

Our Plants, Our Future

6 - 8 December 2021 | University of Birmingham, UK

Programme and Abstracts

British Society for Plant Pathology
European Foundation for Plant Pathology



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Booklet design and layout by Eric Boa.

Cover photo: vegetable farmers in Zimbabwe (while on the hunt for cucurbit viruses)



Welcome from the BSSP President

IT IS ALWAYS A PLEASURE to welcome delegates to the British Society of Plant Pathology's Annual Meeting. All the more so this year, since this is the first such meeting we have held since 2019, and because here in Birmingham (where I did my postgraduate study) we are joined by the European Foundation for Plant Pathology.

There has been a lot of disease in the news yet those that attack plants still lack widespread recognition for the damage and threat they pose. Things are changing, however, as you will discover during one of the most ambitious programmes we have ever assembled. My thanks to the many speakers who are taking part (some remotely) and the many others who have registered to attend in person.

The wide-ranging programme covers many topics and broad themes, from policies on plant health research, diseases on the move and the importance of research partnerships to better management strategies and an increasing emphasis on tree health. Combine this with an exciting array of posters and talks from the next generation of plant health scientists and there's something for everyone – from those at the frontline of research to those working with farmers, foresters and the general public.

The meeting was originally planned for 2020 as a celebration of the International Year of Plant Health. Despite the delay and disruptions I'm delighted that we're getting back together, expanding our knowledge, discussing new ideas and forming new friendships and partnerships.

I hope you all have a stimulating meeting and enjoy your visit to Birmingham.

Nicola Spence

DEFRA

Programme

Monday, 6 December

All talks will take place in The Fry Suite. Sponsor stands, breaks and other displays will be in the adjacent Fry Lounge. Posters will be on show from Monday lunchtime onwards in The Composer Suite on the first floor.

0815-0910	<i>Registration (open 5 December for residential participants)</i>
0910-0915	Welcome by Professor Nicola Spence, BSPP President
Introductory talk	
0915-0930	Plants and net zero Gideon Henderson (Chief Scientific Advisor, DEFRA)
SESSION 1: Emerging Challenges CHAIR: Rob Jackson	
0930-1000	PRESIDENTIAL ADDRESS 1.1 Plant health science and policy in the UK Nicola Spence (DEFRA)
1000-1020	1.2 The global movement of fungal crop pathogens: models, predictions and perils Sarah Jane Gurr (University of Exeter)
1020-1050	1.3 Building resilience to insect-vectored plant pathogens Saskia Hogenhout (John Innes Centre, Norwich)
1050-1120	B R E A K
1120-1150	1.4 Models for emerging and recurrent epidemics Chris Gilligan (University of Cambridge)
1150-1210	Launch of BSPP video Introduced by Pippa Greenwood
1215-1400	BSPP AGM (The Fry Suite, 1215-1245, members only) and LUNCH
SESSION 2: Pest Risks and International Trade CHAIR: David Collinge	
1400-1430	2.1 How do we respond to the emergence of new crop disease threats? Nick Talbot (The Sainsbury Laboratory Norwich)
1430-1450	2.2 Early detection of pathogens: predicting risk for effective control Neil Boonham (Newcastle University)
1450-1510	2.3 Belt and Road Initiative and what it means for plant health Eric Boa (University of Aberdeen)
1510-1530	2.4 Plant health research, working together Clare Trivedi (DEFRA)
1530-1600	B R E A K
PH Gregory Competition CHAIR: Mike Shaw	
1600-1730	Ajisa Muthayli Ali ; Carol N Ibe ; Javier Martínez-Peréz ; Olaide Ogunsaya ; Rachel Murray-Watson ; Tania Chancellor
EVENING MEAL (buffet from 1900 onwards)	

Tuesday, 7 December

SESSION 3: Combatting Plant Health Problems CHAIR: Nicola Spence	
0900-0930	3.1 Genetic solutions: ash dieback and emerald ash borer Richard Buggs (Royal Botanic Gardens Kew and Queen Mary University of London)
0930-0950	3.2 Breeding resistance into plants - successes, disappointments and unknowns Ruth Bryant (RAGT Seeds Ltd)
0950-1010	3.3 Zigzagging towards durable disease resistance Jonathan Jones (The Sainsbury Laboratory Norwich)
1010-1030	3.4 EuroBlight and collaborative efforts to mitigate the impact of evolving populations of <i>Phytophthora infestans</i> (potato late blight) David Cooke (The James Hutton Institute)
1030-1100	B R E A K
SESSION 4: Framing Policies and Setting Strategies for Plant Health CHAIR: Dawn Arnold	
1100-1130	4.1 Tackling a formidable foe: the fightback against a forgotten enemy in Western Europe Diane Saunders (John Innes Centre, Norwich)
1130-1150	4.2 Plant health in Scotland and the work of the Plant Health Centre Gerry Saddler (SASA) and Ian Toth (The James Hutton Institute)
1150-1210	4.3 Global Crop Protection- let's do the simple and cheap things well Richard Oliver (Curtin University, Australia and University of Nottingham)
1210-1230	4.4 Policy approaches to protecting plant health in the UK Richard McIntosh (DEFRA)
1230-1400	L U N C H
SESSION 5: Beyond Pesticides CHAIR: Sophien Kamoun	
1400-1430	5.1 Invasive plants - The enemy of your enemy is your friend Dick Shaw (CABI)
1430-1450	5.2 New targets for biological control of fungal plant pathogens Katherine Denby (University of York)
1450-1510	5.3 Phytophthora communities in UK plant nurseries and links to management practice Sarah Green (Forest Research)
1510-1530	5.4 Developing biocontrol for blackleg disease of potato Ashleigh Holmes (The James Hutton Institute)
1530-1600	B R E A K
SESSION 6: Raising Wider Awareness of Plant Health CHAIR: Gerard Clover	
1600-1630	6.1 Communication and awareness raising of plant health – legacy of the <i>International Year of Plant Health 2020</i> Ralf Lopian (Ministry of Agriculture and Forestry, Finland)
1630-1650	6.2 Access Agriculture: sharing knowledge of plant health in local languages Josephine Rodgers (Access Agriculture)
1650-1710	6.3 Communicating with the public about plant health through gardening Jassy Drakulic (Royal Horticultural Society)

Poster Session	
1715-1845	Posters will be displayed in the Composer Suite (first floor). Judging will take place for the J Colhoun competition

Conference Dinner will begin at 1930.

The winners of the PH Gregory and J Colhoun competitions will be announced.

Wednesday 8 December

SESSION 7: Plant Health Partnerships CHAIR: Vardis Ntoukakis	
0900-0920	7.1 Measuring the “Global burden of crop loss” Cambria Finegold (CABI)
0920-0940	7.2 The story of Plantwise, a global programme fostering stronger plant health partnerships Rob Reeder (CABI)
0940-1000	7.3 A global comparison of fungicide recommendations and what it tells us about their use Phil Taylor (CABI)
1000-1020	7.4 CONNECTED, a community network for African vector-borne plant viruses Neil Boonham (University of Newcastle)
1020-1030	7.5 UK bacterial plant disease initiative Murray Grant (University of Warwick)
1030-1100	BREAK
SESSION 8: Tree Health and Landscape Resilience CHAIR: Saskia Hogenhout	
1100-1130	8.1 Tree Health Resilience strategy – from policy to operations Lisa Smith (DEFRA) and Ana Pérez-Sierra (Forestr Research)
1130-1150	8.2 Real risks and looming threats: the increasing array of tree health problems Steve Woodward (University of Aberdeen)
1150-1210	8.2 Urban tree health and the impact of novel diseases in Colombia Liliana Franco (Universidad Militar Nueva Granada, Colombia)
1210-1240	Career Chats – the opportunity to share and discuss the experiences and insights of leading scientists in small groups (sign up during the conference)
1230-1400	LUNCH
SESSION 9: Plant Health Miscellany CHAIR: Mike Shaw	
1400-1415	9.1 Mind the gap: connecting communities in agritech, agronomy and academia Alex McCormack (CHAP – Crop Health and Protection)
1415-1430	9.2 What deters spotted wing drosophila from egg laying? Trisna Tungadi (NIAB)
1430-1445	9.3 Cucurbit chlorotic yellows virus Infecting groundnut in Western Kenya Anthony Simiyu Mabele (Masinde Muliro University of Science and Technology)
1445-1500	9.4 Rice blast disease outcome is determined by plant and fungal circadian systems George Littlejohn (University of Plymouth)

SESSION 10: RKS Wood Award CHAIR: Nicola Spence	
1510-1515	Introduction to 2021 winner Nicola Spence (DEFRA)
1515-1545	Reflections of a restless plant pathologist Sophien Kamoun (The Sainsbury Laboratory, Norwich)
1545-1600	Thanks and closing ceremony
FINISH	

We thank the following sponsors for their support

CABI
www.cabi.org

CONNECTED community network for African vector-borne plant viruses
www.connectedvirus.net

CHAP – Crop Health and Protection
www.chap-solutions.co.uk



Butternut squash seedlings badly damaged by *Pseudomonas* sp.

Greenfield Nursery, Harare, Zimbabwe

photo Eric Boa

Biographies | invited speakers

Neil Boonham

Neil Boonham is currently Chair of Applied Crop Science at Newcastle University. After graduating with a PhD in Plant Virology from the University of Birmingham he performed post-doctoral research on phytoplasma disease in Asia at Horticulture Research International, he then moved to the Food and Environment Research Agency to lead a research group working on solutions to detection, identification and diagnosis of plant diseases. The aim of this work was to provide practical solutions to real-world problems for growers, agronomists and inspectors to enable them to prevent the introduction and spread of pathogens and the build-up of resistance to crop protection products. His current work includes virus ecology, pathogen resistance and control of pathogens in vertical farming systems.

Ruth Bryant

After working at FERA and obtaining a PhD on cereal diseases from the John Innes Centre in Norwich, I went on to work for plant breeding company RAGT. Here I lead a research team to help improve disease and abiotic stress resistance across the European wheat breeding programmes. My team is also responsible for introduction of novel traits.

Richard Buggs

Professor Richard Buggs is an evolutionary biologist. His research group analyses DNA sequences to understand how plants evolve in nature. His group designs strategies to accelerate plant evolution in response to climate change and new pests and pathogens. His largest research programme is the genetic basis of ash tree resistance to ash dieback and the emerald ash borer. Richard has published on a variety of evolutionary processes including natural selection, speciation, hybridisation and whole genome duplication. He is Senior Research Leader (Plant Health) at Royal Botanic Gardens Kew, and Professor of Evolutionary Genomics at Queen Mary, University of London.

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. Her research 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. Katherine's work is focused on leafy vegetables, using large-scale data and new plant breeding techniques to meet the needs of UK and

Global South agriculture and new production systems (e.g. vertical farming). She is an editor of The Plant Journal and the journal Plants, People, Planet, and an Executive Board member of the Global Plant Council. Katherine was Academic Director of the N8 AgriFood Programme from 2016-2021 (n8agrifood.ac.uk), a multidisciplinary programme across eight UK universities working on sustainable food production, resilient supply chains, diet, consumer behaviour and nutrition to address global food security challenges. She is currently working on FixOurFood (fixourfood.org), a 5-year programme learning how to transform the UK food system to one which prioritises dietary health in young people and builds a more diversified food economy.

Jassy Drakulic

For the last five years Jassy has worked as a Plant Pathologist in the Plant Health team for the RHS. She led a citizen science project on her main research topic, *Armillaria* root rot, and is currently involved in another citizen science project, Check a Sweet Chestnut, mapping sweet chestnuts and the Oriental Chestnut Gall Wasp *Dryocosmus kuriphilus* as part of the EU Horizon 2020 project HOMED (Holistic Management of Emerging and invasive forest pests and Diseases). She regularly contributes to RHS public communications in print, online, via the podcast and on BBC radio. Alongside her research, she provides training and advice on plant health to RHS members and special interest groups. She has an interest in field mycology and advocates for public appreciation and understanding of fungi, recently initiating installation of new interpretation and exhibits about fungi at the RHS. Before joining the RHS in 2016, Jassy studied Plant and Microbial Sciences followed by a Secondary Science PCGE at University of Cambridge, then completed her PhD with Rumiana Ray, Toby Bruce & Matt Dickinson on ecological interactions between agricultural plants, pests and diseases at University of Nottingham and Rothamsted Research.

Cambria Finegold

Cambria Finegold is CABI's Global Director, Digital Development, leading CABI's work on harnessing the power of data, knowledge, and ICTs to support the Sustainable Development Goals. She is a multi-disciplinary social scientist with research interests that weave together rural livelihoods, digital development, nutrition, systems approaches and complexity science, data and modelling, agricultural value chains, geographic information systems, natural resource governance and gender. Prior to joining CABI, she worked for World Fish Center and Oxfam GB,

working primarily in Africa and Latin America. She currently leads the Global Burden of Crop Loss, a new initiative that seeks to generate rigorous, authoritative evidence on impacts, causes, and risk factors of crop loss worldwide. As with the Global Burden of Disease initiative in human health and the Global Burden of Animal Diseases in animal health, the aim is to encourage and facilitate evidence-based decision making to ensure that funding, policy, and research efforts are channelled to where they are most needed.

Chris Gilligan

Professor Chris Gilligan is currently a Director of Research and Head of the Epidemiology and Modelling Group at the University of Cambridge, where he was previously Head of the School of Biological Sciences and Professor of Mathematical Biology. He is a Life Fellow of King's College, Cambridge. Together with his research group and colleagues, Chris Gilligan has developed an extensive epidemiological toolkit with applications in plant and animal disease, including Covid-19. His current research is focused on the development and use of models to predict spread and identify effective strategies for the control of crop disease at scales ranging from on-farm to the landscape, regional and continental scales. Current applications involve models to inform the surveillance and control of crop disease and pests in sub-Saharan Africa (wheat rusts, cassava and banana disease and desert locust), Australia (banana and avocado disease) and India (aflatoxins on maize), Nepal and Bangladesh (wheat rusts) the US (citrus disease) and UK (range of crop and diseases of natural vegetation). He has held a BBSRC Professorial Fellowship and a Royal Society Leverhulme Trust Senior Research Fellowship, and is an Honorary Fellow of the American Phytopathological Society and former President of the British Society for Plant Pathology.

Sarah Gurr

Sarah Gurr studied at Imperial College (BSc, PhD), and awarded The Huxley Medal. She was a post-doc. at St Andrews and thence a Royal Society University Research Fellow. She was elected Lecturer (1993), thence Professor at Oxford (2004), where she held a Leverhulme Trust Royal Society Senior Research Fellowship. Sarah was appointed to the Chair in Food Security, Exeter University in 2013. She was formerly BSCP President (2011) and sat on BBSRC Council (2012 - 2018). She was recently appointed to The International Advisory Board at SLU University, Uppsala; as advisor to Scottish Government on Plant Health (RESAS); Visiting Professor at Utrecht University; Fellow of Canadian Institute for Advanced Research (CIFAR), as Senior Research Fellow at Somerville College; Fellow at The Royal Botanic Gardens, Kew; James Hutton Institute and elected

Fellow of the American Academy of Microbiology (2020). She was awarded the President's medal by British Mycological Society (2018). Her interest is in plant disease - with particular emphasis on fungal infestations / pathogenicity and in their global movement and control. She has authored /co-authored over 150 publications, including 11 high profile papers in Science, Nature, and Nature Journals, being listed amongst the most highly-cited researchers worldwide (Clarivate Analytics 2019).

Gideon Henderson

He became Defra's Chief Scientific Adviser from October 2019 and is a Professor of Earth Sciences at the Dept. of Earth Sciences and a senior research fellow at University College, Oxford. He is also an adjunct associate research scientist at the Lamont Doherty Earth Observatory of Columbia University. In 2013, he was elected a Fellow of the Royal Society. His research uses geochemistry to understand surface earth processes, particularly those relating to climate, the ocean, and the carbon cycle.

Saskia Hogenhout

Saskia Hogenhout obtained her MSc at *de Vrije* University, Amsterdam in 1994 and her PhD at Wageningen University and Research Centre in 1999. She was appointed as Assistant Professor at The Ohio State University, USA in 1999 and obtained tenure as Associate Professor in 2005. She moved her research group to the John Innes Centre, UK, in June 2007, and became Honorary Professor at the University of East Anglia, Norwich, UK, in 2013 and Professor by Special Appointment at the University of Amsterdam, The Netherlands in 2019. Her research has focused on the molecular basis of plant-microbe-insect interactions. She has investigated how virulence proteins of the insect-vectored phytoplasmas modulate plant architecture and development and plant resistance to leafhopper vectors. Her lab has also developed genomics resources for sap-feeding insects of the order Hemiptera, including aphids, leafhoppers and froghoppers, and has studied their interactions with plants (e.g. 2). She led the BRIGIT consortium, a project that brought together twelve UK research institutes to enhance surveillance and response to *Xylella fastidiosa* (www.jic.ac.uk/brigit).

Sophien Kamoun

Sophien Kamoun grew up in Tunisia where he developed a passion and curiosity about nature. He studied genetics in Paris and Davis, California, before working in Wageningen, Ohio and Norwich, where he is currently a Senior Scientist at The Sainsbury Laboratory and Professor of Biology at The University of East Anglia. He is known for his seminal contributions to our understanding of plant diseases and plant immunity. He pioneered genomics and

molecular biology methods to reveal fundamental insights into the biology and evolution of eukaryotic plant pathogens. He discovered virulence effector families from pathogenic oomycetes and fungi, and showed how they can modulate plant immunity. He demonstrated how antagonistic coevolution with host plants has impacted the architecture of pathogen genomes, accelerated the evolution of effector genes, and drove the emergence of immune receptors networks. His inventive work in plant pathology has resulted in new approaches to mitigate some of the world's most serious crop diseases. Professor Kamoun has received many awards and recognitions, notably the Kuwait Prize and The Linnean Medal.

Ralf Lopian

Ralf had been Chief Plant Health Officer for Finland for many years and now as Deputy Chief Plant Health Officer of Finland focuses on international plant health aspects in the Ministry of Agriculture and Forestry. He has held various positions with the Plant Pathology Department at the University of Helsinki, the National Plant Protection Service of Finland and the Secretariats of the European and Mediterranean Plant Protection Organization and the International Plant Protection Convention. He was the chair of the IPPC Commission as well as its vice-chair for several election periods and has been the international champion for the proclamation of the International Year of Plant Health. For six years, he chaired IPPC and FAO steering committees preparing and planning the IYPH.

Richard McIntosh

Richard McIntosh is the Deputy Chief Plant Health Officer in Defra. His role includes leading Defra's plant health policy and risk teams and the UK Plant Health Risk Group. Richard is also UK Controller of Plant Variety Rights.

Richard Oliver

Richard Oliver recently retired as Chief Scientist of the GRDC-supported Centre for Crop Disease Management. He is chair of the Pests and Diseases Expert Working Group of the Wheat Initiative. He is working on various books.

Josephine Rodgers

Josephine Rodgers is the Executive Director of Access Agriculture, with a BSc in Agriculture from University of Leeds and an MA in Mass Communication from University of Leicester. She has been making videos about agriculture for more than 35 years and has been training people to make their own programmes for the past 15 years. Her passion is to enable the use of video to assist smallholder farmers. Having co-founded Access Agriculture in 2012 it has now grown to cover Africa, Asia and Latin America. She works closely with

a number of International Organisations and NGOs to assist with quality video production and distribution. Her belief is that the technology is not important, but the content most definitely is.

Gerry Saddler

Gerry Saddler has a degree in biological sciences from Edinburgh University and a PhD in bacterial systematics from Newcastle. He spent 4 years as an industrial microbiologist, working in drug discovery programmes in Switzerland and Italy, before returning to the UK to take up a post as a bacterial taxonomist at CABI Bioscience, Egham. At CABI he provided a general diagnostic service for bacterial plant pathogens on a wide range of crops and established a research interest in bacterial pathogens of potato. He joined SASA in 2001 and took up his current post as Chief Plant Health Officer for Scotland and Head of SASA in April 2017.

