ECPP 2026

Tuesday, 8 September

All talks & refreshment breaks take place in JIC Conference Centre, Norwich Research Park, Colney Lane, Norwich, NR4 7UH, UK

09:30	Registration desk open: JIC Conference Centre Foyer
10:45	Welcome and Introduction - **Helen Cockerton,** Housekeeping **- Louise Gathercole.** Big Biological Question (BBQ) competition opens
Session A (Chair: Saskia Hogenhout)	
10:55	**Sophien Kamoun** (The Sainsbury Laboratory, Norwich, UK) - A tribute to Eva Sansome.
11:05	Invited Speaker: **Katherine Denby** (Univ. York, UK) - *Re-wiring defence networks to engineer disease resistant crops.*
Session B (Chair: Petra Boevink)	
11:30	**Litsa Ampntelnour** (Warwick Univ, UK) - *The role of ATP-dependent chromatin remodelling complexes in regulation of plant immunity against Fusarium oxysporum.*
11:50	**Ohad Roth** (Weizmann Institute, Israel) - *Plant pathogens degrade TIR-derived signals to suppress plant immunity.*
12:10	**Hayden Burdett** (Univ. Queensland, Brisbane, Australia) - *Self-association allosterically configures the catalytic-site of plant NLR TIR domains.*
12:30	**Lunch**
13:30 - 14:30	**Poster Session**

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Session C (Chair: Trisna Tungadi)	
14:30	**Wei Wang** (James Hutton, Dundee, UK) - *The RXLR–EER Motif is a Molecular Switch that Determines an Unconventional Secretion Pathway*.
14:50	**Mar Marzo** (JIC, Norwich, UK) - *Lineage-Specific Expansion and Diversification of Cathepsin B Effectors in Aphids.*
15:10	**Athira Menon** (Univ. Oxford, UK) - *Pseudomonas syringae inhibits the plant glycosidase PR3 to promote infection.*
15:30	**Refreshment break**
Session D (Chair: Katherine Denby)	
16:00	**Maria Bogino** (SLCU, Cambridge, UK) - *Intracellular Trafficking as a Target of Oomycete Virulence: Functional Characterisation of the REX3 Effector*.
16:20	**Jade Smith** (Rothamsted Res, Harpenden, UK) - *Epigenetic regulation of effectors secreted by Fusarium graminearum.*
16:40	**Chi-Hsin Chang** (Academia Sinica, Taiwan) - *The phytocytokine CAPE9 and its receptor CAPER1 function on plant systemic stomatal immunity*.
17:00 - 18:00	**Poster Session**
18:00	**Sam Mugford** - *Pint of the living dead: brewing with phytoplasma-infected hops. Voting for the Big Biological Question (BBQ) opens*
18:30	**BBQ Aula area of conference centre**
19:30	**Big Biological Questions (BBQ) winner announced**
21:30	**Depart or beer at the Rec (next door to the conference centre)**

Plant Pathology 2026

Wednesday, 9 September

All talks & refreshment breaks take place in JIC Conference Centre, Norwich Research Park, Colney Lane, Norwich, NR4 7UH, UK

08:00	**Registration desk open: JIC Conference Centre Foyer**
Welcome (Chair : Helen Cockerton)	
09:10	Welcome and Introduction - **Helen Cockerton**, Housekeeping - **Louise Gathercole**.
09:20	Directors Address: **Cristóbal Uauy,** Director, John Innes Centre
09:30	**Presidential Address: Saskia Hogenhout** - *Building resilience to insect-vectored plant pathogens*
10:00	KEYNOTE**: Vivianne Vleeshouwers** (Wageningen Univ. Netherlands) - *Integrating EvoMPMI and Effectoromics for Durable Disease Resistance in Potato.*
10:30	**Refreshment break**
Session 1 (Chair : Adrian Fox)	
11:00	Invited: **Olaf Czarnecki** (KWS, Germany) - *Tradition and Innovation: Integrated Research and Breeding for Sugar Beet Pest and Disease Resistance*.
11:30	**Lennart Wirthmueller** (PBP, Halle, Germany) - Profiling substrates of ADP-ribosylating pathogen effectors by proteomics – novel modification types and targets.
11:50	**Doron Teper** (Vulcani Institute, Israel) - *Tissue-Specific Experimental Evolution Reveals Adaptive Trade-Offs in the Plant Vascular Pathogen Clavibacter michiganensis.*
12:10	**Dilantha Fernando** (University of Manitoba, Canada) - *Disabling Susceptibility (S) Genes: A Novel Strategy for Broad-Spectrum Disease Resistance in Canola when two pathogens coinfecting shapes disease dynamics*
12:30	**Lunch & Poster Session (J Colhoun Poster Prize session)**

