BiPS

Black in Plant Science Conference

OFFICIAL PROGRAMME

22ND OCTOBER 2024

SAINSBURY LABORATORY
UNIVERSITY OF CAMBRIDGE
47 BATEMAN STREET,
CAMBRIDGE CB2 1LR

This event is supported by:

GATSBY

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SCHEDULE

09:00 - 09:30	REGISTRATION
09:30 - 10:00	MORNING REFRESHMENTS
10:00 - 10:15	WELCOME AND PROGRAM OF EVENTS
10:15 - 11:00	PLENARY TALK – PROF. STEVEN SPOEL
11:00 - 11:15	BREAK
11:15 - 11:45	MEET THE BLACK IN PLANT SCIENCE INITIATIVE
11:45 - 12:30	CULTIVATE: 2024 BIPS SUMMER STUDENTSHIP AWARDEES
12:30 - 13:40	CONNECT: NETWORKING LUNCH + POSTER SESSION
13:40 - 14:40	CELEBRATE: EXCELLENCE PAST AND PRESENT
14:40 - 15:00	BREAK
15:00 - 16:30	BREAKOUT SESSIONS ***CELEBRATE: YOUR STORY AND HERITAGE THROUGH CREATIVITY*** ***CULTIVATE: HOW TO SECURE FUNDING AND BUILD A CAREER IN PLANT SCIENCE*** ***CONNECT: EXPLORING CAREERS BEYOND ACADEMIA***
16:30 - 17:00	CONCLUSIONS, FEEDBACK AND FINAL REMARKS
17:00 - 19:00	PIZZA AND DRINKS

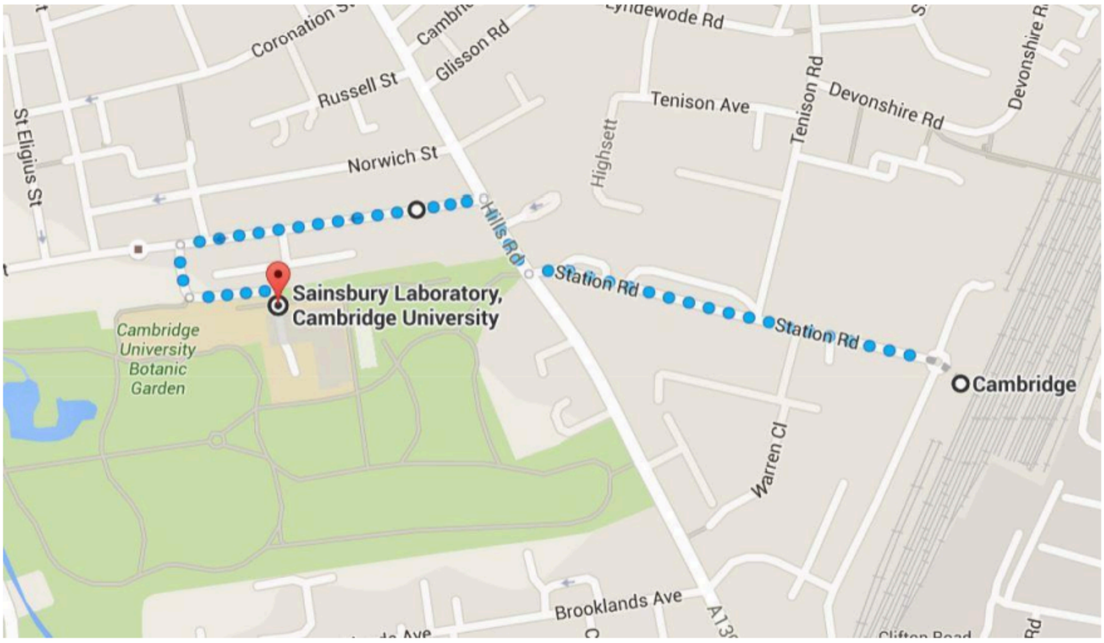
VENUE LOCATION

The Sainsbury Lab entrance is somewhat hidden. The entry is down a driveway next to St Mary's School's Art Centre at 47 Bateman Street. The driveway next to the building leads to the main gates of the Lab. Please ring the Sainsbury Lab reception from the main gates. The security team will let you through, after which, if you turn left, the Lab will be up the driveway on your right.

