UNIVERSITY OF CAMBRIDGE

PLANTS @ CAMBRIDGE

BOTANICON

4th July 2025

St John's College

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Welcome

On behalf of the organising committee, we are delighted to welcome you to the Plants @ Cambridge Botanicon 2025.

This one-day event brings together members of the Cambridge plant biology community to explore the future of research in our field.

Our goal is to encourage meaningful dialogue and spark new collaborations between individuals and institutes. We are also committed to providing a platform for early career researchers to present and discuss their work.

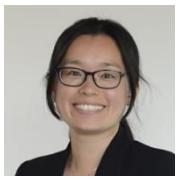
We're excited to connect with you and hope you find the day both enjoyable and inspiring!

Key contacts

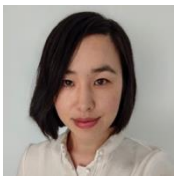
Please email Jeongmin Choi (jc913@cam.ac.uk) and Lida Derevnina (ld645@cam.ac.uk) for further information and questions.

On the day, please contact any of the members of the organising committee listed on the next page (we'll be wearing green bibs).

Botanicon 2025 committee



Jeongmin Choi
Crop Science Centre



Lida Derevnina
Crop Science Centre

Alex Webb
Plant Sciences

Vicki Marshall
Plant Sciences

Elisabeth Burmeister
Sainsbury Laboratory

Ángela Cano
Botanic Garden

Nina Foreman
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Renuka Kolli
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Samaneh Najafi
Niab

Anusree Saha
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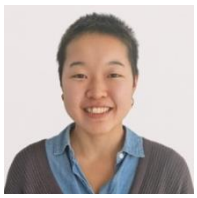
Ludi Wang
Sainsbury Laboratory

Marta Wojnowska
Biochemistry



Karen Uchida
Sainsbury Laboratory

Plants @ Cambridge

Botanicon is an Early Career Researcher community event brought to you by Plants @ Cambridge, a body that co-ordinates plant science activities across the University of Cambridge to ensure better connectivity and to communicate our successes to the wider world. I am very grateful to the organising committee, representing all the constituent components of Plants @ Cambridge, for their hard work in bringing Botanicon 2025 together.

Plants @ Cambridge aims to: facilitate inter- and multidisciplinary research, from molecules to the environment; embed plant science priorities in Cambridge philanthropic fundraising; facilitate interactions with external partners; build partnerships that deliver impact from research to ensure underpinning of future research and teaching; enable knowledge-exchange and develop strategic alliances so that our findings have impact on sustainable technologies, the growing bioeconomy, food security, conservation and biodiversity, and resilience to climate change with nature-based solutions; and raise the profile of plant science in the education system and with the wider public.

Since Botanicon 2024, Plants @ Cambridge has reviewed plant growth facilities across Cambridge and identified areas where coordinated activity can improve the facilities available to all our researchers (guide to the plant growth facilities). The communications teams within Plants @ Cambridge have developed approaches and pipelines for more joined up working to make it easier to share our success stories with each other, and the world. We have recently negotiated with a major international plant science company to provide mentorship for PhD students within the Plants @ Cambridge domain; more details will be released on this exciting programme soon.

Keep an eye out for future events and communications from Plants @ Cambridge, and please get in touch with me if you have any suggestions of things you would like to see supported.

Professor Alex Webb
Director of Plants @ Cambridge

Venue

Great Gate St John's College (1 on map on following page)
Porters Lodge entrance
26-27 Magdalene Street
St John's College
Cambridge

what3words///filer.charmingly.puff

There will be signs directing you from the Porters Lodge to the **Fisher Building**, which is the venue for most of the day.

Palmerstone Room, Fisher Building (2 on map)

You will pass over the Bridge of Sighs when walking to Fisher Building from the Porters Lodge.

Hall (3 on map)

Our poster sessions and lunch will take place in the Hall.

We suggest you keep your valuables with you during the day.

Registration Desk & Poster Drop-off

Please collect your name badge at the Registration desk in the foyer of the Fisher Building when you arrive.

We will have photo consent forms and will be providing lanyards for those who prefer not to have their photo taken during the day.

If you have a poster, this is also where you will hand it in to be put up for you during the morning sessions.

Audio Loop

The Palmerstone Room, where all the talks and panel discussions will be held, is fitted with an audio induction loop amplifier.