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Session 2 (Chair : Vivianne Vleeshouwers)	
14:00	KEYNOTE: **Ryohei Terauchi** (Kyoto Uni, Japan) – *Rice genomics to increase resistance to the rice blast fungus* Magnaporthe oryzae.
14:30	Invited: **Adriaan Verhage** (Rijk Zwaan, Netherlands) - *Genome-enabled lettuce breeding for increased resistance.*
15:00	**Reem Aboukhaddour** (AgriFood, Canada) - *Starship-mediated evolution of virulence and effector mobility in tan spot (Pyrenophora tritici-repentis).*
15:20	**Juan Carlos De la Concepcion** (Univ. Tubingen, Germany) - *Dissecting the structural mechanisms of plant invasion by fungal pathogens with Cryogenic Electron Tomography.*
15:40	**Refreshment break**
16-10-18:00	**SESSION 3: PH Gregory Prize (Chair : Helen Cockerton)** **12 minute slots; 10 minute talk & 2 minute questions**
	Anna Dickinson (Cambridge Univ, UK) - *Reading the Host: How Host Signals Coordinate Effector Expression in the Beet Cyst Nematode.*
	Yao Fu (Dundee Univ., UK) - *Identification and Characterisation of Novel Barley Resistance to Aphids.*
	Chloe Harper (Oxford Univ, UK) - Oxidative stress tolerance in the plant pathogen Pseudomonas syringae.
	Cecilia Longoni (Imperial College, London, UK) - *Engineering immune activation from immune suppression using pathogen effectors as synthetic biology parts.*

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SESSION 3 Continued: PH Gregory Prize – Chair 12 minute slots; 10 minute talk & 2 minute questions	
	David McLean (Univ Dundee, UK) - *Caught Red Handed: Phytophthora infestans targets red light signalling to suppress systemic acquired resistance.*
	Daniel Cincura (Imperial College London, UK) - *From AlphaFold prediction to experimental validation of plant protein interactions*
	Siyu Song (University of East Anglia, UK)- *Simultaneous spatial visualisation of host gene expression and bacterial colonisation in plant roots using PHYTOMap.*
	João Paulo Alves Plácido (Copenhagen, Denmark) - *Endomembrane trafficking disruption suppresses NLR-mediated hypersensitive response via ER stress.*
	Rebecca Thompson (Cambridge Univ, UK) - *Phytophthora infestans suppresses host immune responses by targeting two unrelated helper NLRs*
18:15	**Gather for coaches**
18:30	**Coaches depart to Dunston Hall**
19:00	**Conference dinner at Dunston Hall**
22:15	**Coaches depart for return to JIC**

Plant Pathology 2026

Thursday, 10 September

8:00	**Registration Desk Open**
SESSION 4 (Chair : Ryohei Terauchi)	
9:15	Welcome and Introduction - **Helen Cockerton**, Housekeeping - **Louise Gathercole.**
9:20	KEYNOTE: **Gitta Coaker** (UC Davis, California, USA) *From Recognition to Response in Plant Immunity.*
9:50	Invited Speaker: **Tolga Bozkurt** (Imperial College, London, UK) – *Decoding Immune Recognition and Pathogen Evasion in Plants*
10:10	Invited Speaker: **Cian Duggan** (Resurrect Bio, London) - *Resurrect Bio: Helping crops defeat disease*
10:30	**coffee break**
SESSION 5 (Chair: Saskia Hogenhout)	
11:00	**Diane Saunders** (John Innes Centre, Norwich, UK) - *Leveraging untapped diversity in ancient landraces to tackle a major breakdown of yellow rust resistance in the UK.*
11:15	**Sanu Arora** (John Innes Centre, Norwich, UK) - *Connecting the Dots: Pan-Genome graph reveals structural variation underlying disease resistance in pea.*
11:30	**Rachel Wells** (John Innes Centre, Norwich, UK) - *Novel approaches to oilseed rape protection – moving reduced susceptibility and targeted pest control and from lab to field.*
11:45	**Fabian E. Vaistij** (York Univ., UK) - *Effector-driven defence repression by IAA de-activation.*