Directions from Cambridge Train Station

https://maps.app.goo.gl/7U8dqLQh35KdRGKB9

The Sainsbury Laboratory is located only 1 km, or 0.6 of a mile, from Cambridge Station. Head west along Station Rd | Turn right at Hills Road (A1307) | Turn left at Bateman Street | Turn left at entrance (#47, before 5th bollard)



Please do not try to enter the Botanic Garden to get to the Lab. Please use the 47 Bateman Street entrance only. Please note that there is no parking on-site.

SESSION DETAILS & SPEAKERS

Plenary Speaker – Professor 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

Meet the BiPS Initiative

In this session members of the Black in Plant Science Initiative will share about our vision and mission. Discover who we are, our goals for advancing diversity and inclusion within plant science, and how our work aims to make a difference. Explore how you can benefit from and contribute to our efforts, whether through collaboration, support, or participation in our activities.

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 in the University of La Habana. She completed a PhD in Biochemistry and Molecular Biology in 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.


Yoselin Benitez-Alfonso, PhD


Nicola Patron, PhD

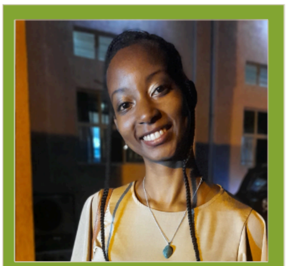

Steven Spoel, PhD


Ayomide Olukorede


Jade Bleau, PhD


Mikhaela Neequaye, PhD


John Baison, PhD


Philippa Walusimbi

SESSION DETAILS & SPEAKERS

Cultivate: Meet our Summer Studentship Cohort

Meet the students from our inaugural 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.

Q&A: Slido

One of our presenters will be joining us remotely. Therefore to please ask your questions directly to them using our online platform, slido:

https://app.sli.do/event/ugHjh9SENuktEDhjKpnUzx

Speak to a member of the event team if you have any issues.

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

Cultivate: Meet our Summer Studentship Cohort

Speaker: Poppy Isabella-Nana Akua Sarpong Cann

Poppy Isabella-Nana Akua Sarpong Cann is a student of Plant Sciences BSc at the University of Bristol. Poppy first got into studying plant sciences due to an interest in ethnobotany, where traditional knowledge and modern science overlap. Poppy is inspired by the vast potential of plants to solve global challenges, from medicine to sustainable agriculture, and the complex relationships they form with other kingdoms. The intricate ways plants adapt and evolve has driven her curiosity to uncover more, with seemingly insignificant plants like the ivy-leaved toadflax thriving in urban environments, showcasing nature's resilience and adaptability. Outside of her studies, Poppy loves to immerse herself in anything creative. From poetry and textiles to meditation and cooking, she loves to try anything to increase self-expression and mindfulness. In the future, Poppy would love to merge her interest in plant science with these hobbies to further explore methods of science communication.

Speaker: Brandon Hinds

Brandon Hinds currently studies Biotechnology with Enterprise at the University of Leeds. What really inspires Brandon about plant sciences is the scope within them for discovering creative solutions to several of the challenges we currently face and will face in the future. Whether it's engineering extreme-climate-resilient cereals, disease-resistant plants, cereals with increased nutritional value, potatoes specialised for use as biofuels, or culturing exotic plants and seeds ex situ to aid conservation efforts, he believes there is so much potential for advancements to be made across agriculture, energy, and health/wellbeing through plant science.

Outside of biotechnology, Brandon enjoys making and performing music with his friends in their band, watching live gigs, graphic design, and skating.

SESSION DETAILS & SPEAKERS

Cultivate: Meet our Summer Studentship Cohort

Speaker: Lyea Rivers

Lyea Rivers is studying BSc Earth & Environmental Studies at Lancaster University. She watched documentaries as a child with her twin sister and this sparked her interests in life & nature including plants and the ecosystems they live in. Learning the biology of plant growth and the ecosystem services they provide inspires Lyea the most! Outside of plant science, Lyea enjoys spending time around pets & wildlife, hiking & swimming in the ocean in her free time.

Speaker: Damilare Shodeinde

Damilare Shodeinde is a student at the University of East Anglia in Norwich, studying for his bachelor's in molecular biology and genetics. Plant science and genetics has always appealed to him since he began to pursue a scientific career.

Damilare believes the science of plants provides vital support to deficient areas of the world such as those undergoing droughts or flooding and areas experiencing nutrient deficiencies. Plant science is viewed as a smaller area of research in the scientific community, and Damilare hopes to not only provide his knowledge to the field but one day inspire others to uptake plant science in their careers.

Outside of science, Damilare's favourite activity is cooking (especially desserts), before he began to study science he originally went to culinary school and still loves to improve his skills, although he has decided to pursue a career in science, cooking will always provide him with a fun and interesting hobby to be improved on.

