BiPS

Black in Plant Science Conference

OFFICIAL PROGRAMME

24TH OCTOBER 2025

HELIX

UNIVERSITY OF LEEDS
E C STONER BUILDING, VERNON ROAD, LEEDS
LS2 9JL

This event is supported by:

GATSBY
SEB
New Phytologist Foundation
UNIVERSITY OF LEEDS
Grow More Foundation

SCHEDULE

09:00 - 09:30	REGISTRATION
09:30 - 10:00	MORNING REFRESHMENTS
10:00 - 10:10	WELCOME AND PROGRAM OF EVENTS
10:10 - 10:50	PLENARY TALK – NICOLA PATRON
10:50 - 11:10	BREAK
11:10 - 11:40	THE JOURNEY OF PLANTS THROUGH BLACK BOTANISTS
11:40 - 12:10	CULTIVATE: 2025 BIPS SUMMER STUDENTSHIP AWARDEES
12:10 - 12:30	FLASH TALKS
12:30 - 13:30	CONNECT: NETWORKING LUNCH + POSTER SESSION
13:30 - 14:20	CELEBRATE: 2025 RESEARCH EXCELLENCE AWARDEES
14:20 - 15:20	BREAKOUT SESSIONS ***CONNECT: DELIVERING IMPACT ON AFRICAN CROPS*** ***CULTIVATE: CULTURALLY SENSITIVE MENTORING*** ***CONNECT: EXPLORING CAREERS BEYOND ACADEMIA***
15:20 - 15:35	BREAK
15:35 - 16:15	PLENARY TALK – KEVIN COX
16:15 - 16:30	CONCLUSIONS, FEEDBACK AND FINAL REMARKS
16:30 - 18:00	POSTERS AND DRINKS

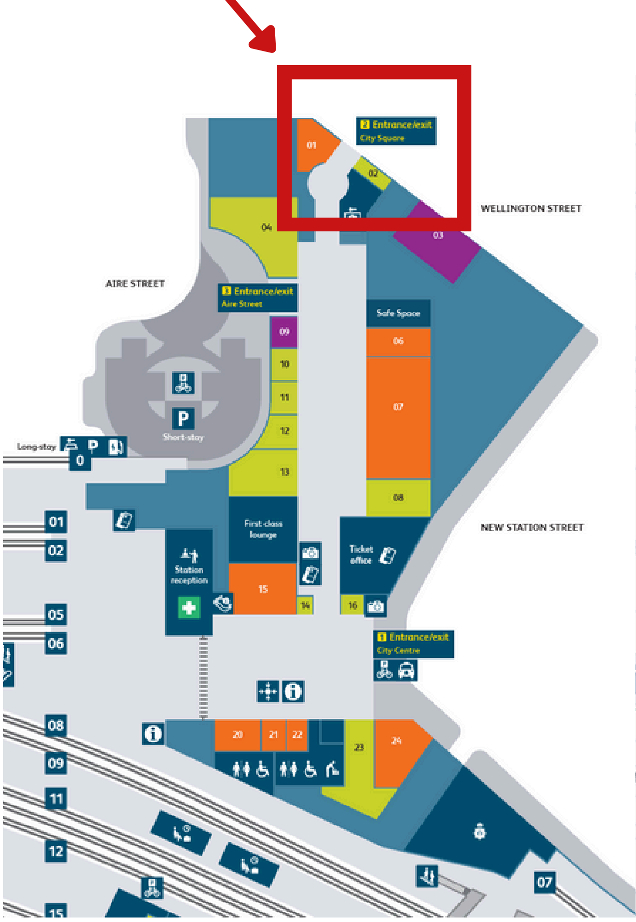
VENUE LOCATION

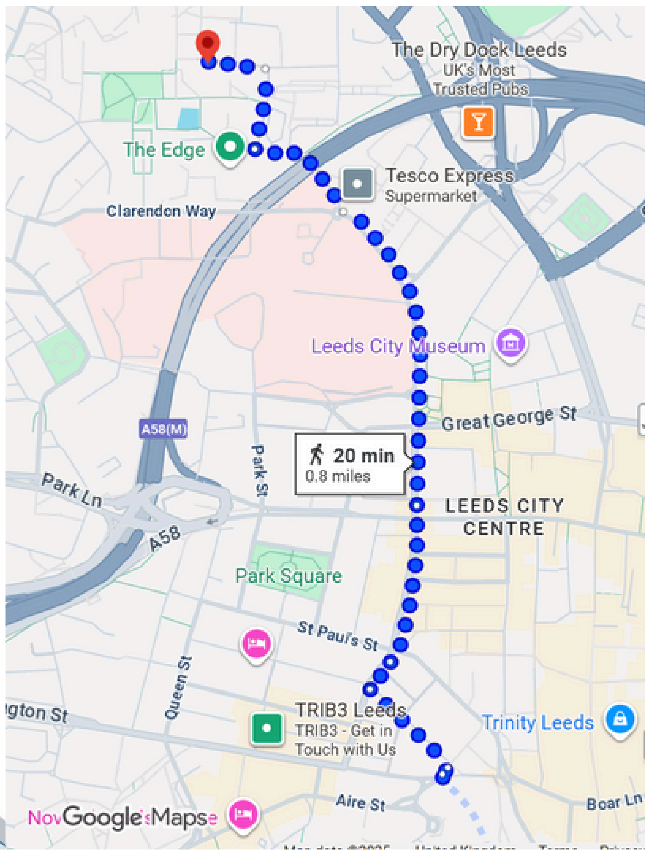
The Helix Venue entrance is somewhat hidden. HELIX can be found on Level 7 of the EC Stoner building on the University of Leeds campus. Lookout for our BiPS volunteers in white shirts who will be giving directions. **What3Words: arrow.vibes.lush**

Directions from Leeds Train Station

https://maps.app.goo.gl/uGNeAch7jaHfxWYs9

Exit Leeds Train Station via the City Square exit to follow google maps.





SESSION DETAILS & SPEAKERS

Plenary Speaker – Nicola Patron

Nicola is an Associate Professor in the Department of Plant Sciences, University of Cambridge using synthetic biology approaches to understand the production of plant specialised metabolites, and to investigate how quantitative plant traits emerge from network functions. Her lab develops tools and technologies for plant biotechnology, with the aim of driving innovation in agriculture and biomanufacturing. Nicola has a PhD in plant molecular biology and did post-doctoral research on plastid metabolism at the John Innes Centre and the University of British Columbia. As a SynBioLEAP fellow, she was recognised as an emerging leader in synthetic biology. Nicola is a co-founder of Black in Plant Science.

SESSION DETAILS & SPEAKERS

Plenary Speaker – Kevin Cox

Kevin is a HHMI Hanna Gray Fellow who is an Assistant Professor in Biology at WashU and an Assistant Member/Principal Investigator at the Donald Danforth Plant Science Center. Kevin earned his Bachelor's (B.S.) in Biology at the University of Missouri-St. Louis in 2013. He earned his Ph.D. in Plant Pathology at Texas A&M University in Libo Shan's lab in 2018, where he studied the molecular mechanism of a cotton disease called Bacterial Blight of Cotton. Afterwards, he joined the Danforth Center for his post-doctoral experience in Blake Meyers' lab, where he focused on developing methods to study spatial gene expression in plants. Kevin started his role as a joint faculty member at WashU and the Danforth Center in July 2024. His lab is interested in understanding how genes are spatially organized in plant tissues and how cells use those genes to communicate with other cells, especially in response to stresses.

SESSION DETAILS & SPEAKERS

The Journey of Plants through Black Botanists

Join us for an inspiring and educational panel exploring the profound connections between plants, people, and the powerful legacy of Black botanists throughout history and today.

In The Journey of Plants through Black Botanists, we'll trace the scientific, cultural, and spiritual journeys of plants across continents and generations—through the lens of Black scholars, horticulturists, and plant lovers who have shaped our understanding of the natural world.