Diane Saunders

Dr. Diane Saunders is a Group Leader at the John Innes Centre, Norwich, UK. Her research focuses on (re-) emerging plant pathogens that pose a significant threat to agriculture. Diane received her BSc degree from Exeter University where she continued her studies to PhD level, studying the genetic mechanisms that regulate plant pathogen development. She then joined The Sainsbury laboratory to pursue her interest in the molecular mechanisms that underpin plant-pathogen interactions. In 2014, Diane started her own research group, with her long-term goal to dissect the molecular mechanisms that drive pathogen evolution and adaptation to prevailing selective pressures and ultimately use this new knowledge to develop host varieties with enhanced disease resistance. She has worked on three of the world's most important plant diseases, rice blast, potato late blight and cereal rusts. Diane is particularly well known for her pioneering research on the wheat rust pathogens, where she developed innovative genomic-based approaches to improve disease surveillance including the "field pathogenomics" and "MARPLE diagnostics" techniques, leading to her award as the BBSRC innovator of the year in the international category in 2019. Her research has many practical applications for agriculture, particularly improving resilience against the wheat rust pathogens in the UK and beyond.

Richard Shaw

Richard (Dick) Shaw is CABI's Senior Regional Director for Europe and the Americas as well as being Director for CABI's UK Centre in Egham. The teams in this region have expertise in microbiology, invasive species, biocontrol, biopesticides trade and commodities and extension support and pest diagnosis under CABI's flagship Plantwise programme. CABI has a global reputation in weed biocontrol, a field

Dick has worked in for 26 years with fieldwork in 20+ countries. His focus is on weeds that have an impact on aquatic and riparian habitats in Europe including Japanese knotweed which he has been studying since the last Century! He is also particularly interested in the public perception of invasive species and weed biocontrol.

Lisa Smith and Anna Brown

Lisa Smith is Head of Tree Health Policy and Plant Health Evidence and Analysis in Defra, leading an interdisciplinary team of policy makers, natural scientists, statisticians, economists and social scientists that provide evidence to inform policies on the health of plants, trees and managed bees. Anna is Head of plant health forestry and contingency at the Forestry Commission and leads a team delivering plant health forestry operations for Great Britain, and Tree Health operations in England. Previously she spent three years as the Head of Tree Health Policy and Practice for Forestry Commission Scotland and 15 years as a pathologist at Forest Research.

Nicola Spence (BSPP President 2019-2021)

Nicola is Defra's Chief Plant Health Officer (CPHO) and advises ministers, industry and others about the risks posed by plant pests and diseases, and ensuring that measures are in place to manage those risks and minimise their impact, as well as leading the operational response in the event of a disease outbreak. Nicola is an experienced research plant pathologist and worked on virus diseases of horticultural crops in the UK and internationally for over 20 years. She is an expert in plant health and international plant trade and was previously the Head of Plant Health and then Chief Scientist at the Food and Environment Research Agency near York. She is a Fellow of the Royal Society of Biology, Honorary Professor at the University of Birmingham, Visiting Professor at Harper Adams University and a Trustee of The Royal Horticultural Society and The Yorkshire Arboretum. She has a BSc in Botany from the University of Durham, an MSc in Microbiology from Birkbeck College, University of London and a PhD in Plant Virology from the University of Birmingham. The subject of her PhD was Bean Common Mosaic Virus in Phaseolus beans in Africa.

Nick Talbot

Nick Talbot received his PhD from the University of East Anglia and following postdoctoral research at Purdue University in the USA, he moved to the University of Exeter as a Lecturer, later becoming Professor of Molecular Genetics, Head of the School of Biosciences, and Deputy Vice Chancellor for Research. He joined The Sainsbury Laboratory (TSL)

as Executive Director in 2018. Nick's research is focused on understanding plant infection by the rice blast fungus, which causes the most serious disease of cultivated rice. He is particularly interested in how *M. oryzae* uses specialised infection cells called appressoria to infect rice plants. His research has contributed to understanding how appressorial turgor is generated and how autophagic cell death is necessary for plant infection. Nick's research group also studies how rice tissue is invaded using special structures called transpressoria that enable the fungus to move between rice cells, and how effector proteins suppress immunity. His work is funded by BBSRC, The Leverhulme Trust, Halpin Scholars programme, and Gatsby. Nick has supervised 40 PhD students to date. He is a Fellow of the Royal Society of Biology, a member of EMBO, a member of Academia Europaea, and a Fellow of The Royal Society.

Ian Toth

After completing his PhD on blackleg disease (caused by the bacterial potato pathogen *Pectobacterium atrosepticum*) at the University of Warwick and working on product discovery at the biotechnology company Novo Nordisk in Denmark, he took up a Principal Investigator position at the Scottish Crop Research Institute (now the James Hutton Institute) in Dundee in 1995. Since then he has continued to study blackleg and other bacterial plant diseases with the aim of reducing disease problems for industry. In 2018 he became Director for the Scottish Centre of Expertise for Plant Health where he is involved in helping to coordinate plant health knowledge and overseeing the Centre's project delivery and translation to stakeholders.

Steve Woodward

Forty years of experience in tree health research mainly on pathogens attacking woody plants in temperate and tropical forest ecosystems, funded by the EU, UK Research Councils and various charities. Currently, my research is focused on alien invasive pathogens, their detection, the damage they cause, how they spread globally and mitigation methods that can be used to reduce their impacts on natural ecosystems. A major interest is in how plants in populations respond to infection, with a view to finding genotypes that may be less susceptible to pathogens and, therefore, could be used in repopulating ecosystems damaged by invasive alien pathogens. I am also examining the potential use of biological control agents against diseases caused in plants by fungi and Oomycetes. I have many long-standing collaborations both within the UK and globally, which have enabled me to work on a full range of pathogens that are already or may, in the future, become invasive.

Talks and Posters

abstracts arranged alphabetically by presenter



Moroccan Watermelon mosaic virus on squash, Zimbabwe

Genetic basis of partial resistance against *Pyrenopeziza brassicae* in oilseed rape

Ajisa Muthayil ALI, Stotz, H

University of Hertfordshire

Light leaf spot (LLS) caused by *Pyrenopeziza brassicae* is the most damaging disease of oilseed rape (*Brassica napus*) in the UK. The disease accounts for up to £160M yield loss annually in England and Wales, despite expenditure of £20M on fungicides, and the severity of the disease is much greater in Scotland. In the UK, the disease has been increasing as a national problem in recent years rather than just being confined to Scotland and Northern England. LLS is currently controlled by a combination of cultivar resistance, fungicide applications and cultural practices. However, resistance mechanisms of the oilseed rape plant against *P. brassicae* are not well understood. Furthermore, fungicide control is problematic as the disease remains asymptomatic from autumn until spring and the pathogen has developed insensitivity to triazole and MBC fungicides. Thus, it is necessary to identify the genes involved in quantitative resistance of *B. napus* to design an improved and durable control strategy against LLS. The aim of this project is to better understand the genes involved in quantitative resistance against *P. brassicae* in oilseed rape. A phenotypic screen for LLS susceptibility was done in glasshouse experiments using 195 accessions of *B. napus*. In collaboration with the John Innes Centre, this screen was used together with an associative transcriptomics pipeline to identify gene expression markers (GEMs). Scanning electron microscopy (SEM) were used to monitor the pathogen during infection process and to determine time points for gene expression analysis. SEM showed that the pathogen germinates 1-day post-inoculation (dpi) on leaf surfaces, penetrates the cuticle by 2dpi and colonises the subcuticular layer by 8 dpi. Eight GEMs were expressed differently in accessions susceptible or resistant to *P. brassicae*. Characterisation of gene expression and function will aid crop breeders to develop oilseed rape with better protection against *P. brassicae*.

Viral diversity and coevolution with fungal and oomycete pathogens

Alexander ALLMAN, Silva G, Seal S, Armitage A

1. Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent, UK

Fungal and oomycete plant pathogens pose a significant threat to food security. However, viruses of these filamentous organisms (VFOs) display potential as biocontrol agents. Despite many viral infections appearing cryptic with no apparent effect on their hosts, some VFOs such as *Cryphonectria hypovirus 1* (CHV-1) elicit hypovirulence, reducing the ability of the pathogen to cause disease. Just over 200 mycoviruses have been described to date, and consequently, a great proportion of viral diversity remains uncharacterised (Gilbert et al., 2019). This project takes advantage of the vast amount of publicly available sequence data to identify and characterise novel viruses. The project focuses on viral diversity within the *Alternaria*, *Phytophthora* and *Fusarium*, representing genera of filamentous plant pathogens across the Sordariomycete, Dothideomycete and Oomycete classes. We have developed a pipeline based upon de novo transcriptome assembly coupled with hidden Markov models and BLAST searching to identify the viral presence in fungal RNA-Seq data. Results are promising with the positive identification of essential viral RNA dependent RNA polymerase (RdRP) sequences from data known to contain viruses. Furthermore, we identify additional hits from sequencing projects where the virus status is unknown. Initial analysis indicates that these may represent novel viral genomes. The next step will be to characterise the remaining viral diversity present within *Fusarium* spp.

Diversity of *Botrytis* species pathogenic on legume crops

Biruta BANKINA (1), Brauna-Morževska E (1), Kaņeps J (1), Stoddard F (2), Bimšteine G (1), Roga A (3), Fridmanis D (3)

(1) Latvia University of Life Sciences and Technologies, LV3001, Latvia; (2) University of Helsinki, P.O. Box 4, Finland; (3) Latvian Biomedical Research and Study Centre, LV1067, Latvia

Diseases of legumes are poorly studied, especially in northern Europe, in spite of the growing importance of legumes in cropping systems. *Botrytis* spp. are important pathogens of legumes, including chocolate spot of faba beans and grey mould of many legumes. *B. fabae* and *B. cinerea* are well described pathogens. Recent research has shown that the spectrum of *Botrytis* species in the legumes is more complex than considered before (Bankina et al., 2021; Plesken et al., 2015). We obtained 278 isolates of *Botrytis* spp. from faba bean, lupin, chickpea, common bean and red clover. By using the DNA sequences of three definitive genes (RPB2, HSP60 and G3PDH), we identified these to *B. cinerea*, *B. fabae*, *B. pseudocinerea*, *B. fabiopsis*, *B. euroamericana*, *B. prunorum* and *B. medusae*. Three isolates were not assigned to any known *Botrytis* species. Pathogenicity and virulence of 29 isolates were determined in vitro on faba bean, pea, narrow-leafed and broad-leafed lupin and soybean. All tested specimens infected one or more hosts, but virulence varied significantly between isolates, pathogen species and host species. We continue work on recognition and description of species and to clarify possible hosts.

References: Bankina B., Stoddard F.L., Kaņeps J., Brauna-Morževska E., Bimšteine G., Neusa-Luca I., Roga A., Fridmanis D. 2021. *Botrytis* four species associated with chocolate spot disease of faba bean in Latvia. *Zemdirbyste-Agriculture*, 18(4) – in Press; Plesken C., Weber R. W. S., Rupp S., Leroch M., Hahn M. 2015. *Botrytis pseudocinerea* is a significant pathogen of several crop plants but susceptible to displacement by fungicide-resistant *B. cinerea* strains. *Applied and Environmental Microbiology*, 81 (20): 7048–7056.

POSTER

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Mini-chromosomes as horizontal gene shuttles in the multi-host blast fungus

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The blast fungus *Magnaporthe oryzae* is a devastating plant pathogen infecting multiple staple crops. A major challenge in developing blast resistant crops is the ability *M. oryzae* has to quickly adapt to its plant host and overcome disease resistance. Mini-chromosomes, i.e. small, supernumerary chromosomes, can contribute to adaptive evolution in *M. oryzae*. Recent analyses on rice-infecting *M. oryzae* strains collected in Italian rice fields revealed the presence of distantly-related “alien” mini-chromosomes, which are most similar to *M. oryzae* lineages infecting wild grasses. In addition, some of these mini-chromosomes carry predicted virulence genes, suggesting a role in disease. These observations led us to hypothesize that mini-chromosomes may facilitate horizontal transfer of genetic material between *M. oryzae* lineages, thereby acting as gene shuttles and promoting the pathogens ability to infect its host plant. Using comparative genomic approaches of *M. oryzae* populations infecting a variety of wild and cultivated plant hosts in Italy’s Po Valley, I will identify the origin of the “alien” mini-chromosomes and then experimentally determine their impact of host virulence.

POSTER

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Using sequencing technologies to identify different *Fusarium oxysporum* forma speciales within the associated microbiome

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Fusarium oxysporum is a ubiquitous soil-borne fungus that is a major pathogen of cultivated plants worldwide. Different pathogenic strains are designated as formae speciales (ff. spp.) depending on their host range with over 120 forms described. However, within the *Fusarium oxysporum* species complex (FOSC) there are also endophytes and saprophytes, some of which are even used as biocontrols against other fungal plant pathogens. Many ff. spp. have now been sequenced and comparative genomic studies have revealed the FOSC genomes consist of a core genome with little variation between strains as well as lineage-specific (LS) and pathogen-specific (PS) chromosomes that are enriched for effectors and transposons. However, identification of ff. spp. from environmental samples remains difficult as there is so little variation between them. Accurate diagnostics are important for plant pathogen surveillance and agronomic planning. It is also important to be able to investigate the wider soil community and how plant pathogens interact with and are affected by other

microorganisms and by agronomic practices. Amplicon sequencing is often employed to identify soil microorganisms to genus and occasionally species level using 16S for bacterial and ITS for fungal identification. TEF1alpha amplicon sequencing can be used to distinguish between *Fusarium* species but so far it has not been possible to distinguish FOSC pathogens from non-pathogens or between pathogenic ff. spp. using this approach. By targeting effector genes shared between ff. spp. we have developed a novel Illumina amplicon-based approach that has the potential to identify and distinguish between different ff. spp. present in the same soil sample. In addition, to enable use of the whole genome for identification and to avoid PCR, a new long-read approach based on Oxford Nanopore is also currently being developed.

POSTER

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***Leptosphaeria biglobosa* inhibits the production of secondary metabolite sirodesmin PL by *L. maculans* in planta**

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Phoma stem canker is an economically damaging disease of oilseed rape (*Brassica napus*), caused by two co-existing fungal pathogens *Leptosphaeria maculans* and *L. biglobosa*. Interactions between these pathogens affect disease severity. *L. maculans* produces a non-host selective epipolythiodioxopiperazine (ETP) phytotoxin, called sirodesmin PL, allowing the pathogen to have a competitive advantage over other invading pathogens. Results of our recent in vitro studies indicated that simultaneous inoculation with *L. biglobosa* inhibits the production of sirodesmin PL by *L. maculans*. This study aimed to determine whether this inhibition by *L. biglobosa* also occur in planta. Cotyledons of oilseed rape cultivar Charger were inoculated with *L. maculans* only, *L. biglobosa* only, *L. maculans* and *L. biglobosa* simultaneously, or sterilised distilled water as a control. Secondary metabolites from the lesions were extracted 26 days post inoculation, using ethyl acetate. Through analytical chemistry techniques such as HPLC and LC-MS, the presence of sirodesmin PL was confirmed only in extracts from cotyledons inoculated with *L. maculans* only. These results indicate that *L. biglobosa* inhibits the production of sirodesmin PL by *L. maculans* in planta, if both are inoculated simultaneously. There is a need to further investigate the mechanisms of this inhibition by *L. biglobosa*. Understanding the interactions between *L. maculans* and *L. biglobosa* can provide new strategies for effective phoma stem canker control, alongside resistant cultivars and fungicide applications.

Monday | Talk 2.3

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The Belt and Road Initiative and what it means for plant health

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The Belt and Road Initiative (BRI) – the ‘project of the century’ – is a greatly expanded version of the Silk Road. Launched by China in 2013, around \$4 trillion (estimates vary) investments in physical and digital infrastructure in more than 130 countries have far-reaching consequences. The most obvious impact on plant health is through plant-related trade, but there are other implications relating to the scientific and technical capacity of nations and the ability of countries to detect and respond to new pests and diseases and new outbreaks. We will reflect on the possible implications and outcomes of the BRI for plant health in the Kyrgyz Republic, Tajikistan and Uzbekistan.

Tuesday | Talk 3.2

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CONNECTED: a community network for African vector-borne plant viruses

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The CONNECTED Network (Community Network for African Vector-Borne Plant Viruses) builds multidisciplinary research capacity to tackle crop diseases spread by insects in Sub-Saharan Africa, contributing to food security and reducing poverty. The Network brings together plant pathology and entomology research communities to tackle the complex problems of vector-borne crop diseases. The CONNECTED Network comprises 1500 members across 84 countries, this community represents a valuable resource of technical expertise and knowledge, and is a pool of potential international collaborators. CONNECTED has partnered with a range of international partners (including IITA in Nigeria and BecA-ILRI Hub in Kenya) to fund international research, provide innovative training, and run networking events primarily for early career researchers. The CONNECTED Network has funded a portfolio of 20 innovative international projects involving 14 countries, 11 different crops, and collaborations of 55 researchers in 34 institutions, each representing a new productive collaboration between UK and African institutions. The Network has delivered over 100 training opportunities awarded for multidisciplinary courses or educational visits for delegates from 18 different countries. The Network is free to join and members can access a programme of conferences, workshops, seminars and online resources, including training manuals and other educational materials.

References: Silva G, Tomlinson J, Onkokesung N, Sommer S, Mrisho L, Legg J, Adams IP, Gutierrez-Vazquez Y, Howard TP, Laverick A, Hossain O, Wei Q, Gold KM, Boonham N (2021) Plant pest surveillance: from satellites to molecules (2021) *Emerging Topics in Life Sciences* 5 (2), 275

Tuesday | Talk 3.2

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Early detection of pathogens: predicting risk for effective control

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Pests and diseases can significantly impact food systems and the environment, the impact has been accelerated in recent years due to global trade moving pests out of natural ranges at an accelerated frequency, climate change extending the range of pests and the diseases they vector and resistance to control measures (e.g. agrochemicals) has made control more difficult. Early detection is critical to facilitate the deployment of timely intervention measures. Whilst molecular diagnostics have improved our ability to rapidly identify pests and disease, early detection and effective surveillance are a more complex proposition, requiring an integration of technologies incorporating the steps from sampling through to data reporting. No single technology can be used to achieve these aims and effective surveillance systems incorporate a range of technologies operating at different spatial and temporal scales. Collecting more data is key to effective surveillance, though the associated costs and uncertainty compared with conventional approaches can limit uptake. As a result, automation is likely to be an increasing trend facilitating deployment. Here we will present some recent innovations in several different cropping systems, exploring how early detection and automation can help to get ahead of diseases and initiate more effective control measures.

References: Silva G, Tomlinson J, Onkokesung N, Sommer S, Mrisho L, Legg J, Adams IP, Gutierrez-Vazquez Y, Howard TP, Laverick A, Hossain O, Wei Q, Gold KM, Boonham N (2021) Plant pest surveillance: from satellites to molecules (2021) *Emerging Topics in Life Sciences* 5 (2), 275

POSTER

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Engineering tolerance to *Botrytis* in strawberries

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Botrytis cinerea is a virulent necrotrophic pathogen with a wide array of infection mechanisms, enabling it to evade host responses, cause disease and subsequently infect neighbouring plants. In strawberries, *B. cinerea* is responsible for causing soft fruit rot both pre- and post-harvest. Consequently damaging crops throughout the production, transport and retail stages. Strawberries are a high value crop, hence harvest losses at all stages of production have an economic impact and resistance to fungicides is increasing (1). The aims of this project are to identify novel strawberry susceptibility or resistance factors to *B. cinerea*. Through preliminary pathogenicity

tests an optimal spore concentration of 5×10^5 was shown to reveal the most variation in virulence between isolates, therefore this concentration will be used in a large-scale pathogenicity test. This pathogenicity test will be conducted on the less complex, diploid, woodland strawberry (*Fragaria vesca*) and the cultivated strawberry (*Fragaria x ananassa*; octoploid) to observe variation in virulence between 31 isolates; determining what isolates will be utilised for subsequent experiments. To investigate strawberry susceptibility factors, an ethyl methanesulfonate population of *F. vesca* plants will be produced; this will be a population of plants with random mutations throughout their genomes. Pathogenicity tests will then be carried out on these mutated plants with representative isolates. Any changes observed in susceptibility or resistance to *B. cinerea* infection may imply a factor associated with these phenotypes was mutated; the corresponding plant will have its genome sequenced to identify mutations. This experiment will reveal factors that are paramount to the success of *B. cinerea* as a strawberry pathogen and will reveal targets for further investigation in cultivated strawberry.

Reference: 1) Leroch, M., Kretschmer, M., Hahn, M. Fungicide Resistance Phenotypes of *Botrytis cinerea* Isolates from Commercial Vineyards in South West Germany. *J. Phytopathol.* 159, 63–65 (2011).