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Plant Pathology 2026

Thursday, 10 September

Session 5: Continued	
12:00	**Urooj Fatima** (Kaust, Saudi Arabia) - *Conserved rust fungal pathogen ligands trigger non-host disease resistance in cereal crops.*
12:15	**Federica Locci** (Cologne, Germany, Parker lab) - *Beyond local cell death: emerging roles of plant TIR-domain proteins.*
12:30	**Lunch and Poster session**
SESSION 6 (Chair: Gitta Coaker)	
14:00	Invited: **Adrian Fox** (Fera, York, UK) – *Tomato brown rugose fruit virus: what is the biological relevance of your detection?*
14:20	Invited: **Sergio de la Fuente van Bentem** (ENZA Zaden, Netherlands) - *HREZ confers high resistance to the tomato brown rugose fruit virus in tomato.*
14:50	**Boyoung Kim** (Research Institute of Agriculture and Life Sciences, Seoul National University, Republic of Korea) - Paracidovorax citrulli employs multiple effectors to suppress NbPtr1-triggered cell death in Nicotiana benthamiana
15:10	**Mauricio Contreras** (Tubingen Univ, Germany) - *A conserved structural logic underlies sensor–helper NLR communication in the NRC immune receptor network.*
15:30	**coffee break**
SESSION 7 (Chair: Helen Cockerton)	
16:00	Prize giving and announcements of Presidents
16:15	RKS Wood Prize Talk: **Nick Talbot** (Sainsbury Laboratory, Norwich, UK) - *Breaking and Entering - The biology of plant infection by the blast fungus.*
17:00	**The Rec (next door to the conference centre) is open for congratulating the award winners and finding colleagues for dinner**

Plant Pathology 2026

Friday, 11 September

9:00	Registration Desk Open
9:15 - 12:00	Three Parallel sessions
Parallel session 1: Workshop: Launching Ventures: Strategy, Story, and Scale.	
Room: G36/G37 Wilkins/Franklin	
9:15	Introductions: **Cian Duggan** (Chair) and **Saskia Hogenhout**
9:30	**Ross Hendron** (Wild Bio, Oxford) *Wild Bio: Evolving seeds for a changing planet*.
9:45	**Rosario Campilongo** (PfBio, Norwich) - *PfBIO: Sifting Nature for Agricultural Allies.*
10:00	**James Canham** (GetGenome, Norwich, UK) *GetGenome: A mission-driven venture enabling global research capacity*.
10:15	**Cian Duggan** (ResurrectBio)
10:30	**Coffee break**
11:00	Panel session: **Cian Duggan** (ResurrectBio, Chair), **Ross Hendron** (WildBio), **Jake Malone** (PfBIO founder), **Ashima Wadhawan** (EngBio Accelerator Programme, Biotech Consultant), **James Canham** (GetGenome), **Dr Sarah Garland** (Triple Helix)
Ask our experienced panellists about the stories behind their ventures—covering funding, team-building, intellectual property, mission, governance, timelines, lessons learned, and how to get started while balancing a research career—as well as any other questions you may have.	