Chair: Mikhaela Neequaye

Mikhaela Neequaye, PhD, is a Post-doctoral Research Assistant in the newly established Byers Lab at the John Innes Centre. She is a chemical ecologist, with a background in crop genetics, currently studying the regulation of plant-pollinator interactions. Mikhaela is a British-Ghanaian and a recent recipient of the Rosalind Franklin Society Award in Science.

SESSION DETAILS & SPEAKERS

The Journey of Plants through Black Botanists

Speaker: Jade Bleau

Jade Bleau, PhD, is a Postdoctoral Research Assistant at the University of Dundee/James Hutton Institute. After finishing her BSc at the University of Leeds, she completed her MRes in Plant and Microbial Biology at the University of Sheffield (UK), working with the vegetable breeding company Enza Zaden (Netherlands). She completed her PhD at the University of Edinburgh and is currently at the University of Dundee, researching the molecular mechanisms behind plant-aphid interactions.

Jade is one of the founding members of Black Botanists Week, a campaign first organised in 2020 to promote, encourage, create a safe space for, and find more Black people who love plants across the globe. In addition, alongside the committee members of Black Botanist Week, she produced a seminar series called Growing Black Roots: The Black Botanical Legacy which consists of eleven lectures delving into the many ways one can be a botanist and use botanical knowledge.

As well as this, Jade contributed significantly to the inception of the Black in Plant Science Network and continues to serve as a valued member of the committee.

SESSION DETAILS & SPEAKERS

The Journey of Plants through Black Botanists

Speaker: Jessica Ashman

Jessica Ashman (b.1986) is a Jamaican British interdisciplinary artist, based in London. Her practice is informed by the hidden histories of the Black British Jamaican diaspora communities she was raised in, archive as a social political force and Black radical feminist theory and speculative fiction. Ashman is also a keen gardener, allotment holder and trainee horticulturalist, connecting this to her artist practice by exploring Black existence in relation to land, nature, and colonial botanical history.

Ashman's work combines painting, animation, music and sound into transformative and visceral installations and performances. A Royal College of Art graduate, her work has been supported by Animate Projects, Arts Council England, Focal Points Gallery, New Art Exchange and 198 Contemporary. Ashman has recently finished a 15-month residency at Bristol Museum and Art Gallery, as part of UAL's 20/20 Programme, resulting in her 2025 solo exhibition 'Those that do not smile will kill me'.

SESSION DETAILS & SPEAKERS

The Journey of Plants through Black Botanists

Speaker: Christine Eyene

Christine Eyene is an art historian, critic and curator. She is Senior Lecturer in Contemporary Art at Liverpool John Moores University and Research Curator at Tate Liverpool. From 2012 to March 2022, she was Research Fellow in Contemporary Art at the University of Central Lancashire where she worked on Making Histories Visible, a multidisciplinary visual arts research project led by multiple award-winner artist Lubaina Himid CBE RA. In this framework, she developed new research into feminism, sound art, and photography. In 2023 she completed her PhD at Birkbeck, University of London, on the relationship between African literature and visual representation in the work of South African photographer George Hallett (1942-2020) under the supervision of Professor Annie E. Coombes.

Eyene's areas of research and curatorial practice encompass contemporary African and Diaspora arts, feminism, photography, and non-object-based art practices notably sound art. Her other interests include: socially-engaged initiatives, urban culture, music, design, and new media.

SESSION DETAILS & SPEAKERS

Cultivate: Meet our Summer Studentship Cohort

Meet the students from our second iteration of our Summer Studentship Programme! Join us to hear directly from these emerging talents about their experiences and insights gained over the summer. Discover the impact of the programme and celebrate the achievements of the next generation of plant scientists.

Chair: Steven Spoel, FRSE

Born to parents from Suriname and the Netherlands, Steven Spoel is Professor of Cell Signalling and Proteostasis at the University of Edinburgh. After completing an MSc at Utrecht University (Netherlands), he moved to Duke University (USA) for his PhD degree and subsequently was awarded an EMBO Long-Term Fellowship and a Netherlands Science Foundation Rubicon Fellowship for postdoctoral work at the University of Edinburgh. In
2010 he started his lab with a Royal Society University Research Fellowship. He has served as Director of the Institute of Molecular Plant Sciences (2018-2023) and currently is Director of Research for Biological Sciences. Steven has been a recipient of the New Phytologist Tansley Medal, the Early Excellence in Science Award from the Bayer Foundation, and two consecutive grants from the European Research Council and was elected Fellow of the Royal Society of Edinburgh (FRSE). He serves the community in various external roles, including as a member of BBSRC's Council and as Gatsby Plant Science Advisor.

SESSION DETAILS & SPEAKERS

Cultivate: Meet our Summer Studentship Cohort

Speaker: Hamda Hassan

Hamda Hassan, is an undergraduate student at King's College London studying Biochemistry. What has always interested her most about Plant Biology is the uncovering of the ways in which
microbial communities interact with plants and their respective ecosystems; how this influences plant health, and even human health by means of discovering medicinal the benefits plants resistant to pathogenic microorganisms have. All forms of plant- microbial interactions fascinate me, whether pathogenic or symbiotic. Hamda firmly believes research into Plant health and Biology is arguably one of the most important areas of scientific research, sitting at the intersection of driving innovation for Biotechnology, Genomics, Microbiology and reforming Agriculture. She wishes to become a proficient Microbiologist, and understanding the ways in which microbes interact with our environment first sits at the very foundation of this path.

Outside of Science, she's a bit of a cinephile and greatly enjoys watching many movies, especially international ones. She's interested in the ways in which film captures culture, history and the exploration of identity through storytelling.

SESSION DETAILS & SPEAKERS

Cultivate: Meet our Summer Studentship Cohort

Speaker: Noir Tucker

Noir Tucker is currently a Plant Science Bsc student at the University of Bristol. Noir's interest in plants stemmed from their extremely adaptive abilities across the Earth's varying climates and environments. Once they discovered Ethnobotany, this interest shifted to how plants are used by indigenous people, their benefits, and how plants should be thought of as their own beings with systems and communication methods instead of stand still organisms.

Within Plant Science, plant development and growth is what Noir finds most thought provoking since within it, lies the answer to how plants are able to be so adaptable, ranging from; their flower construction and morphology, leaf shape, root architecture and so forth.

Diverging from Plant Science, they have an interest in herbology mixed with cooking and how these both infused can make the body feel fuelled. They are also interested in creative fields such as; fabric arts like crochet and music, which they utilise during times of relaxation, synonymous with how plants are able to evoke relaxation.

SESSION DETAILS & SPEAKERS

Celebrate: Research Excellence Award

Meet this year's award winners of the Research Excellence Award!
Learn more about their contributions to the plant sciences from the beginning of their careers to date. Including their most recent experience at ICAR 2025.

Chair: Ayomide Olukorede

Ayomide Olukorede is a PhD candidate at the John Innes Center, Norwich, (UK) in the PhD rotation program in Plant and Microbial Science. She completed her Master's in Plant Science and Biotechnology at the University of Leeds, UK and served as a research assistant in the Benitez-Alfonso laboratory. Ayomide is interested in using a creative, curiosity-led approach to answer fundamental questions in bioscience and translating that knowledge into societal benefits and innovations in plant science. She is concerned about improving food security in Africa and passionate about contributing her knowledge and skills to improving bioscience education for early career scientists who have limited opportunities, ensuring that they are on par with their global counterparts and can reach their maximum potential.

SESSION DETAILS & SPEAKERS

Celebrate: Research Excellence Award

Speaker: Crispus Mbaluto

Dr. Crispus Mbaluto is a Senior Research Officer at the University of Essex. His research focuses on understanding mechanisms underlying interaction of plants with their environment. Within this broad topic, he is pursuing: (1). Interactions and optimization of multiple stress responses, specifically between aboveground and belowground herbivores, through systemic induced plant-responses. (2). System biology approach to discover novel elements in plant immune systems involved in beneficial microbes – induced resistance, and to model the response of microbes-induced resistance against herbivores. He earned his PhD from the German Centre for Integrative Biodiversity Research (iDiv) and Friedrich-Schiller-University-Jena in Germany, where he investigated systemic-induced plant responses underpinning interaction between nematode and herbivores in tomato. Following his PhD, he joined Dr. Sharon Zytynska group at the University of Liverpool as a postdoctoral researcher, studying beneficial multi-species interactions in cereal crop system. Dr. Mbaluto was awarded a prestigious MSCA fellowship, to investigate how beneficial microbes boost plant immunity and thereby stimulate plant health. His work generates useful knowledge on plant responses, and so we can apply this knowledge to create sustainable agrifood systems.