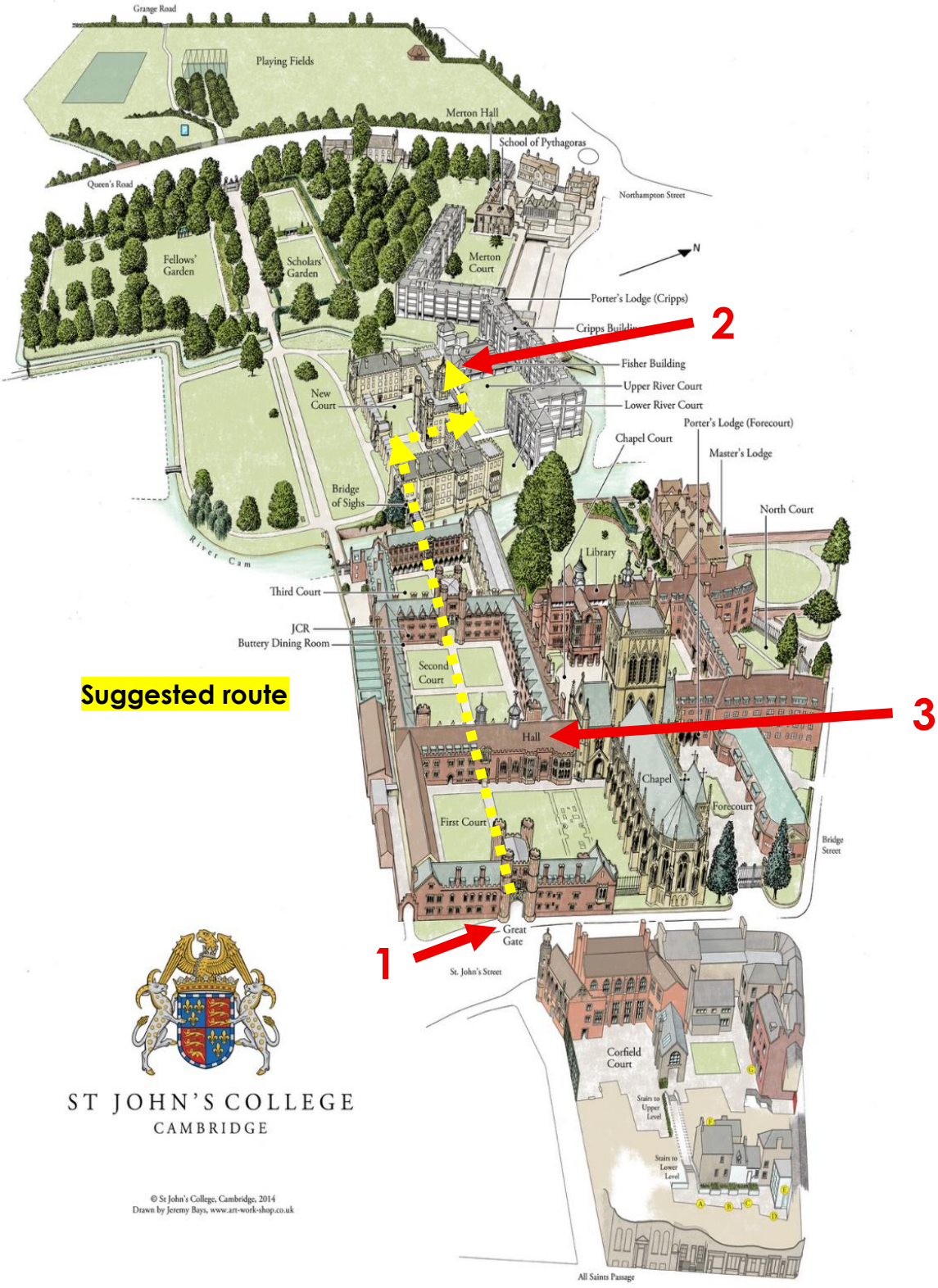
Blue Badge Parking

Blue Badge holders can request a parking space at St John's College. Please email Vicki Marshall (vjm35@cam.ac.uk) with your vehicle registration number to reserve a spot.

Bicycle Facilities

There is no bicycle parking onsite. There are some bike parking spaces along St John's Street, but they are very popular. The other nearest bicycle parking is the Grand Arcade Cycle Park.

Map



Creating an inclusive and respectful meeting

Professional and respectful etiquette

We are looking forward to many productive and invigorating discussions at the Plants @ Cambridge Botanicon. In order to create a space that fosters open dialogue and where everyone feels welcomed, respected and safe we expect that all Symposium participants will treat others with consideration and professionalism. To help create a meeting that welcomes free expression of ideas, please:

- Listen to the contributions of everyone with respect and appreciation.
- Be open to other participants' opinions. Critique ideas, not people.
- Give feedback constructively and with kindness.
- Share your thoughts and be mindful that time is limited, and others may wish to speak.

Quiet Working Rooms

We have access to one additional room in the Fisher Building (the Drawing Room) that can be used during the day as a quiet room or working area. This room is at the top of the Fisher Building, and there is stair and lift access. Please ask at the Registration Desk for directions.

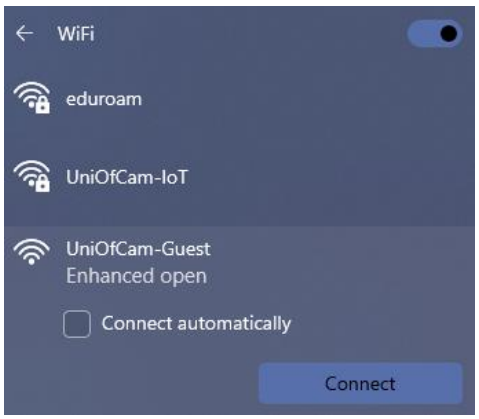
Catering and dietary requirements

For people with specific allergy/dietary requirements, your food will be plated separately. Please ask the caterers for your food, which will be labelled.

Smoking

Smoking is strictly prohibited in any buildings and onsite at St John's College.

Wi-Fi



If you are an existing member of the University with a valid CRSid, please use **Eduroam** or **UniOfCam-IoT**. Visitors and guests of St. John's College can connect to the **UniOfCam-Guest Wi-Fi** network using their email address or a social media account, such as Facebook.

The University's Information Services (UIS) team provides detailed, up-to-date instructions for connecting devices to the **UniOfCam-Guest** network. To access these instructions, please follow this **link.**

Schedule

08:30-09:00 **Registration**

09:00-09:05 Welcome (Lida Derevnina & Jeongmin Choi)

09:05-09:10 Plants @ Cambridge Introduction (Alex Webb)

09:10-09:20 Special Botanicon 2025 award announcement (Ludi Wang & Humberto Herrera Ubaldo)

09:20-10:20 Careers panel I (Chairs: Dominic Leach & Anusree Saha)

- **Cristina Sales** - Industry
- **Neha Bhatia** - Academia
- **Alan Wanke** - Academia
- **Sam Brockington** - Collections
- **Christopher Surridge** - Editor

10:20-10:30 Flash Talks I (odd numbers)

10:30-11:00 **Morning coffee break**

11:00-11:50 Short Talks (Chair: Nina Foreman)

- **Tianshu Sun**, Plant Sciences
- **Donghwi Ko**, Sainsbury Laboratory
- **Julia Lambret Frotte**, Niab
- **Harry Taylor**, Plant Sciences
- **Alex Guyon,** Sainsbury Laboratory
- **Darren Johnson**, Careers Service

11:50-12:00 Flash Talks II (even numbers)

12:00-12:05 Group photo

12:10-13:50 **Lunch (Hall)**
Poster sessions to run during lunch

12:10-12:50 Poster session I (odd numbers)

13:10-13:50 Poster session II (even numbers)

14:00-15:00 Hot techniques (Chair: Karen Uchida)

- **Tally Wright,** Niab - GWAS
- **Min-Yao Jhu**, Crop Science Centre - Spatial Transcriptomics
- **Elise Laurelle**, Sainsbury Laboratory - Segmentation

15:00-16:00 Careers panel II (Chairs: Zara Guppy & Nina Foreman)

- **Giles Yeo** - Communication, Media
- **Raphaella Hull** - Science education
- **Sarion Bowers** - Policy
- **Sonja Dunbar** - Education
- **John Pierrepont** - Animal and Plant Health Agency (Government)