POSTER

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Genetic based resistance to aphids in wheat

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Sap-sucking aphids detrimentally impact plants through direct feeding and the secretion of sucrose rich honeydew, promoting saprophytic fungi and reducing the photosynthetic ability of a colonised host. Combined with their ability to readily transmit devastating plant viruses, aphids represent a notable threat to important crop species. Common wheat, *Triticum aestivum*, is one such species affected by aphids and the viruses they transmit, most prominently Barley yellow dwarf virus (BYDV). In terms of both worldwide distribution and economic significance, BYDV is one of the most important viral diseases affecting cereal crops. BYDV-attributed wheat grain yield losses of 13-45 kg ha⁻¹ have been reported per 1% increase in disease incidence. Overall yield reductions range from 5% to 80%. Current methods for controlling cereal aphids/BYDV depend upon removing aphid vectors through insecticides. There are, however, increased reports of resistance(s) evolving against key insecticide classes whilst indiscriminate pesticide usage may be having severe environmental implications. New legislative restrictions also limit the arsenal of insecticides available for effective use. Genetic sources of resistance to aphids may provide an alternative, reliable, environmentally friendly and more economically attractive control solution. Such valuable genetic resistances have been identified in the diploid species *Triticum monococcum* yet remain unexploited. This ancestral progenitor of modern hexaploid wheat has been the focus of research aiming to introgress valuable traits, including aphid resistance, into a commercial wheat genetic background. However, genotyping options/informative molecular markers for both marker-assisted selection and quantitative trait locus (QTL) mapping using *T. monococcum* have been limited. Here, the work of Hammond-Kosack et al. (1) has been employed to develop germplasm-specific KASP markers for future QTL analyses and exploration of potential genes underlying valuable aphid resistance. Some features of the aphid resistance phenotype will also be described and discussed.

Reference: (1) <https://doi.org/10.1111/pbi.13672>

Tuesday | Talk 3.2

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Breeding resistance into plants – successes, disappointments and unknowns

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In plant breeding, introducing novel resistance traits or new genetic diversity is a long and difficult process. Often novel traits come with negative effects such as yield drag or poor quality from the exotic donor. In the case of resistance genes, you have the added complication of not knowing if, or how soon they will be overcome. Here is an outline of where we find novel traits for a wheat breeding programme, the difficulties in breeding them in, and some case studies of resistance introductions with various outcomes.

Genetic solutions: ash dieback and emerald ash borer**Richard JA BUGGS***Royal Botanic Gardens Kew, Richmond, TW9 3DS and Queen Mary University of London, London, E1 4NS*

If a new plant pest or pathogen overcomes biosecurity and eradication measures, the only sustainable long-term solution may be the enhancement of its host's resistance by breeding. This is challenging when the host is a tree, due to the long generation time and large size of trees. Modern genetics provides two complementary methods for accelerating tree breeding. (1) Discovery of the genetic basis of resistance allows genomic prediction of the level of resistance present in juvenile offspring within breeding programmes, allowing accurate early selections. (2) Trees may be genetically engineered to flower at a young age, allowing rapid cycling through several generations, with the engineered genes eliminated from the progeny before they are deployed into the wider environment. Together these methods could allow the rapid development of more resistant trees, in cases where there is already a low level of resistance found within the species. I will outline progress that my research group is making to identify the genetic basis of resistance to the ash dieback fungus and the emerald ash borer in ash trees [1,2]. I will describe current and future strategies for applying this knowledge to the long-term flourishing of European ash populations.

References: [1] Stocks JJ et al (2019) Genomic basis of European ash tree resistance to ash dieback fungus. *Nature Ecology & Evolution* 3: 1686-1696. [2] Sollars SA, et al. (2017) Genome sequence and genetic diversity of European ash trees. *Nature* 541: 212-216

POSTER

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Extracellular recognition and immune evasion of bacterial pathogens in plants**Pierre BUSCAILL** (1), Sanguankiatichai N (1), Kaschani F (2), Lee YJ (1), Ichinose Y (3), Preston G (1), van der Hoorn RAL (1)*(1) Department of Plant Sciences, University of Oxford, UK. (2) ZMB Chemical Biology, University of Duisburg-Essen, Germany. (3) The Graduate School of Environmental and Life Science, Okayama University, Japan.*

New crop protection strategies are essential to feed a growing world population. Plant pathogens decrease food production, and these losses are expected to increase with climate change and reduced agrochemical use. Plants recognise conserved flagellin fragments as a signature of bacterial invasion. These immunogenic elicitor peptides are embedded in the flagellin polymer and require hydrolytic release before they can activate cell surface receptors. Although much of flagellin signalling is understood, we know little on the release of immunogenic fragments. Recently, we discovered that plant-secreted β -galactosidase-1 (BGAL1) of *Nicotiana benthamiana* promotes hydrolytic elicitor release and acts in immunity against pathogenic *Pseudomonas syringae* strains only when they carry a terminal modified viosamine (mVio) in the flagellin O-glycan. In counter defence, *P. syringae* pathovars evade host immunity by using BGAL1-resistant O-glycans or by producing a BGAL1 inhibitor. Polymorphic glycans on flagella as well as polymorphic sequences represent an important determinant of host immunity to bacterial pathogens. Our work stresses the role of apoplastic events in plant-bacteria interactions and has increased our interest on investigating the release of flagellin immunogenic peptides during bacterial infection. This talk will present the latest progress on this subject.

POSTER

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Identification and characterisation of novel bacteriocins as a treatment for *Xanthomonas* infections**Ray CHAI**, Walker D, Milner JJ*University of Glasgow, G12 8QQ*

Xanthomonas is a genus of bacterial phytopathogens that infects more than 400 species of plants including those that are of significant economic importance. Notable infections include citrus canker (*X. citri*), tomato and pepper plants (*X. perforans*) as well as numerous brassica species (*X. campestris*). Once infected, the only option is to have the infected plants destroyed to limit the spread of disease. In order to prevent potential outbreaks growers are pre-emptively spraying their plants with antimicrobials such as streptomycin, a last resort

medically important antibiotic. To limit the spread of antibiotic resistance there is a desperate need for novel antimicrobials to treat these infections. One possible solution is the use of bacteriocins, proteinaceous antibiotics produced ubiquitously by bacteria to outcompete closely related species. As a result of targeting a small range of bacteria there is less selective pressure to develop resistance compared to broad spectrum antibiotics that are commonly used as well as having a minimal effect on the local microbiota. In our group we have identified several putative bacteriocins harboured by *Xanthomonas* using homology searches against well-defined bacteriocins. A selection of these were shortlisted and cloned into *E. coli* for expression. Following purification, several were found to have strong antimicrobial activity against multiple *Xanthomonas* species. Here we describe their characterisation and the challenges involved in the process of developing bacteriocins as an antimicrobial.

Monday | PH Gregory competition

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Exploiting the family feud: a fungal endophyte for the control of take-all disease in wheat

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Take-all disease, caused by the soil-borne ascomycete fungus *Gaeumannomyces tritici*, is the most economically important root disease of wheat in the UK and worldwide. Yield losses of up to 60% have been reported in the UK but are typically in the range of 5-20%(1). The fungus invades the roots and destroys the vascular tissue, hindering the plants ability to uptake water and nutrients from the soil. Current control methods include crop rotation, later sowing of crops at risk and the use of partially effective fungicide seed dressings. Closely related species in the Magnaporthaceae family, such as *G. hyphopodioides*, occur naturally in arable and grassland soils and have considerable potential to suppress take-all disease(2). Through detailed microscopy analyses we have identified a strong lignification response in roots colonised by *G. hyphopodioides*. In addition, we found that *G. hyphopodioides* produces “sub-epidermal vesicles” in planta. Transmission electron microscopy (TEM) revealed that these structures share key characteristics with fungal chlamydospores, and may be formed in response to upregulated plant defences. Co-inoculation bioassays demonstrated that effective take-all control is achieved when *G. hyphopodioides* colonises the root system first, further strengthening the hypothesis that *G. hyphopodioides* induces a plant defence response, thereby preventing future infection by *G. tritici*. By performing a comparative transcriptome analysis via dual-RNAseq we have elucidated crucial defence pathways implicated in take-all disease resistance in wheat, shedding light on the biocontrol mechanism of *G. hyphopodioides*.

References: (1) Bateman, G., Gutteridge, R., Jenkyn, J. (2006). Take-all in winter wheat: management guidelines, HGCA, AHDB, 1-7. (2) Osborne, S. J., McMillan, V. E., White, R., Hammond-Kosack, K. E. (2018). Elite UK winter wheat cultivars differ in their ability to support the colonization of beneficial root-infecting fungi. *J of Experimental Botany*, 69(12), 3103-3115.

Tuesday | Talk 3.4

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EuroBlight and collaborative efforts to mitigate the impact of the evolving population of *Phytophthora infestans* (potato late blight)

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The sustainable protection of European crops against potato late blight depends on knowledge of the effectiveness of agrochemicals, host resistance and alternative practices (i.e. biocontrol) against current populations of *P. infestans*. An evolving pathogen population indeed challenges control methods and threatens the sustainability of integrated pest management (IPM) strategies. A co-ordinated industry-wide approach to investigate the genetic diversity of *P. infestans* has thus been pursued by EuroBlight, a network of academic, government and industry research scientists specialising on blight research and crop protection, with each season's results communicated to the industry to optimise late blight management. Since 2013, we have genotyped more than 12000 samples of *P. infestans* contributed by partners across 35 countries in Europe, and submitted standardised data to the EuroBlight pathogen database held at Aarhus University. We used simple

sequence repeat (SSR) genotyping of DNA either from live cultures or stored on FTA cards and have shown that the pathogen population is complex and dynamic. In some regions, the population was dominated by relatively few, locally adapted and fit asexual clones which survived from one season to the next and initially spread locally, and then sometimes internationally. In other areas, highly diverse sexually reproducing populations comprising ephemeral, local genotypes predominated. A turn-over was also observed in the clonal populations with, for example, a recent decline of the triploid EU_13_A2 clone that was first detected in 2004 and its displacement driven by the emergence of the EU_37_A2, and now the EU_36_A2 genotypes. We describe these patterns of local, national and international change, and how the data generated each season continues to have a real impact on both short-term changes in late blight IPM as well as longer-term strategic changes in priorities for future disease management utilising for example, more durable host resistance.

POSTER

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Untangling the role of histone acetyltransferases in plant homeostasis

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Climate change, unstable environmental conditions, rapid increase in human population and scarcity of resources are creating food insecurity. A sustainable strategy to prevent such losses is to create plants with enhanced tolerance to plant pathogens. Reversible epigenetic changes, including histone acetylation, are emerging as an important regulatory junction between genomic, transcriptional, translational and metabolic responses. Histone acetylation is mediated by histone acetyltransferases (HATs) that catalyze the transfer of an acetyl group from acetyl-CoA to lysine residues within histones. HATs are recruited to particular loci by sequence specific transcription factors. The aim of this project is to investigate the role of *A. thaliana* HATs; HAC4 (AT1G55970) and HAC5 (AT3G12980) in plant homeostasis. Using a yeast two-hybrid and in planta assays, we identified the transcription factor Auxin response factor 2 (ARF2) as a HAC5 specific interactor. The loss-of-function mutants of both HAC5 and ARF2 have increased responses to abscisic acid (ABA). They show enhanced defence responses against *Botrytis cinerea* and delayed dark-induced senescence.

Tuesday | Talk 3.1

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New targets for biological control of fungal plant pathogens

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Lytic polysaccharide monoxygenases (LPMOs) are enzymes discovered in the last decade that can oxidise bonds in recalcitrant polysaccharides such as cellulose and chitin, enabling hydrolytic enzymes to further degrade the polymers. Multiple classes of LPMOs have been identified and recently a LPMO in the AA17 class was shown to degrade pectin and play a crucial role in infection of potato by *Phytophthora infestans* (Sabbadin et al. Science, 2021). In our research we are asking whether LPMOs play a similar virulence function in the fungal pathogens, *Botrytis cinerea* and *Sclerotinia sclerotiorum*. We have used transcriptome data to identify target LPMOs, and RNAi to silence the expression of these genes during early pathogen infection. We have identified a number of LPMO encoding genes from different classes whose expression is essential for full pathogen virulence on both lettuce and Arabidopsis.

POSTER

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Genetic dissection of the roles of effectors and toxins in the pathogenicity of *Pseudomonas syringae* towards cherry

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Cherry canker is commonly caused by three distinct pathogens of *Pseudomonas syringae*, pv *syringae* (Pss) and pvs *morsprunorum* races 1 and 2. Compared with the *morsprunorum* races, Pss has a reduced repertoire of type III effectors but greater capacity for production of the toxins, syringomycin, syringopeptin (both encoded in one

cluster syrsyp) and syringolin A (sylA)1. Genome analysis showed that Pss strain 9644, was found to harbour 1) the conserved effector locus (CEL) identified in most *P.syringae* pathogens, hopAA1, hopM1 and avrE1, 2) a CORE of effectors common to *P. syringae* phylogroup 2, hopAG1, hopAH1, hopAI1 and hopI1, 3) a FLEXIBLE set within the phylogroup, hopAF1, hopAZ1 and hopBE1, and, 4) a set of PRUNUS effectors closely associated with pathogens of stone fruits hopAR1, hopH1, hopA2, hopAE1 and avrRpm1. In addition, Pss 9644 contains the genes for biosynthesis of Syrsyp and SylA. Mutants were created with gene deletions in each of the effectors and toxins and pathogenicity tested on detached leaves and immature cherry fruits². Results obtained demonstrated that the mutants fell into three categories, no change in pathogenicity, intermediate scores and symptoms reduced to those of a non-pathogenic strain. The toxins, in particular syrsyp, were found to have a key role in disease development in fruits but were of less significance in leaves. The presence of hopAF1 was found to be required for full virulence but other effectors in the FLEXIBLE group were not essential. Similarly, deletion of the CEL, CORE and PRUNUS effector sets alone had surprisingly little effect on symptom development, notably in fruits if the toxins were still present. Our results so far highlight the niche-specific differential role of toxins on leaves and fruits and the complexity of effector redundancy in the cherry pathogen. Reconstruction of a strain pathogenic on leaves from the non-pathogenic combined CEL, FLEXIBLE, PRUNUS deletion mutant should allow the key effectors to be further identified.

References: 1. Hulin MT, Armitage AD, Vicente JG, Holub EB, Baxter L, Bates HJ, Mansfield JW, Jackson RW, Harrison RJ (2018) Comparative genomics of *Pseudomonas syringae* reveals convergent gene gain and loss associated with specialization onto cherry (*Prunus avium*). *New Phytol.* 219(2):672-696. 2. Hulin MT, Jackson RW, Harrison RJ, Mansfield JW (2020) Cherry picking by pseudomonads: After a century of research on canker, genomics provides insights into the evolution of pathogenicity towards stone fruits. *Plant Pathol.* 69(6):962-978.

Tuesday | Talk 6.3

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Communicating with the public about plant health through gardening

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Public understanding of plant health issues is valuable in many ways, from gaining support for evidence-based policies and control practices to accessing the power of numbers to spot invading pests or diseases. As a large and long-established gardening charity, the Royal Horticultural Society (RHS) is a voice for plant health through various media streams, whereby we aim to communicate clear messaging through diverse channels to reach as many people as possible. The RHS primarily communicates to our 600,000 members through our gardening advice service, monthly magazine and weekly podcast. Most of the 30 million gardeners in the UK are non-members, and the RHS engages with them by providing freely available online resources and social media content. The member's advice service also enables us to stay relevant, as certain issues change in their importance to gardeners over the years, and the topics of greatest concern can be communicated to visitors of RHS gardens through interpretation boards and family activities. To reach new audiences, it is essential to engage the national press, and we do so to promote our changing practices, share scientific findings and recruit for citizen science projects about specific organisms of concern. We can learn from communications work done in the conservation sector to ensure our messaging evades common pitfalls which transform what could be meaningful scientifically sound information into clickbait. Conversely, we can also learn from social media to find creative ways to make messages concise yet evocative, encouraging people to take a deeper interest. As plant health scientists, we can all be advocates for public acceptance of and respect for plant health issues. Through positive messaging we can all contribute to building public trust in scientists and ensuring that plant health is valued and protected for future generations.

POSTER

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Characterising the UK population of *Bremia lactucae*

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Lettuce Downy Mildew (LDM), caused by the biotrophic oomycete *Bremia lactucae*, is a foliar disease of lettuce which negatively affects crop value through reduced yield and quality. LDM management strategies are usually preventative, employing fungicides in conjunction with resistant cultivars to maintain crop foliar quality. There is an ongoing risk of the emergence of new strains of *B. lactucae* that can overcome host resistance genes or have reduced sensitivity to fungicide active ingredients. Monitoring and characterising the diversity in the *B. lactucae* population would therefore be useful to help inform LDM management strategies. One aim of this study is to examine the genotypic and phenotypic diversity of the UK population of *B. lactucae*. The development of a set of Simple Sequence Repeat (SSR) markers and their use to genotypically profile isolates collected from commercial lettuce crops is described. Seventeen candidate SSR markers were selected from a screening of the *B. lactucae* genome (Fletcher et al., 2019) and tested for their ability to identify genotypic (allelic) diversity in UK and other reference isolates. Evidence of discrimination of UK isolates from reference strains using the SSR markers is presented. Associations between isolate genotype and phenotypic traits including virulence profile (race), assessed using a lettuce host differential set, and fungicide sensitivity will be examined in combination with information on geographical location and host cultivar. DNA from UK isolates collected 2019-2020 will be utilised to further assess the genetic diversity of the population and to design a simple multiplex SSR marker for future use. Additionally, aspects of the epidemiology, detection, and control of LDM will be investigated, with the long-term aim of providing a range of tools to aid in LDM management strategies.

Reference: Fletcher, K., et al., (2019). Genomic signatures of heterokaryosis in the oomycete pathogen *Bremia lactucae*. *Nature Communications*, 10. doi:10.1038/s41467-019-10550-0

POSTER

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Use of a disease screening technique to identify a resistant trait associated gene in oilseed rape

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With increasing disease incidence, reductions in oilseed growing area, and increased environmental demands to reduce agricultural inputs, there is a need to produce sturdier crop varieties that can combat disease without the use of fungicides (GAIN, 2021). One of the most economically damaging diseases of oilseed rape, light leaf spot (LLS), responsible for crop losses over £80 million a year across the UK (cropmonitor.com) it is also becoming insensitive to most of the commonly used fungicides (Carter, et al. 2014). Because infection symptoms are not produced until late into the fungal growth cycle it makes timing the use of fungicides difficult and often ineffectual. Using disease screening results from controlled environment experiments in a generalised linear association model, we have identified SNPs that are strongly associated with trait variation. These can be used as molecular markers for early selection and identification of genes that could be involved with a plant's resistance or susceptibility to disease.

References: Global Agricultural Information Network (GAIN). (2021). *United Kingdom: Oilseeds and Products Annual*. Carter, H. E., et al. (2014). Alterations in the predicted regulatory and coding regions of the sterol 14 α -demethylase gene (CYP51) confer decreased azole sensitivity in the oilseed rape pathogen *Pyrenopeziza brassicae*. *Molecular Plant Pathology*. <https://doi.org/10.1111/mpp.12106>

Wednesday | Talk 7.1

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Measuring *The Global Burden of Crop Loss* to increase food security, protect the environment and secure livelihoods

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Keeping pace with growing demand for food is one of the defining challenges of our time. Between population growth, urbanisation, and increased meat consumption, we need to produce significantly more food as the population heads towards 10 billion by 2050 (1). Yet, crops are exposed to growing threats including climate

change, pests, and ineffective agricultural practices. FAO estimates that pests reduce global crop production by 20% to 40%. While it's clear that crop loss causes significant impacts, and that reducing losses represents a major opportunity to increase yields without increasing the environmental footprint of agriculture (2) we lack robust evidence. Data on the scale, scope, and drivers of loss are outdated, lacking in granularity, or unavailable. Without knowing how much of our food we are losing or what we are losing it to, actors across the plant health system lack clarity on how to take effective action. The *Global Burden of Crop Loss* aims to provide rigorous, authoritative evidence on impacts, causes, and risk factors of crop loss. Evidence-based decision making across the plant health system will enable resources and efforts to be directed where they're most needed, resulting in more targeted research, better investments, and more effective interventions. Inspired by the *Global Burden of Disease* in human health, a system that provides comprehensive data on the impact of hundreds of diseases and has transformed the public health agenda, we aim to have a similarly transformative impact in plant health.