SESSION DETAILS & SPEAKERS

Celebrate: Excellence Past and Present

Speaker: Charlene Dambire

Dr Charlene Kunaka Dambire, PhD, is a Zimbabwe-born plant scientist and Research Fellow at the University of Nottingham's School of Biosciences, working in Professor Michael Holdsworth's lab. She holds a BSc Hons in Microbiology (cum laude) from the University of Fort Hare, an MSc in Zoology (Evolutionary Genomics, cum laude) from Stellenbosch University, and a Doctorate in Agriculture from Aberystwyth University. Dr Dambire's research explores plant proteostasis, with a focus on N-degron pathways that regulate protein stability under environmental stress. She is internationally recognised for her groundbreaking work on oxygen sensing and plant adaptation to altitude, published in leading Nature journals. Her research is driven by a passion for enhancing crop resilience, aiming to improve food security and livelihoods. In recognition of her achievements, she received the 2025 UK Black in Plant Science Research Excellence Award. Beyond her scientific work, Dr Dambire founded Ideas2Careers, a mentorship platform empowering Black girls in STEM, reflecting her dedication to diversity, inclusion, and nurturing the next generation of scientists.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Culturally sensitive mentoring

Cultivate: Inclusive Academic and Professional Growth

In today's diverse research and academic environments, mentoring must go beyond one-size-fits-all approaches. This interactive workshop equips mentors with the tools to engage meaningfully across cultures. Participants will explore identity, bias, and communication strategies to foster inclusive, supportive mentoring relationships that empower mentees from all backgrounds.

Chair: Yoselin Benitez-Alfonso

Yoselin Benitez-Alfonso, PhD, is a Professor of Plant Sciences and UKRI Future Leaders Fellow at the University of Leeds. She is originally from Cuba and studied at the University of La Habana. She completed a PhD in Biochemistry and Molecular Biology at the University of Cordoba, Spain and did postdoctoral placements at Cold Spring Harbor Laboratory (New York, USA) and at the John Innes Centre (JIC) (Norwich, UK). Yoselin's research focuses on investigating the mechanisms regulating intercellular communication in plants using biological, physical and mathematical approaches.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Culturally sensitive mentoring

Panellist: Chloe Lewis

Chloe Lewis is the award winning founder and Programme Director of The Catalyst Collective, mentoring organisation that pairs Black teenage girls with Black women mentors for high impact mentoring experiences. Launched in 2020 with just 6 pairs, this year The Catalyst will match 125 Black girls up with professional Black women to help achieve their dreams (www.thecatalystcollective.co.uk).

Chloe is also Strategic Adviser to the Director for Fair Access and Participation at the Office for Students, the higher education regulator in England. Prior to this, she held policy, procurement and private office roles at the Department for Education. Before joining the Civil Service, Chloe worked in various education charities and settings across the UK and abroad.

Finally, Chloe is final year, part-time doctoral researcher at the University of Cambridge researching the experiences of Black British PhD students and in particular, examining the dynamics of their relationships with their supervisors.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Culturally sensitive mentoring

Panellist: Katharine Hubbard

Dr Katharine Hubbard is a National Teaching Fellow and Principal Fellow of Advance HE, and is currently Director of Learning Enhancement and Academic Practice (LEAP) at Buckinghamshire New University. See Biography for more details.

Katharine is a leading expert in areas including equity within HE, awarding gaps, effective pedagogies within STEM subjects and career support for education focussed academics, including in the Scholarship of Teaching and Learning (SoTL). She publishes impactful educational research and scholarship in international peer-reviewed journals (Katharine's GoogleScholar profile).

She is the author of a sector leading Inclusive Education Framework, funded by the Quality Assurance Agency and highlighted as excellent practice in reports by both QAA and AdvanceHE.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Culturally sensitive mentoring

Panellist: Sally Osei-Appiah

Dr Sally Osei-Appiah is currently the EDI Learning and Development Manager at the University of Leeds, responsible for developing and implementing an institutional, strategic EDI Learning and Development Plan, including behaviour change interventions and EDI-related leadership development programmes. Prior to this role, Sally had served in both academic and professional services' roles, the most recent being leading the institutional Postgraduate Research (PGR) Diversity project for student success, aimed at addressing systemic barriers faced by PGRs from underrepresented groups. A certified coach, Sally also Co- Chairs the Black Female Academics' Network, a global network that seeks to empower and support the careers and leadership of Black females in higher education.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Delivering Impact on African Crops

Connect: Working with African crops and scientists.
This workshop will feature a panel of plant scientists focussed on resilient and nutritious crops for Africa. They will discuss the challenges, opportunities, and rewards of researching African plants, collaborating with African scientists, and their contributions to capacity building and the integration of innovative technologies into African research.

Chair: Nicola Patron

Nicola Patron, PhD, is an Associate Professor in the Department of Plant Sciences, University of Cambridge. Her group used synthetic biology approaches to investigate plant gene expression and metabolism. Of Trinidadian descent, Nicola was born and educated in the U.K. She did her first plant science experiments on seeds that had visited the International Space Station. After a PhD in plant molecular biology, she completed postdoctoral placements at The John Innes Centre, UK and The University of British Columbia, Canada. As a SynBioLEAP fellow, Nicola was recognised as an emerging leader in synthetic biology with a desire to help innovations in the laboratory have a positive social impact. Nicola started her research group in 2016 at the Earlham Institute, Norwich and relocated to the University of Cambridge in February 2024.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Delivering Impact on African Crops

Panellist: Katherine Denby

Professor Katherine Denby is a member of the Centre for Novel Agricultural Products (cnap.org.uk) in the Biology Department at the University of York. The research in her group focuses on plant disease resistance, novel bio-control strategies and crop improvement for disease resistance, yield and quality traits through integrating genomics, transcriptomics, network analysis and quantitative genetics. Her lab works mainly on leafy vegetables, using large-scale data and new plant breeding techniques to meet the needs of sustainable agriculture in the UK and Global South and new production systems, such as vertical farming. She is also Editor in Chief of The Plant Journal.

Panellist: Oluwaseyi Shorinola

Oluwaseyi (Seyi for short) Shorinola is an Assistant Professor of Plant Biology at the University of Birmingham. His research harnesses the power of genomics and genetics to uncover the molecular basis of productivity and quality traits in crops, with experience spanning over ten crops. Seyi is particularly passionate about promoting the improvement and adoption of underutilised crops to enhance global nutritional diversity. He recently led a major initiative to develop reference and population genomic resources for four African crops: tef, yam bean, lablab, and kei apple. His work not only advances scientific understanding but also supports sustainable agriculture and food security across diverse regions.

BREAKOUT SESSIONS & SPEAKERS

Workshop: Delivering Impact on African Crops

Panellist: Dr Beatrice Ifie

Dr Beatrice Elohor Ifie is a Senior Research Fellow in Plant Breeding at the Institute of Biological, Environmental and Rural Sciences (IBERS), Aberystwyth University, Wales, United Kingdom. She leads the Miscanthus Breeding Programme at IBERS. Beatrice uses innovative plant breeding approaches to accelerate genetic gains in crops for high yield, resilience to stress, and quality traits. Before joining IBERS, she was a Senior Lecturer at the University of Ghana and Leader, Maize Breeding Programme at West Africa Centre for Crop Improvement (WACCI), UG. Beatrice has contributed to the training of Plant Breeders at the Master of Philosophy and PhD levels in Africa. She developed an instructor guide and applied learning activities for the plant breeding e-learning in Africa (PBEA) in partnership with faculty at Iowa State University, USA.