16:00-16:30 Awards & concluding remarks

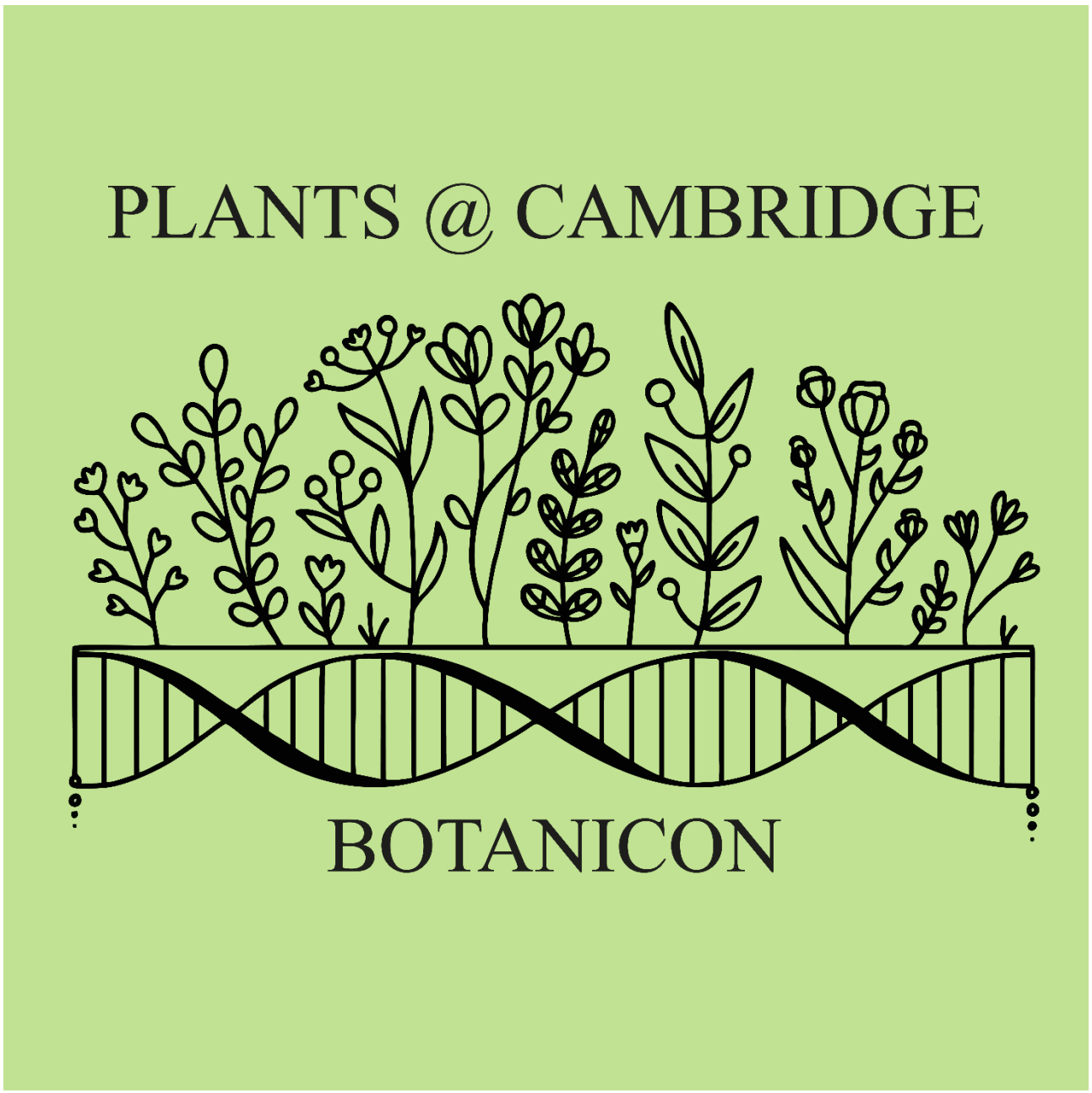
16:30-18:00 Drinks and snacks

Poster presenters

1. **Katie Jeal**, Sainsbury Laboratory
2. **Polly Bridges**, Crop Science Centre
3. **Julia Stewart-Wood**, Plant Sciences
4. **Emily Oren**, Sainsbury Laboratory
5. **Adela Jezierska-Suwińska**, Crop Science Centre
6. **Ángela Cano**, Botanic Garden
7. **Mareyam Mukhtar**, Niab
8. **Zhengao Di**, Plant Sciences
9. **Lijun Zhou**, Plant Sciences
10. **Chetan Pandey**, Sainsbury Laboratory
11. **Darius Kosmützky**, Sainsbury Laboratory
12. **Amir Porat**, Sainsbury Laboratory
13. **John Palmer**, Plant Sciences
14. **Jinpeng Gao**, Crop Science Centre
15. **Miguel Santos**, Crop Science Centre
16. **Jibril Lubega**, Niab

Session I: Odd numbers

Session II: Even numbers



Short talk abstracts

Tianshu Sun

Understanding the Molecular Basis and Evolution of C4 Photosynthesis via Single Nucleus Analysis of Eleven *Flaveria* Species

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[1]Department of Plant Sciences, University of Cambridge, UK

C_4 photosynthesis, which enhances carbon fixation by compartmentalising the pathway between mesophyll and bundle sheath cells to reduce photorespiration, is one of the most prominent examples of the convergent evolution of a complex trait. The C_4 pathway has evolved independently across multiple plant lineages and is thought to have arisen through a stepwise manner. However, the molecular mechanisms underlying each transitional stage remain unclear. To address this, we performed comparative single-nucleus transcriptomic analyses across 11 closely related *Flaveria* species representing C_3, C_3–C_4, C_4-like, and C_4 evolutionary stages. Our study reveals the molecular changes underpinning each step of the transition and highlights three key findings: 1) The preferential expression of several core genes is already established at the C_3 stage; 2) Additional genes acquire differential expression between mesophyll and bundle sheath cells at later stages, using distinct regulatory strategies; 3) Enhanced cell-to-cell connectivity may play a crucial role in optimising the C_4 pathway. This work provides a valuable roadmap for understanding the molecular establishment of C4 photosynthesis and may inform the practical engineering of crops with enhanced photosynthetic efficiency.

Donghwi Ko

Recruitment of bifunctional thermospermine to methylated ribosomes directs xylem cell fate decision

Ko D[2]*, Ruonala R[1], Faille A[3], Hellmann E[1], Warren AJ[3], Kirpekar F[4], Helariutta Y[1]

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[1]Organismal and Evolutionary Biology Research Programme, Viikki Plant Science Centre, University of Helsinki, Finland
[2]The Sainsbury Laboratory, University of Cambridge, UK
[3]Cambridge Institute for Medical Research, UK
[4]Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark

Polyamines are often associated with ribosomes and thought to stabilise their integrity. In plants, the polyamine thermospermine induces translation of SUPPRESSOR-OF-ACAULIS51 (SAC51) and SAC51-LIKEs (SACLs) that inhibit heterodimerisation of LONESOME-HIGHWAY (LHW) and TARGET-OF-MONOPTEROS5 for xylem fate, but its mode of function has remained elusive. Here, we present a methyltransferase, OVERACHIEVER, responsible for a methylation of a uridine in the peptidyl transferase centre (PTC) of the 25s rRNA. The base methylation stabilises thermospermine binding to a specific site in the PTC. This interaction bifunctionally facilitates the translation of SACLs and inhibits that of LHW, thereby inhibiting xylem vessel differentiation. This study uncovers the dependency between a conserved rRNA base methylation and a polyamine in orchestrating cell fate decisions, highlighting a role for the ribosome chemical landscape in translational regulation and vascular development.