SESSION DETAILS & SPEAKERS

Celebrate: Excellence Past and Present

In this session, we will be honouring the outstanding achievements and contributions of Black people in plant science to date. This event will spotlight both historical and contemporary successes, recognising the impact of pioneering work and celebrating the ongoing excellence of current researchers and innovators. Don’t miss this opportunity to reflect on past triumphs and be inspired by present accomplishments.

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.

Speaker: Hannah Cusworth

Hannah Cusworth is a PhD researcher with English Heritage and former Head of History.

She began teaching in 2012 and taught in a number of London academies. As Head of History, Hannah led the creation of a curriculum that embraced migration stories and the history of empire and race.

She is currently researching the hidden history of mahogany in three English Heritage properties.

She regularly contributes to CPD in the history and heritage community and creates resources for teachers across the country to use with their students.

SESSION DETAILS & SPEAKERS

Celebrate: Excellence Past and Present

Speaker: Thelma Madzima

Dr. Madzima is an 1855 Associate Professor in the Department of Plant Biology at Michigan State University.

She received her Ph.D. in 2009 in Plant Molecular and Cellular Biology from the University of Florida. She subsequently joined the laboratory of Dr. Karen McGinnis at Florida State University as a postdoctoral scholar.

The overarching goal of her research program is to understand how epigenetic mechanisms facilitate growth, development, and response to abiotic stress stimuli in crop plants.

Dr. Madzima is dedicated to broadening the participation, recruitment and retention of individuals from groups underrepresented in STEM. In recognition of her efforts, she was awarded the 2021 University of Washington Bothell School of STEM Inclusive Service Award, the 2022 Maize Genetics Cooperation Leadership Award, 2022 American Society of Plant Biologists (ASPB) Excellence in Diversity and Inclusion Award and the 2022 ASPB Excellence in Education Award.

SESSION DETAILS & SPEAKERS

Celebrate: Excellence Past and Present

Speaker: Jade Bleau (winner of BiPS Research Excellence award)

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.

Speaker: Bernice Waweru (winner of BiPS Research Excellence award)

Bernice Waweru is a PhD student at John Innes Centre (University of East Anglia), she is originally from Kenya where she completed her bachelor's and master's degrees. She has already established a long track record of research excellence – studying a variety of different genomes, assembling those genomes and annotating them.

Bernice has been involved in numerous EDI activities throughout her career, being a voice for gender equality in recruitment. She is currently at the John Innes Centre as part of the Rosalind Franklin Women in Wheat Champions programme as a mentee and is an active member of the Women in Crop Science network.

BREAKOUT SESSIONS & SPEAKERS

Celebrate: your story and heritage through creativity

Engage in a creative writing and visual art workshop that delves into our roots and envisions our future. This session invites you to explore personal and collective histories through art and storytelling, while also shaping our shared and personal visions for what lies ahead.

Facilitator: Philippa Walusimbi

Philippa Walusimbi is an experienced project coordinator, producer and workshop facilitator and singer-songwriter whose main passions lie in music and film. In each of these areas she is interested in how organisations and creatives are responding to the challenges we face as local and global communities.

Facilitator: Besiana Sinanaj

Besiana Sinanaj is an eclectic artist navigating the planes of art, science and education. Born in Albania but raised in the lush tropics of Nigeria, the crispy temperate region of Libya and the scorching desert of Saudi Arabia, her experience and love of diverse cultures and ecosystems fuels her art. Besiana obtained her Biology PhD degree from the University of Leeds in 2022, where she focussed on exploring plant-fungal interactions. Since then, she has completed postdoctoral work at the University of Sheffield and currently works as a researcher at the John Innes Centre, UK.

BREAKOUT SESSIONS & SPEAKERS

Cultivate: how to secure funding and build a career in Plant Science

Join us for a panel discussion on securing a successful career in plant science, with a focus on funding and making an impact. Hear from experts who will share their experiences—both struggles and successes—in obtaining research funding. Gain valuable insights and practical tips, including advice from a funding representative, to help you navigate the challenges and opportunities in this field.