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Friday, 11 September

Parallel session 2: Green-shielding our food security: Endophyte discovery and applications in plant pathology	
Room: Main Auditorium	
9:15	**David Collinge** (Univ. Copenhagen, Denmark) - *Fungal endophytes for disease control in cereals.*
9:30	**Richard Johnson** (Bioeconomy Science Institute, New Zealand) - *Establishment of functional symbioses between Epichloë endophytes and hexaploid wheat (Triticum aestivum).*
9:45	**Gustaf Fredell** (The James Hutton Institute) - *Utilising Native Endophytes for Pathogen Inhibition in Barley*
10:00	**Tingyu Duan** (Lanzhou University, China) - *Endophyte symbiosis reduces disease severity and restructures the phyllosphere bacterial community of perennial ryegrass*
10:15	**Nyambura Mwangi** (Harper Adams University) - *Festulolium–Epichloë symbiosis: Suppressing stubby root nematodes and delivering nematotoxic plant metabolites*
10:30	**Coffee Break**
11:00	**Carolyn Young** (North Carolina State University) - *Invisible Defenders: Harnessing Endophytes for Sustainable Plant Protection*
11:15	**Van Schepler-Luu** (The International Rice Research Institute, Philippines) - *Genetic links between rice immunity, phyllosphere microbiome assembly and bacterial blight resistance*
11:30	**Lorena I Rangel** (James Hutton, Dundee, UK) - *EndoReg: drawing consensus on future governance of UK endophyte-enabled crops*
12:00	**Session Ends and Lunch**

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Friday, 11 September

Parallel Session 3: Surveillance and Decision Support in Action	
Room: G34/G35 McClintock	
9:15	**John Clarkson** (University of Warwick) INVITED SPEAKER - *Enriching pathogens: development of a commercial diagnostic for Fusarium basal rot risk assessment and management in onion*
9:45	**Jade van Wijk** (Earlham Institute, UK) - Airborne cereal pathogen surveillance using AirSeq
10:00	**Levente Kiss** (University of Southern Queensland) - *Powdery mildews everywhere: Where do all the new species come from?*
10:15	**Richard Oliver** (University of Nottingham) - *Out of sight and out of mind; fungicide resistance monitoring in low- and middle-income countries.*
10:30	**Coffee Break**
11:00	**Kyran Moloney** (SAC Consulting) INVITED SPEAKER - *How the UK Seed Potato Industry is Responding to a Changing Potato Leaf Roll Virus Challenge*
11:30	**Yuk Woon Cheung** (The University of Dundee) - *Genetic analysis of potato late blight R genes in differential sets*
11:45	**Rita Domingues Carvalho** (John Innes Centre) - Gene expression polymorphism linked to virulence diversification in wheat yellow rust
12:00	**Lunch**
13:00	**Ross Haffenden** (Optigene) INVITED SPEAKER - *Translating the complexity of plant disease understanding to produce on-farm, real-time diagnostic tools that enable large scale positive impact*

Plant Pathology 2026

Friday, 11 September

Parallel Session 3: Surveillance and Decision Support in Action	
Room: G34/G35 McClintock	
13:30	**Antonio Deidda** (University of Sassari) - *Detection of Acute Oak Decline-associated bacteria in declining cork oak trees in Sardinia (Italy)*
13:45	**David Studholme** (University of Exeter) - *PhytoBacExplorer: A Genomic Platform for Plant Pathogen Population Genomics, Surveillance and Diagnostic Development*
14:00	**Yue Lin Loh** (Fera Science Limited) - *Targeted intact whole genome sequencing as a diagnostic tool to indicate virus viability*
14:15	**Moozhan Serpoush** (Leibniz Institute of Plant Genetics and Crop Research) - *Rapid Seedling-Based Screening of Fusarium Root Rot Resistance in Wheat Using Automated Imaging*
14:30	**Morgan Wodring** (RSB PHUG Studentship) - *Using bees as surveillance sentinels for pollen-transmitted viruses: detection of a novel nepovirus isolated from Tilia in hive debris and pollen*
14:45	**Jack Rich** (University of Reading) *A Likelihood Framework for Estimating Infection Efficiency in Inoculation Experiments*
15:00	**Gosia Jedryczka** (Polish Academy of Sciences, Poznan) *Genomes of the pathotypes of Plasmodiophora brassicae causing clubroot on winter oilseed rape in Poland*
15:15	**Discussion & Close**