BREAKOUT SESSIONS & SPEAKERS

Connect: Working Beyond academia, different routes

Academic careers are just one path among many. This workshop guides participants through the varied landscape of professional opportunities beyond the university setting. From industry to policy, entrepreneurship to NGOs, learn how to identify transferable skills, build relevant networks, and confidently pivot into fulfilling careers.

Chair: John Baison

John Baison, PhD, is a UKRI Future Leaders Fellow and cereal geneticist based at RAGT Seeds Ltd. focusing on the implementation of genomic selection methods in cereal breeding programmes, and liaison with breeders and statisticians to ensure delivery of molecular genetics and bioinformatics analyses. John completed his PhD on the application of genetic and genomic tools in Apple breeding at the ARC in South Africa. In June 2015, John was awarded a Postdoctoral Fellowship from the Karl Kemp Foundation to join the Bio4Energy project at Umea Plant Science Centre (UPSC), Sweden as a bioinformatician. This was followed by a Postdoctoral Fellowship from The Swedish Foundation for Strategic Research (SSF) in the Forest Genetics group at UPSC as lead bioinformatician.

BREAKOUT SESSIONS & SPEAKERS

Connect: Working Beyond academia, different routes

Panellist: Brian Chimzinga

Brian is a crop scientist and certified seed inspector specialising in cereals and pulses, currently working with the Animal and Plant Health Agency (APHA). His work focuses on import inspections, plant health surveys to support pest and disease status declarations (including “not known to occur” claims), and horizon scanning for emerging threats. With a strong background in regulatory plant health, Brian is also pursuing a postgraduate study in Plant Health and Biosecurity at Harper Adams University. He is passionate about building visibility for Black and other ethnic minorities professionals in the plant science sector.

Panellist: LDM

Professor Lisa-Dionne Morris is a distinguished UK-based Black female leader in STEMM (Science, Technology, Engineering, Mathematics, and Medicine), industrialist, and business strategist who is transforming the landscape of leadership, equity, and diversity in academia and beyond. Her commitment to driving Research Equity, Diversity, and Inclusion (EDI) has led her to found and direct the Black Female Academics’ Network, a powerful global network dedicated to championing EDI across sectors. As a dynamic advocate, she invites business leaders, entrepreneurs, and allies to join her vision of an equitable future where diversity and inclusion are foundational to success in STEM and beyond.

BREAKOUT SESSIONS & SPEAKERS

Connect: Exploring Careers Beyond Academia

Panellist: Bharat Pokhrel

Dr Bharat Pokhrel is a Research Development Manager at the University of Leeds, where he supports the development of large-scale research and innovation proposals in engineering and physical sciences. With a background in biology, biochemistry, and biotechnology, he holds a PhD in Molecular and Cellular Biology.

Bharat's career has taken him from academic research into science funding and strategy. Before joining Leeds, Bharat worked at UKRI's Engineering and Physical Sciences Research Council (EPSRC) as a Portfolio Manager, helping shape strategic investments and support national research portfolios. In his current role, he works closely with academics and partners to develop collaborative funding proposals and align university capabilities with emerging funding opportunities.

Black in Plant Science Conference 2025

POSTER ABSTRACTS

Flash Talks

1

Optimising Agroinfiltration and Investigating Cuticular Wax Genes for Improved Plant Production of VOCs

*Assia Ibrahim**

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Volatile organic compounds (VOCs) play central roles in plant biology, from pollinator attraction and defence against herbivores to stress adaptation1. Their biosynthesis can be elucidated and studied by expressing enzymes involved in their production in heterologous hosts such as *Nicotiana benthamiana*, which may also provide a route to access to high- value VOCs2. However, the rapid evaporation of VOCs from plant leaves limits our ability to quantify target products. To improve the production and retention of VOCs within plant cells, we need to optimise gene delivery and expression systems. In this study, we aimed to refine agroinfiltration methods in *N. benthamiana* to increase throughput and reliability of gene delivery. We will also investigated if the overexpression of cuticle biosynthesis genes could enhance wax deposition and reduce VOC diffusion, thereby improving retention and yield.

To refine agroinfiltration methods we compared whole-leaf infiltration approaches and developed a leaf disc–based system. Using reporter constructs (YFP, RFP) we benchmarked transformation efficiency for vacuum infiltration of leaf disks or syringe infiltration with and without 6-benzylaminopurine (BAP). We found that syringe infiltration consistently yielded higher expression with marginal increases in expression with the addition of BAP. We then tested the effect of wax biosynthesis production by expressing cer1, cer26, lasc4, and the transcription factor win1, on increasing VOC yields in *N. benthamiana*. Light microscopy was used to assess phenotypes such as stomatal closure and density. Co-expression of lavandulol synthase with wax biosynthesis genes produced phenotypes consistent with enhanced wax production, including indirect stomatal closure3. At the time of writing, the quantification of yields by GC–MS has yet to be assessed. By optimising gene delivery and developing methods for volatile stability, this work supports engineering strategies to improve plants for the production of VOCs.

References:

1. *Tissier, A., Morgan, J.A. and Dudareva, N. (2017) Plant volatiles: going 'in' but not 'out' of trichome cavaties. Trends Plant Sci., 22 pp. 930-938. doi: 10.1016/j.tplants.2017.09.001.*
2. *Golubova, D., Tansley., C, Su, H., and Patron, N.J. (2024) Emerging strategies for engineering natural product biosynthesis in Nicotiana benthamiana. Current Opinion in Plant Biology. 81;102611 doi: 10.1016/j.pbi.2024.102611*
3. *Hunt L, Amsbury S, Baillie A, Movahedi M, Mitchell A, Afsharinafar M, Swarup K, Denyer T, Hobbs JK, Swarup R, Fleming AJ, Gray JE. (2017) Formation of the Stomatal Outer Cuticular Ledge Requires a Guard Cell Wall Proline-Rich Protein. Plant Physiol. 174(2):689-699. doi: 10.1104/pp.16.01715.*

2

Sunshine Tomatoes: Can a Bowl of Soup Boost Your Vitamin D levels?

B.K. Mionki[1,2], J. Lie[1], Jennifer Ahn-Jarvis[2], Antonietta Hayhoe[2], T. Robertson[3], S. Lanham-New[3], M. Warren[2], C. Martin[1]

[1]John Innes Centre, Norwich Research Park, UK.
[2]Quadram Institute, Norwich Research Park, UK,
[3]University of Surrey, Guildford, UK

Vitamin D_3 is essential for various cellular and bodily functions. While sunlight triggers its synthesis, dietary intake or supplementation is the most reliable way to meet recommended levels throughout the year.

Plants are poor sources of vitamin D although they would play a crucial role in curbing deficiency as they are widely consumed and affordable. To address this, genome editing was used in tomato plants to engineer the accumulation of pro-vitamin D_3 by targeting the cholesterogenesis pathway. Specifically, CRISPR-Cas9 technology was used to knock out the Sl7-DR2 gene, responsible for converting 7-dehydrocholesterol (7-DHC) - pro-vitamin D_3 - to cholesterol. Disruption of Sl7-DR2 led to a significant accumulation of 7-DHC in both the leaves and fruits of the mutant plants. MALDI imaging confirmed the presence of 7-DHC in both the flesh and peel of the fruit. Upon UV exposure, 7-DHC was converted to vitamin D_3, with a single tomato providing up to 2 µg of vitamin D, demonstrating the potential of using plant metabolic engineering as a sustainable strategy for biofortification.

This study optimises UV-mediated conversion of pro-vitamin D3 to vitamin D3 in tomatoes and develops biofortified tomato soups to evaluate their nutritional efficacy. In a 4-arm, double-blind trial, healthy volunteers will consume soups containing a test dose of 10 µg vitamin D3, with plasma 25(OH)D and cholesterol levels measured to assess bioavailability and effectiveness in maintaining vitamin D status. This represents the first human intervention study to test biofortification of tomatoes as a sustainable dietary strategy to combat global vitamin D deficiency.