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

Cultivate: how to secure funding and build a career in Plant Science

Panellist: Faith Uwadiae, PhD

Faith is a Research Culture and Communities Specialist at the Wellcome Trust. Her vision is for academic research to be more positive and inclusive, enabling everyone to thrive. Sadly, this is not currently a reality, but she is working on it. Faith works on specific Wellcome research culture initiatives, advises teams across Wellcome on how they can redesign their funding opportunities to drive better cultures and collaborates with other industry stakeholders to incentivise and transform the research and innovation sector. Faith also leads Wellcome's work to support Black-led initiatives which enhance the careers of Black-heritage researchers. Before joining Wellcome, Faith spent 10 years in academic research, this included completing a PhD in Immunology at Imperial College London and working as a post-doctoral researcher at the Francis Crick Institute. It is this time in academia, the people she met and their stories and experiences that fuel her passion to revolutionise and change the system for the better.

Panellist: Steven Spoel

Bio as above.

BREAKOUT SESSIONS & SPEAKERS

Cultivate: how to secure funding and build a career in Plant Science

Panellist: Marianna D’Arco

Marianna obtained her PhD in Neurobiology in 2008 in Trieste (Italy). She then moved to UCL to take up her research fellowship. Upon completion of her project, Marianna decided to transition into a career in research funding, driven by her passion for supporting researchers to achieve their potential. Her first job outside of academia involved managing the “L’Oréal-UNESCO For Women in Science Programme”. Marianna joined the Royal Society in 2015, where she currently holds the position of Head of UK Grants with responsibility for shaping the Society’s funding schemes for Early Career Researchers (ECRs) and overseeing the delivery of the engagement activities for research fellows. Over the past 9 years, Marianna has contributed to new strategies of funding and support for ECRs. Under her leadership, Marianna’s team recently established the Career Development Fellowships, a pilot scheme that aims to increase retention in STEM Academia of talented researchers from underrepresented background.

Panellist: Yoselin Benitez-Alfonso

Bio as above.

BREAKOUT SESSIONS & SPEAKERS

Connect: Exploring Careers Beyond Academia

Discover how plant science research can lead to diverse career paths outside academia. In this session, professionals who have successfully transitioned from research to roles in education, policy, industry, and more will share their journeys. If you're considering a career shift, join us to gain insights on navigating change and seizing new opportunities.

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.

Panellist: Rupesh Paudyal

I am Funding Policy Lead for UK Research and Innovation (UKRI) where I develop policies related to research grant funding working across policy, strategy and operations. I am a plant scientist by training with PhD in cell and chemical biology from the University of Leeds. I also worked as a Postdoctoral Research Fellow in Leeds and Programme Manager at the National Institute for Health Research (NIHR) before I joined UKRI. Note: I am participating in the event in personal capacity and not representing my employer.

BREAKOUT SESSIONS & SPEAKERS

Connect: Exploring Careers Beyond Academia

Panellist: Maiara Piovesana Roberti

Maiara Piovesana Roberti is a Senior Portfolio Manager with the Private Office and Corporate Development team of the Engineering and Physical Sciences Research Council (EPSRC), part of UK Research and Innovation (UKRI). A passionate plant sciences enthusiast, Maiara is a trained plant molecular biologist who has transitioned from a career in academia to work with science funding and policy in the public sector. Maiara obtained a BSc in Molecular Biotechnology from Universidade Federal do Rio Grande do Sul (Brazil) and later completed her PhD studies through a partnership between Rothamsted Research and The University of Exeter. Following a one-year postdoc at The University of Edinburgh investigating the role of redox signalling in biotic and abiotic stress responses in Arabidopsis thaliana, Maiara joined EPSRC/UKRI as a Portfolio Manager, later moving on to her current role.

Panellist: Ines Alvarez-Garcia

After graduating with a degree in Zoology, Ines moved to Cambridge and became very interested in molecular biology and development while she worked as a Research Assistant in a Drosophila lab. She was awarded a PhD from the University of Cambridge and moved to Harvard University as a Postdoctoral Fellow. After a short collaboration at the European Molecular Biology Laboratory in Heidelberg, she moved back to Cambridge to do a second postdoctoral fellowship. She joined the PLOS Biology team in April 2008, and has since enjoyed collaborating closely with scientists to help them share their results.

Black in Plant Science Conference 2024

POSTER ABSTRACTS

Patterns of Diversity and Richness in the Hill Flora of Bangladesh

Ishrath Jahan

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Loss of primary forest cover is a serious threat to the biodiversity of Bangladesh, hindering all other efforts towards sustainable development. Evergreen forests of Chittagong and Sylhet alone comprise about 85% of the total forest cover within the country, playing a significant role in species conservation and carbon sequestration. Understanding the pattern of species distribution and associated environmental variables is crucial for making an effective conservation plan. This research aimed at building a complete distribution model of 372 tree species (collected from 297 forest plots) of these regions and predict the pattern of diversity and richness and how it will change under future climatic scenarios. It has been observed that species richness and diversity are higher in the northern part of Chittagong and the southern part of Sylhet. Analysis of variable contribution has shown that annual precipitation contributes the highest to species distribution in these areas compared to other selected variables. Projection of prediction results to different future climate scenarios has shown some significant shifts in the total suitable areas, which aligns with the assumption of an increase in the rate of annual precipitation in future. This outcome will help formulate suitable recommendations for conservation and further investigation to enhance species' resilience to climate change.