Julia Lambret Frotte

DNA-free gene editing in potato

Lambret Frotte J[1]*, Wallington EJ[1]

*julia.lambret@niab.com

[1]Niab, Cambridge, UK

Potato is one of the world's most important food crops. However, its genetic complexity - being polyploid, vegetatively propagated, and highly heterozygous - poses significant challenges for traditional breeding approaches. Modern gene-editing tools, such as CRISPR/Cas, offer a promising alternative for precise trait manipulation aimed at crop improvement. With the UK's new Precision Breeding Act permitting the cultivation of precision bred crops produced through gene editing technologies, novel strategies for crop improvement have become increasingly viable.

In cereal species like rice wheat and barley, we typically perform CRISPR/Cas editing via *Agrobacterium*-mediated transformation, followed by T-DNA segregation through sexual reproduction. However, these methods are not easily applicable to potato due to its complex heterozygous genome. An alternative approach involves the use of protoplasts for the transient delivery of CRISPR/Cas components, enabling genome editing without stable DNA integration.

At Niab, we have developed a pipeline for the efficient isolation, transfection, and regeneration of potato protoplasts in potato. This platform lays the groundwork for producing gene-edited potato lines that comply with current regulatory frameworks and hold promise for agronomic improvement. The success of this protocol marks a major step forward in applying gene editing to complex, vegetatively propagated crops, paving the way for more sustainable and resilient agricultural practices.

Harry Taylor

Epigenetic Regulation of Disease Resistance in Tomato: Characterizing the Role of H3K9me2 and Developing Targeted Epigenetic Editing Tools

Harry Jack Taylor[1]* & Jake Harris[1]

*hjt53@cam.ac.uk

[1]Department of Plant Sciences, University of Cambridge, UK

Pathogen infections pose a severe threat to plant health and global crop production. Epigenetic mechanisms, including DNA methylation, histone modifications, and chromatin remodelling are central to the transcriptional regulation of plant defence responses. How these epigenetic mechanisms facilitate enhanced, long-lasting resistance following exposure to a given stressor - otherwise known as priming - is an area of recent intensive investigation. My research focuses on understanding how transcriptionally repressive epigenetic marks, particularly H3K9me2 and DNA methylation, underpin immune priming in tomato (*Solanum lycopersicum*). My findings reveal that priming with the pathogen-associated molecular pattern (PAMP) flg22 triggers significant gene upregulation of immunity-related loci, with many of these genes residing in epigenetically repressed regions in wild-type plants prior to flg22 perception, i.e., in the naïve state. These loci are enriched with WRKY motifs in their promoters, which exhibit local spikes in chromatin accessibility that may facilitate a poised chromatin state ready for transcriptional activation. Interestingly, mutation of *KRYPTONITE* (KYP, also known as SUVH4) - which reduces genome-wide H3K9me2 deposition and DNA methylation in the CHG context - causes tomato (cv. M82) to lose its priming response to flg22. *kyp* plants also exhibit increased basal resistance to the bacterial plant pathogen, *Pseudomonas syringae*, implicating H3K9me2 as a repressive mark that can modulate inducible immune responses. To further explore whether chromatin states can be artificially manipulated to control gene expression, we have engineered constructs to recruit histone methyltransferases for H3K9me2 and H3K27me3 deposition at targeted genomic loci using the dCas9-SunTag system. This research highlights the dynamic interplay between chromatin modifications and immune responses, contributing to a deeper understanding of plant defence mechanisms, as well as establishing a novel tool for targeted epigenetic silencing in plants.

Alex Guyon

Mycorrhiza symbiosis alters phosphoinositide signatures at pathogen interfaces and increases resistance to *Phytophthora*

Guyon A[1,2]*, Staps T[1,3], Badot L[1,4], Schornack S[1,2]

*alex.guyon@slcu.cam.ac.uk

[1] Sainsbury Laboratory, University of Cambridge
[2] Department of Plant Sciences, University of Cambridge
[3] Martin-Luther-University Halle-Wittenberg
[4] ENS Paris Saclay

Intracellular microbe-host interactions result in pathogenesis or symbiosis, with the enveloping host membrane acting as a critical interface. Membrane identity is partly determined by the distribution of a family of membrane lipids, the phosphoinositides, with a polar inositol head group that can be modified at various positions, giving rise to a range of PIP species. However, whether phosphoinositide signatures at membrane interfaces with pathogens and symbionts change during co-colonization remained unexplored. We generated *Nicotiana benthamiana* plants with PI4P or PI(4,5)P_2 biosensors, enabling simultaneous root interaction analysis with pathogenic (*Phytophthora palmivora*) and symbiotic (arbuscular mycorrhiza fungus *Funneliformis mosseae*) microbes. Binary plant-microbe interactions revealed distinct patterns: PI(4,5)P_2 was uniquely tip-enriched around mutualist structures but evenly distributed along pathogen structures. Meanwhile, PI4P was largely excluded from extrahaustorial membranes but present at periarbuscular membranes of the mutualist fungus. Significantly, mutualist pre-colonization rendered roots more resistant and altered the membrane identity around subsequent pathogen haustoria, recruiting PI4P. These findings show distinct phosphoinositide compositions define pathogen vs. symbiont interfaces. Furthermore, membrane identities are dynamic and modulated during co-colonization, likely influencing microbial interaction outcomes.

PLANTS @ CAMBRIDGE

BOTANICON

Poster abstracts

1. Katie Jeal

Investigating awn development and diversity within the grasses

Jeal, K[1]* & Bartlett, M[1]

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In the grass family, Poaecae, awned lemmas have been repeatedly gained and lost with both awn function and morphology differing between species. The awns are likely homologous to the leaf blade and the genes responsible for awn development may be the same as those responsible for leaf blade development. This suggests that developmental constraint has driven the emergence of awns with the expression of leaf blade genes in the lemma providing a mechanism for the repeated emergence of awns in different grass species. This developmental constraint suggests that the genes regulating awn development might be conserved across species, despite their independent origins and differing morphologies.

Barley awn mutants are being used as an experimental system to identify genes regulating awn emergence and mediolateral awn constriction. If the developmental programs of the grass leaf and awn are conserved, then genes downregulated in the awnless barley mutant lemma compared to wildtype are likely to be involved in both awn and leaf development. A developmental series of wildtype and awn mutants in barley will determine when their developmental trajectories diverge, providing further insight into the developmental programs underlying awn development. Additionally, loss-of-function mutants of homologues of known barley awn development genes are being generated in the grass model species brachypodium. This will test the hypothesis that the genetic mechanisms regulating awn development are conserved across the grasses.