UV exposure studies have shown that UVB is more effective than UVC for conversion of provitamin D to vitamin D and heating the samples after UV exposure further increases vitamin D levels. Unlike previous beliefs, freeze-dried tomato powders have similar conversion efficiency as fresh tomatoes, which further simplifies the large-scale conversion of 7DHC to vitamin D in tomatoes not only for the human study but also for market production of vitamin D biofortified tomato products. The human study is scheduled to start December 2025.

3

Potato Tuber Protoplast Isolation for High Throughput Screenings

Chinemerem Akamihe[1], Melissa Salmon[11], Davide Annese[1], Erica Hawkins[1], Carolina Grandellis[1]

[1]Earlham Biofoundry, Earlham Institute, Norwich Research Park, Norwich, Norfolk, NR4 7UZ, United Kingdom

Plants have huge potential to solve food insecurity and mitigate the climate change crisis. Conventional plant breeding methods cannot meet the growing demand for secure and sustainable food systems therefore radical innovations are needed to develop resilient crops more swiftly. Advances in synthetic genomics have enabled the construction of synthetic genomes in bacteria and yeast, and applying these breakthroughs to plants is the next logical step. As part of a multidisciplinary team, the Earlham Biofoundry aims to develop a pipeline for the routine generation and testing of synthetic plant artificial chromosomes (synPACs) in potato (*Solanum tuberosum*). Engineering synthetic genetic pathways requires characterised regulatory elements capable of modulating expression levels and providing spatial and temporal control. The project aims to develop an automated platform for high throughput testing of tuber-specific DNA elements *in vitro* grown minituber protoplasts (cv Désirée) to understand how they influence gene expression. Candidate regulatory elements identified from a potato tissue atlas built by the Hall group (EI) will be tested using the developed protocol. Promising results will be correlated with *in planta* assays to understand protoplasts behaviour compared with the whole plant. These screening tools are one step on the way to enable the rapid and efficient programming of plants with improved, or entirely novel functions and will pave the way to deploy this engineering pipeline to other plant species.

4

Exploring Larval Resistance to Cabbage Stem Flea Beetle in Brassica napus Using Sinapis alba as a Genetic Resource

*Damilare Shodeinde**

**damilare.shodeinde16@gmail.com*

The cabbage stem flea beetle (CSFB, *Phylliodes chrysocephela L.*) poses a major threat to oil seed rape (Brassica napus) cultivation, particularly following the EU ban on neonicotinoid seed treatments. Developing resistant cultivars offers a sustainable alternative for managing this pest. this study explored the potential of sinapis alba (White mustard), a wild brassica relative, as a potential source of genetic resistance to the larval stage of CSFB. Two lines of *S. alba* (53, 57) and one of B. napus cultivar (Castille) were artificially infested with larvae and assessed over four weeks. Plant size traits (area, stem thickness, height) showed no significant effect on larval growth, suggesting resistance is not linked to resource availability. In contrast, larval performance differed strongly across hosts. Larvae on both *S. alba* lines exhibited significantly reduced growth and higher mortality compared to those on B. napus. No significant differences were observed between the two *S. alba* lines, nor in larval instar distribution, although variation was high. These results indicate that *S. alba* possesses traits that negatively impact CSFB larvae, likely through chemical mechanisms, and highlight its potential as a resistance donor for oilseed rape breeding.

Grounding ("knowledge graphs") Energies

David Nii Kwartei Quartey[1]

[1]*Encouraging Tangents*

Presenting work in progress emerging from time spent in the interdisciplinary ecology of postgraduate study in science, art and design, David Nii Kwartei Quartey presents on Renewable Energy through the collaborative culture of nurturing soil as microbial fuel cells.

The work in progress is considering Knowledge Graphs as informational maps, where sample collection, measured performance/ character, construction method and microscopy recognition are mapped in a reflective texture of interconnected aspects (or networked dataset architectures).

Renewingurea is the practice of exploring ways that nitrogen-carbon integration in soil systems supports (super)electrogenic bacteria, capable of powering low power electrical appliances. Through a multidisciplinary cultural perspective, Renewingurea is positioning ways of grounding knowledge graphs into generative forms of library knowledge for iterative development and insight sharing. Translating an industrial perspective stemming from Biopharma 4.0 into bioprocessing that prioritises abundant biological life and activity, this presentation recaps and introduces the microbial collaborators and material interactions that could pave ways for heightened attention on plant and soil bioelectrochemistry as a deep ecology context for energy transition ideals.

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Unmasking Root-Knot Nematodes: Identification and characterisation of their core effectorome

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Root-knot nematodes (RKNs, *Meloidogyne* spp.) cause substantial agricultural losses, surpassing billions of dollars annually. To successfully parasitize their hosts, RKNs produce and secrete effectors to suppress the plant immune system and reprogram host physiology. The majority of effectors are synthesized in the nematode's oesophageal gland cells and injected into plant cells via a syringe-like stylet. Despite their central role in pathogenicity, only a few RKN effectors have been functionally characterized. Comparative transcriptomics of infected roots identified 3- and 5-days post-inoculation as key early parasitic stages, marked by transcriptional shifts and effector gene enrichment indicative of stage-specific regulation. Analysis of predicted secreted proteins across multiple RKN species has also revealed conserved orthogroups that likely underpin RKN parasitism. To enable refined effector discovery, gland cell isolation techniques for RKNs have been optimised to facilitate targeted transcriptomics of the effector-producing cells themselves. Sequencing of the gland cells at key parasitic stages will allow us to define the effector repertoire in RKNs with unprecedented spatial and temporal precision. Together, these approaches lay the foundation for defining an RKN effectorome, identifying conserved parasitism genes and dissecting the molecular mechanisms underpinning nematode infection.

Investigating the role of F-group bZIP transcription factors in barley Zn homeostasis

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Zinc (Zn) is an essential micronutrient for all living organisms. Human Zn deficiency is a serious health concern in many populations around the world, particularly those of South-East Asia and Sub-Saharan Africa. This is due partly to the heavy reliance on nutrient-poor cereal crops as a main calorie source, which are often grown on Zn-poor soils. Developing cereal crops that maintain high yields and suitable grain Zn content without intensive fertilizer application is important for sustainable agriculture. To achieve this, and ultimately improve human health and food security, a more comprehensive understanding of crop Zn homeostasis is required. This research investigates Zn homeostatic regulation in cereal crops by studying the barley Zn-deficiency response as a model. It particularly investigates the role of F-group bZIP transcription factors, which are suggested in model systems such as *Arabidopsis*, to play a key role. Barley has an expanded number of F-group bZIPs but it is not clear if all play a role in Zn homeostasis. In *Arabidopsis*, bZIP19 and 23 regulate Zn homeostasis under low Zn conditions by binding to Zn-Deficiency Response Elements (ZDREs) in the promoters of ZIP transporter genes, thereby increasing Zn uptake and distribution within the plant1. Using CRISPR/Cas9 genome editing, we demonstrate that F-group bZIPs, HvbZIP56 and 62 are involved in the barley Zn-deficiency response. The *bzip56bzip62* double mutant shows detrimental growth effects on low-Zn conditions, in the form of pronounced stunted growth, chlorosis and necrosis. Increasing Zn concentration rescues this hypersensitive phenotype to WT levels. Functional complementation studies showed HvbZIP56 and 62 to partially rescue the Arabidopsis bzip19bzip23 Zn-deficiency phenotype [2]. We also show that over-expressing another barley F-bZIP, HvbZIP10, leads to improved performance under Zn deficiency. Additionally, gene expression analysis in bzip56 single mutants illustrates that, under low Zn, HvbZIP56 directly regulates the expression of fellow F-group members *HvbZIP10* and *1*, suggesting hierarchal regulation within the F-group. Furthermore, HvbZIP56 directly regulates ZDRE-containing genes of varying physiological function, including *HvZIP7 & 8*, and *RNA-Binding Protein1*. CRISPR single and double mutants of the remaining F-bZIPs, *HvbZIP55, 57, 58 and 1*, did not demonstrate detrimental growth effects on low-Zn. Additionally, ZDRE-gene expression in these mutants was not affected, suggesting these F-bZIPs may be involved in regulating other candidate genes not investigated in this research, or in other roles within the plant. Overall, this research provides further evidence that F-group bZIPs are involved in the barley Zn-deficiency response.