Understanding the role of the Sterile Alpha Motif (SAM) domain containing protein Vts1 during rice blast disease

Prince B. Amoah[1], Neftaly Cruz-Mireles[1], Barakat Obadara[1], Neha Sahu[1], Paul Derbyshire[1], Lauren S. Ryder[1], Mark Jave Bautista[1], Adam Bentham[1], Alice Eseola[1], Xia Yan[1], Iris Eiserman[1], Weibin Ma[1], Frank L.H. Menke[1] and Nicholas J. Talbot[1]

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Rice blast disease, caused by the filamentous fungus Magnaporthe oryzae, poses a significant threat to global food security, accounting for nearly 30% of lost rice production. To cause infection, M. oryzae needs to undergo a sequence of morphogenetic changes to develop a specialized infection structure called appressorium. Different studies indicate that regulation of gene expression is essential for controlling the formation of the appressorium. However, the underlying mechanisms regulating such specialised cell during infection-related development are not completely understood. Here, we investigate the function of the putative post-transcriptional regulator protein, Vts1. A recent study has discovered that the sterile alpha motif (SAM) domain containing protein Vts1 associates with Pmk1 MAPK during early appressorium morphogenesis, and it is required for vegetative growth, appressorium development and pathogenicity. Interestingly, truncation of Vts1 SAM domain (Vts1-SAM) has shown to impair pathogenicity and germ tube formation. Using structural homology and a phylogenetic approach, we have identified that Vts1 SAM domain is a putative RNA-binding protein. Using Immunoprecipitation coupled to Mass Spectrometry (IP-MS) and a Yeast-Two-Hybrid (Y2H) screening approach, we have also identified a set of Vts1 interactors with RNA binding and cytoskeletal regulatory functions. We have also identified a set of genes which regulate mRNA binding and stability that are downregulated in the transcriptome of the null mutant of Vts1 during mycelium growth, spores (0h), incipient appressorium (4h) and mature appressorium (24h) stages. To investigate Vts1 role (s) in further detail, we have generated a series of Vts1 mutants fused to eGFP and 3xFLAG for localisation and biochemical studies in the blast fungus. Overall, we aim to determine how an RNA-binding protein regulates rice blast disease.

Determining the Significance of Non-Foliar Photosynthesis on Development, Yield, and Nutritional Value in Fruit Crops with a Focus on *Solanum lycopersicum*

Alexander Williams [1] [2], Prof. Erik Murchie[2], Dr Andrew J Simkin [1] [3]*

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[2]*School of Biosciences, University of Nottingham, UK*
[3]*School of Life Sciences, University of Essex, UK*

During the early stages of fruit development, many fruits contain high quantities of chlorophyll along with the apparatus required to successfully carry out photosynthesis. Studies have shown that in species such as Solanum lycopersicum (tomato), 29% of all photosynthetic electron transport activity occurs in non-foliar organs such as the green fruit, supporting tissues and calyces. With the improvement of a fruit's photosynthetic and carbon assimilation ability, it may be possible to significantly increase its nutritional value, size and postharvest quality.

We aim to explore methods of determining the contribution of fruit photosynthesis by overexpressing enzymes involved in the Calvin-Benson-Bassham cycle (CBB) such as SBPase which is involved in regulating the regeneration of the principal CO2 acceptor Ribulose 1,5-Bisphosphate (RuBP). The literature shows the upregulation of SBPase and similar enzymes in leaf tissue resulted in the plant's photosynthetic capacity being significantly increased as a result of an increased turnover of the CBB cycle. We aim to differentially express such CBB cycle enzymes in tomato fruit with fruit-specific promoters to determine the significance of fruit photosynthesis and its impact on fruit characteristics. Additionally, we aim to manipulate chlorophyll biosynthesis as well as alter the optical cross-section of the light-harvesting (antenna) complex through the differential expression of the related genes with the use of fruit-specific promoters. This will allow us to create transgenic tomato plants with fruit that have an enhanced ability to harvest light in specific light conditions over wildtype.