2. Polly Bridges

Investigating the function and conservation of nuclear pore complex components in rice arbuscular mycorrhizal symbiosis

Bridges P[1]*, Ferreras Garrucho G[1], Wallington E[2], Paszkowski U[1]

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[1]Crop Science Centre, Department of Plant Sciences, University of Cambridge, Cambridge, UK
[2]Niab, Park Farm, Histon, Cambridge, UK

Arbuscular mycorrhizal (AM) symbiosis is an ancient and incredibly widespread plant-fungal mutualism, and a promising target for sustainable crop improvement. Its establishment and maintenance requires a molecular dialogue between the plant and fungus, as well as numerous signalling processes in both partners, many of which are not fully understood. Three components of the nuclear pore complex, nucleoporins NUP85, NUP133 and NENA, play an unknown, symbiosis-specific role in the model legume Lotus japonicus, with the mutants showing severe, temperature-sensitive defects in AM colonisation. We aim to determine whether the symbiotic role of these nucleoporin genes is conserved in rice, a key cereal crop and a model for the study of AM symbiosis, as well as unpick their specific molecular role in AM signalling. We have generated CRISPR/Cas9 mutant lines for all three rice orthologues of these genes, and confirmed that their AM colonisation phenotypes are highly consistent with Lotus, exhibiting a drastic reduction in colonisation levels and similar fungal morphology, confirming that their symbiotic role is conserved between the two species. Work is now underway to determine the degree of temperature-sensitivity these mutants exhibit in rice. We have additionally established, and are characterising, the genetic material needed to investigate the nup85/nup133 double mutant phenotype, as well as the interplay between these NUPs and other key rice symbiotic signalling pathways.

3. Julia Stewart-Wood

It's about time: Conserved and divergent functions of EARLYFLOWERING 3 in wheat circadian oscillators

Stewart-Wood J[1]*, Pingarron-Cardenas G[1], Upadhyay A[2], Locke JCW[2], Webb AAR[1]

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[1]Department of Plant Sciences, University of Cambridge, United Kingdom
[2] Sainsbury Laboratory, University of Cambridge, United Kingdom

Plant circadian oscillators regulate numerous pathways underlying yield-related traits, including photosynthesis, flowering time, and temperature responses. EARLY FLOWERING 3 (ELF3), a key circadian oscillator component, integrates environmental signals into circadian oscillators and regulates these downstream pathways. Crop plants including wheat, have differences in *ELF3* transcriptional dynamics and protein structure relative to well-studied model plants. ELF3 is a critical component of wheat circadian oscillators. However, the mechanisms underlying its different transcriptional timing relative to *Arabidopsis* and the impact its altered structure has on the protein's functions in temperature responses and photoperiod-dependent flowering time remain unclear.

Here, we present an analysis of *ELF3* at the transcriptional, molecular, and physiological levels. We hypothesize that wheat *ELF3* is regulated by the circadian oscillator transcription factor TOC1, contrasting with CCA1-mediated regulation in the model plant *Arabidopsis thaliana*. Furthermore, we have explored the roles of ELF3 in regulating circadian oscillations in photosynthesis through chlorophyll fluorescence imaging and found that the role of ELF3 in integrating light and temperature signals into circadian oscillators is not impaired by heat stress. *In vivo* assays have also indicated that the abilities of the ELF3 protein to interact with *A. thaliana* circadian clock proteins and proteins involved in temperature responses are partially conserved in wheat. Overall, these findings enhance our understanding of the roles of ELF3 in wheat circadian biology, offering insights for optimizing photoperiod-dependent flowering and temperature resilience in wheat breeding programs and understanding the impact that a changing climate may have on this key crop.

4. Emily Oren

Cell Division as a Mechanical Regulator of Arabidopsis Growth

Oren E[1]*, Robinson S[1]

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[1]Sainsbury Laboratory, University of Cambridge, United Kingdom

Plants grow and develop throughout their lives, creating complex morphology through cell expansion and cell division. How plants control these processes is a pressing and unanswered question in the field of developmental biology. This project seeks to investigate the regulatory relationships between three factors known to impact plant growth: hormonal signalling, mechanical feedback, and cell division. While all three factors are known to contribute to growth regulation, how each feeds back on the others is currently unclear. To begin to unravel this complex process, cell division was studied in Arabidopsis hypocotyls, an organ with very little endogenous division, and manipulated using inducible lines that increase cell division frequency. Hormonal activity was manipulated directly through exogenous hormone and inhibitor treatments, and indirectly through environmental conditions such as far-red light. Mechanical properties were quantified using Atomic Force Microscopy (AFM) and Automated Confocal Micro Extensometer (ACME). AFM allows for cell wall scale measurement of stiffness, while ACME operates at the whole organ scale. Inducing excess cell divisions in the Arabidopsis hypocotyl results in altered growth behaviors: increased growth after treatment with BR, and decreased growth in shade mimicking conditions. These differences appear to be due to changes in wall modification responses to the stimuli, not due to mechanical constraints caused by the presence of extra walls. Future work will focus on whether this is due to changes in cell identity, hormone movement, or some other factor.

5. Adela Jezierska-Suwińska

By the Order of the Root: Plant Signals in Nematode Parasitism

Jezierska-Suwinska, A.G.[1,2]*, Damm, A.[1], Pellegrin, C.[1], Sperling, A.L.[1], Molloy, B.[1], Shin , D.S.[1], Long, J.[1], Brett, P.[3], Chisom Iguh, T.[1], Desikan, P.[1], Senatori, B.[1], Vieira, P.[4], Meijas, J.[6], Kumar, A.[6], Masonbrink, R.E.[7], Mayer, T.R.[6], Baum, T.J.[7], Eves-van den Akker, S.[1]

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[5]The Data Analysis Group, School of Life Sciences, University of Dundee, Dow St, Dundee DD1 5EH
[6]Department of Plant Pathology, Entomology and Microbiology, Iowa State University, 2213 Pammel Dr., Ames, IA, 50011, USA
[7]Genome Informatics Facility, Iowa State University, 448 Bessey Hall, Ames, IA 50011, USA

Plant-parasitic nematodes, as with many plant pathogens, have evolved a diverse arsenal of effector molecules designed to manipulate host cells, suppress plant immune response, and promote successful colonization. The production of these effectors is spatially confined to two specialised sets of gland cells and is tightly regulated by two gene homologues: the Subventral Gland Regulators: SUGR-1 and Dorsal Gland Regulator 1 (DGR-1). SUGR-1 and DGR-1 are nuclear hormone receptors, which together orchestrate the expression of 160 effector genes. These transcription factors are therefore crucial determinants in the successful establishment of a parasitic interaction. The SUGR/DGR regulatory pathway is hyperactivated by the presence of plant-derived small molecules: "effectostimulins". To investigate the natural variation in effectostimulin production and identify the signals involved, we treated nematodes with root extracts from over 100 different lines of the Multiparent Advanced Generation Inter-Cross (MAGIC) population of Arabidopsis thaliana. This approach revealed natural variation in effectostimulin levels and allowed the integration of phenotypic data with genotype information to perform a Genome-Wide Association Study (GWAS). These findings provide new insights into the genetic underpinnings of plant effectostimulin-induced hyperactivation of parasite effector production, laying the groundwork for future targeted approaches in crop protection from nematodes.