References: (1) Tilman, D; Balzer, C; Hill, J; Befort BL (2011) Global food demand and the sustainable intensification of agriculture. *Proceedings of the National Academy of Sciences* 108 (50) 20260-20264. (2) Savary, S; Willocquet, L; Pethybridge, SJ; Esker, P; McRoberts, N; Nelson, A (2019) The global burden of pathogens and pests on major food crops. *Nature Ecology & Evolution* 3, 430-439

POSTER

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A RiPPing time: exploring a novel peptide from *Zymoseptoria tritici*

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The fungal capacity for production of anthropogenically useful compounds has been recognised by mankind for several decades, with peptides formed by non-ribosomal peptide synthetases (NRPS), including penicillin, cephalosporin, and the cyclosporines, transforming modern medicine and undoubtedly extending human lifespans. It is therefore unsurprising that continued interest lies in fungal peptides. Fungal ribosomally synthesised and post-translationally modified peptides (RiPPs), were first characterised in 2007 following analysis of amanitin, despite the application of bacterial and animal RiPPs commercially prior to this. Subsequently, more and more peptides have been re-evaluated in terms of their biosynthetic mechanism, resulting in the re-classification of peptides, previously designated as products of NRPS, as RiPPs formed by post-ribosomal peptide synthesis. Importantly, RiPPs can be synthesised by plant pathogens such as *Cochliobolus victoriae*, *Ustilaginoidea virens* and *Phomopsis leptostromiformis*. For these pathogens, RiPPs take action as virulence factors or have mammalian toxic functions, while other fungal RiPPs show nematocidal activity. The wheat pathogen *Zymoseptoria tritici* produces a similar RiPP. Ongoing studies aim to discover the role of this RiPP in the biology of this important plant pathogen. Functional investigations carried out to date, into plant virulence, insect toxicity and antibiotic activities have each provided negative results. In addition, the mechanism of biosynthesis of this RiPP is being studied. The RiPP in IPO323 has 9 copies of the repeat YVIPVD within its precursor peptide, but the repeat number varies between different strains indicating the presence of some level of selection on the peptide, the direction of which is currently unknown. Knockout strains of the biosynthetic genes for the RiPP are currently in development and may facilitate a deeper understanding of fungal RiPP production more widely.

Wednesday | Talk 8.3

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Urban tree health and the impact of novel diseases in Colombia

Liliana FRANCO

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Trees are a vital part of the urban landscape in Andean cities yet little attention is made to their vitality and impact of pests and diseases. It was only relatively recently that a major disease was identified on Urapán (*Fraxinus uhdei*), the dominant roadside and parkland tree in Bogotá. This prompted further investigations by researchers at my university and the discovery of a wide range of other urban tree species affected by the same phytoplasma. I will talk about overcoming the multiple challenges of tackling entrenched attitudes to

misdiagnosis and official indifference to the discovery of the diseases. I will also report on progress on documenting the problems affecting urban trees in other cities in Colombia and the importance of paying close attention to maintaining their vitality.

POSTER

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Understanding insect host plant selection and modelling

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The cabbage stem flea beetle, *Psylliodes chrysocephala*, (Coleoptera, Chrysomelidae), is an important Brassicaceae feeding pest throughout the UK and Europe. Since 2018, the EU has banned the three main neonicotinoids (clothianidin, imidacloprid and thiamethoxam) for all uses outdoors. Without effective chemical protection approaches, the CSFB accounts for between 5-15% of the crop being lost, or around £70m per year. Here, we apply a comparative genomics approach of CSFB to examine the evolution of genes putatively involved in plant-insect interactions. Owing to the diversity of the beetle family, the phylogenetic analysis also has been challenging. We designed a phylogenomic pipeline for accurate tree building, from careful data compilation including single-copy orthologue identification to tree reconstruction. Through insect dynamic modelling, we can develop better IPM (Integrated Pest Management) methods. In the genomic age, this work answers questions in the evolution of CSFB, provides new directions for designing new classes of insecticide molecules, pest risk maps and models, and novel pest management strategies to help farmers control this major agricultural pest.

Wednesday | Talk 7.1

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Models for emerging and recurrent epidemics

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Epidemics continue to threaten food security. Here I shall focus on staple crops, first with a summary of some major pest and disease threats in sub-Saharan Africa (SSA) and South Asia (SA), and then illustrate how epidemiological modelling is helping to prepare for and respond to emerging and recurrent epidemics in SSA and SA. We begin by introducing an epidemiological framework that can be adapted to model the spread and management of a range of fungal, viral and bacterial pathogens, insect vectors and pests. I shall explain how the framework is being adapted for two markedly different classes of transboundary plant pathogen: wind-dispersed wheat rusts and cassava brown streak virus, which is dispersed on planting material and by insect vectors. By coupling a meteorologically driven spore-dispersal model with epidemiological models it is possible to identify countries at risk from new races of wheat rust and to provide a real-time early warning and advisory system now active in Ethiopia, Nepal and Bangladesh. Meanwhile we are using a model for CBSV transmission to identify likely arrival times for westward spread of the pathogen from East Africa to major cassava production countries in West Africa. The model is also used to screen options for management, and to optimise surveillance for early detection. We conclude by measuring progress against with a G.E. Box's maxim that 'All models are wrong - but some are useful'.

References: Meyer M, Cox JA, Hitchings MDT, Burgin L, Hort MC, Hodson DP, Gilligan CA. 2017. Quantifying airborne dispersal routes of pathogens over continents to safeguard global wheat supply. *Nature Plants* 3: 780-786. Ferris AC, Stutt ROJH, Godding D, Gilligan CA. 2020. Computational models to improve surveillance for cassava brown streak disease and minimize yield loss. *PLOS Computational Biology* 16: e1007823.

Wednesday | Talk 7.5

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The UK Bacterial Plant Disease Initiative

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Bacterial phytopathogens can cause widespread and severe economic, environmental and societal impacts on landscapes and ecosystems. Despite excellent fundamental research, key skills in bacteriology and applied

research have been eroded. Superimposed on this, the UK has seen increased impacts from bacterial diseases, particularly those of trees, and the consequential broader threat to biodiversity within the environment. The Bacterial Plant Diseases Programme was established by UKRI, Defra and Scottish Government to address current and emerging bacterial threats to UK agriculture, woodlands and wider environment. Nine projects were funded including the recently completed BRIGIT Xyella project. Here we introduce the eight projects funded by the BPD that started in 2020. BAC-STOP takes a holistic approach to understanding and controlling Acute Oak Decline, investigating the microbial and vector biology as well as the community impact of AOD. DES-BL explores how nematodes vector *Pectobacterium atrosepticum*, the causal agent of potato blackleg disease and aims to build a robust decision support tool for growers. CALIBER investigates the biology and societal impact of insect vectored *Candidatus liberibacter solanacearum*, examining the influence of biology, the environment and agricultural practice on this phyto bacterium. DISEASE SUPPRESSIVE MICROBES seeks to harness beneficial bacteria isolated from disease-suppressive soils, combining these with novel synthetic soils for sustainable, low-input horticulture. FUTURE OAK targets the oak microbiome to identify beneficial microbes that might be applied to 'future-proof' this iconic tree. PSEUDOMONAS-PRUNUS is a multidisciplinary project investigating the interactions between *Pseudomonas* spp. and bacterial canker of UK cherry trees. RALSTONIA-PHAGE CONTROL deploys phage therapy developed in the tomato-*Ralstonia* model system as a tool to control pathogens in the plant rhizosphere microbiome. XANTHOMONAS THREATS exploits unique collections to investigate the genetics, genomics, demography and diagnosis of *Xanthomonas* spp. aiming to mitigate emerging and future threats to UK agriculture.

Tuesday | Talk 5.3

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***Phytophthora* communities in UK plant nurseries and links to management practice: opportunities for mitigation through accreditation**

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The PHYTO-THREATS project was an interdisciplinary collaboration of seven institutions addressing risks to UK forest and related ecosystems from *Phytophthora*. One key objective of this three year project, which started in April 2016, was to examine the diversity of *Phytophthora*s across a range of UK plant nurseries operating different management practices. The project team together with Plant Health inspectors collected over 4000 water and root samples from plant nurseries located across Britain. These included fifteen partner nurseries intensively sampled in a 'fine-scale' survey and a further 118 nurseries sampled as part of a 'broad-scale' survey. Samples were tested for the presence of *Phytophthora* DNA using an Illumina metabarcoding approach. Approximately 50% of all samples were positive for *Phytophthora*, with 63 *Phytophthora* species identified across all samples including quarantine regulated pathogens and species not previously reported in the UK. Some of the most diverse *Phytophthora* assemblages were found in river water used to irrigate plants and in open reservoir irrigation sources, as well as in puddles which formed around plant stock, confirming that effective water treatment and good drainage are essential components of *Phytophthora* management. *Phytophthora*s were also detected in diseased shelterbelt or landscape trees present at some nurseries, acting as additional inoculum reservoirs. In some cases, native plant stock being raised from seed collected from ecologically sensitive sites and destined for planting back out at these sites were found to be harbouring damaging *Phytophthora* species. These findings have considerable implications for the proposed massive expansion of UK woodland. Evidence generated from the nursery sampling is being used to underpin a 'management standard' being developed as part of the 'Plant Healthy' certification scheme currently being rolled out in the UK to raise the baseline of plant biosecurity in UK plant production systems.

***Xanthomonas* plant diseases: mitigating, existing, emerging and future threats to UK agriculture**

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The *Xanthomonas* threats consortium is part of the Bacterial Plant Diseases program and aims to address *Xanthomonas* threats to UK agriculture, with a particular focus on black rot of brassicas caused by *Xanthomonas campestris* pv. *campestris* (Xcc). Black rot is the most damaging disease of vegetable Brassica oleracea crops worldwide. Xcc also infects other important brassica crops such as swede, oilseed rape (*Brassica napus*), brown mustard (*B juncea*), Chinese cabbage and turnips (*Brassica rapa*). Control of black rot is challenging due to the lack of effective bactericides and varietal resistance. The project has four integrated work packages covering *Xanthomonas* genomics, identification of host resistance, imaging infection dynamics of xanthomonads with different lifestyles, diagnostics and biosecurity threats. Initial screening of Warwick's Brassica Diversity Fixed Foundation Sets (DFFS) - capturing the genetic diversity of ~6000 Brassica accessions in a few hundred lines - has identified resistance to one or more of the most important Xcc races 1, 4, 5 and 6. In parallel, we are sequencing >900 xanthomonads, including ~700 *X. campestris* (Xc) isolates from the NCPPB and Warwick's unique *Xanthomonas* collections, to identify genetic determinant of Xc virulence, pathovar and race type as well as to better define Xc classification. So far, genome analysis of selected NCPPB isolates supports the transfer of 20 Xc pathovars into *X. euvesicatoria* and two Xc pathovars into *X. citri*. Genomics will support diagnostic development and underpin studies dissecting *Xanthomonas* infection dynamics using whole plant and sub-cellular imaging and effector deletion and exchanges between races. We are also investigating the use of the beneficial fungus *Trichoderma hamatum* and bacteriophages for IPM control of Xcc in brassicas and assessing the future risk of other xanthomonads like *X. fragariae* and *X. vasicola* pv. *vasculorum* to UK strawberry and maize production.

Monday | Talk 1.2

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The global movement of fungal crop pathogens: models, predictions and perils.

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Over the past centuries crop diseases have led to the starvation of the people, the ruination of economies and the downfall of governments. Of the various challenges, the threat to plants of fungal (and oomycete) infection outstrips that posed by bacterial and viral diseases combined. Indeed, fungal and oomycete diseases have been increasing in severity and scale since the mid 20th Century and now pose a serious threat to global food security and ecosystem health (Fisher *et al.*, 2012 *Nature* 484 185). We face a future blighted by known adversaries, by new variants of old foes and by new diseases. Modern agricultural intensification practices have heightened the challenge - the planting of vast swathes of genetically uniform crops, guarded by one or two inbred resistance (R) genes, and use of single target site antifungals has hastened emergence of new virulent and fungicide-resistant strains. Climate change compounds the saga as we see altered disease demographics - pathogens are moving poleward in a warming world (Bebbler *et al.*, 2013 *Nature Climate Change* 3 11). This presentation will highlight some current notable and persistent fungal diseases of both calorie and commodity crops. It will consider the evolutionary drivers which underpin emergence of new diseases and man-made "accelerators" of spread. I shall set these points in the context of our recently published disease modelling meta-analyses, which show the global distributions of crop pathogens; their predicted movement and crop disease saturation. I shall present a new mechanistic model for predicting Septoria Tritici Blotch disease risk on wheat grown in temperate climes, parametrised with experimentally-derived data for temperature and wetness-dependent germination, growth and death in *Zymoseptoria tritici*. I shall conclude with some thoughts on future threats and challenges, on fungal disease mitigation (and the jeopardy of fungicide resistance) and of ways of enhancing global food security.

Molecular tools for UK hop - fast tracking disease resistance breeding

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To date, breeding of new hop varieties has been achieved through classical breeding practices, where individual hop plants are selected solely based on their expressed phenotypes such as resistance to diseases. However, the use of modern breeding techniques, including marker assisted selection (MAS), could add value to the national hop breeding programme and to the UK hop industry. In current hop breeding, artificial infection assays are used to screen for resistance to three major hop diseases: downy mildew (DM), Verticillium wilt (VW) and powdery mildew (PM) at different stages of the breeding programme. Hop breeders could leverage molecular markers to bypass the labour-intensive and expensive phenotype-based selection methods which involves the artificial inoculation of the target organism onto mature, clonally propagated hop plants. Marker assays could be used as simple, low-cost laboratory tests on young hop seedlings and would decouple the need for extensive phenotyping from confirming disease resistance/susceptibility of breeding lines. We established a bi-parental mapping population segregating for disease resistances between parents 'Pilgrim' and '316/1/10'. The mapping population and parental genotypes were screened for PM R2 resistance. Powdery mildew R2 resistance has been hypothesised to be under single major dominant gene action. The observed segregation of R2 resistance was tested against a chi-squared distribution and no significant deviation from the expected 1:1 segregation between resistant and susceptible phenotypes was found. In total, parents and 171 individuals from the mapping population were genotyped with high-throughput DArT sequencing technology. We refined an initial set of 9562 DArT-SNP markers to 1465 segregating markers providing high-quality markers for QTL analysis and linkage map construction. Kruskal-Wallis mapping of powdery mildew R2 resistance identified two SNPs that were significantly associated with PM resistance. These co-localised on the same linkage group within our linkage map, meaning that the two SNP markers are potentially representing the same QTL. Next generation sequencing reads generated for the parental genotypes will allow us to identify putative resistance genes in the region. This study aims to provide foundation for the characterisation of genetic background of pathogen resistances, and to develop transferrable molecular breeding tools for UK hop.

Plant pandemic study: Ug99 stem rust: the breakdown and rebuilding of durable disease control

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In the late 20th Century, resistance against stem rust of wheat seemed to be one of plant breeding's big success stories. After some earlier failures when single resistance genes were overcome due to the selection of virulent rust pathotypes, varieties with a combination of resistance genes had proven more durable. However, individual resistance genes within the stacks had been gradually breaking down, and so when a rust lineage with virulence against the Sr31 gene appeared in Uganda in 1999, widely-grown wheat varieties were suddenly susceptible. Renewed breeding efforts began urgently, racing to find and deploy new rust resistance as Ug99 spread through East Africa and towards key wheat producing areas in Asia. Breeders now aim to combine multiple resistance genes effective against Ug99 in each wheat variety, but ongoing virulence monitoring is still needed. There are clear parallels between the breakdown of resistance genes against stem rust, and the emergence of fungicide resistance in many major pathogens. For genetic control as with fungicides, no single control measure can be a sustainable solution to a diverse and evolving pathogen population. Increased diversity is needed at all levels from gene to landscape: in crop gene pools, in the crop protection toolbox, and in farming and cropping systems as a whole. We also need to move from reactive to pre-emptive management of the breakdown of crop protection measures. This means anticipating the risk of control breakdown before it occurs, deploying crop

protection measures in a durable way before control-breaking strains emerge, and monitoring for shifts in the pathogen population.

POSTER

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Developing genomic resources for powdery mildew affecting horticultural crops

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Powdery mildew fungi are amongst the most serious pathogens affecting UK horticultural crops. Current control measures rely heavily upon frequent fungicide application, however this practice may be unsustainable given increasing legislative restrictions and emerging fungicide resistant strains. The performance of different control measures could be better tracked given effective molecular diagnostics for these pathogens. There is an immediate need for improved diagnostic testing of orchard diseases. Specifically, a test is required that can provide quick and simultaneous diagnosis for a panel of common orchard diseases, at a low cost to growers. This test also needs to be precise enough to identify key pathogen characteristics such as resistance to certain fungicides and virulence. Unfortunately, there is a lack of genomic information available for powdery mildew pathogens on horticultural crops. This project leverages advances in next generation sequencing technologies to develop some of the first genomic resources for *Podosphaera leucotricha*, which affects apple and pear trees, and *P. aphanis*, which affects strawberry and a range of Rubus crops. Draft genome assemblies have been generated for powdery mildew infecting UK apple (49.4 Mb), strawberry (56.2 Mb) and raspberry plants (51.6 Mb). Powdery mildews are known to be highly host specific. We are using comparative genomics to identify the genetic basis of this host specification. This will lay the groundwork for a diagnosis by sequencing method for these pathogens.

Monday | Talk 1.3

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Building resilience to insect-vectored plant pathogens

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Sap-feeding insects of the order Hemiptera, such as aphids, psyllids, leafhoppers and froghoppers, are vectors of a wide range of plant pathogens, including viruses, phytoplasmas, *Liberibacter* species and *Xylella fastidiosa*. These pathogens are spreading globally and are a threat to UK agriculture and landscapes. Whereas excellent progress has been made with understanding mechanisms involved in plant-pathogen interactions, it is equally important to gather knowledge on the insect vectors. Research in my lab has demonstrated that phytoplasmas have evolved sophisticated mechanisms to modulate plant development and suppress plant defence to sap-feeding insects. However, genome sequence data of phytoplasma insect vectors were essential for the identification of a phytoplasma Achilles' heel that we were able to exploit for increasing plant resistance to these bacteria and their insect vectors (1). Recent advances in low-input next generation sequencing technologies have enabled us to generate genomic and transcriptomic resources for ± 40 mostly small hemipteran insect species, including many insect vectors, in just the past few years (e.g. 2). One of these species is the *X. fastidiosa* insect vector *Philaenus spumarius*, known as the meadow spittlebug, which is one of the most common insects in the UK. Our data gave insights into how *P. spumarius* dispersed globally. Moreover, we found that the *P. spumarius* populations that occur in the *X. fastidiosa* outbreak regions of southern Italy belong to a different haplogroup and have higher migration rates, distinct phenology and a different plant host preference compared to UK populations. This research has provided key information that will help to reduce the likelihood of arrival and potential impacts of *X. fastidiosa* outbreaks in the UK and elsewhere. Taken together, we demonstrate that gathering information about sap-feeding insects is essential for building resilience to vector-borne plant pathogens.

References: (1) Huang et al. 2021. *Cell* 184: 5201-14. (2) Mathers et al. 2021. *Mol. Biol. Evol.* 38: 856-75

Developing bacteriophage biocontrol for blackleg disease of potato

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Potato is the third most consumed crop in the world but is at risk to substantial losses through disease, damage and failure to meet market specifications. There is a need for a sustainable, biocontrol solution for the most-damaging bacterial disease of potatoes; blackleg and associated tuber soft rot, caused by *Pectobacterium* species. The technology is based on bacteriophage (phage); naturally occurring viral pathogens of bacteria that provide an effective, low risk solution to bacterial pathogens of crops, increasing productivity and decreasing waste and associated carbon emissions. Our project aims to follow phage movements within plants to inform mode of action and explain efficacy results for a commercial product, Biolyse®. To determine whether phage treatment affected bacterial colonisation of the stem or roots of potato plants, we developed a model for investigating bacteriophage/bacterial host/plant interactions using sequenced phage M1, which infects *Pectobacterium atrosepticum* strain SCRI_1043. Confocal fluorescence microscopy was used to investigate the localisation of stained phage and bacteria expressing red fluorescent protein (RFP) on potato roots. The model phage M1 did not affect the numbers of Pba_1043-GFP colonising the stem or roots of potatoes grown in the glasshouse or hydroponically. We compared staining of the M1 phage with SYTOX(TM) and SYTO(TM) 9 nucleic acid stains. Using confocal fluorescence microscopy to observe interactions between labelled M1 phage and host bacteria during colonisation of potato roots highlighted potential issues for in planta studies with this staining approach. The impact of bacteriophage treatment on the development of blackleg disease on potato is more complex than phage induced lysis of susceptible bacteria. We will be investigating this further through a new project, funded by Innovate UK.