Exploiting Effectostimulins and Effectosuppressins for plant protection

Tochukwu Chisom Iguh, Anika Damm and Sebastian Eves-van den Akker*

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Successful parasitism in plant-parasitic nematodes is driven majorly by effectors, small molecules deployed by nematodes to manipulate their host. These effectors are primarily produced in two pharyngeal glands – one dorsal and two subventral gland cells. Localised in these gland cells are transcription factors (TFs) that regulate effector production. Unlike effectors which are at the interface of pathogen-host interactions in nematode infections, these TFs are hidden from the plant immunity and have no direct interaction with host plants, making them an attractive target for durable nematode control. Two TFs, SUGR1 and SUGR-like, have been identified to regulate effector production in the pharyngeal gland cells of the model cyst nematode (*H. schachtii*). Understanding the regulatory mechanisms underlying the expression of these two parasitism genes may open opportunities for nematode control. In this study, host root extract (effectostimulins) known to influence nematode behaviours and infection biology was evaluated for its short-term and long-term effect on *sugr1* and *sugr-like* expression, and on the infectivity of second-stage juvenile (J2) nematodes. Short-term treatment of J2s in effectostimulins induced transcriptional activation of *sugr-like* which consequently promoted J2 infectivity, while no effect was recorded for *sugr1*. The transcriptional expressions of both TFs were upregulated by long-term effectostimulin treatment which was accompanied by a downward trend in J2 infectivity. Furthermore, non-host root extract (effectosuppressins) investigated for its effect on *sugr1, sugr-like* and J2 infectivity in this study showed no influence on *sugr1* expression and J2 infectivity, while *sugr-like* expression was significantly upregulated.

Identification of novel signalling components of the phytosulfokine pathway

Michael Agbodo[1], Markus Draeger[1], Clinton Asare[1], Paul Derbyshire[1] and Frank L.H. Menke[1]

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Plants use peptide ligands as signaling molecules to integrate their development with external biotic and abiotic stimuli. These endogenous peptides are perceived through cell-surface receptor kinases. The pentapeptide Phytosulfokine (PSK), which is one of the numerous endogenous peptides encoded by plant genome, is recognized by the leucine-rich-repeat receptor kinase PHYTOSULFOKINE RECEPTOR 1 (PSKR1). PSK signaling promotes growth and suppresses plant immunity, and therefore plays an important role in plant microbiome homeostasis (Song et al., 2023). Although several PSK signaling outputs are known, the downstream signaling components of this pathway remain poorly understood. Here we report on the immune-suppressive function of PSK and identification of novel signaling components of the PSKR1 pathway. We show that PSK suppresses PATHOGEN/DAMAGE ASSOCIATED MOLECULAR PATTERN (PAMP/DAMP)-induced production of reactive oxygen species (ROS), one of the earliest immune responses. In addition, using a transcriptomics approach, we show that PSK treatment strongly suppresses immunity- and salicylic acid-related gene expression. Using PSKR1-GFP as a bait in affinity purification mass-spectrometry (AP-MS) experiments we identified 23 proteins with increased abundance in PSKR1-GFP pull-downs after PSK treatment. Those interactors include known interactor BRI1 ASSOCIATED KINASE (BAK1), as well novel potential interactors such as MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 7 (MKKK7), Zink finger C3HC4 RING-finger type family protein (MUP24), TRANSMEMBRANE KINASE 1 (TMK1), MILDEW RESISTANCE LOCUS 0 (MLO1), and Protein S-acyl transferase 09 (PAT09).

In conclusion, the immune-suppressive function of PSK, together with the AP-MS data shown here, provides clues for the future characterization of the signaling pathway downstream of PSKR1. Characterization of the PSKR1 pathway will help to understand how plants suppress immune responses and interact with non-pathogenic microorganisms. Ultimately, this knowledge will help guide breeding strategies to optimize the growth-defense balance, enhancing yield while leveraging the benefits of plant-associated microbes.