6. Ángela Cano

How can Cambridge University Botanic Garden support your research?

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At Cambridge University Botanic Garden (CUBG), we grow over 14,000 plants representing 5,700 species from across the globe and the taxonomic spectrum. With a palette that includes economically important, native, exotic, threatened, and ornamental species, the primary goals of our collections are to support research, education, and conservation. As such, they are accessible to researchers from any academic institution. We offer multiple forms of support to researchers—whether by providing specimens, granting access to our landscape for field studies, hosting experimental plantings in our facilities, or sourcing unique species. In addition to our living collections, we house the Botanic Garden and Cambridge University herbaria—where Darwin deposited specimens collected during his voyage on the *Beagle*—as well as a library specialising in botanical publications and a seed bank. All of these resources are available to researchers and educators. We also run a variety of courses through our Adult Learning Programme, including a 1-week intensive course on Plant Systematics (with bursary places available), and shorter courses on native plant identification, tropical botany, mycology, botanical illustration, and gardening. Additionally, we offer the *Botany Hour* course from late September to early July—a 1-hour weekly session that guides students through the plant tree of life, exploring over 60 plant families and their evolutionary relationships, while introducing botanical terminology. CUBG is in the heart of Cambridge and the University. It is a place for wellbeing and recreation, while also serving as a hub for multidisciplinary research supported by our uniquely diverse collections.

7. Mareyam Mukhtar

Genome-Wide Identification of DOMON Domain Genes in Rice (*Oryza sativa*) in Stress Responses and Functional Characterization of *OsDomon4.1* in Response to *Magnaporthe oryzae*

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Understanding plant defense against rice blast disease is vital for sustainable crop production. Here, we present the first comprehensive genome-wide analysis of the DOMON domain gene family in *Oryza sativa* and their roles in stress responses. We identified 15 DOMON genes, many co-occurring with cytochrome b561 domains and transmembrane helices, suggesting roles in redox regulation and membrane-associated signaling. Promoter analysis showed enrichment of stress-responsive cis-elements (WRKY, NAC, ERF, MYB), especially in the blast-resistant cultivar Tetep. Several OsDOMON genes were upregulated after *Magnaporthe oryzae* infection, with *OsDomon6.1* and *OsDomon4.1* showing the highest induction at 6 hours post-infection, indicating involvement in early defense. Tissue-specific expression showed constitutive expression of *OsDomon1.4* and *OsDomon6.1*. Functional validation through overexpression of *OsDomon4.1* in the susceptible TP309 background enhanced resistance in multiple infection assays. Confocal microscopy confirmed plasma membrane localization, and histochemical staining revealed increased ROS accumulation and reduced cell death. Additionally, specific DOMON genes responded to abiotic stresses: *OsDomon3.3* (drought), *OsDomon9.1* (heat), and *OsDomon9.2* (salt), particularly in Tetep. Overall, our findings identify *OsDomon4.1* as a key contributor to blast resistance and highlight the broader potential of the DOMON family in enhancing multi-stress resilience, offering promising targets for molecular breeding and crop improvement.

8. Zhengao Di

Cell-type specific elucidation and targeted engineering of plant nitrate-responsive gene circuits

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Nitrogen (N) is a critical nutrient for plant growth and yield. While external N has facilitated modern agriculture, over-application of N-containing fertilisers has drastic ecological and environmental consequences. Quantitative traits in crops are typically determined by the actions of suites of genes working combinatorially within complex gene regulatory networks (GRNs), which often contain partially redundant nodes and numerous network motifs that define and fine-tune network dynamics. In a recent project, we elucidated a regulatory circuit acting upstream of the critical *NIN-LIKE PROTEIN-7 (NLP7)* transcription factor and its conservation and divergence in plant lineages. An outstanding question is how the regulatory networks function across cell types to coordinate changes in root development and nitrogen metabolism. By applying single-cell RNA sequencing, we observed the enrichment of *NLP7*-related sub-networks in specific groups of cells in the root. The resulting network models provide a framework for targeted engineering to increase plant nitrogen use efficiency. To this end, we are applying Cas-based transcriptional activators and repressors with cell-specific promoters to investigate the importance of observed cell-specific expression patterns, and precisely manipulate the N-responsive networks within the most relevant cells.

9. Lijun Zhou

Iridescence in Flowers - How and Why? Insights from *lisa* mutant

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Colouration in nature arises not only from pigments but also from physical phenomena, which are known as structural colours. Iridescence, a change in colour due to changes in viewer position, is generated in the epidermis from a cuticle that buckles, creating arrays of regularly spaced ridges on the petals in *Hibiscus trionum*. However, the process remains poorly understood and its ecological significance is still unclear.

We identified a mutant line, lisa, derived from an EMS-mutagenized *H. trionum* population, which exhibits a significant reduction in iridescence and the nanoscale ridges on the petal surface fail to develop normally. These changes prevent the ridges from functioning as an effective diffraction grating. Therefore, we plan to 1) check the mechanical reason underlying the defects in ridge formation by analyzing the cuticle layers features; 2) check chemical differences in cuticle composition and pigments; 3) explore molecular mechanism by identifying the mutated gene. Finally, to study how iridescence affects plant-pollinator interactions, we are using the iridescent artificial flowers and lisa mutant flowers to test bee preferences. We hope to offer new insights about the formation of nanoridges in the petals, which, in the future can help the generation of biologically-inspired, structurally-colored materials for diverse applications.

10. Chetan Pandey

Vesicular Trafficking Rewired: Role of *EXO70.3* gene in coordinating arbuscular mycorrhiza symbiosis and photomorphogenic control in *Marchantia paleacea*

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Plant growth and development as well as interactions with microbes rely on cellular processes. For example, spatially controlled exocytosis is regulated by the exocyst, an octameric protein complex that tethers vesicles to the plasma membrane before fusion. This is crucial for cellular activities like tip growth, auxin transporter polarization, cell plate formation during cell division, and autophagy, as well as plant responses to both pathogenic and symbiotic microbes. Studies in *Arabidopsis thaliana* and other angiosperms show that the exocysts' most diverse component is EXO70, where the paralogs have distinct roles. In the context of plant-microbe interactions, the EXO70.3 subfamily, including EXO70G and EXO70I clades, is of particular interest.