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Beyond plant genetics: Recruitment of the soil microbiome for survival by naturally drought-tolerant crops

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Climate change imperils agricultural crop productivity, particularly in the global south, where the compounding effects of severe soil degradation and drought have impoverished millions. While plant breeding efforts have yet to succeed in tackling drought, existence of drought-tolerant crops indigenous to Africa proves that nature holds the solution. However, research focusing on plant genetics alone has not unveiled the molecular basis for natural drought tolerance in such crops. Our hypothesis is that natural drought tolerance is enabled by the soil microbiome. We have demonstrated that cowpea (Vigna unguiculata) loses its natural drought tolerance when the associated soil microbiome is disrupted. This paved way to the isolation and identification of cowpea-associated microbes showing phenomenal resistance to simulated drought. Amending a degraded soil with these bacterial isolates boosted crop drought tolerance. We show that soil microbes prime plant molecular responses to drought, thereby enabling a swift stress-adaptive response not found in drought-sensitive plants. Our results suggest that soil health holds the key to sustainable agricultural productivity in the face of climate change.

Arabidopsis Gene Networks: Mapping G-Box & W-Box Regulation with Single-Cell Data

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Gene regulatory networks (GRNs) offer powerful frameworks for uncovering how transcription factors (TFs) coordinate plant growth, development, and responses to the environment. Building on Ara-BOX-cis, a bulk RNA-seq–based network, we generated an updated GRN by integrating single-nucleus RNA-seq data across Arabidopsis seed-to-seed developmental stages. This high-resolution approach captures expression dynamics at the cell-type level, enabling a more precise view of motif–TF relationships across developmental transitions.

We focused on two highly conserved promoter motifs: the G-box (bound by bHLH/bZIP TFs), central to light signalling, circadian rhythm, and stress response; and the W-box (bound by WRKY TFs), key to immunity, germination, and senescence. Centrality analyses revealed TFs with persistently high betweenness and alpha scores, suggesting their roles as regulatory hubs bridging distinct developmental states. Gene Ontology enrichment highlighted convergence on light signalling, ABA-mediated hormone response, and defence pathways underscoring their functional importance.

Our study demonstrates that single-cell–informed GRNs reveal influential regulators that are not easily detectable with bulk approaches. By identifying master regulators of plant development and stress adaptation, this work provides insights that could be extended to crop systems, informing strategies for resilience breeding and sustainable agriculture.

African Underutilized Legumes: Nutritional, Environmental, and Economic Contributions to Sustainable Food Security

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Africa's quest for sustainable food security is increasingly threatened by rapid population growth, climate variability, political instability, and fragile agricultural systems. The continent's heavy reliance on a narrow range of staple crops, namely rice, maize, and wheat, which together account for nearly 60% of global dietary energy, has created a nutritionally inadequate and environmentally vulnerable food system. This dependence has intensified malnutrition, particularly among smallholder farmers, women, children, and indigenous communities whose livelihoods traditionally depend on diverse cropping systems. Underutilized legumes, often referred to as orphan crops, represent a critical but overlooked resource with the potential to transform African food systems. Species such as African yam bean (Sphenostylis stenocarpa), Bambara groundnut (Vigna subterranea), Kersting's groundnut (Macrotyloma geocarpum), pigeon pea (Cajanus cajan), winged bean (Psophocarpus tetragonolobus), Lima bean (Phaseolus lunatus), Hyacinth beans (Lablab purpureus) and rice bean (Vigna umbellata) are characterized by superior nutritional profiles, including high protein, micronutrient density, and functional bioactive compounds. Beyond their nutritional value, these legumes demonstrate significant ecological resilience, including drought tolerance, nitrogen fixation, and adaptability to marginal soils, thereby contributing to soil fertility, climate change mitigation, and sustainable land management. Their phytochemical richness also underscores their potential for functional food innovation and nutraceutical applications. Despite these advantages, underutilized legumes remain marginalized due to limited research investment, weak policy support, poor market integration, and low farmer awareness. These constraints have accelerated genetic erosion and hindered their adoption in mainstream agriculture. This review highlights the strategic importance of incorporating underutilized legumes into modern farming systems as a pathway toward diversified, climate-resilient, and nutritionally robust food systems. Advancing this agenda requires coordinated efforts among researchers, policymakers, and development practitioners to unlock the genetic, nutritional, and economic potential of these crops. Repositioning underutilized legumes from peripheral to central roles in agricultural development can reduce Africa's dependence on food imports,
strengthen resilience against environmental and economic shocks, safeguard indigenous knowledge, and accelerate progress toward the Sustainable Development Goals on zero hunger, climate action, and biodiversity conservation.

Keywords: Underutilized legumes; orphan crops; food security; nutrition; climate resilience; agrobiodiversity; sustainable agriculture; nitrogen fixation; functional foods; Africa

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POSTER ABSTRACTS

Poster Presentations

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Rhizoctonia solani AG2-1 modifies the host-auxin response network for increased root pathogenesis of Arabidopsis thaliana

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Rhizoctonia solani AG2-1 is a soil-borne fungal pathogen that causes damping off on several important crops, including oilseed rape and potatoes. The pathogen produces the auxins, indole acetic acid (IAA) and phenylacetic acid (PAA), at varying levels, however, the role of these auxins in host pathogenesis remains unclear.

Here, we used auxin-responsive reporter lines of *Arabidopsis thaliana* to investigate how pathogen-derived auxins influence root auxin dynamics during infection by three isolates of R. solani anastomosis group (AG) 2-1. A mathematical model was developed to predict root auxin signalling in response to pathogen-derived IAA and PAA, and our model predictions were experimentally validated using exogenous hormone treatment of the reporters.

Our results revealed that pathogen-derived auxins triggered measurable auxin responses in roots prior to direct contact, including accelerated DII:VENUS degradation and enhanced DR5:VENUS activation. Exogenous auxins affected isolates' growth in vitro, with IAA inducing a biphasic response in all isolates. In planta, IAA increased the disease severity of isolate 1927, whereas PAA stimulated host growth without enhancing infection. Reporter assays revealed that IAA strongly induced auxin signalling via the canonical TIR1 pathway, while PAA competitively attenuated IAA-induced response, consistent with our model predictions. Additionally, TIR1 abundance declined after prolonged auxin treatment and during infection, suggesting dose- and time-dependent modulation of receptor levels.

Together, these results showed that *R. solani* AG2-1 manipulates host auxin signalling through differential secretion of IAA and PAA, and this could be mediating auxin perception and response via the TIR1 pathway. This study highlights that auxin signalling has a critical role in pathogen virulence and could be employed for developing tolerant crops to *R. solani* AG2-1.

Wheat stem rust back in the UK: Enhancing plant disease models with new Pgt environmental responses

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Fluctuations in environmental conditions driven by climate change are altering the distribution and aggressiveness of plant pathogens, posing a significant threat to future agricultural productivity due to disease-related yield losses. One pressing concern is the (re-)emergence of historically devastating crop diseases [1].

In the United Kingdom (UK), reports of wheat stem rust caused by Puccinia graminis f. sp. tritici (Pgt) have recently increased, signalling a potential resurgence of this historically devastating pathogen in the region [2]. Given Pgt's thermal requirements, disease development is expected to be influenced by warming temperatures. Previous efforts to model wheat stem rust epidemics have largely relied on experimental data from the last century [3]. However, as climate conditions shift and pathogen populations adapt, there is a critical need to update these models with data from contemporary Pgt isolates.