Under attack by a cereal killer: the identification of critical host pathways required to support wheat yellow rust colonisation

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Wheat rusts pose a major threat to global food security, particularly in developing countries where 50% of global wheat production are harvested annually. Developing new forms of disease resistance against wheat rust pathogens is urgently required to reduce wheat yield losses and to sustainably increase global wheat production. We previously conducted RNA-seq analysis to study the interaction between wheat and the yellow rust pathogen, *Puccinia striiformis* f.sp. *tritici* (Pst), using bread wheat (*Triticum aestivum*) varieties with different levels of susceptibility. This revealed several differentially expressed genes including an isocitrate lyase (TaICL) gene. Here, we generated a Taicl (B genome) disruption mutant and found this mutant line had significantly enhanced resistance to Pst and elevated pathogenesis-related (PR) gene expression during infection compared to the wild-type. Microscopic analyses of fungal invasive structures revealed a severe compromise in fungal penetration of host stomata in Taicl B genome mutants compared to the wild-type, suggesting that TaICL is required in the initial stages of Pst colonisation. Considering the known function of ICL in converting fatty acids to carbohydrates through the carbon-conserving glyoxylate cycle, we speculate that Pst may be exploiting its host carbon metabolic pathway to accelerate its invasion and proliferation. Further studies will delineate the specific metabolic pathways involved in the disease process and how this may be manipulated to enhance Pst resistance in wheat.

How does *Fusarium graminearum* acquire zinc during wheat infection?

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Fusarium Head Blight (FHB) is the number one floral disease of cereals, including wheat, and is principally caused by the ascomycete fungus *Fusarium graminearum*. Infection contaminates the cereal grain with trichothecene mycotoxins, posing a threat to human health and global food security. Currently, there is no effective method to control FHB. Thus, an enhanced understanding of the molecular determinants of FHB is needed. Nutrient acquisition from the host is crucial for fungal pathogenesis [1]. Zinc is an essential micronutrient, but how *F. graminearum* acquires zinc from its wheat host during infection is unknown. Phylogenetic and transcriptomic analyses suggest that *F. graminearum* uses multiple zinc transporters (ZIPs) to acquire zinc during wheat infection. A library of *F. graminearum* mutants lacking individual ZIPs was generated and shows the importance of the ZIPs during fungal growth under zinc stress and during wheat infection. Complementation of a ZIP-deficient *S. cerevisiae* strain with select *F. graminearum* ZIPs provided supporting evidence that these ZIPs function as zinc importers. Transcriptomic analyses revealed that the expression of the ZIPs and a transcription factor were dependent on environmental zinc levels. RNA-sequencing demonstrated the ZIP expression was dependent on a zinc-responsive transcription factor, which was ultimately shown to be essential to growth under zinc stress and during wheat infection. These on-going investigations continue to define the importance of novel metal ion acquisition systems to *F. graminearum* growth, stress-responses, mycotoxin production and virulence.

References: [1] Johns, L.E., Goldman, G.H., Ries, L.N, Brown, N.A., 2021. Nutrient sensing and acquisition in fungi: mechanisms promoting pathogenesis in plant and human hosts. *Fungal Biology Reviews*, 36, pp.1-14.

Wednesday | Talk 9.2

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Zigzagging towards durable disease resistance

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Plant resistance (R) genes usually encode intracellular NLR immune receptors, and polymorphism in NLR repertoires is important for their efficacy. Plant populations are continuously selected for R gene variants that can resist aspiring microbial colonists, and pathogen populations are selected for races that can evade the mechanisms evolved by plants to avoid being a good host. Successful parasites often specialize to colonize only particular host species, with related species that resist the parasite designated as "non-hosts". A better understanding of mechanisms of "non-host" (or species-specific) resistance might enable further enhancement of crop disease resistance. What would it take to convert crop plants into non-hosts for their most important pathogens? We investigate the extensive within- and between-species diversity in plant NLR-encoding repertoires using DNA sequence capture, and apply these methods to recruit and deploy multiple genes for resistance to potato late blight caused by *Phytophthora infestans*. Pathogens carry a battery of effectors to suppress immunity; we have also used sequence capture to investigate diversity in effector repertoires and reveal new recognized effectors. Knowledge of recognized effector diversity is crucial to wise custodianship of useful R genes (1). Some resistances require two NLR proteins. One (the sensor) detects effector action, while the other (helper) NLR transduces the signal. Arabidopsis RPS4 and RRS1 genes, encoding TIR-NLR proteins, confer recognition of two bacterial effectors. We used this system to reveal mutual potentiation between the immune mechanisms activated by intracellular and cell surface receptors (2). These insights suggest stacking multiple immune receptors result in synergistic elevation of resistance, and that these mechanisms might underpin non-host resistance.

References: (1) <https://pubmed.ncbi.nlm.nih.gov/33574576/>. (2) <https://pubmed.ncbi.nlm.nih.gov/33692545>

Reflections of a restless plant pathologist**Sophien KAMOUN***The Sainsbury Laboratory, Norwich, NR4 7UH*

A fundamental concept in plant pathology is that most plants are actively resistant to most pathogens and pests. Plants fend off biotic foes primarily through immune receptors that detect invading pathogens to trigger a robust immune response. The conceptual basis of such interactions was elegantly articulated by Harold Flor, who back in 1942 proposed the hypothesis that single genes in plants and pathogens define the outcome of their interactions. Flor's gene-for-gene model turned out to be hugely insightful and influential—it has, ever since the mid-twentieth century, helped to guide applied and basic research on disease resistance. However, recent findings are taking the field far beyond this binary view of plant-pathogen interactions. Plants turned out to carry diverse repertoires of immune receptors that are interconnected in complex ways. The emerging paradigm is that dynamic webs of genetic and biochemical networks underpin early stages of plant-pathogen interactions. I will discuss our work on NLR networks and explore the implications of this systems view of plant-pathogen interactions. We have postulated that Flor's intuitive gene-for-gene model is superseded by the systems view that plant immune receptors form networks with complex topology. Current activities aim at decrypting the regulatory pathways that modulate receptor network wiring. Ultimately, an improved knowledge of plant immune systems would enable optimal deployment of immune receptors in agriculture.

References: Kamoun S., Talbot NJ, Islam MT 2019. Plant health emergencies demand open science: Tackling a cereal killer on the run. *PLoS Biology*, 17:e3000302. <https://doi.org/10.1371/journal.pbio.3000302> Kamoun S. 2021. NLR receptor networks: filling the gap between evolutionary and mechanistic studies. *Zenodo* doi.org/10.5281/zenodo.5504059

POSTER

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Understanding components of resistance to an apple tree pathogen**Amanda KARLSTRÖM** (1), Gómez-Cortecero A (2), Nellist CF (2), van de Weg E (3), Dunwell J (4) Ordidge M (4), Harrison RJ (2)

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The fungal pathogen *Neonectria ditissima* infects a wide range of broadleaved hardwood species, causing trunk cankers, dieback and branch lesions in its hosts. The fungus is especially damaging in commercial apple orchards where it causes a disease called European canker. This work was carried out to facilitate the breeding of new apple varieties with improved resistance, and to understand how host resistance may be modulated by nitrogen fertilisation. The genetic basis of resistance to *N. ditissima*, was studied in a multiparental population of apple scions using several disease phenotyping methods and a pedigree-based quantitative trait locus (QTL) analysis. The analysis revealed a total of seven QTL with a small to moderate effect on disease resistance. Due to the quantitative nature of disease inheritance, genomic prediction models were assessed as a tool for selection for European canker resistance. To further understand the modulation of *N. ditissima* host resistance by nitrogen fertilisation the pathogen colonisation rate was studied in a resistant and susceptible apple cultivar grown under different fertilisation rates of NH_4NO_3 . The rate of nitrogen application had a significant effect on disease progression after two years of differential fertilisation, with trees grown under low nitrogen showing a reduced disease expression.

POSTER

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The influence of *Pectobacterium* (blackleg) loads and Irrigation practices on soil microbial community dynamics**Ciara KEATING**, C. (1), Kilbride E (1), Laird J (1), Stalham M (2,3), Smart S. (3), Humphries S (4), Milner J (1), Toth I (4), Ijaz, UZ (1), Mable BK (1)

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Potato crops in GB have estimated losses of £50M each year from blackleg disease, attributed to the pathogens *Pectobacterium atrosepticum*. Recent studies have suggested that bacterial transmission could occur through the soil rather than only through seed potatoes, as previously assumed. However, it is not known how management interventions to reduce blackleg affect soil community composition. Using field trials we investigated the influence of *Pectobacterium* load, seed variety, and irrigation treatments on disease symptoms, *Pectobacterium* prevalence and associated microbial community dynamics. We used three seed stock varieties with varying levels of *Pectobacterium* prior to planting (Jelly - high load; Jelly- low load: Estima minitubers without evidence for *Pectobacterium*) and grew them under four different irrigation regimes that differed in the timing and level of watering. Soil microbial community dynamics were assessed by extracting DNA from the soil before planting, soil from the ridge and root at potato harvest, and performing amplicon sequencing of the 16S rRNA gene V4 region. The field trials recorded blackleg symptom prevalence at a maximum of 16% in both Jelly varieties and 5% in Estima. Increased irrigation led to increased symptom prevalence but in the soil microbial community, we found that the most abundant taxa in the soil microbiome (inc. species of Nitrososphaeraceae, Beijerinckiaceae, Vicinamibacteraceae and Chloroflexi) were remarkably stable across irrigation regimes throughout the experiment. However, when phylogenetic relationships were taken into account, potato variety/*Pectobacterium* load altered soil bacterial community diversity, with the most susceptible variety showing distinct differences compared to the other two. A PERMANOVA test of beta-diversity showed significant differences between time-points sampled and stock variety but not between irrigation treatments. We conclude that different potato varieties and / or their *Pectobacterium* load before planting could have more substantial effects on soil community dynamics than irrigation regime.

POSTER

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Infectivity of Faba bean necrotic yellows virus cloned genome components in *Nicotiana benthamiana* and their reconstitution

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Faba bean necrotic yellows virus (FBNYV) (genus Nanovirus; family Nanoviridae) has a genome comprising eight individually encapsidated circular single-stranded DNA components each of about 1 kb and encoding only one protein. *Aphis craccivora* and *Acyrtosiphon pisum* are two insect vectors of FBNYV. It has frequently been reported infecting faba bean (*Vicia faba* L.) and chickpea (*Cicer arietinum* L.) from Azerbaijan, Egypt, Iran, Morocco, Spain, and Syria etc. In our study, 1.1-mers infectious clones of full-length FBNYV DNAs were constructed. All eight DNAs were agro-inoculated for reproducing FBNYV-like symptoms in *Nicotiana benthamiana*. Characteristic symptoms of FBNYV infection i.e., necrosis and leaf yellowing were observed in the host plants i.e., cowpea. Following that, reconstitution of a fully infectious nanovirus from its cloned DNAs was successfully done by using total extracted DNA as template for PCR amplification with DNA segments specific primers, respectively. Southern blot hybridization was accomplished as well using [³²P]-radiolabeled PCR amplified products of 1 kb of DNA R (Rep), DNA S (capsid protein) as probe that showed the typical double-stranded and single-stranded appearance of the respective DNAs. So, in this study, we are introducing a new simple and efficient nanovirus infectious clones' construction method which can be valuable in understanding the intriguing aspects of nanoviruses.

POSTER

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Rapid and sensitive detection of rice stripe virus by RT-RPA and qRT-RPA methods

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Rice (*Oryza sativa*) is the main crop in East Asia, and infection with various pathogens has been reported. Rice stripe virus is a virus that mainly occurs in China, Japan, and Korea, and is transmitted by the small brown planthopper (*Laodelphax striatellus*). In Korea, intermittent outbreaks have been reported mainly by migrated insects from China. We tried to develop a diagnostic technology that can quickly and reliably diagnose RSV in

the field based on the Recombine polymerase amplification (RPA) method. TwistAmp® Basic kit was used after adding RevertAid Reverse Transcriptase (Thermo scientific) to diagnose RSV through one-step RT-RPA without additional cDNA synthesis step from RNA. After designing at least 5 sets of primers from RNA dependent RNA polymerase coding sequence, the primer set showing the clearest amplicon was selected, and then optimized conditions for temperature, time, magnesium ion concentration, etc. was confirmed. After that, to identify real-time amplification, Miami Green, a DNA-Binding Fluorescent, was added to the reaction compounds, and amplification curves were described using real-time PCR equipment. Through qRT-RPA, it was observed that the amplification product was confirmed in 6-7 cycles (about 120-140 seconds). Through this, it was confirmed that this method can be usefully used for quantitative analysis of RSV within a short time.

POSTER

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Virome analysis from *Cnidium officinale* and *Thrips nigropilosus* based on next-generation sequencing in Korea

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In Korea, *Cnidium officinale* is cultivated as a medicinal plant, mainly cultivated in the highland regions of Gangwon-do and northern Gyeongsangbuk-do. Viruses such as apple stem grooving virus (ASGV), cucumber mosaic virus (CMV), cnidium vein yellowing virus 1 (CnVYV1), and cnidium vein yellowing virus 2 (CnVYV2) have been identified and reported in cultivated *C. officinale*. During May and June 2021, *C. officinale* plants grown in four cities (Hoengseong, Samcheok, Bonghwa, and Yeongyang) located in the eastern part of South Korea and *Thrips nigropilosus* living therein were collected. Mainly samples in which symptoms of vein clearing and chlorotic spots observed in leaves, and thrips occurring in nearby areas were also used for analysis. Total RNA was extracted the complementary DNA libraries were generated. Next-generation sequencing (NGS) was performed using an Illumina Novaseq 6000 (100 bp paired-end read), and then analyzed raw read data with CLC Genomic Workbench. CnVYV1, CnVYV2, CMV, and ASGV previously reported in Korea were commonly identified in *C. officinale* leaf samples, and cnidium virus X was also identified in all but one region. In addition, sequences of viruses suspected to be novel viruses belonging to the Solemoviridae and Betaflexiviridae families have been additionally identified. In thrips, reads for CnVYV1, CnVYV2 and CMV were confirmed. Nucleic acid sequence similarity among trimmed and rearranged contig sequences identified in each region was analyzed. Thereafter, to recheck, virus infection was verified through RT-PCR using a primer set capable of specifically diagnosing each virus.

POSTER

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Development of diagnostic methods based on RPA and RT-RPA techniques that can quickly and accurately identify viruses mainly occurring in tomatoes in Korea

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Unlike PCR, isothermal amplification reaction methods have been used for various diagnostics because they can produce amplification products that can be used for diagnosis under one temperature condition without a complicated process. Recombinase polymerase amplification (RPA) is also a type of isothermal amplification reaction, which usually produces sufficient amplification products with a reaction time of less than 30 minutes at a temperature of 37 degrees. We developed an RPA-based diagnostic method for five major viruses that occur mainly in tomatoes grown in Korea [tomato yellow leaf curl virus (TYLCV), tomato chlorosis virus (ToCV), cucumber mosaic virus (CMV), tomato mosaic virus (ToMV), and tomato spotted wilt virus (TSWV)]. TwistAmp® Basic kit was directly used only in the case of TYLCV, which has DNA as its genome, and RevertAid Reverse Transcriptase (Thermo scientific) was added to the reagent to diagnose the rest of the viruses

through RT-RPA directly from RNA. After designing at least 5 sets of primers for each virus, the primer showing the clearest amplification product was selected. For viruses with multiple segments, primer sets targeting different genes were prepared and selected. Afterwards, each diagnostic condition (temperature, time, magnesium ion concentration, etc.) was optimized. After that, in order to perform real-time diagnosis, Miami Green, a DNA-Binding Fluorescent, was added to the reaction, and then a method was also developed to confirm the amplification product through the amplification curve using real-time PCR equipment.

POSTER

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First report of citrus leaf blotch virus 2 infecting mandarin (*Citrus reticulata*) in Korea

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Citrus reticulata is an economically important fruit in Korea, and more than 90% of them are produced in Jeju Island. In July 2021, we collected leaves from five trees with virus-like symptoms in Jeju Island to determine the presence and degree of citrus virus infection. Each sample's total RNA was extracted the complementary DNA libraries were generated. Next-generation sequencing (NGS) was performed using an Illumina Novaseq 6000 (100 bp paired-end read). We analyzed the NGS data with CLC Genomic Workbench and found that apart of sequence read mapping Citrus tristeza virus (CTV) and Citrus leaf blotch virus 2 (CLBV 2). CLBV 2 was first reported in China in 2018 and appear to have originated through RNA recombination between members of two distinct citrivirus species. The full-length genome was assembled by mapping of the Illumina reads on a reference Viral DataBase (RVDB) (21.0 June 2021) with high similarity were identified and had 99.49% sequence identity with the CLBV 2 CN-2 isolate (MH558590) 99.54 to 99.72% amino acid identity within the translated region. RT-PCR was used for further validation with two primer pairs, CLBV2-1-F(5'-TCATCCAGAAGGGTATCTCGGA-3')/CLBV2-1-R(5'-CCCTCCTCACCTTCCCCATA-3') and CLBV2-2-F(5'-GGGTCAAGAAGCACGTCAGA-3')/CLBV2-2-R(5'-CGTTCACATCCATTGAAGGAC-3') designed from identified contig sequence and successfully amplified 588bp (partial replicase protein) and 780bp (partial coat protein) fragments were amplified and products were cloned into the pGEM-T Easy vector and the sequences of the clones were analyzed. To the best of our knowledge, this is the first report of CLBV 2 in Korea, and further investigation is needed to determine the extent and effect of infection in Korea.

POSTER

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Analysis of host siRNAs response to multistrain viral infection in strawberry

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A mixed viral infection with two cytorhabdoviral species, strawberry crinkle virus (SCV) and strawberry virus 1 (StrV-1), and a stramovirus, strawberry mottle virus (SMoV), was recently identified in a single strawberry plant (1,2). Peculiarity of the infection was that each of viruses was represented by several distinct genotypes. Four daughter plants of the CRM isolate of *Fragaria ananassa* were subjected to extraction of small RNAs. Three to four leaf samples were collected per a plant and processed individually. The sequencing libraries were prepared using NEBNext Small RNA Library Prep Set for Illumina (NEB, USA) and processed using NovaSeq6000 (IAB, Czech Republic). High-throughput sequencing of small RNAs was complemented with RT-qPCR estimation of viral levels. In this work, we estimated abundance of distinct viral RNAs, compared with amount of plant-produced small interfering RNAs. Plant response measured in a number of virus-specific small RNAs did not always correspond with levels of specific viral RNAs. The strongest response was documented for SMoV, quantified as the most abundant agent. Both SCV and StrV-1 triggered significantly comparable production of specific siRNAs, although StrV-1 had several folds higher titers. Further, pattern of siRNA hotspots was compared between samples of both intra-plant and inter plant samples.

References: (1) Koloniuk et al., 2018. *Arch Vir* 163 9:2539-42. (2). Fránová et al., 2019. *Viruses* 11 11:982.

NLR immune receptor-nanobody fusions confer plant disease resistance

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Plant pathogens cause recurrent epidemics that threaten crop yield and global food security. Efforts to retool the plant immune system have been limited to modifying natural components and can be nullified by the emergence of new pathogen races. Therefore, there is a need to develop made-to-order synthetic plant immune receptors with resistance tailored to the pathogen genotypes present in the field. Here we show that plant immune receptors can be used as scaffolds for VHH nanobody fusions that bind fluorescent proteins (FPs). The receptor-nanobody fusions signal in the presence of the corresponding FP and confer resistance against plant viruses expressing FPs. Given that nanobodies can be raised against virtually any molecule, immune receptor-nanobody fusions have the potential to generate resistance against all major plant pathogens and pests.