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POSTER INDEX

Tuesday 8 September — ECPP 2026 Poster Session

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2 Valeria Denisse Palma Encinas — *Contrasting physiological and transcriptomic responses highlight cultivar-specific tolerance to Peronospora variabilis in cañahua and quinoa*

3 Miguel Angel Corrales Gutierrez — *Where is FHB resistance in Oats? An exploratory study with Fusarium culmorum*

4 Sarah Thorne — *The Protective Role of Silicon in Grasses Against Fungal Pathogens Depends on Infection Mechanism*

5 Jay K Goldberg — *The desert thorn apple (Datura discolor) genome reveals an unexpected contraction of the NRC immune receptor network*

6 Gracie Thomas — *Towards structural and functional characterisation of lectins from the twayblade orchid (Neottia ovata)*

7 Trisha McAllister — *Bacterial hormone mimicry in potato blackleg disease*

8 Junli Wang — *Spatiotemporal dynamics of NRG1-mediated cytoplasmic and nuclear calcium signaling in TNL-ETI*

9 Hazel McLellan — *Identification of MARVELlous Protein Markers for Phytophthora infestans Extracellular Vesicles*

10 Federico Gabriel Mirkin — *Engineered bacterial effector allows for ubiquitin-independent degradation of custom targets*

11 Alba Pacheco-Moreno — *Decoding Peronospora viciae: Do repeats and genome size drive virulence?*

12 Evangelia Niki Pentari — *Investigating Histone Acetylation Dynamics During Plant Immune Responses*

13 Nuria Fontdevila Pareta (1) — *Insights into insect vectors and SBR-associated pathogens in Swiss sugar beet and potential reservoir crops*

14 Tao-Ho Chang — *RNP-Based CRISPR/Cpf1 Gene Editing Platform for Rapid Isolation and Characterisation of Fusarium oxysporum Mutants*

15 Jade Bleau — *Investigating the role of the Myzus persicae effector complex Mp1-Mp58 in targeting host cellular trafficking*

16 Diana Gómez De La Cruz — *Leveraging molecular mimicry of a pathogen virulence target to engineer multiple disease resistance by an NLR*

17 Mishi Vachev — *Identification and validation of candidate genes for resistance to mildew diseases in pea*

18 Chongjing Xia — *An AlphaFold3-predicted rhizobia-legume interactome identifies new factors required for symbiotic accommodation*

19 Yi Liu — *A BDBBX21–BDSK1 regulatory module connects shikimate-derived metabolism with salicylic acid-associated immunity in bamboo*

20 Thomas Waksman — *Structure and Mechanism of a Conserved Aphid Effector Complex*

21 Xinyi Liu — *Proteogenomic insights into transposable elements of Blumeria hordei*

22 Wanxin Chen — *Mutation of Sucrose: Fructan 6-fructosyltransferase (6-SFT) in Hexaploid Wheat Reduces Susceptibility to Fungal Disease without Compromising Growth or Yield*

23 Sebastian Samwald — *Physical barrier formation to protect the root vasculature from pathogen entry*

24 Katie Hawkins — *Exploiting Wheat-Wild Relative Introgression Lines as a Source of Barley Yellow Dwarf Virus (BYDV) Resistance*

25 Hannah Blyth — *Heat mobilises the fungal accessory genome and remodels lipid metabolism in the wheat–Zymoseptoria tritici interaction*

26 Mariama D. Carter — *Nutritional warfare: effector targeting of nutrient deficiency pathways in plants*

27 Mikail Bayrak — *Comparative genomics and cross-pathogenicity in brassica-infecting Fusarium oxysporum strains*

28 Nicolas Trenk — *Resolving the century-old mystery of Fusarium wilt resistance in pea*

29 Matteo Gravino — *AI-guided discovery of plant resistance genes*

30 Cesar Franco Padilla-Castro — *Identifying drivers of bud rot disease incidence in oil palm: a work in progress*

31 Zsuzsanna Revesz — *From mechanism to symptoms: effector-mediated reprogramming of development turns plants into zombies*