To address this, we conducted controlled experiments using current UK Pgt isolates to assess the effects of temperature and leaf wetness duration on key pathogen life cycle stages. Specifically, we examined in planta growth, latent period, and sporulation dynamics across a range of environmental conditions. Our findings provide updated estimates of cardinal temperatures and minimum leaf wetness duration for Pgt development. These parameters are now being incorporated into climate-based disease models to refine predictions of future wheat stem rust risk in the UK. By building upon the pioneering work of rust pathologists, this research enhances the UK's readiness for the resurgence of this wheat disease.

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A look into plant immunity: dissecting the roles of heat, copper, and ADR1 localization in NLR-mediated immune responses.

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Plants are equipped with a multi-layered intricate immune system network, that contains nucleotide-binding leucine-rich repeat (NLR) receptors; these are responsible for sensing pathogen effectors and triggering an immune response, for example a programmed cell death called hypersensitive response (HR). In this project, we investigated how various environmental factors influenced immune signalling outcomes. This project was categorised into 3 main projects, 2 of which investigated how different environmental factors. Project 1 explored the effect of copper treatment on NLR mediated immunity. For this experiment we used a fixed concentration of copper solution injected into wild-type plants of equal age, via agroinfiltration-based HR assay. Cell death responses were then compared between copper-treated and non-treated (control) plants through leaf imaging, observing cell death trends. Our result for this part of the project found no significant difference between the copper and non-copper induced cell death, suggesting either copper does not play a crucial role in NLR-mediated responses, or, more likely, the concentration of copper was too low for any difference to be seen. For our second project, we examined the effect of heat on NLR-mediated immune response within both old and young wild type leaves, via agroinfiltration-based cell death assays and incubation of half the leaves in heat, and the other half (control) in regulated temperature standardised for the plants. Here we observed no difference in the immune response for the hea-treated leaves, which showcased equal levels of cel death. This finding could be significant as it could be potentially useful in agriculture within regions of the world largely affected by global warming, as plants still may sustain their immune response in rising temperatures. Lastly the third experiment was part of a wider project investigating whether ADR1 activates a transcriptional change instead of cell death unlike nrg1. We used an auto active version of ADR1 tagged with GFP to see if it entered the nuclear envelope, and the conditions to induce ADR1 localisation within the nuclear envelope. Here we did agroinfiltration and confocal microscopy, where we observed bright rings indicating ADR1 localisation to the nuclear envelope, which supported our hypothesis. This is important as it showcases a role ADR1's may have in transcriptional changes. Overall these experiments help us better understand NLR immune responses within plants.

The Effect of Herbal Teas on Microbial Metabolism

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Introduction

Microbial metabolism shapes human health by influencing nutrient uptake, immune function, and disease progression. While herbal teas are widely consumed for their flavour and potential health benefits, evidence of how their phytochemicals affect clinically relevant bacteria is scarce. This study examined how a commercially available herbal tea, alongside diverse nutrient sources, modulates the volatile metabolic outputs of Escherichia coli, Streptococcus mutans, and Streptococcus pyogenes across lag and stationary growth phases.

Methods

Bacterial cultures were grown in a laboratory-grade medium (BHI), distilled water (DW), and tea at 0.8&5%. Volatile organic compounds (VOCs) were collected using solid-phase microextraction gas chromatography–mass spectrometry (SPME-GC-MS).

Results

BHI supported a broad range of microbial metabolites, while no VOCs were detected in DW. The herbal tea introduced phytochemicals that bacteria transformed or depleted. At 0.8%, bacterial metabolism was highly active, producing dimethyl sulfide, β-butyrolactone, and pyrazine derivatives. At 5%, tea-derived volatiles dominated, indicating a concentration-dependent effect. Each species exhibited distinct metabolic shifts between growth phases.

Conclusion

By demonstrating how herbal teas modulates bacterial VOC profiles in a dose- and phase-dependent manner, this work offers novel insights into using natural phytochemicals to influence microbial communities, with potential implications for functional food development and non-antibiotic interventions.

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Impact of Cell Wall Crosslinking on Plant Freezing Tolerance

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One of the biggest questions facing plant scientists around the world is how climate change will impact plant growth and development. The major challenge lies in the unpredictability of environmental conditions. For instance, the occurrence of early or late frosts poses a significant threat to plants during vulnerable stages of development. The damage caused by freezing temperatures arises mainly from the formation of ice crystals in spaces around cells. Susceptibility to freezing stress significantly contributes to global crop yield losses, necessitating the development of stress resistance strategies. While research in Arabidopsis thaliana has elucidated many molecular mechanisms underlying plant freezing tolerance over the past three decades, there has been limited focus on the structural features of plants that influence how readily ice forms and spreads. One such structural feature is the cell wall, which serves as a physical barrier around the cell. It comprises of cellulose, pectin, and proteins, which provides structural integrity while enabling flexibility, extensibility, and growth. My research aims to explore how differences in cell wall properties influence the likelihood of ice formation and spread within Arabidopsis tissues. I will demonstrate that alterations in cell wall pectin and pectin crosslinking correlate with freezing damage. Additionally, I will show how ice propagates in these pectin crosslinking mutants using a novel high-speed cryo-microscope to visualize individual cells during the freezing process. These findings provide valuable insights into the relationship between alterations in cell wall characteristics, such as strength and flexibility, and variations in ice spread and freezing damage.

Characterising Trypsin Inhibitor Activity in the orphan crop Vicia faba

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Vicia faba (faba bean) is a legume of high nutritional value and agronomic importance. Its wide array of uses in food systems are overshadowed by the presence of large quantities of trypsin inhibitors in the grains. This trypsin inhibitor activity reduces the bioavailability of proteins in the digestive tract,
decreasing amino acid consumption in consumers. *Vicia faba* is an orphan crop, with wide-scale genome data becoming available only in 2023 after sequencing.

This project aims to quantify trypsin inhibitor activity in a range of plant tissues in order to verify and complement publicly available datasets. Furthermore, the trypsin inhibitor levels in twelve pangenome varieties of *Vicia faba* will be assessed to determine which varieties are nutritionally superior. *Vicia faba* trypsin inhibitor genes are not yet fully annotated in available resources, thus a variety of bioinformatic approaches were implemented in order to compile a list for this project's use. Analysis of the publicly available RNA-Seq data was used to determine which trypsin inhibitor genes are more highly expressed.

RNA extraction of the Hedin (reference variety) tissues, as well as the grains of eleven other varieties were used for downstream qPCR. These results were compared to the RNA-Seq data. qPCR data from pangenome varieties was analysed to assess relative gene expression, showing which varieties have lower trypsin inhibitor gene expression.

The Effect of Light and Prosthetic Rhizosphere on Nitrogen Metabolism of Hydroponic Grown Plant

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The increasing global population and the negative effects of climate change demand a more sustainable approach to food production. Controlled Environment Agriculture (CEA), particularly hydroponics, is a viable option for solving these challenges through its efficient resource, yield and environmental management compared to traditional systems. However, conventional hydroponics lack rhizosphere interactions that in natural systems are vital for nutrient-cycling, stress resistance, and microbial interactions, which raise concerns about its sustainability. Furthermore, reliance on unsustainable artificial nutrient solutions and external energy sources limits its viability.

This research aims to develop a circular Hydroponic-Bioelectrical System (BES) for urban agriculture; a convergence of Microbial Fuel Cells (MFCs) and hydroponics to form a prosthetic rhizosphere. This will improve nitrogen metabolism and support plant growth, yield and quality with fewer inorganic inputs, by using atmospheric CO2, light, and nutrient-rich household wastewater as critical inputs. The prosthesis captures nutrients from wastewater, provides energy for lights and pumps, and produces beneficial organic compounds like those of the natural rhizosphere through the integration with Microbial Electrosynthesis Cells (MECs).

Basil is used as test crop and cultivated hydroponically using the nutrient film technique (NFT). Nitrogen metabolism is being evaluated through integrated biochemical and molecular approaches, including enzymatic assays of key N-assimilation enzymes, transcriptome profiling, and quantification of protein. Metabolic responses will be characterized by comprehensive analysis of volatile and non-volatile compounds, pigment profiling, and phenotypic trait assessment.