This research has identified the *EXO70.3* gene as a molecular player in arbuscular mycorrhiza symbiosis and developmental responses in the liverwort *Marchantia paleacea*. Loss of function *Mpaexo70.3* mutants display a pronounced delay in the colonization by the arbuscular mycorrhizal fungus *Funneliformis mosseae* indicating an essential role for *EXO70.3* in the early stages of fungal accommodation within the storage cells of the bryophyte liverwort. Additionally, *Mpaexo70.3* mutants exhibit skotomorphogenesis in the dark, suggesting disrupted dormancy compared to wild-type plants. Under low fluence conditions, mutant thalli remain significantly shorter, further implicating the role of *EXO70.3* in photomorphogenic growth and shade avoidance.

Understanding how plant-microbial interactions intersect with developmental processes in liverworts enables comparisons with similar mechanisms in vascular plants and provides insights into their evolutionary origins.

11. Darius Kosmützky

The transcription factor Mp*GRAS7* is a novel susceptibility factor with a role in reproductive development in *Marchantia*

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While it is known that vascular plants integrate biotic and abiotic signals for their development, knowledge of this in non-vascular plants is lacking. The transcription factor Mp*GRAS7* from the model bryophyte *Marchantia polymorpha* has recently been found to respond to abiotic stresses such as drought and far-red light. Furthermore, Mp*GRAS7*shifts the balance of reproductive strategy of *M. polymorpha* towards the sexual rather than asexual mode. Here we show that in addition to the responsiveness to abiotic signals, infection of *Marchantia* with the pathogen *Phytophthora palmivora* leads to increased systemic expression of Mp*GRAS7*. Treatment of *Marchantia* with *P. palmivora* cell-free supernatant was sufficient to elicit a similar increase in expression, confirming that the causal agent is a molecule rather than infection structures. Knock-out mutants of Mp*GRAS7* in *M. polymorpha* and *M. paleacea* showed increased resistance to infection by *P. palmivora,* implicating Mp*GRAS7* as a susceptibility gene. Mp*GRAS7* therefore functions as a positive regulator of infection and is nevertheless maintained in *Marchantia* due to its role in coordinating reproductive development. Future work will determine the integration of these functions.

12. Amir Porat

Integrating Growth, Mechanics, and Genetic Control in Self-similar Plant Morphodynamics

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Plant morphodynamics arises from an interplay between growth, mechanics, and genetic regulation. Focusing on two self-similarly growing organs - the apical hook and the shoot apical meristem (SAM) - we pose an "inverse morphoelastic problem" (IMP): inferring possible growth laws and elastic properties directly from observed shape dynamics and morphogen distributions.

Assuming a strain-based growth law and employing "natural coordinates" - a curvilinear system aligned with flow and principal stress directions - the IMP is analytically tractable, enabling estimation of coarse-grained elastic strain profiles based on morphogen-dependent growth laws. While the origin of strain remains uncertain - possibly reflecting variations in stiffness, turgor pressure, or structural incompatibility - the model yields predictions testable via mutants, treatments, and mechanical measurements.

In the SAM, we explore how the WUS-CLV3 gene regulatory network may interact with tissue mechanics to regulate size, tip growth, and phyllotactic patterning. In the apical hook, combining our framework with morphoelastic rod models recapitulates experimental growth rates, identifies autotropism as critical for shape robustness, and highlights the possible role of residual stress in the growth-driven motion.

This integrative framework offers new tools to probe morphogen-mechanical feedback in plant development.

13. John Palmer

How does nutrient limitation inform arbuscular mycorrhizal induced gene expression?

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In order to make informed decisions about when, and to what extent they engage with AM fungi, it follows that plants need to be able to integrate information about their own carbon and nutrient status. In practice, integration of information could take many forms, including effects on transcription mediated by changes to *cis* and *trans* regulation as well as more complex chromatin-based changes.

Previously, AM-related *cis*-elements have been characterised through promoter deletion techniques as well as bioinformatics- based approaches however changes to the chromatin accessibility of these elements throughout symbiosis and at a cell specific level has yet to be explored in significant detail. Widespread changes to DNA methylation landscapes upon AM contact, as well as AM fungal effector proteins targeting histone modifications add confidence to the idea that epigenetic modifications may play an underappreciated role in AM symbiosis. To establish the links between transcriptional mechanisms and nutrient regulated symbiotic gene expression, I will focus on utilising single-nuclei approaches to illuminate the cell specific differences in the transcriptional and chromatin landscape in *Medicago truncatula*. Currently a complete snRNA-seq dataset has been generated including nutrient replete, starved and mycorrhized root transcriptomes. This has allowed for the beginnings of exciting insights into nutrient regulated symbiotic gene expression at a cell specific level, as well as preliminary investigations into epigenetic regulation.

14. Jinpeng Gao

AI-driven structural modelling reveals the interkingdom interactome during rhizobial symbiosis

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Beyond to engaging with diverse microorganisms, legumes have evolved mutualistic relationships with nitrogen-fixing rhizobia to overcome nitrogen limitation. While the host genetic determinants governing nodulation processes are characterized, the molecular dialogue between rhizobia and their host plants, particularly inside the nodules, remains poorly understood.

In this study, we employed AlphaFold3-based structural prediction to systematically screen cross-kingdom interactions between 634 rhizobial secreted proteins and 227 known nodulation regulators (encoding >330 transcript variants). Computational screening of over 209,000 protein pairs identified hundreds of high-confidence putative interactions. Among these interactions, we found that more than 20 rhizobial proteins were predicted to associate with *DEFECTIVE IN NITROGEN FIXATION* (DNF), a key regulator of bacteroid persistence and defense responses within nodules. In addition, *NODULE-SPECIFIC PLAT DOMAIN* (NPD) proteins, essential for rhizobia accommodation and differentiation, also showed potential interactions with many rhizobial effectors. Using bimolecular luciferase complementation assays, we confirmed a couple of interactions in a heterologous system. Knockout and overexpression will be used to validate the nodulation phenotype associated with these interactions during *Medicago-rhizobium* symbiosis.

Collectively, our findings reveal a comprehensive interactome of rhizobial proteins and nodulation regulators, providing a mechanistic resource for understanding high-efficiency nitrogen fixation. Our work establishes an AI-driven, scalable framework for decoding molecular plant-microbe interactions, with broad implications for engineering sustainable crop production.