Improving cowpea development and physiology for growth in phosphorus-deficient African soils

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[2]*International Institute of Tropical Agriculture, Kano, Nigeria.*

Cowpea is a staple crop in tropical and subtropical regions of the world. However, yields for subsistence farmers in Africa are often poor due to low soil phosphorus (P). We tested soils from Nigerian savannah and found that the soils are extremely depleted of P in all forms. An immediate approach for yield improvement will therefore require affordable external P inputs and cowpea varieties with high Phosphorus Uptake Efficiency and Phosphorus Utilisation Efficiency (PupE and PUtE). In the longer term, soil nutrients must be managed (particularly P). Whilst Sokoto rock phosphate is cheap and accessible in Nigeria, the P therein is not bioavailable. To address this limitation, we are identifying cowpea genotypes that can mobilise, uptake and utilise fixed P in Sokoto rock phosphate and exploring the potential of P-solubilising rhizobacteria (PSR). We have grown 52 cowpea genotypes under low and high Pi supply and have identified high PupE and PUtE genotypes. However, a trade-off exists between these efficiency metrics. We have also isolated rhizobacteria and are screening for PSRs able to solubilise Sokoto rock phosphate. As field-grown cowpeas are nodulated, we have isolated N2 fixing Bradyrhizobia and currently investigating the potential impact of microbial association in mitigating the observed trade-off. Additionally, we are applying transcriptomic and metabolomic analysis to understand the molecular pathways that underpin PupE and PUtE in cowpea. These resources will be used to identify cowpea genotypes and PSRs that can grow well and maintain effective rhizobia N2 fixation, in low P soils amended with Sokoto rock phosphate.

Investigating the temporal regulation of miR156 expression in Arabidopsis thaliana

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Vegetative phase change describes the transition from the juvenile to the adult phase of vegetative development and is a widely conserved developmental phenomenon. The timing of vegetative phase change is regulated by master regulator – the microRNA miR156. High miR156 levels during juvenile vegetative development repress the expression of members of the SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) family of transcription factors, which promote adult phase traits. As miR156 levels decline during development, SPL expression increases, promoting vegetative phase change. While previous studies have identified some environmental and endogenous factors that influence overall levels of miR156, the molecular mechanisms that regulate the timing of this decline remain unclear. My research aims to elucidate the clock like mechanism that governs the temporal repression of miR156. To do this I am carrying out two complementary approaches: a semi-unbiased screening method to identify new cis-regulatory motifs and a focused candidate gene approach to characterise a candidate activator of miR156 expression. Understanding what is controlling this molecular clock will provide insights into how plants coordinate developmental phase transitions and adapt to environmental cues. In breaking this ‘clock’ the project will contribute to the broader understanding of plant development.

Manipulation of Plant NAD + Metabolism by Bacterial Effectors

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Pseudomonas syringae is responsible for diseases in many economically important crops. *P. syringae* delivers virulence proteins, called type III effectors (T3Es), into plant cells to cause disease. Nicotinamide adenine dinucleotide (NAD+) metabolism plays a crucial role in plant immunity and is therefore an attractive target for T3Es. We recently identified two T3Es, HopAM1 and HopBY, with NADase TIR domains. To investigate the intrinsic enzymatic function of HopAM1, we mutated residues in the NAD-binding pocket of HopAM1 to match those of the NAD-binding pocket in HopBY. The resulting chimera along with HopAM1 and HopBY were delivered into Nicotiana *benthamiana* by an effectorless *P. syringae* strain for metabolite analysis using HPLC-MS. NAD+ hydrolysis by the chimera changed HopAM1's enzymatic product from 3'cyclic ADP-Ribose (cADPR) to 2'cADPR. Therefore, the catalytic residues of HopAM1 are critical for determining enzymatic specificity and maybe virulence.

METACASPASE9gated diverse substrates of the Ndegron pathways in Arabidopsis thaliana

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The Ndegron pathways of the Ubiquitin Proteasome System (UPS), target proteins for proteasomal degradation, depending on the aminoterminus (Ndegron) of the protein substrate. Although Ndegron pathways are highly conserved in eukaryotes, few physiological substrates have been identified in plants. This is primarily because there is a scarcity of data on intracellular protease targets in plants. An exception was the publication of a degradome dataset derived from Nterminal proteomic analysis of targets of METACASPASE9 (AtMC9) in A. thaliana. Following cleavage of proteins by AtMC9, amino (N) and carboxyl (C) terminal proteolytic proteoform fragments are produced. For Cterminal proteoforms this results in a novel Nterminal residue that can be targeted, dependent on the nature of the residue, by Ndegron pathways. The published AtMC9 degradome in A. thaliana seedlings was used to define new substrates of the wider Ndegron pathways. Here we show that 12 out of 18 selected AtMC9 derived Cterminal proteoforms, from cleavage of 18 different proteins, are in vivo substrates of the PRT6/Ndegron pathway. We identified the first in vivo plant substrate of the enzyme Nterminal glutamine amidohydrolase 1 (NTAQ1; At2g41760). Previously, only substrates of the PLANT CYSTEINE OXIDASE (PCO) Ndegron pathway have been shown to have a pathwayassociated physiological role dependent on conditional stability. Here we show in A. thaliana that AtMC9 cleavage of one of its targets, produces a conditionally stable Cterminal proteoform carrying Glutamic acid as a destabilizing residue. This proteoform has novel functions in plant growth and developmental processes, revealing a previously uncharacterised link between METACASPASE9gated cleavage of proteins and the PRT6/N degron pathway in controlling growth and development.