The research outcome is expected to provide novel insights into sustainable hydroponic methods that lead to a more nutritious vegetables with little reliance on unsustainable inputs and external energy sources. The expected findings will promote circular nutrient use and also provide clear insights regarding the integration of renewable energy solutions within CEA systems. This will inform light manufacturers and CEA users about a more sustainable production method.

Developing Turnip Mosaic Virus Resistance in Brassica oleracea via CRISPR-Cas9-Mediated Editing of *eIF(iso)4E*

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Durable disease resistance is a key goal in crop protection. While resistance mediated by dominant R genes have been widely deployed, such resistance is often short-lived as it is eventually overcome by evolving pathogen races. Alternatively, host susceptibility (S) genes– those required for successful infection–can confer a broader and more durable type of resistance when they have undergone loss-of-function processes and are therefore targets for resistance in crop protection.

Turnip mosaic virus (TuMV) is a major threat to Brassica spp. worldwide, however, no extreme forms of resistance to TuMV are known in Brassica oleracea (B. oleracea) vegetable types. The identification of recessive resistance gene, retr01, and its mode of action in conferring the broad-spectrum, potentially durable resistance to TuMV in B. rapa show potential for achieving the same in other Brassica spp. Both B. rapa and B. oleracea possess three copies of eukaryotic translation initiation factor isoform *4E (eIF(iso)4E)* which are known host targets of TuMV making them ideal gene-editing candidates for disease resistance.

This project utilises CRISPR-Cas9 technology to alter these susceptibility alleles in B. oleracea 'rbroc'– a cultivar not previously transformed or regenerated. CRISPR-Cas9 vectors targeting *eIF(iso)4E.a* and *eIF(iso)4E.c* were assembled using Golden Gate cloning and introduced into rbroc via Agrobacterium tumefaciens-mediated transformation using two explant types. To-date regeneration of B. oleracea 'rbroc' has been achieved, and optimisation of transformation protocols is ongoing. We aim to develop T-DNA free, homozygous eif(iso)4e mutant lines and evaluate their resistance to a range of TuMV isolates.

The project also aims to establish optimised in vitro transformation and regeneration protocols that can be used to breed new B. oleracea varieties and to demonstrate the capability to edit finished B. oleracea vegetable varieties to deliver broad-spectrum, potentially durable resistance to TuMV, circumventing the need for lengthy crossing and back-crossing programmes.

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

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Optimising root phenotypes for improved resource capture under drought conditions, 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. Root growth angle (RGA) is a significant agronomic trait and a major component of root system architecture. Knowledge of the molecular mechanisms underlying the effect of drought on root growth angle during drought remain limited. Sorghum is a naturally drought-adapted crop and a good model for investigating drought-mediated RSA changes. Here, we investigate mechanistic pathways underlying sorghum RGA regulation under drought conditions. We screened root traits using high-throughput phenotyping protocols in sorghum genotypes in varying drought water-stress and control conditions followed by high-throughput transcriptomic and gene expression analyses. Our results reveal that root architectural traits vary dramatically across genotypes that have differing drought adaptability. Further analyses shows that the nodal root growth angle 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, that may play a crucial role in regulating root architecture in response to drought stress. Our data provide a mechanistic and 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.

LAZY but effective: The role of LAZY genes in regulating lateral root gravitropic setpoint angle

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Overall plant architecture (consisting of the number, spacing and angle of secondary root and shoot branches) determines the efficiency of crops to capture essential resources such as water and nutrients below-ground, and light above-ground. Plant architecture is critically regulated by gravitropic growth, and recently, members of the highly conserved LAZY gene family have been demonstrated to play crucial roles in regulation of branching angle, a key determinant of plant architecture. We identified a novel dominant point mutation in AtLAZY4, (described as lazy4D) through an EMS mutagenesis screen in the model plant, Arabidopsis. Lateral roots in the lazy4D mutant demonstrate extremely steep rooting. However, the mechanistic basis for LAZY4 dependent-regulation of root angle remains uncharacterised. Using live cell bioimaging and molecular genetic techniques, we determined that the lazy4d protein shows increased targeting to the amyloplasts and polarises strongly to the lower plasma membrane in in LR gravity sensing cells. Finally, we show that the region of AtLAZY4 containing the dominant mutation (termed D3X) is highly conserved across land plants and that an equivalent mutation in a wheat LAZY gene (qSOR1-B) also leads to steep rooting. Since this is a hight highly desirable trait that maximises nitrogen uptake, drought tolerance and carbon sequestration in cereal crops, LAZY genes are attractive targets for gene-editing to engineer deeper rooting in crop plants.

Using embryonic monocot grafting as a tool for physiological trait transfer in Oryza sativa

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Grafting is an ancient horticultural practice of physically joining two plants so that they can grow as one. This technique has long been used to transfer desirable traits between different rootstock and scion, both within and across species. Recently, Reeves et al. (2022) overturned the longstanding consensus that monocotyledonous plants cannot be grafted. They demonstrated that several monocot species, including cereals and grasses, can be successfully grafted at the embryonic root-shoot interface, thereby opening new possibilities for studying root–shoot communication and transferring desirable traits in these crops. Here, we aimed to test whether the transfer of physiological traits from a photosynthetically efficient rootstock to a less efficient scion can improve whole-plant photosynthesis and water-use efficiency. We used non-invasive, digital high-throughput phenotyping technique (Phenospex-Planteye), alongside infra-red gas exchange measurements (LICOR-6800), to screen a sub-panel of eight Asian rice cultivars (*Oryza sativa L.*) for photosynthetic performance and biomass accumulation. Among these, Azucena, (tropical japonica subspecies), and Sarali, (indica 2 subspecies), exhibited high photosynthetic performance and biomass accumulation, whereas IR64 (indica 1 subspecies) showed reduced performance in both traits. Further, we generated Azucena/IR64 and Sarali/IR64 grafts that will be used for comparative assays with the respective non grafted controls to assess the role of grating in transferring desirable traits in rice.

Molecular Labelling Tool for Cereal Genetic Resources Management Derived from Barley and Wheat Genebank-Genomic projects

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Globally, a total of 5.94 million accessions are conserved in 867 genebanks, with 41.5% (2.47 million) of these being cereal crop accessions. Only a small proportion of the conserved germplasms have been marker-genotyped or genome-sequenced. Accurate identification of genebank accessions is critical to enhance the global efficiency and effectiveness of genebanking. It is key for preserving the associated legacy knowledge attached to the germplasm and for ensuring a prolonged value for contemporary plant science and breeding endeavours. Current common practices can be largely divided into two groups: either expensive and complex or inefficient, labour-intensive, and inaccurate. The first group relies on high-resolution genomic sequences or saturated markers, and the latter on morphological comparisons of regenerated plants with historical records. To address this, we present a low-cost, simple, reliable, and rapid genotyping approach based on a minimal set of Single Nucleotide Polymorphism (SNP) markers. We identified a minimal set of SNPs sufficient to distinguish between genebank accessions of barley (*Hordeum vulgare and Hordeum spontaneum*) and durum wheat (*Triticum durum*) conserved in the custodianship of the Germplasm Resources National Capability at the John Innes Centre, UK. This method offers a simple, automatable, and affordable alternative to traditional genebank crop descriptors used as identifiers during seed regeneration and distribution. By defining the minimal genomic resolution required to differentiate genetically distinct accessions, we demonstrate that as few as 25 carefully selected SNP markers can effectively distinguish between individual accessions, capturing a broad naturally occurring gene-pool diversity in the studied barley and wheat collections. Unlike morphology-based identification methods, which can identify mislabelling or contamination errors but can rarely prevent or correct them, our SNP *molecular labelling* approach allows for the correction of such errors and the recovery of lost germplasm identity. This study demonstrates the enhancement of accuracy and reliability of germplasm management without the need for expensive whole-genome sequencing and computationally intensive analysis. We discuss the implications of this method for improving quality assurance within genebanks and its broader utility for the user community.

Key Words: DNA fingerprint, DNA Barcoding, Genebank, KASP Marker, Minimal Marker Set