Mini-chromosomes as drivers of genetic diversity and host-adaptation in the blast fungus *Magnaporthe oryzae*

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Cereal blast is one of the most threatening plant diseases worldwide and impacts the most common cereal crops, including rice, wheat, and barley. Despite a prevalent lack of sexual recombination in most natural populations, the blast fungus continuously adapts to its host plants which can lead to host-jumps and recurrent pandemics. A major driver of host-adaptation is rapid genomic changes that lead to a gain and loss of effector genes. However, the molecular details that enable rapid genomic changes are not well understood. We established a state-of-the art, multidisciplinary approach to analyse structural variations including mini-chromosomes and identify mini-chromosome associated genes that likely contribute to virulence of the blast fungus. Mini-chromosomes in wheat- and rice-infecting blast fungus isolates contribute to their genomic diversity by horizontal mini-chromosome transfer and inter-chromosomal recombination with core-chromosomes leading to lineage- or isolate-specific genome arrangements that involve effector candidates. These structural changes in the genome facilitate gene gains or losses of virulence factors and ultimately enable rapid adaptation to varying host conditions. Using this approach, we identified several effector candidates that differentiate two sub-lineages of a pandemic wheat blast lineage. Our results suggest that mini-chromosomes are major drivers of genetic diversity and host adaptation in the blast fungus. We will leverage this knowledge to identify novel virulence genes and to identify potential sources of resistance against the blast disease.

Rice blast disease outcome is determined by plant and fungal circadian systems

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Rice blast is a devastating fungal disease of cultivated rice, causing the destruction of 10-30% of the global rice crop, or enough to feed 60 million people annually. *Magnaporthe oryzae*, the causative agent of rice blast disease, displays strongly circadian behaviour in conidiation, where spores are produced at night. We have observed that rice blast disease severity is dependent on the timing of inoculation relative to dawn, where dawn inoculations cause more severe disease symptoms than seen on plants infected at dusk. These observations suggest the entrainment of the plant circadian clock plays a substantial role in the pathogenicity of *M. oryzae* on rice. We used CRISPR-Cas9 to generate a white collar 2 (*wc-2*) mutant in *M. oryzae* which does not exhibit circadian sporulation behaviour and which is impaired in its capacity to cause disease. We conclude that both the plant and fungal circadian systems are important in determining rice blast disease outcome. The

development of strategies to control plant pathogens is crucially dependent on a firm understanding of the interaction between both partners of the pathosystem and the importance of abiotic factors such as growing medium, chemical and physical environmental conditions, the light environment as well as time of day, inoculation timing, and the circadian clock in the outcome of plant infection are key to characterising disease interactions.

POSTER

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Investigating mycovirus-mediated systemic resistance in oilseed rape

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Oilseed rape, *Brassica napus*, is an important and popular food crop for making canola oil, rapeseed meal for cattle and is used increasingly by the biofuels industry. The crop is ravaged by many fungal diseases globally causing £100 million worth of yield losses annually (Fitt et al., 2006), namely light leaf spot (caused by *Pyrenopeziza brassicae*) and phoma stem canker (caused by *Leptosphaeria maculans* and *L. biglobosa*). Previously a quadrivirus (LbQV-1) was characterised that infects *L. biglobosa* and interferes with *L. maculans* pathogenicity (Shah et al., 2020). Additionally, plant response genes were differentially expressed to combat enhanced pathogenicity. My project involves screening and characterising viruses in *L. maculans*, *L. biglobosa* and *P. brassicae* and quantifying how rape recognises and responds to each fungus. Virus-infected and -free isogenic lines of the Chinese *L. biglobosa* isolate (W10) have been resurrected to conduct challenge assays in planta. RT-PCR conditions were optimised, and LbQV-1 specific primers were used to confirm the virus presence previously ascertained by dsRNA isolation. Endemic field isolates were collected and, to date, 26 *L. maculans*, 16 *P. brassicae* and 1 *L. biglobosa* isolates have been screened. Apart from *L. biglobosa* isolate WH17-WHY-1, which contained LbQV-1, none of the other fungi appeared to be virus infected. In order to gain insight into the molecular mechanisms underpinning the observed phenotypes, samples will be collected from different parts of challenge inoculated plants (i.e., stem, leaf, root, petiole etc.) and compared in terms of gene regulation using next-generation sequencing and quantitative PCR.

Reference: Fitt BDL et al., (2006). *E. J. Plant Pathol.* 114, 3-15. Shah UA et al., (2020). *Mol. Plant Micro Int.* 33, 98-107.

Tuesday | Talk 6.1

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Communication and awareness raising of plant health – legacy of the International Year of Plant Health 2020

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Communication and information exchange technology has dramatically changed in particular since the start of the third millennium. The developments in information technology must be considered revolutionary have led to a change in how human societies communicate. In particular, the internet and social media have created unprecedented opportunities for people being informed about any subject. At the same time, the oversaturation of the information available may have led to a situation where individuals chose their information not according to the factual precision or accuracy of it, but rather to confirm own beliefs and preferences, or because celebrities have endorsed it. This in turn may well lead to a change of how international and national policies are developed and justified and how political power is attributed and exercised. These developments have enormous impacts on scientists, such as plant health experts. It becomes more and more important that plant health information is generated and distributed in forms, which are easily accessible to the public and inform understandably and accurately about risks to plant health, ways on how to mitigate these risks and the role the public can play in this mitigation. To raise the awareness of plant health and to promote it the international community declared 2020 as the International Year of Plant Health (IYPH) (1)). The IYPH communication efforts, which were primarily based on internet and social media channels, reached over 473 million accounts and had a media coverage for potentially 4.4 billion readers. In order to mainstream the importance of plant health into the challenges humanity faces today, the IYPH 2020, in particular,

highlighted the importance of plant health to food security and biodiversity conservation, and stressed the impact of climate change on plant health issues. To continue the awareness raising activities an international day of plant health has been proposed to the United Nations. It is of paramount importance that the IYPH 2020 is considered as the start to a continuous and intensified public information campaign to inform about plant health issues. One of the legacies of the IYPH 2020 must be that plant health scientists and regulators must make sure that research and risk findings do not stay within the plant health community only.

Reference: (1) IYPH 2020 final report at: <https://www.fao.org/documents/card/en/c/cb7056en>

POSTER

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Identifying novel powdery mildew susceptibility and resistance genes in strawberry

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The biotrophic pathogen powdery mildew (*Podosphaera aphanis*) is a major disease on strawberry. Strawberry powdery mildew is a global problem, infecting the leaves, flowers and fruit and resulting in high economic losses due to unmarketable fruit. Control of this disease is regulated by the application of fungicide sprays; however, the continued application of fungicide has caused concerns regarding fungicide insensitivity and resistance. Generating disease resistant cultivars offers a favourable solution to reduce the impact of powdery mildew on strawberries. This project will characterise disease development and identify tissue specific resistance/susceptibility alleles and genes for use in breeding. This will be achieved through conducting a genome-wide association study (GWAS) on a field trial consisting of 350 different cultivars with five replicates and using natural infection. The genotyping will be performed using an Affymetrix IStraw 35 array to facilitate identification of candidate genes associated with response to powdery mildew. Associated genes identified will be subject to gene editing using both HIGS and CRISPR/Cas9 techniques to quantify the gene function and the disease phenotype of resulting transformants will be validated through pathogenicity testing. Furthermore, this project is focusing on characterising the tissue specificity of powdery mildew in a variety of different strawberry genotypes. Tissue specificity will be assessed by pathogenicity tests incorporating advanced hyperspectral, multispectral and fluorescent imaging technology to assess disease progression on the strawberry foliage and fruit.

Tuesday | Talk 4.4

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Policy approaches to protecting plant health in the UK

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Protecting plant health is an important Government priority, leading to economic, social and environmental benefits. There are many potential threats to UK plant health which need to be identified at an early stage, to assess the scale of threat and agree priority actions. The UK Plant Health Risk Register is the key screening tool used by the UK Plant Health Risk Group to analyse potential threats and agree policy responses. The role of the Risk Register and work of the Plant Health Risk Group will be described, including their contribution to meeting strategic objectives on protecting plant health, with practical examples of how the Register has been used to mitigate specific threats.

Wednesday | Talk 9.1

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Mind the gap: connecting communities in agritech, agronomy and academia

Alex McCormack

CHAP – Crop Health and Protection, York Biotech Campus, York

I will discuss how CHAP, one of the four Agri-Tech Centres in the UK, connects and facilitates discussions between researchers, government stakeholders and industry to advance innovation and promote sustainable agriculture practices. I will showcase how for CHAP, it is crucial to foster collaborations to transform the Agri-Tech innovation process to tackle present and future challenges faced by farmers. Ultimately, supporting

growers and farmers to make informed decisions is vital, as innovations in this sector can support the development of a more sustainable, resilient, nutritious and climate positive crop production in the UK. Additionally, a series of ongoing collaborative case studies and projects will be discussed where CHAP aims to address leading challenges in the agriculture sector. The vision for CHAP is to be a global leader in the progression of sustainable applied agri-technologies and in its latest campaign, Making Connections, the aim is to engage and reach the wider sector and drive forward the adoption of innovative solutions that can help the industry meet the net zero target set by the government. CHAP seeks to build lasting and trusting collaborations which can secure a safer, more sustainable future for crop production.

Wednesday | Talk 9.3

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Prevalence, host range and management of cucurbit chlorotic yellows virus infecting groundnut (*Arachis hypogaea*) in Western Kenya

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Groundnut or Peanut (*Arachis hypogaea*) is an important oilseed legume crop in Kenya but yields are declining due to pests and diseases. Cucurbit chlorotic yellows virus (CCYV) (genus: Crinivirus, family: Closteroviridae) causing cucurbit chlorotic yellows disease (CCYD), causes upto 68-97% yield loss. CCYV is characterized by typical interveinal yellowing symptoms in leaves with vein banding, veinal chlorosis, yellow vein mosaic, leaf brittleness and plant vigor reduction affecting flower, peg and pod formation. CCYV is transmitted by whitefly (*Bemisia tabaci*). Limited information is available on the prevalence, host range and serological diagnosis of CCYV in western Kenya. This study determined the occurrence, prevalence, host range and serological bioassays of CCYV. Two disease diagnostic surveys were conducted during the short and long rain seasons in six counties growing groundnut in western Kenya. Disease incidence and severity was scored on the disease diagnostic score sheet. The data collected was subjected to analysis of variance using SAS Software. Serological bioassays were done with double antibody sandwich-enzyme linked immunosorbent assays (DAS-ELISA). CCYV was distributed in all the surveyed groundnut farms in Bungoma, Busia, Homabay, Kakamega, Siaya and Vihiga Counties. The mean CCYV incidence ranged between 61-97%. The Mean CCYV incidence was highly distributed during the short rains season than the long rains season and varied significantly among the counties. The severity of CCYD increased with increase in incidence. Serological results on *Cucumis pepo*, *Datura stramonium* and *Psidium quajava* leaves exhibiting typical CCYV viral symptoms, tested positive with DAS-ELISA. Visual symptom observation in some groundnut varieties needs a belt with serological bioassays, molecular diagnostics and bioinformatics braces approach to limiting virus incidence and severity in the field through breeding for resistant/tolerant cultivars.

References: Amer, MA (2015). Serological and molecular characterization of Cucurbit chlorotic yellows virus affecting cucumber plants in Egypt. *International Journal of Virology*. 11:1-11. Mabele AS, Were HK, Ndong'a MFO, Mukoye B (2020). Occurrence and genetic diversity of groundnut rosette assistor virus in western Kenya. *Crop Protection*. 139:1-7.

POSTER

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The role of the rhizosphere in the development of acute oak decline

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Acute Oak Decline (AOD) is a complex decline disease affecting the British oaks *Quercus petraea* and *Q. robur*. The disease can be fatal in 3-5 years of symptom development and has a concerning distribution throughout the UK [2]. Records of similar cases involving the same bacterial species are being confirmed in Europe, with new records and on other broadleaf trees reported from the Middle East, marking a worrying turn in forest health. *Brenneria goodwinii* and *Gibbsiella quercinecans* have been identified as key agents of disease while *Rahnella victoriana* and *Lonsdalea britannica* play secondary roles in disease development, but their origins remain unidentified [2]. The aims of the study were to identify if AOD bacteria were present in the rhizosphere soil of oaks and identify other differences in plant growth-promoting bacteria (PGPB) and soil pathogens between healthy and diseased oaks rhizosphere. Using high-resolution melt analysis and enrichment culturing, G.

quercinecans and *R. victoriana* have been identified and isolated from healthy and diseased oak rhizosphere soil samples from Hatchlands National Trust site. This provides evidence that soil could be a reservoir for pathogens contributing to the development of AOD symptoms. To compare differences in PGPB and pathogens synthetic long-read 16S rRNA V1-V9 will be used to identify groups of interest based on their potential role in the rhizosphere. Amplicon sequencing will then be used to contrast key bacterial groups at the species level. Several potential novel bacterial species of the order Enterobacterales have also been identified from the Hatchlands soil samples. These will be further classified using a polyphasic approach based on genotypic and phenotypic assays.

References: [1] Brady, C, et al. (2017) *World Journal of Microbiology and Biotechnology* [online]. 33 (7), pp. 1-11. [2] Denman, S, et al. (2018) *ISME Journal* [online]. 12 (2), pp. 386-399.

POSTER

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Phylogenomics reveals a complex evolutionary history of Fabaceae NLR immune receptors

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The legume family (Fabaceae) is the third largest angiosperm family and is considered one of the most important crop families. Biotic stress constrains legume yield, and resistance gene breeding is currently considered the most sustainable management method to deal with pathogen pressure in the field. Many legumes share the same pathogens, but whether they share the same resistance genetic basis is currently unknown. To address this question, our initial goal was to identify resistance (R) genes in the Fabaceae family. As a first step towards uncovering the Fabaceae resistance genes repertoire, we undertook a phylogenomic analysis of nucleotide-binding leucine-rich repeat proteins (NLRs) in 23 legume species. These analyses uncovered large variation in overall NLR abundance as well as in distribution of the different NLR classes. The distribution of the NLR classes did not always match the species phylogeny. For instance, pea (*Pisum sativum*) and grass pea (*Lathyrus sativus*) have significantly different NLR repertoires, despite being closely related. The Fabaceae NLR repertoire will be an important tool for comparative resistance mapping studies and for R gene enriched Genome-Wide Association Studies. The outcome of these analyses will be used to accomplish the long-term goal of my project: to develop tools to assist legume breeding programs for durable resistance.

Monday | PH Gregory competition

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Unlocking the biocontrol potential of kiwifruit *Pseudomonas*

Javier MARTÍNEZ-PÉREZ (1,2), Chandra G (1), Vanneste J (3), Truman (A 1), Malone J (1)

(1) John Innes Centre, Norwich (2) University of East Anglia, Norwich (3) Plant & Food Research, Hamilton, New Zealand

Pseudomonas syringae pv. *actinidiae* (Psa) is the major threat to the world kiwifruit industry since 2008. Just in New Zealand, cumulative yield losses are well over £1B since 2010. Currently, copper compounds and antibiotics are the most common and efficient treatments but are a ticking bomb. Psa has evolved rapidly since its introduction by exchanging mobile genetic elements with the local bacterial populations, leading to copper and antibiotic resistance. Therefore, spraying these agrochemicals, is a short-term solution for New Zealand kiwifruit growers. With my project, I am aiming to provide kiwifruit growers with an effective, sustainable, and environmentally friendly crop protection agents to control Psa. To do so, I am examining how the naturally occurring population of kiwi-associated *Pseudomonas* responds to Psa infection, to exploit this knowledge, discover and characterise novel anti-Psa treatments. From a representative 6,000 epiphytic *Pseudomonas* collection, 1,000 strains have been tested using laboratory-based assays. As a result, there were identified 33 biocontrol candidates. Additionally, more than 100 genomes were whole genome sequenced between suppressive and non-suppressive Psa strains. This data has been of great value for identifying that published copper resistance genes are missing from most copper resistant strains, suggesting new unknown mobile genetic elements may become a future problem. Also, thanks to their analysis with AntiSMASH and transposon mutagenesis libraries, we have very successfully identified a wide variety of known and unknown natural

product (NP) potential within the strains. From the biocontrol candidates, at least four *Pseudomonas* strains strongly suppress *Psa* infection in planta by around 3-log. Lastly, I have identified a novel NP cluster responsible for strongly suppressing *Psa* and I am in the process of characterising the molecule and examining the impact of the key NP by making and testing deletion mutants in the NP gene cluster.

Monday | PH Gregory competition

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Modelling the interaction between human behaviour and crop disease management.

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While the spread of plant disease depends strongly on biological factors controlling transmission, epidemics clearly also have a human dimension. Disease control depends on decisions made by individual growers, which are in turn influenced by a broad range of factors. However, control of many diseases requires co-ordinated management between growers, who must all co-operate to be successful. Despite this, human behaviour has rarely been included in plant epidemic models. Considering cassava brown streak disease (CBSD; a viral disease of cassava) as a case study, we model how access to information, the risk aversion of growers, and the perceived benefit of disease control influence participation in disease management. CBSD can be transmitted within season by a whitefly vector, and between seasons via vertical transmission. The former means that the outcome of one grower depends on the actions of others as whitefly vectors can travel between fields and spread infection, providing an ideal case study for co-ordinated control schemes. In sub-Saharan Africa, clean seed systems (CSS) have been proposed as a means of limiting the vertical transmission of CBSD. Though broadly beneficial, CSS are susceptible to freeloaders who benefit from control measures without incurring any costs. This threatens the long-term success of such schemes. We study the system in both a spatial and non-spatial setting, with the behavioural component included as both a game-theoretic assessment of payoffs for each control strategy as well as the spread of information between growers. Importantly, we investigate which factors ensure sustained participation in CSS, since oscillations in participation may lead to periodic disease incursions.

POSTER

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Elucidating the role of small RNAs in *Alternaria alternata* tomato pathosystem.

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Fungal infections make up most of the crop losses in the agricultural industry. Chemical pesticides have been used largely to prevent crop losses due to fungal infections. However, use of pesticides bring further problems such as fungal resistance to pesticides, harm to the farmers and ecological damage to the surrounding area from run off. The growing technology of RNA silencing shows great potential in alleviating this problem, providing a method of specific pathogen targeting, an adaptable system that can be updated to account for new pathogen systems and account for pathogen resistance. Use of small RNAs have been explored in HIGS and SIGS systems. To further the field of sRNA silencing, this project has focused on a specific pathosystem, *Alternaria alternata* and tomato, with an aim to decipher the small RNAs present and what role they play in the interactions. The small RNA libraries from fungi, plant, and infected tissue were used to identify sRNAs that are up regulated during infection and potentially capable of silencing genes in their respective counterpart. sRNA sequences were bioinformatically analysed and their relative expression level were determined. In addition, we wanted to determine the viability of Chitin Syntheses as a target for sRNA-mediated fungal control. There are 11 CHS genes in *A. alternata*. Gene specific siRNAs targeting CHS gene were used to treat fungal spores and the effect of the treatment observed. The results showed that sRNA targeting each sRNA caused a significant increase in spore tube length, production of spores and little reduction in germination rate. In conclusion, targeting individual CHS genes is unlikely to be a viable target for sRNA mediated gene

silencing, but revelations into the sRNA interactions may reveal new gene targets and sRNA that may show a promising effect.

Monday | PH Gregory Competition

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Identification of causative pathogen responsible for foliar and pod diseases of African yam bean (*Sphenostylis stenocarpa*) in Nigeria

Olaide OGUNSANYA (123), Michael A (1), Clement A (2), Ortega-Beltran A (1), Armitage A (3), Colgan R (3), Thompson T (3)

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African yam bean (AYB; *Sphenostylis stenocarpa*) serves as a security crop, which can be used for food, feed, medicine, and its insecticidal properties (Adewale and Odoh, 2013; Okafor and Usman, 2013). Despite the nutritional value of AYB, low grain yield as a result of fungal diseases deters farmers from large-scale cultivation (Ogah, 2011). The causal agents of AYB pod blight, flower bud rot and leaf blight are largely uncharacterised. To investigate the prevalence of AYB fungal diseases in Nigeria, a disease survey was conducted in 2018 in major AYB-growing areas in Nigeria. Morphological and molecular assays were conducted to identify the causal agents and diseases responsible for low grain yield in this crop. The 143 fungal isolates collected from diseased AYB leaves, flower buds and pods were identified by morphology and sequencing of the Internal Transcribed Spacer (ITS4 and 5). *Colletotrichum gleosporioides* complex (52%), *Neopestalotiopsis* sp. Asebi Neo (18%), *Curvularia akaii* (18%), *Fusarium oxysporum* (40%) were recovered from the leaves whereas *C. gleosporioides* complex (2%) and *C. truncatum* (97%) were collected from the pods. *F. oxysporum* (10%) and *C. truncatum* (90%) were collected from flower bud. Koch's postulates were satisfied for the most commonly isolated fungi, *C. truncatum* and *C. gleosporioides* complex, both of which caused progressive dark lesions on healthy detached AYB leaves, pods, and flower buds. Other fungal pathogens did not produce any symptoms on the aforementioned AYB tissues. This investigation confirms *Colletotrichum* spp. as the causal agents of these diseases. Given the importance of AYB in Western- and Eastern-Nigerian diets, accurate pathogen species identification is vital to understand disease epidemiology. Furthermore, it is a pre-requisite to screening for crop resistance, which will aid the development of integrated disease management. Thus, further study is required to accurately identify and delimit *Colletotrichum* spp.