32 Eva Anna Burgunder — *Future climate conditions increase severity of soilborne diseases in table beets*

33 Nanne W. Taks — *Mapping the proteome of rare PRIMER cells in plant immunity*

34 Valentina León — *NLRome characterisation of potato cv. Spunta reveals an expanded NRC4 helper clade*

35 Maria Serrano Hernandez — *Developing an experimental system to study Starship Transposon-Mediated Horizontal Gene Transfer in Fungal Wheat Pathogens*

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37 Lisa Humbert — *Silencing the Rust: Virus-Induced Gene Silencing (VIGS) for functional genetic studies in Asian Soybean Rust*

38 Victor Soria-Carrasco — *The Entomology and Insectary Platform at the John Innes Centre: Advancing Research on Plant–Invertebrate–Pathogen Interactions*

39 Nathan J Williams — *HMAking Sense of Tandem Kinase Proteins as Plant Immune Receptors*

40 Sayali Bakore — *Fungal Endogenous Ethylene Signalling Machinery Plays a Key Role in Pathogenesis in the Cereal Blast Fungus*

41 Łukasz Florkowski — *NOSH-A, a multicomponent signalling donor, primes systemic acquired resistance in potato against Phytophthora infestans*

42 Juan Martin Azcue — *A singleton integrated-domain NLR scaffold enables modular plant immune receptor design*

43 Jack Yu — *The Effect of Temperature on Xanthomonas ROS Tolerance*

44 Benjamin Tremblay — *Cell-state-specific cis-regulatory logic of pattern-triggered immunity with csRNA-seq and snMultiome*

45 Joey Lau — *From gene to field: accelerating crop trait discovery and validation, illustrated by Wild Bioscience's WB-01 soybean trait*

46 Vangeli Geshkovski — *Chromatin regulation during plant immune responses*

47 Eleftheria Seira — *A buttery smell makes plants strong: Volatile-Mediated Priming of Resistance against Root Pathogens*

48 Natalia Arango Lopez — *Non-host resistance genes – new sources for durable rust resistance?*

49 Davide Danzi — *Thermal modulation of virulence in the Xanthomonas-pepper interaction*

50 Hsuan Pai — *Visualising Plant-Microbiome interactions at single-cell resolution using PHYTOMap*

51 Jung Kum Park — *Bacterial community profiles associated with Kimchi cabbage cultivated in South Korea*

52 Isabel Faci — *Rapid response to major yellow rust resistance breakdown in UK wheat*

53 Boyoung Kim — *Paracidovorax citrulli employs multiple effectors to suppress NbPtr1-triggered cell death in Nicotiana benthamiana*

54 Sarah Amy Blackburn — *Characterisation of quantitative Verticillium wilt resistance in hop using GWAS*

55 Fiona Fitchett — *Harnessing compost microbes for new crop protection products against foliar diseases*

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Wednesday 9 September — J Colhoun Prize Poster Session

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3 SAFDI Nour El Houda — *Shotgun Metagenomic Characterization of Rhizosphere Microbiomes in Opuntia Ecotypes*

4 Anna Narduzzo — *Dissecting Plant-Microbe Interactions in Grapevine Trunk Disease: a genotype-focused approach*

6 Alice McCallister — *Enhancing Genetic Resistance to Downy Mildew in Pea*

7 Gaia Galiberti — *Molecular basis of higher-order septin assembly during infection by the blast fungus Magnaporthe oryzae*

8 Sheetal — *HAG5/HAM2 a tool to engineer resilient crops?*

9 Amber Gentle — *HIPP43 interacts with immune response proteins and may be targeted to p-bodies by blast effector PWL2*

10 Harry Aston — *Improving crop yields through mycovirus-mediated resistance*

11 Theresa Staps — *Coordination of Xanthomonas secretion systems during plant disease*

12 Cesaree Morier-Gxoyiya — *Modelling environmental suitability of wheat stem rust in the UK: temperature and leaf wetness responses of Puccinia graminis f. sp. tritici*