15. Miguel Santos

Evolution of receptor (D14L) signalling specificity for symbiosis and development

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The DWARF14-LIKE (D14L) signalling pathway is important for arbuscular mycorrhizal (AM) symbiosis development. In rice, D14L plays a dual role in regulating both developmental processes and symbiosis competence. Specifically, activation of D14L facilitates the degradation of the negative regulator SMAX1, leading to de-repression of symbiosis signalling and thereby promoting symbiosis development. While D14L is relevant for proper symbiotic regulation in angiosperms, its apparent lack of involvement in AM symbiosis in early-diverging land plants suggests that this function is a derived trait in later plant evolution. This project aims to reconstruct the evolutionary trajectory of the D14L signalling pathway and to identify key determinants of its recruitment into symbiotic signalling. To achieve this, a high-resolution metagenomics approach was employed to identify potential components associated with symbiosis signalling either upstream of the D14L pathway, via conserved cis-regulatory motifs, or downstream, using relevant differential transcriptomic data obtained from mutants of the *D14L* complex. After obtaining a comprehensive list of candidate genes using this approach, the future goal is to functionally characterise them in both rice and *Marchantia paleacea*, offering comparative insights into the molecular evolution and regulation of plant–fungal interactions across both early and late-diverging plant lineages.

16. Jibril Lubega

Validation and role of avirulence effectors produced by the wheat stem rust pathogen

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*), has long been one of the most devastating wheat diseases in many wheat growing regions worldwide. This biotrophic pathogen establishes successful host interactions by deploying a vast repertoire of effectors, which facilitate infection by suppressing host immunity and/or altering host metabolism and physiology. The *Pgt* genome is predicted to encode over 1,300 candidate effectors, however, only a few have been identified as being recognised by corresponding stem rust resistance (*Sr)* genes. In this study, we applied virus-based protein overexpression (VOX) in wheat to validate newly identified variants of known avirulence effectors (e.g. AvrSr50 and AvrSr27) identified through comparative genome sequencing, as well as novel effectors (e.g. AvrSr13, AvrSr22, AvrSr33) discovered via pooled effector library screenings in wheat protoplasts. Additionally, we investigated the role of these effectors during wheat infection in the absence of the respective *Sr* gene. To achieve this, we used yeast two-hybrid screens and protein co-IP followed by GC-MS/MS analysis, to identify host proteins that interact with and may be targeted by *Pgt* effectors. Several candidate interactors were identified, and we are validating these interactions for AvrSr22, AvrSr33 and AvrSr50 using the in planta split GAL4 RUBY assay. To further investigate their functional significance, we plan to silence the validated host interactor genes using VIGS in wheat and assess whether silenced plants exhibit increased susceptibility to *Pgt*. We hypothesise that enhancing the expression of these host proteins or modifying them to prevent effector targeting could contribute to improved disease resistance.

Pump-Priming Funding - CALL FOR APPLICATIONS

The Plants @ Cambridge Botanicon is an annual event designed to empower early career researchers (ECRs) in plant sciences across Cambridge institutes. To celebrate our third anniversary and foster collaborations beyond the event, we are launching the **Botanicon Pump-Priming Funding Competition**.

Who can apply:

The call is open to postdoctoral researchers, undergraduate and postgraduate students, and technicians working in plant-related areas within:

- Department of Plant Sciences
- Crop Science Centre
- Sainsbury Laboratory Cambridge University
- Niab
- Biochemistry
- David Attenborough Building
- Cambridge University Botanic Garden

What we fund & how proposals will be assessed:

We will award **two grants of up to £1000 each** for projects lasting **6–12 months**. The funds are intended to seed **independent collaborations** between researchers from at least two different buildings, focusing on:

- **Career development**: advancing the careers of participants
- **New collaborations**: establishing connections across institutes
- **Originality and innovation**: supporting novel ideas
- **Tangible outcomes**: generating clear, measurable deliverables
- **Independence**: projects led by ECRs without direct PI input (Funding can be managed through a PI's account, but the PI should not contribute to the project)

Eligible costs include reagents, synthesis of molecules (e.g. DNA, peptides), equipment or tools, software/hardware, and access to specialised equipment or services.

Application process:

Submit a single PDF (max 3 pages) including:

1. The Team

- Project leader's name, host laboratory, expected contract end date.
- Names of team members from at least one different building.

2. The Project

- Introduction to the proposed project with a title and a short summary (150 words).
- Objectives and approach (maximum 2 pages, including images). Please compose the text to be accessible to a cross-disciplinary panel. Images can be included in this and the following section if this aids clarity.
- Details of the intended use of the award funds. Please include a draft budget (with cost breakdown of funding being requested) and indication of the time required for completion of the award. We are expecting that most awards will run for 6-12 months.

3. Expected outcomes Please highlight any opportunities that you see:

- for scientific or technical advances (generation of useful resources, or wider community benefits)
- for advancement of the participants careers

Additional requirements:

1. You will need to provide a note of support from the head of the host laboratory (this can be a short email or signature), to confirm that the proposed project is compatible with your existing work, and that they will sponsor establishment of a grant account for the award funds. All award expenditure will be drawn from this account held at the department of the project leader and must follow standard university rules.

2. The project activities will be documented to encourage follow-on and outreach. This could include (subject to commercialisation and IP plans):
    - Publishing a short half-way progress report for the Departmental website and newsletter
    - Providing a short presentation to be shown during Botanicon 2026.

3. At the end of the funding period, you will be expected to provide a 1-2 page summary of your progress with a representative image. This could be shared via the Departmental website and newsletter.

Submission deadline:

- Email your application to Ludi Wang (**lw821@cam.ac.uk**) and Humberto Herrera (**hh585@cam.ac.uk**) by **Friday 5 September 2025**
- Results will be communicated by **3 October 2025** via email

Hot techniques

Genome Wide Association Study (GWAS)

Tally Wright
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Spatial transcriptomics

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Segmentation

Elise Laurelle
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Career Panellists

Morning session (9:20-10:20)

Neha Bhatia
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Sam Brockington
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Cris Sales
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Christopher Surridge
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Alan Wanke
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Afternoon session (15:00-16:00)

Sarion Bowers
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Sonja Dunbar
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Careers Service

Our advice is confidential, tailored and impartial.

Who we are

The University of Cambridge Careers Service helps you to prepare for your future. Whether you are an undergrad, masters student, PhD student, or a postdoc, our experienced and impartial team is here to support you at Cambridge and beyond.

We'll work with you from day one to explore options, connect with employers, and navigate the complex job market – saving you time and maximising your employability prospects. Whether you have no idea what to do next, a few ideas or a definite plan, we offer plenty to help you take the next step: one-to-one guidance consultations; 14 major careers events each year; an extensive programme of briefings and skill sessions; coordinated employer presentations; a free book on CVs and Applications; and a database of graduate-level job vacancies in Handshake.

Attendees: names and contact details

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