POSTER

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Exploring *Bacillus* species to control downy mildew pathogens in pulses

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Food security is the major challenge that humankind faces at present, which is to worsen with the increase in climate change, land degradation and world population. In order to sustain the world population in 2050, it is projected that global food production has to rise by 60–110%. Use of chemical pesticides in crop production has increased yields of global crops, but they cause a lot of hazards particularly to the environment and human health. Research investigations are increasingly focusing on exploitation of untapped potentials of microbial biological control agents (MCBA) for managing plant diseases in an eco-friendly and sustainable manner. Among the mostly studied and used MCBA, Rhizobacterium *Bacillus* species have been shown to suppress wide range of plant pathogens. However, no commercialised MCBA has been reported for effective controlling of downy mildew diseases in pulses. We have been investigating the effectiveness of different strains of *Bacillus* in controlling downy mildews in pulses. In-vitro antagonism bioassays of different concentrations of *B. subtilis* as well as varying concentrations of filtrates on *Peronospora viciae* f. sp. *pisi* (Pvp) that attacks pea showed 100% inhibitory activity on Pvp spore germination compared to the control. In-planta antagonism assays were performed, and the results showed significant suppression of Pvp sporulation in peas treated with *B. subtilis* or

its filtrates using foliar application technique. The reduction in sporulation obtained using different concentrations of *Bacillus* culture and their filtrates ranged from 62.2 to 99.6%. Drenching the soil with *Bacillus* was also tested, but no significant reduction in Pvp sporulation was observed. This suggests that foliar application of using *Bacillus* cultures and their filtrates could be an effective method against Pvp. Latest results will be presented.

Tuesday | Talk 4.3

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Global crop protection- let's do the simple and cheap things well

Richard OLIVER

Adjunct Curtin University and special professor University of Nottingham

There are four broad methods to control plant diseases – agronomy, chemistry (crop protection products), genetics and biosecurity – but disease losses remain persistently high; at least 20%. The research, development and exploitation of these methods differs markedly in cost effectiveness. The most effective are CPPs and genetics. Both suffer from evolution in pathogen populations to overcome effective defences but there is good evidence that fungicides protect genetics and vice versa. Globally, regionally and nationally, we lack basic resources that would enable the elongation of the effective life of CPPs and genetic packages conferring resistance. I argue that a modest investment a global molecular diagnostic network and in accessible isolate collections would provide a strong foundation for reducing losses to acceptable levels. Diagnosis (where?) and isolates (what) are the key tools needed to breed crops that carry appropriate genetic resistance and would warn of loss of efficacy of CPPs. Such a strategy would insure against harmful biosecurity breaches. I illustrate this concept focussing on the needs of the wheat crop.

POSTER

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Take-all disease: a model study system to investigate root-infecting fungal pathogens of cereals

Javier PALMA-GUERRERO, Chancellor T, Canning G, Hammond-Kosack K

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Roots are essential organs constantly in contact with the soil and its microbiome consisting both of beneficial and pathogenic organisms. These rhizosphere interactions can have a strong effect both on plant health and the environment. Global diseases caused by root-infecting fungal pathogens routinely impact crop yield and quality of vegetables, fruits and major grain crops, including wheat. However, the molecular interactions between pathogenic fungi and plant roots have been understudied compared to the above-ground interactions. Take-all disease of wheat is caused by the soil-borne ascomycete fungus *Gaeumannomyces tritici*, previously known as *Gaeumannomyces graminis* var. *tritici*. Take-all is considered to be the most important disease of wheat roots worldwide. No resistance against take-all disease has been found in commercial wheat cultivars so far, and control measures predominantly rely on using break crops in the cereal rotations. Chemical control is inadequate because not all isolates of the fungus are sensitive to the available fungicides. Therefore, a better understanding of the “hidden” below ground interactions between wheat roots and their associated microorganisms is crucial to protect wheat from take-all disease. We are currently investigating new sustainable control strategies against this fungal pathogen. We have identified new sources of genetic resistance to take-all by exploring wheat relatives and other resistant cereal crops. We also have achieved a better understanding of the role of the soil microbiome in the disease outcome, and we are currently investigating the potential of natural wheat root colonisers in take-all disease suppression. Our findings are aiding the development of novel sustainable control strategies against take-all disease while providing a model study system for root-infecting fungal pathogens of cereals.

Reference: Palma-Guerrero J, Chancellor T, Spong J, Canning G, Hammond J, McMillan VE, Hammond-Kosack KE (2021). Take-all disease: new insights into an important wheat root pathogen. *Trends in Plant Science*, doi: 10.1016/j.tplants.2021.02.009.

Phytopathogens and their influence to the invasion development of alien plant species

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Biological invasion is one of the greatest environmental challenges of the 21st century. Displacement of native taxa, economic losses and even threat to human health are just some of the effects of the expansion of alien species. The main aim of the research was to determine the mycobiota composition inhabiting three invasive plant species: *Acer negundo*, *Padus serotina* and *Spiraea tomentosa*, and to determine the pathogenicity potential of selected species of fungi isolated from the infected tissues. The research was conducted throughout 2017-2019 in three locations in Poland: in Wrocław, in Bory Dolnośląskie and in the Wigry National Park. Based on monthly field observations, the diversity and dynamics of disease symptoms appearance were determined. Strains isolated from green tissues and seeds were genetically analyzed, based on ITS fragments. Using GLMM models, the disease index, mycobiota of seeds and the biodiversity of fungi were analyzed in relation to climatic factors, air pollution and habitat conditions. In total 1980 colonies were isolated from parts of green plants (31 taxa), and 17,647 colonies from the spermosphere (51 taxa). New *Fusarium* strains have been identified causing dieback of the shoots of the ash-leaf maple in Europe. This is the first comprehensive study to identify the mycobiota of invasive plants in Poland and one of the first of such kind in Europe.

The impact of elevated CO₂ on the resistance of oak seedlings to powdery mildew

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Levels of atmospheric carbon dioxide (CO₂) are at the highest point in 2 million years due to human activity. One part of the solution is the ending of deforestation and an increase in tree planting. In the UK planting includes oak species. However, young oak success is highly restricted by the biotrophic fungal pathogen *Erysiphe alphitoides*, the causal agent of oak powdery mildew (PM), which is considered a limiting factor in oak woodland regeneration. Previous work in our group has shown that elevated CO₂ (eCO₂) causes seedlings to become more susceptible to the infection, which could have devastating future impacts. This work uses metabolomic analysis to understand the molecular basis for the increased susceptibility state in naturally regenerated seedlings at the Birmingham Institute of Forest Research Free Air CO₂ Enrichment (BIFoR-FACE) experiment. Leaves were collected from seedlings growing in both ambient and eCO₂ arrays that were either healthy or infected with PM. Samples were extracted and run on an LC-ESI-QTOF-MS. Analysis of data was done using Metaboanalyst and MARVIS packages to provide tentative identification of significant compounds. eCO₂ appeared to drive most differences in samples. However, it was the combined impact of eCO₂ and PM infection that provided the most dramatic differences from the control. No metabolites were shared between all conditions showing an element of specificity in the responses. Enrichment analysis showed that monoterpenoid, glucosinolate and flavonoid biosynthesis pathways play a role in CO₂ and PM infection, suggesting that eCO₂ may act to trigger an atypical defence response in oak seedlings, which is less effective against PM. Work in underway to understand the effect of eCO₂ in mature oak tree and compare differences between tree developmental stages.

The story of Plantwise, a global programme fostering stronger plant health partnerships**Rob REEDER***CABI, Egham, TW20 9TY, United Kingdom*

The world's 800 million smallholder farmers produce most of the world's food, but the rural communities where they live often lack access to science-based information about crop health. The CABI-led, Plantwise programme increases food security and improves rural livelihoods by reducing crop losses and helping countries to improve their plant health systems, so that they can prevent and manage pest outbreaks more effectively. The Plantwise programme began in 2011, but its origins date back to the early 2000s and the first plant clinic held in Bolivia. Plant clinics operate in rural locations and function in a similar manner to human health clinics. The 'patients' attending plant clinics are diseased plants, brought by farmers for diagnosis and management recommendations. Clinics are staffed by plant doctors, sourced from existing agricultural advisory staff and trained through the Plantwise programme. Farmers receive a written prescription describing how to manage the plant health problem. In addition, information about the farmer and the problem are recorded in an online database, accessible to country stakeholders and the Plantwise programme. Plant clinics are the entry point to strengthening the partnerships necessary for better functioning plant health systems. The clinic data helps to inform stakeholders about current problems and drives the interactions between extension, research, policy and agro input suppliers. Over the past decade the Plantwise programme has established over 5,000 plant clinics in 33 different countries and trained more than 13,000 plant doctors. Studies indicate that participation in plant clinics results in significant yield and net income gains and that plant clinic users have better and more detailed knowledge about pests and diseases. Building on the lessons learnt through Plantwise the new PlantwisePlus programme is focusing on issues relating to excessive and/or hazardous pesticide use, food safety, lack of access to effective/affordable low-risk alternatives and better pest surveillance and response.

Sharing knowledge of plant health in local languages**Josephine RODGERS***Access Agriculture, 1050 Brussels, Belgium*

Having just won the FAO Innovation Award for Sustainable Food Systems - Access Agriculture is about to celebrate ten years of "farmer to farmer" training videos in local languages. These farmer experience videos are based upon strong field research and checked with experts, so that smallholder farmers can increase their incomes sustainably. From beginnings in Africa, Access Agriculture now has videos in more than 90 languages across Africa, Asia and Latin America. In order to assist with distribution of the videos there is now a team of more than 70 Entrepreneurs for Rural Access using solar powered Smart Projectors to show the videos in remote areas. These young people are making a business of showing the videos without the need for electricity, internet connection or mobile phone signal. This is an example of using digital tools both offline and online in order to reach smallholder farmers improving plant health, livelihoods and the environment.

Plant health in Scotland and the work of the Plant Health Centre**Gerry SADDLER (1), Ian K TOTH(2)***(1) SASA, Edinburgh, EH12 9FJ. (2) The James Hutton Institute, Dundee, DD2 5DA*

Scotland has a unique set of plant health needs which are overseen at the policy level by the Office of the Chief Plant Health Officer for Scotland. To assist with this function, in 2018 the Scottish government established Scotland's Plant Health Centre (PHC), which links closely with similar government-funded centres on animal health, water, climate change and knowledge exchange. The PHC is a virtual centre that brings the plant sectors for forestry, horticulture, environment and agriculture together to share plant health skills, ideas, solutions and knowledge exchange. While our main customer is the Scottish Government, we work closely

with other stakeholders including public bodies, industry and the public to provide scientific evidence to help them make important decisions about plant health threats to Scotland. The Centre's Directorate is headed up by the James Hutton Institute, and has sector leads from Scotland's Rural College (agriculture), Royal Botanic Garden Edinburgh (horticulture and environment) and Forest Research (forestry). It also has a Science Advisory and Response Team (SART) from the above organisations as well as partners from the universities of Edinburgh, Exeter and Strathclyde, Centre for Ecology & Hydrology and Biomathematics and Statistics Scotland (BioSS), each bringing unique skills across a range of plant health related disciplines, from understanding public perceptions to modelling and genomics.

POSTER

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Can oaks express priming of defence?

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Plants are continually exposed to multiple stresses that can negatively affect their growth, productivity and survival. However, they have developed highly sophisticated strategies to fight against these threats. One strategy is known as priming of defence, a sensitisation of defence mechanisms for a faster and stronger activation upon subsequent attack. Many chemicals can trigger priming and studies have demonstrated wide spectrum effectiveness. However, studies in oak seedlings are lacking. This work aims to determine whether oak seedlings can express chemical-induced priming. Oak seedlings were treated with salicylic acid (SA), jasmonic acid (JA) and β -aminobutyric acid (BABA) 7 days before infection with *Erysiphe alphitoides*, the causal agent of powdery mildew (PM), to which oak seedlings show extremely high vulnerability. Treatments with SA and BABA result in enhanced resistance to PM and JA in enhanced susceptibility. Resistance by SA and BABA was based on priming of SA-dependent gene expression and callose deposition, respectively. To investigate the mechanisms behind specific SA and BABA priming, an untargeted metabolome analysis was performed. Green leaves were collected at 0, 1 and 2 dpi and subjected to LC-MS/MS. Spectra were filtered using the XCMS R script and MarVis was employed to putatively identify metabolites and pathways. 17865 and 9408 putative masses were detected in positive and negative modes, respectively. Subsequently, a MANOVA analysis showed 3837 significant global differences ($p < 0.05$): 1147, 1295 and 1395 at 0, 1 and 2dpi respectively. Fold changes versus water treatment were applied to isolate primed metabolites. A total of 272 for SA and 313 for BABA masses were observed. Pathway enrichment analysis determined that BABA priming is mostly dependent on alkaloids biosynthesis, whereas SA failed to identify any specific pathways. The next steps in the project are to identify the metabolites responsible for priming by BABA and SA.

POSTER

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Understanding host resistance to improve control of light leaf spot on winter oilseed rape in the UK

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Light leaf spot, caused by the fungal pathogen *Pyrenopeziza brassicae*, is the most economically damaging disease of winter oilseed rape (*Brassica napus*) in the UK, with annual yield losses of > £100M. Control of light leaf spot is challenging because it is a polycyclic disease, with epidemics starting in autumn by ascospores. Subsequently, conidia produced by asexual sporulation on infected leaves cause secondary infections on all parts of the plant. Current control relies on fungicides; however, insensitivity development highlights the need for non-chemical controls like host resistance. Host resistance against *P. brassicae* is poorly understood; the aim of this project is therefore to improve our current knowledge by researching virulent races in pathogen populations, identifying candidate resistance genes, and investigating mechanisms of host resistance. This is a HKEP (Hertfordshire Knowledge Exchange Partnership) funded project in collaboration with the Perry Foundation and the industrial partner ADAS. Effects of plant age, incubation condition and inoculum concentration on light leaf spot disease severity have been investigated using cultivar Charger. *P. brassicae* isolates from the 2020/2021

season were obtained from crop samples through single-spore isolation. Results showed that older plants and higher inoculum concentration produced the most severe symptoms. Additionally, plants that received the higher inoculum (105 spores/ml) were significantly shorter by 5 cm than those with lower inoculum concentration (104 spores/ml), suggesting possible correlations between fungal inoculum concentration and plant growth. This hypothesis will be investigated in future work. Over 25 *P. brassicae* field isolates have been collected from oilseed rape and kale cultivars across England. Those isolates will be further screened for virulence.

Tuesday | Talk 4.2

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Tackling a formidable foe: the fightback against a forgotten enemy in Western Europe

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Emergent plant pathogens threaten modern agriculture and ecosystem stability. Today, one disease of significant concern for re-emergence in Western Europe is wheat stem rust. This disease has been associated with crop failures throughout history. However, during the green revolution, plant pathologists and wheat breeders achieved the almost impossible: They prevented any significant stem rust epidemics in the major wheat growing areas worldwide in the last half of the 20th century, including Western Europe. Then, in 2013, pathologists in Germany raised the alarm about the re-emergence of this previously vanquished disease. Since, increasing episodes of wheat stem rust have been recorded across Western Europe, including the first UK record for over 60 years in 2013. Furthermore, we found that 80% of current UK wheat varieties are susceptible to wheat stem rust and climatic conditions over the past 25 years have become increasingly conducive to supporting infection. With pathologists at the forefront of Europe's fightback, pathologists and legislators much once again work hand-in-hand to tackle this re-emergent threat. Historically, one area where legislation was critical in curbing wheat stem rust outbreaks, was managing the prevalence of the pathogens alternate host, *Berberis*. This hedgerow shrub can act as an infection reservoir, spreading the disease into neighbouring cereals. However, as stem rust has been in abeyance for many decades in Western Europe, legislation to restrict *Berberis* planting has long since lapsed. Using latest advances in high-speed videography, mathematical modelling and basic biology we finally unravelled the long-standing mysteries surrounding how spores are liberated and dispersed from *Berberis*. This new knowledge can now aid farmers and legislators to assess the current local risk of dispersal and develop modern-day policy on *Berberis* planting. It also facilitates development of sophisticated epidemiological models to potentially curtail stem rust epidemics originating on *Berberis* and help bridle the onslaught of this formidable foe.

Tuesday | Talk 5.1

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Invasive plants - the enemy of your enemy is your friend

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Most people consider that green is good and plants are much less of a threat to economies and habitats than insects for example. However, whether it is in an agricultural or environmental setting, weeds can have very significant impacts. It is no coincidence that herbicides account for almost half of the global pesticide, almost as much as insecticides and fungicides combined. If the weed in question is non-native and problematic outside of the rapidly disturbed arable field then it is likely to have arrived without its natural enemies that kept it in check in its native range. There are plenty of valued British native plants that have become serious invaders in the new world for just this reason. There are also many examples of such weeds that have come under control after reassociation with one of more of their native natural enemies. Classical biocontrol relies on co-evolved arthropods or fungal pathogens to bring about long-term and sustainable control often at a very large scale. This is only possible and permissible after extensive safety testing to ensure there is no significant threat to native species or crops. This presentation will summarise the steps in a biocontrol project from field survey to eventual release with particular reference to plant pathogen agents. The particular requirements and peculiar

public understanding of pathogens will be highlighted as will the spectacular successes that persist to this day. Finally, the recent and current weed biocontrol activities in the UK will be reviewed and the conclusion drawn that this tried and tested approach is in its infancy in Europe but that the UK is leading the way.

Wednesday | Talk 8.1

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Tree health resilience strategy - from policy to operations

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In 2018, Defra published the Tree Health Resilience Strategy. Founded on research by Fuller and Quine (2016) it defines three resilience outcomes - Resistance (risk reducing activities), Response & Recovery (from adverse events) and Adaptation (long term transformation leading to an increase in the extent, connectivity, condition and diversity of our treescape). Since that publication, the government has committed to invest over £600m in tree planting, with a target of 30,000ha per year across the UK by the end of this parliament. Trees are now at the forefront of the Government's plans to achieve net zero emissions by 2050, to help to bend the curve of biodiversity loss and to create thousands of green jobs. But the threat from tree pests and diseases is significant and growing due to globalisation and climate change. Thirty per cent of the 1200 pests on the UK plant health risk register are a threat to trees. In 2021, we are responding to outbreaks of two new pests and pathogens in the UK - *Ips typographus* and *Phytophthora pluvialis*. The latter being the first detection in Europe and on an unpublished host species - Western Hemlock. This presentation will explore government action to combat the escalating threats to tree health and safeguard our trees for future generations.

Reference: Fuller and Quine, 2016, Resilience and tree health: a basis for implementation in sustainable forest management, *Forestry: An International Journal of Forest Research*, 89 (1)

Monday | Presidential Address - Talk 1.1

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Plant health science and policy in the UK

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The plants and trees of this country are precious natural resources. They contribute to our food supply, our rural economy, and are essential to the biodiversity of the country. They shape the landscape, provide timber, they are part of our heritage and support our health and wellbeing providing much enjoyment. Yet the threat to the health of our plants and trees from pests and diseases is real and increasing. Globalisation of travel and trade and demands for a greater variety of plant species mean threats are ever-present. While we cannot eliminate all threats from occurring, we can strengthen protection, minimise impact and enhance the ability of our plants and trees to resist pressures. In the UK we have worked hard to improve standards of biosecurity for plants and trees. We have established a risk-based approach, world leading science and research, enhanced protection, surveillance, and inspection. Yet the threat level is constantly evolving, and we must take further action to keep pace with changing threats. By working collectively, we can minimise the risks and strengthen our approach for example from potential threats like *Xylella* and Emerald Ash Borer. We all have a part to play to limit the spread of pests and diseases through simple actions when travelling, buying plants or visiting our woodlands and parks.

POSTER

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Unmasking a cereal killer: what triggers 3LysM effector expression in a fungal wheat pathogen?