13 Julia Forsbacka — *RootSock: A Microflidic Platform to Study Pathogen-Root Interactions*

14 Nick Eilmann — *AI-Guided Immune Receptor Discovery and Engineering*

15 Harry Meades — *Providing an Alternative Approach to Disease Management via Engineered Biocontrols*

16 Qijun Liu — *Quantifying early immune signalling at scale using BY-2 cell packs*

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18 Silvia Favia — *Phytoplasma-induced pectin remodelling in sieve elements: a possible trade-off between defence and phloem mass flow*

19 Samuel Bruty — *Mendelian Mishaps: How breeding has shaped the rhizosphere microbiome and disease resistance in pea.*

20 Enrico Jugadora — *Transcriptomic profiling of the barley fungal pathogen Ramularia collo-cygni reveals virulence-associated secreted enzymes and candidate effector proteins*

21 Heike Beukes — *Branch invaders: Investigating the Botryosphaeriaceae in South African avocados*

22 Sougata Saha — *Investigation of the Role of Cytokinin Biosynthesis and Degradation Pathways in pathogenesis of Pyrenopeziza brassicae*

23 Junior Lusu Kika — *Opposing transcriptional programs define pre-parasitic activation and sustained parasitism in Meloidogyne enterolobii*

24 Tanicha (Fah) Duangta — *Do plants recognise Aphid Chitin? Functional Analysis of CERK1 and LYR4 in Medicago truncatula*

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26 Xiaoxue Xu — *Rachis tip dieback: a phenology-driven, multi-pathogen disease of macadamia racemes*

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28 Sophie Powell — *Elevated CO_2 Under Climate Change Affects the Metabolite Profiles of Quercus robur Leaves.*

29 Feixue Liao — *Engineering Gene Regulatory Networks to Design Disease Resistant Lettuce*

30 Gregory Knight — *Frustration guided design of plant TIR domains to introduce ground up functionality.*

31 Gaurav Adhikari — *A harmonized annotation resource of 305 Fusarium genomes prioritizes conserved cytoplasmic effectors for resistance breeding*

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36 Longfei Cui — *Stress and Hunger Drive Pathogen Survival at the Host Interface: Gene Expression and Regulation in Powdery Mildew Haustoria*

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40 AmirAli Toghani — *AI-guided discovery of atypical protein assemblies*

41 Andrea Vadillo-Dieguez1 — *HopBZ1, a novel Type III Effector Protein in Pseudomonas syringae confers virulence in plants using two enzymatic domains*

42 Mpho Matsetela — *Development of molecular markers for rapid identification and detection of macadamia husk rot pathogens*

43 Naina Korotania — *Development of Phage therapy to treat Ash canker*

Thursday 10 September — Main Poster Session

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2 Christian Gäele NEMBOT FOMBA — *Modelling Cocoa-Phytophthora megakarya (causal agent of the black pod disease) metabolic interaction to weaken plant-host compatible relationship*

3 Anna Pedroncelli — *Silent but present: do asymptomatic grapevines contribute to Flavescence dorée spread and which tissues best reveal phytoplasma infection?*

4 Deborah Schönegger — *RPN10 paralogs as potential resistance modulators in apple*

5 Kwang-Hyung Kim — *A Generic Multiplication–Dispersal Modeling Platform for Predicting Diverse Bacterial Plant Diseases*

6 Mattia Tabarelli — *Visible effects, invisible helices: NMR Insights into SAP11CaPm*

7 Zhi-Yuan Chen — *Reducing aflatoxin contamination in maize through host induced gene silencing*

8 Lavinia Carlini — *Hijacking the Host: Do SAP05-RPN10 Interactions Shape Phytoplasma Susceptibility in Apple?*

9 Ayesha Senanayake — *One crop disease, two causal agents, and both developing resistance to registered fungicides: Changes in mungbean powdery mildew populations in Queensland, Australia*

10 Sam T. Mugford — *Aphid cathepsin B effector CathB6 targets the MORF–GUN–GLK axis to suppress SA immunity and sustain photosynthetic nuclear gene expression.*

