berkeley	United States
Selected speaker	Pravesh	Kundu	CSIR-IHBT Palampur	India
Poster presenter	Novalia	Kusumarini	University of Birmingham	Indonesia
Poster presenter	Lucrezia	Laccetti	University of Naples Federico II	Italy
Local organising committee	Lisa	Lamberte	University of Birmingham	United Kingdom
Poster presenter	Hana	Leontovycova	Institute of Experimental Botany AS CR	Czechia
Selected speaker	Jiaze	Li	Imperial College London	United Kingdom
Poster presenter	Shey Li	Lim	The University of Hong Kong	Hong Kong
Mentor	Keith	Lindsey	Durham University	United Kingdom
Mentor	Claire	Litchfield	University of Birmingham Enterprise	United Kingdom
Mentor	Marjorie	Lundgren	Lancaster University	United Kingdom
Selected speaker	Julien	Luneau	University of Lausanne	Switzerland
Local organising committee and keynote speaker	Rob	MacKenzie	BIFoR, University of Birmingham	United Kingdom

Poster presenter	Rachel	Mailes	University of Birmingham	United Kingdom
Poster presenter	Lamya	Majeed	University of Birmingham	United Kingdom
Keynote	Nokwanda (Nox)	Makunga	Stellenbosch University	South Africa
Poster presenter	Vishwadeep	Mane	Indian Institute of Science	India
Local organising committee and poster presenter	Diego	Márquez	University of Birmingham	United Kingdom
Staff	Holly	Martin	University of Birmingham	United Kingdom
Poster presenter	Ana	Medina-Fraga	University of Buenos Aires	Argentina
Poster presenter	Lilian	Melo	Uppsala University	Sweden
Poster presenter	Jacopo	Menconi	Sant'Anna School of Advanced studies	Italy
Selected speaker	Sara	Mendes	Consejo Superior de Investigaciones Científicas (CSIC)	Spain
Selected speaker	Carey	Metheringham	University of Dundee	United Kingdom
Poster presenter	Kali	Middleby	IRD Occitanie	France
Poster presenter	Abdelrahman	Mohammad	University of Birmingham	United Kingdom
Selected speaker	Ayla	Mongès	Lund University	Sweden
Mentor	Matthew	Naish	University of Cambridge	United Kingdom
Mentor	Carl	Ng	University College Dublin	Ireland
Local organising committee	Rich	Norby	University of Birmingham	United States
Selected speaker	Expedito	Olimi	University of Southampton	United Kingdom
Selected speaker	Monika	Opatíková	Palacký University Olomouc	Czech Republic
Keynote	Maarja	Öpik	University of Tartu	Estonia
Mentor	Rory	Osborne	University of Birmingham	United Kingdom
Poster presenter	Antonia	Otte	University of East Anglia	United Kingdom
Mentor	Ralph	Panstruga	RWTH Aachen University	Germany
Poster presenter	Rajni	Parmar	Tennessee State University	United States
Poster presenter	Alicia	Perera-Castro	University of Hohenheim	Germany

Staff	Christine	Phillips	The New Phytologist Foundation	United Kingdom
Selected speaker	Charlotte	Phillips	University of Portsmouth/ RBG Kew	United Kingdom
Poster presenter	Matteo	Pivato	University of Verona	Italy
Local organising committee	Andy	Plackett	University of Birmingham	United Kingdom
Poster presenter	Ilian Giordano	Ponce-Pineda	Umeå Plant Science Centre	Sweden
Poster presenter	Serena	Qiao	University of Oxford	United Kingdom
Selected speaker	Julian	Radford-Smith	Western Sydney University	Australia
Poster presenter	Annette	Raffan	University of Aberdeen / JHI	United Kingdom
Poster presenter	Rini	Rahiman	National University of Singapore	Singapore
Poster presenter	Ram Sevak	Raja Kumar	Max Planck Institute	Germany
Mentor	Anja	Rammig	Technical University of Munich	Germany
Poster presenter	Jesamine	Rikisahedew	Estonian University of Life Sciences	Estonia
Poster presenter	Abhishek	Roychowdhury	University of Hyderabad	India
Poster presenter	Caio	S. Ballarin	São Paulo State University	Brazil
Mentor	Ari	Sadanandom	Durham University	United Kingdom
Poster presenter	Svenja	Saile	Plant Health Institute of Montpellier	France
Poster presenter	Jenny	Saile	Wageningen University & Research	The Netherlands
Local organising committee	Rosa	Sanchez-Lucas	University of Birmingham	United Kingdom
Mentor	Tina	Schreier	University of Oxford	United Kingdom
Poster presenter	Marili	Sell	University of Tartu	Estonia
Poster presenter	Rachel	Selman	The University of Edinburgh	United Kingdom
Keynote	David	Seung	John Innes Centre	United Kingdom
Invited guest	Brigita	Simonaviciene	University of Leeds	United Kingdom
Selected speaker	Dhriti	Singh	Umeå Plant Science Centre	Sweden
Mentor	Pallavi	Singh	University of Essex	United Kingdom
Mentor	Holly	Slater	New Phytologist Foundation	United Kingdom

Poster presenter	Lina	Spiller	University of Würzburg	Germany
Poster presenter	Erin	Stroud	University of Warwick	United Kingdom
Poster presenter	Keiri Winnie	Swann	Reading University and Vertical Future	United Kingdom
Poster presenter	Kohsuke	Tanigawa	Swedish Univ. of Agricultural Sciences	Sweden
Poster presenter	Lizzie	Telford	University of Sheffield	United Kingdom
Poster presenter	AmirAli	Toghani	The Sainsbury Laboratory	United Kingdom
Poster presenter	Anastasia	Tõnisson	University of Tartu	Estonia
Mentor	Rosie	Trice	John Wiley & Sons Ltd	United Kingdom
Local organising committee	Sami	Ullah	University of Birmingham	United Kingdom
Local organising committee and poster presenter	Andrea	Vadillo Dieguez	University of Birmingham	United Kingdom
Mentor	Mariana	Vale	Fed. Univ. Rio de Janeiro/UoB	Brazil
Poster presenter	Cas	Verbeek	Naturalis Biodiversity Center	The Netherlands
Selected speaker	Antonia	Vukmirović	University of Zagreb	Croatia
Mentor	Catherine	Walker	Nature Plants	United Kingdom
Mentor	Jo	Wood	Wiley	United Kingdom
Poster presenter	Ziqi	Ye	Laurentian University	Canada
Selected speaker	Haopeng	Yu	John Innes Centre	United Kingdom
Poster presenter	Selin	Zeyrek	University of Cambridge	United Kingdom
Poster presenter	Chongzhe	Zhang	Nanjing Agricultural University	China
Selected speaker	Min	Zhao	Western Sydney University	China
Poster presenter	Hao	Zhou	Lancaster University	United Kingdom
Selected speaker	Leonardo	Ziccardi	Michigan State University	United States
Poster presenter	Sibongile	Zimba	University of Bristol	United Kingdom