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The fungal pathogen *Zymoseptoria tritici* is responsible for septoria leaf blotch disease on wheat (*Triticum aestivum*). This devastating disease is associated with high fungicide use and yield losses of up to 50%. Current management strategies do not provide full control of *Z. tritici*. An effector protein essential for *Z. tritici*

virulence on wheat, Zt3LysM, may be useful in developing future control strategies. Zt3LysM sequesters chitin fragments, preventing their recognition by wheat immune receptors and 'masking' the pathogen. Little is known about how Zt3LysM expression is controlled. This work aims to investigate what triggers the expression of Zt3LysM and how this is regulated. Preliminary experiments were conducted in planta and in vitro using *Z. tritici* strains expressing GFP under the control of the Zt3LysM promoter. We found GFP expression was affected by nutrient source (nutrient-rich, nutrient-poor or plant-derived) and changed temporally during wheat leaf infection. GFP intensity was also affected by Zt3LysM promoter length, adding evidence for the existence of an upstream regulatory sequence. Future work will verify these observations, and use a yeast one-hybrid approach to identify proteins involved in Zt3LysM regulation. Investigation into how Zt3LysM expression is controlled could lead to new disease management strategies blocking the secretion of the effector. This would allow wheat to mount a full immune response to *Z. tritici*, preventing septoria leaf blotch disease and associated yield losses.

POSTER

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Epigenetics of long-lasting post-harvest resistance in tomato

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Tomato is a major crop world-wide with an annual retail value in the UK of £175 million, however its production is heavily limited by *Botrytis cinerea*, the causal agent of grey mould. Due to the toxicity of post-harvest pesticide application, alternative control methods are required. An attractive method for future integrated disease management is priming, a phenomenon that sensitises defence mechanisms for a faster, more efficient defence response upon subsequent attack. Priming typically resulting in broad spectrum resistance at minimal cost. In tomato fruit we have demonstrated that priming by the chemical β -aminobutyric acid results in long lasting resistance against *B. cinerea*. Priming is associated with epigenetic changes such as DNA methylation which ultimately alter gene expression. Our work has shown that priming seedlings (2 weeks old) results in both long lasting and transgenerational resistance which is not observed when BABA treatments are applied to older plants (12 weeks). This work explores how changes in DNA methylation mark long lasting priming in fruit and explores the hypothesis that young plants display a greater epigenetic imprinting capacity. Using whole genome bisulphite sequencing analysis (WGBS), changes in DNA methylation were observed depending on the timing of priming stimuli. Differentially methylated regions (DMRs) specific to the phenotype of long-lasting resistance have been identified. Our results illustrate that BABA treatment impacts CHH context methylation depending on timepoint of application. Additionally, CHH methylation is revealed to be highly dynamic over time. Furthermore, a transcriptomic analysis on *B. cinerea* infected fruit from early and late BABA treated plants identified differentially expressed genes (DEGs) associated with resistance against *B. cinerea*. By overlapping our DEGs of interest with our resistance associated DMRs we aim to ultimately identify markers of long-lasting priming in tomato fruit which could serve for targets of durable resistance in other cultivars or crop species.

POSTER

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Pathogenicity testing of pseudomonads isolated from epiphytic populations

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Pseudomonas syringae is an economically devastating plant pathogen affecting many Prunus species (1). Cherry canker is caused by *P. syringae* pathovars *syringae* (Pss) and *morsprunorum* race 1 (Psm1) and 2 (Psm2) and can affect leaves (shot-hole), stem (cankers discharging gummy sap) and also fruit (necrosis). Type III secreted effectors and toxins have been implicated as key virulence factors for the pathogens. Members of the leaf surface microbiome (epiphytes) include strains of Pss and Psm that were isolated from healthy plants where symptoms were not observed. However, many of these strains harbour type III secretion systems suggesting they

may be pathogens or have the potential to cause disease. Therefore, several *P. syringae* epiphytic strains were tested for pathogenicity by infiltration into detached cherry leaves (Sweetheart variety), and analysis of symptoms and population counts. Most of the epiphytes caused little or no tissue discoloration or disease symptoms compared to control pathogenic strains. However, population counts showed that several of the epiphytes could grow equally as well, or better, than the pathogens. This suggests the epiphytic strains have optimised in planta growth without causing disease symptoms. How this occurs is unclear and needs further investigation. Crucially, an important question arises around whether these strains could rapidly evolve to cause disease symptoms and analysis of a larger collection of strains and their genomes should enable this.

References: (1) Hulin MT, Jackson RW, Harrison RJ, Mansfield JW (2020). Cherry picking by pseudomonads: After a century of research on canker, genomics provides insights into the evolution of pathogenicity towards stone fruits. *Plant Pathology*; 69:962–978; doi: 10.1111/ppa.13189

Monday | Talk 2.1

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How do we respond to the emergence of new crop disease threats?

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Fungal diseases affect many of the world's most important crops and represent a significant threat to global food security. The forces of globalisation and the climate emergency have combined to increase the frequency with which diseases are spreading across the world. We are studying the pathogenic fungus, *Magnaporthe oryzae*, which is best known as the causal agent of rice blast disease. This disease affects rice cultivation across the world. In the last two decades, however, as demand for rice has grown in sub-Saharan Africa, blast disease has emerged as a very significant threat to rice production. An international project has utilised knowledge of the prevailing blast fungus population to guide a resistance breeding programme to identify the most important resistance genes for deployment. *M. oryzae* is, however, capable of infecting many grass hosts and undergoing host jumps. A relatively recent host jump has led to wheat blast (Brusone) disease in S America. This disease has, however, now spread to Bangladesh and most recently to Zambia. I will present recent work that is aimed at developing durable disease resistance to rice blast in sub-Saharan Africa and an open science initiative that is providing solutions to the emerging threat of wheat blast disease.

References: Mutiga SK et al. (2021). Integrated strategies for durable rice blast resistance in sub-Saharan Africa. *Plant Disease* doi.org/10.1094/PDIS-03-21-0593-FE. zenodo.org/communities/openriceblast/?page=1&size=20. www.openwheatblast.net

Wednesday | Talk 7.3

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A global comparison of fungicide recommendations and what it tells us about their use

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There is poor documentation with regard the types of fungicide used in LIMCs especially with regard small holder farmers. Using data collated from the Plantwise Online Management System we catalogued which fungicides are used in the various regions of the world. There were 87 commercially available active ingredients recorded in the data representing 30 FRAC. The most widely represented FRAC code were the Triazoles (FRAC 3) with 19 active ingredients. Some active ingredients were poorly represented and 16 of the 87 were represented less than 5 times in the whole data set. Regional differences were apparent, FRAC 1 (MBC fungicides) was well represented in South (SA) and South East Asia (SEA) where 29 and 23 % of the records contained this group of chemicals whereas they were rarely used in Latin America and Caribbean (LAC) (9%) and Sub Saharan Africa (SSA) (5%). The Strobilurins were more widely used in LAC (16%) with LAC and SSA

using them in only 3% of cases and almost never recommended in SA. In all regions Mancozeb and Copper salts are the mainstay of disease control. In SSA 55% of all fungicide recommendations contain one or both of these chemicals whereas SA and SEA were at 31% and LAC 26%. The blending of active ingredients is encouraged to prevent resistance but despite this 70% of recommendations from SA contained a single active ingredient. The region which blended most frequently was LAC; half of the recommendations contained two or more active ingredients. Fungicides are generally referred to by tradename only in all regions but LAC and SSA over 70% of recommendations contain the trade name in isolation. The proportion of recommendations containing highly hazardous pesticides were found to be over half in all regions except for LAC.

POSTER

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Network analysis of *Zymoseptoria tritici* transcriptional profiles during infection reveals gene networks involved in pathogenicity

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Zymoseptoria tritici is an important fungal pathogen of wheat. Differences in infection and lifecycle stages between isolates have been linked to differences in gene expression (1). Previous efforts have focussed on generating large-scale sequencing data to identify genes involved in pathogenesis. Much of this work has used differential expression, pairwise comparison or looked at genes in isolation to identify potential candidates involved in disease processes. However, organising these data into co-expression networks can reveal much about the functional organisation of an organism (2). Co-expression networks can be used to identify modules (groups of highly connected genes), annotate uncharacterised genes, and importantly, detect differences in module expression that correlate with phenotypic traits including disease progression. In this study, we apply these methods to publicly available *Z. tritici* data to identify (i) module expression changes during infection, with notable modules peaking in expression at the lifestyle transition from biotrophic to necrotrophic growth, (ii) differences in module expression between strains, with strain Zt10 showing the most divergent expression programme, and (iii) modules whose expression correlates with differences in timing of disease progression, specifically the timing of pycnidia development. Our approach enables identification of modules associated with disease progression and allows us to generate hypotheses about the functions of the genes in these modules, particularly those genes that are uncharacterised. These genes can be prioritised and targeted for experimental validation to confirm their role in disease progression.

References: (1) Haueisen J et al.. Highly flexible infection programs in a specialized wheat pathogen. *Ecology and evolution* 2019, 9, 275–294. (2) Zhang B; Horvath S. A general framework for weighted gene co-expression network analysis. *Statistical applications in genetics and molecular biology* 2005, 4.

POSTER

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Improvement of plant growth and immunity by impediment of MYST histone acetyltransferases

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Part of plant immune responses to pathogens is reprogramming of gene expression. Acetylation of the N-terminal tails of histones by histone acetyltransferases (HATs) and deacetylation by histone deacetylases (HDACs) can regulate transcriptional responses. Arabidopsis HAM1 together with its close homologue HAM2 belong to the MYST-HAT family. According to previous studies, AtHAM1 and AtHAM2 work redundantly to regulate gametophyte development and flowering time. Our results show that the two MYST-HATs interact with distinct set of transcription factors and have different functions. AtHAM1 regulates immunity against *Verticillium dahliae* while AtHAM2 regulates plant growth and immunity against *Pseudomonas syringae* pv. *tomato*. Interestingly, not all plant species have two homologues of MYST-HATs. Tomato (*Solanum lycopersicum*) has a single copy but Brassica (*Brassica oleracea*) has two copies of MYST-HATs, which raise the question if a single copy of MYST-HAT can perform both functions of MYST family. To address this question we have generated mutants of Brassica plants and performed an in silico screen to identify chemical inhibitors of tomato and Brassica MYST-HATs.

Plant health research: working together**Clare TRIVEDI**

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Protecting Plant Health is an important Government priority, leading to economic, social and environmental benefits. Robust evidence, brought together from a wide range of disciplines and perspectives, underpins our risk-based decision making in plant health and is an integral part of the GB Plant Biosecurity Strategy and the Tree Health Resilience Strategy. To ensure that Plant Health policy is driven by evidence, we support both long-term strategic research with more applied responsive research that has been developed in collaboration with others across the UK and beyond. The presentation will provide an oversight of both the scope and content of this research and how it is delivered in partnership.

Exploration of the origin of interspecific oviposition deterrence in *Drosophila***Trisna TUNGADI** (1), Powell G (1, 4), Shaw B (1), Farman D (2), Bray D (2), Harte S (2), Hall D (2), Wijnen H (3), Fountain MT (1)

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The invasive fruit pest, *Drosophila suzukii*, lays its eggs in fruit before harvest causing fruit collapse and significant economic loss (Asplen et al., 2015). Soft and stone fruit production in the UK and worldwide are severely affected by *D. suzukii* infestation, leading to significant economic losses. Currently, control method relies primarily on foliar insecticide applications, but this is not a sustainable long-term solution due to regulatory restrictions, incompatibility with integrated pest management programmes for control of other pests, and potential insecticide resistance. We showed previously that *D. suzukii* females were deterred from ovipositing on artificial media or fruit where eggs have been laid by *D. melanogaster*, but not where eggs had been laid by conspecific females (Shaw et al., 2018). A series of laboratory choice experiments on artificial media have now been done to elucidate the mechanism of oviposition deterrence and the lifestage involved. Presence of the larval stage of *D. melanogaster* exerted a strong oviposition deterrent effect on *D. suzukii*, and the cuticular hydrocarbons (CHCs) of *D. melanogaster* were considered to be potential deterrents. Hexane extracts of larvae and adults of both *D. melanogaster* and *D. suzukii* were analysed by GC-MS, and the compositions of the CHC's of larvae were found to be similar to those of the conspecific adults, although present in much lower quantities. Furthermore, the CHC profiles of the two species were confirmed to be markedly different, providing a basis for intraspecific discrimination. However, in laboratory bioassays neither natural CHC extracts from *D. melanogaster* nor blends of the synthetic CHC's specific to *D. melanogaster* consistently deterred *D. suzukii* from laying eggs. The significance of these results for future work is discussed. The potential to utilise these findings to improve *D. suzukii* control methods is explored.

References: Asplen, M.K et al., (2015). *J. Pest. Sci.* 88 : 469-494; Shaw, B. et al., (2018). *Pest Manag. Sci.* 74 : 1466-1471

Identifying candidate resistance genes against acute oak decline and oak powdery mildew using transcriptome sequencing**Thomas E WELCH**, Kettles G

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The genomes of woody tree species frequently exhibit expansion and diversification of gene families related to disease resistance, such as receptor-like kinases (RLKs) and nucleotide-binding leucine-rich repeat (NLR) proteins. Such expansion has been observed in the genomes of Eucalyptus, Citrus, and most recently Oak, leading to speculation that large cohorts of resistance (R)-genes are an important facet of the long life-span of woody perennials (!). The role of such gene families in immunity is well studied among model and crop plants, but not in trees; a significant knowledge gap considering their ecological importance and the increasing threat trees face from invasive diseases. English Oak (*Quercus robur*) is under threat from diseases like Oak powdery

mildew (OPM) and Acute oak decline (AOD) in the UK and parts of Europe. Exapted resistance to their causative pathogens exists in the *Q. robur* population, but no *Q. robur* R genes have been characterised (2). Our project aims to identify R-genes that contribute to successful immune responses to OPM and AOD. *Q. robur* seedlings resistant and susceptible to AOD and OPM were identified using novel and adopted screening assays respectively. For AOD, many seedlings clear bacterial infection almost completely, whilst in a smaller proportion of plants AOD bacteria proliferate. For OPM, we find that significant differences in resistance exist in oak seedlings sourced across several UK provenances. We also confirm Bartholome et al's (2019) findings, that a large number of oaks are resistant to OPM infection at the seedling stage. Differences in transcriptional responses between resistant and susceptible plants is currently being assessed using RNA-seq. Our most recent progress will be reported.

References: (1) Plomion et al. 2018. Oak genome reveals facets of long lifespan. *Nature Plants*. (2) Bartholomé, J et al, 2019. The genetics of exapted resistance to two exotic pathogens in pedunculate oak. *New Phytologist*.

Wednesday | Talk 8.3

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Real risks and looming threats: the increasing array of tree health problems

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Establishing the UK risk register and employing the Chief Plant Health Officers were milestone events in assuring political recognition that invasive alien pests and pathogens are significant and real challenges to cultivated and natural ecosystems in Britain. Although the problems caused by Dutch Elm Disease, Ash Dieback and *Phytophthora ramorum* received considerable media attention, many other potentially damaging pathogens are known, including some already present though less well known in Britain and some established elsewhere in Europe. In this talk, I will illustrate the threats posed by some of these organisms, based on experiences in other regions. Examples will include canker stain disease of *Platanus* species, pine pitch canker, pine wilt nematode and *Xylella fastidiosa*. Less well-known problems, in media terms, already established and active in Britain include, amongst many others, *Phytophthora cinnamomi*, *Phytophthora lateralis*, sweet chestnut canker (*Cryphonectria parasitica*), box blight (*Calonectria pseudonaviculata*, *C. henricotiae*) and the recently reported *Phytophthora pluvialis*. The reason for these invasions is clear: all revolve around human activities. Demand for novel ornamental plants shows no sign of abating. Global trade has taken a shock from the covid-19 pandemic, but will recover and continue its relentless growth thereafter. Climate change will impact on pathogen incidence and severity, with decreases in some regions, counterbalanced by increases in others. Serious political will is required to address the causes of invasions by alien pests and pathogens, as well as the potentially disastrous consequences of climate change.

POSTER

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Dynamic changes of the Prf/Pto tomato resistance complex following effector recognition.

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A common plant pathogen virulence strategy is the secretion of effector proteins inside the host cell, with the goal of compromising plant immune responses. In turn, plants have evolved nucleotide-binding leucine-rich repeat (NLR) immune receptors that recognise pathogen-derived effector proteins and initiate effector-triggered immunity (ETI). However, the molecular mechanisms that link NLR mediated effector recognition and downstream signalling are not fully understood. By exploiting the well-characterised tomato Prf/Pto NLR resistance complex, we identified the 14-3-3 proteins TFT1 and TFT3 as interacting partners of both the NLR complex and MAPKKKa. Moreover, we identified the helper NRC proteins (NLR-required for cell death) as integral components of the Prf/Pto NLR recognition complex. Notably our studies revealed that TFTs and NRCs interact with distinct modules of the Prf/Pto complex and, following effector recognition, dissociate to facilitating downstream signalling. Thus, our data provide a mechanistic link between activation of immune receptors and initiation of downstream signalling cascades.

Diversity, pathogenicity and stability of *Pseudomonas* population over distance, time and environment

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Pseudomonas syringae is a widespread bacterial pathogen of a variety of plant species, cherry included. Despite the advances in disease control, *P. syringae* remains of great concern to the security of cherry production. Some *P. syringae* strains, such as *P. syringae* pathovars *syringae* (Pss) and *morsprunorum* (Psm), are known pathogens which infect and cause canker symptoms on cherry trees whilst some *P. syringae* bacteria proliferate silently as epiphytes without causing symptoms. Epiphytic *P. syringae* populations also play a potential role in the emergence of outbreaks of canker in cherry. In the previous sampling across cherry orchards around the UK a diversity of non-pathogenic *P. syringae* strains were isolated from the leaf and shoot surface of undiseased trees. Intriguingly, these non-pathogenic epiphytes were extremely widespread and display the hallmarks of a pathogenic strain, although they had not been described as a pathogen in prior studies. Moreover, interesting regional variations in *P. syringae* populations were observed. Extending the previous work, the current study further investigates the diversity, heterogeneity and pathogenicity of environmental *P. syringae* in cherry trees via multi-year, multi-site samplings from orchards in four regions in the UK. In addition, as varied levels of resistance to *P. syringae* has been found in wild cherry, the sampling also includes the wild cherry in the woodlands nearby. In the May and September samplings in 2021, a total of 6000 bacterial strains have been isolated from leaves and shoots samples. A multiplex PCR method has been devised to identify the potentially pathogenic *Pseudomonas* bacteria. By using repeated sampling and genome sequencing of these environmental isolates, we aim to enrich the insights on the temporal and spatial variation in the epiphytic populations of pathogenic and potentially pathogenic *P. syringae* in cultivated and wild cherries.

Pyrenopeziza brassicae: azole fungicides sensitivity screening and investigation of molecular mechanisms of insensitivity within CYP51 gene

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Light leaf spot (LLS) of Brassicas, caused by *Pyrenopeziza brassicae*, is amongst the most damaging diseases of winter oilseed rape (OSR) (*Brassica napus*) and a significant threat to Irish crops. As not much is known about the epidemiology of the disease and no fully resistant OSR cultivars are available, the control relies upon the use of fungicides, with sterol 14 α -demethylase (CYP51) inhibitors (azoles), representing the main class of fungicides used. A shift in the sensitivity towards azole fungicides has been already documented for different European *P. brassicae* populations, including Ireland. Therefore, to confirm the presence of strains with reduced sensitivity to azoles and to determine the degree of sensitivity for the Irish populations, we aimed to assess the sensitivity of *P. brassicae* isolates from 2019-2020 to tebuconazole and prothioconazole-desthio and confirm the presence of the resistance mechanisms within the CYP51 gene. The screening *in vitro* of three Irish representative populations established in 2019 and two extensive collections of *P. brassicae* isolates revealed a change in sensitivity to azoles for the Irish populations. Consequently, the CYP51 gene and its promoter region, targeted by this class of fungicides, were genotyped for the populations investigated. Two substitutions were identified within CYP51 (G460S and S508T) and an insert of different sizes in the promoter region. Compared to wildtype isolates, those carrying G460S or S508T were less sensitive to tebuconazole and prothioconazole-desthio, and when the alterations were present with an insert, the reduction of sensitivity to azoles was increased. A glasshouse experiment was developed to confirm the reduction of sensitivity *in planta*. Although the fungicides showed high efficiency, the results support using the azoles in mixture with fungicides having a different mode of action, such as QoI/SHDI fungicides, to control LLS and to delay the deployment of insensitivity.