The Genetics of Carpel Suppression in Grass Flower Development and Evolution

Terice Kelly, Amber de Neve, Hailong Yang, Elizabeth Kellogg, Madelaine Bartlett and Benedikt Nuesslein.

Maize flowers are unisexual —an adaptation associated with wind pollination that has evolved independently many times. Maize belongs to the grass family, where floral sexuality is diverse. This diversity is, in part, caused by floral organ suppression. In maize, flowers initiate both stamens and carpels, but only stamens persist in the tassel to form staminate flowers, and only the carpels persist in the ear to form pistillate flowers. *RAMOSA3 (RA3)* and *GRASSY TILLERS1 (GT1)* regulate this carpel suppression: gt1;ra3 double mutants have large pistils in tassel flowers. Here, we aim to determine if RA3 has a conserved role in controlling floral organ suppression. In addition, since all grass grains come from pistils, knowledge of specific genes that influence pistil development can guide crop development efforts.

The late blight pathogen, *Phytophthora infestans*, suppresses core nodes of the plant immune system to promote virulence

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In Solanaceous plants, the Nucleotide-binding leucine-rich repeat receptor (NLR) Required for Cell death (NRC) network mediates immunity to diverse pathogens, by connecting disease resistance genes (sensor NLRs) and cell surface receptors to helper NLRs within the NRC clade. Despite being an agriculturally important food crop, very little is known about the NRC network of potato (*Solanum tuberosum*). Given that *Phytophthora infestans* is an important pathogen of potato, we hypothesized that many effectors have evolved to target NRCs to perturb the potato immune system. In this study, the *P. infestans* effector, PITG_06246, was confirmed to suppress two sequence divergent potato NRCs (StNRC1 and StNRC4e). A coimmunoprecipitation experiment revealed that PITG_06246 and the NRCs it suppresses did not associate *in planta*. This suggests that PITG_06246 is targeting an unknown host protein to perturb the function of the two NRCs. Additionally, PITG_06246 truncation studies revealed that the C-terminal LWY motif is required for its virulence activity. Further experiments to determine the target of PITG_06246 are underway. Better mechanistic understanding of how effectors function will enable us to generate novel strategies to control plant pathogens and grow healthier crops.

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.

Variation at the major facilitator superfamily (MFS) ZIFL1 gene influences Zinc content of barley grain

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Keywords: micronutrients, genome-wide association study, quantitative trait loci, zinc

Food and nutritional security are global challenges exacerbated by an increasing human population and impacted by climate change. Barley is among the top cereal crops grown worldwide and is a strategic crop for food and nutrition security in several geographical domains. However, barley grains are generally limited in iron and zinc, two major micronutrient deficiencies affecting billions of people around the world, but particularly women and children in developing countries. One promising strategy to enhance crop micronutrient status is via biofortification, the identification and use of nutrient-rich natural variants in crop genetic improvement. Germplasm assessed as being rich in essential nutrients are used as parental materials in traditional breeding strategies. While simple in theory, directly assessing grain nutrient content as a phenotype in a crop breeding program is not trivial, particularly in lesser developed geographies. As an alternative, genetic diagnostics can simplify the identification of desirable progenies and accelerate the breeding process. We explored natural variation for grain zinc content within 296 Ethiopian and Eritrean barley landraces using a genome-wide association study and found strong associations with two SNPs, both of which were located within the barley ortholog of a tonoplast-associated major facilitator superfamily (MFS) transporter gene of Arabidopsis thaliana (AtZIFL1). Sequence-based haplotype analysis of the barley gene (HvZIFL1) extended this association to a 153-162 bp deletion in a non-coding region. The favourable haplotype, associated with higher grain Zn content (23-50% increase), was found in ~20% of Ethiopian and Eritrean barley germplasm. Validation experiments revealed that the effect size of the favourable haplotype was robust but influenced by growing environment. Markers are designed to the diagnostic SNPs for use as Marker-Assisted Selection (MAS) in breeding for Zn-enriched crop variety development.

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