11 Kara Boyd — *Two peas in a pod? Identification of allelic resistances to downy mildew in pea.*

12 Ashleigh Holmes — *Microbiome responses to Soil Amendments in Potato systems*

13 Hana Azuma — *Viral manipulation of aphid behaviour: cucumber mosaic virus has differential effects on specialists versus generalist aphids*

14 Henriette Laessle — *Cross-kingdom activity of diverse NLR immune receptor N-terminal signalling domains*

15 Susan Breen — *Investigating why PAMPs associate with EVs during infection*

16 Yongju Huang — *Challenges of screening for host resistance against the light leaf spot pathogen Pyrenopeziza brassicae in oilseed rape*

17 Adam Bryning — *Not resting on our laurels – Findings from over 10 years of surveillance for Xanthomonas arboricola pv. pruni in the UK*

18 Sohini Deb — *The extrahaustorial membrane in the barley/powdery mildew fungal interaction depends on plant lipid transfer*

19 Teniade Adeyemo — *Understanding patterns of Leptosphaeria maculans and Leptosphaeria biglobosa ascospore release and oilseed rape cultivar resistance*

20 In Woong Park — *Novel virulence proteins of the Gram-positive bacterium Clavibacter michiganensis responsible for symptom development in host plants*

21 Jacob Malone — *Control of Type III effector export and disease symptom development during Pseudomonas syringae plant infections*

23 Laura Silva Ferreira Regalado — *One pathogen, two paths: Genomic and metabolic distinction of Portuguese Erwinia amylovora lineages*

24 Marco Pautasso — *An overview of rapid pest risk assessment schemes*

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37 Guillermo Merino Martin — *Temporal dual RNA-seq resolves Phytophthora capsici infection programs and accession-specific effector responses in pepper*

38 Giulia Semenzato — *Streptomyces sampsonii strain C4: a promising candidate for leguminous plant protection*

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42 Marine Folgoas — *Population genomics of the root fungal pathogen causing wheat take-all disease using a global pangenome framework*

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44 Sascha JJenkins — *Transforming Crop Protection Through Early Fusarium Detection*

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47 Javier Palma-Guerrero — *The Role of Berry Skin Traits in Botrytis cinerea Susceptibility of Fungus-Resistant PIWI Grapevines*

48 Van Vlierberghe Lies — *Unlocking the diverse Sarocladium lifestyles through CRISPR-Cas9 and live imaging*

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53 Hoan X. Dinh1, Nola K. D'Souza1, Julie A. Lawrence1, Elzette Palmiero1, Simon R. Ellwood1 — *Fine mapping of a centromeric locus on barley chromosome 6H reveals a candidate gene underlying the net form of net blotch susceptibility*

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57 Riccardo Scotti *Microbial Consortia Modulate Chickpea Root Microbiomes under Rhizoctonia solani Disease Pressure*

ECPP 2026 Oral Abstract 1

The role of ATP-dependent chromatin remodelling complexes in regulation of plant immunity against Fusarium oxysporum

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Fusarium wilt is one of the most destructive and economically important fungal diseases, severely affecting the quality and yield of plants worldwide. Although ATP-dependent chromatin remodelers are well-established regulators of leaf immunity, their role in root-pathogen interactions remains largely unexplored. Here, we show that the Arabidopsis thaliana chromatin remodeler mutants *chr8* and *chr9* exhibit enhanced tolerance to the soilborne pathogen *Fusarium oxysporum*. Phylogenetic analysis reveals that these remodelers are closely related to CHR25, a yeast RAD54 homologue involved in DNA damage repair (DDR). Comet assays revealed that under zeocin induced genotoxic stress, both mutants paradoxically accumulate more DNA lesions than wild-type plants yet maintain superior root growth. This finding challenges the conventional growth-arrest model suggesting that these mutations alter how the cell perceives DNA damage. Moreover, *chr8* shows increase resistant to Fusarium mycotoxin Fumonisin b1, highlighting a potential role in tolerance to pathogen-associated genotoxic stress. Ongoing work examines how CHR8 physically restructures chromatin architecture and nucleosome positioning to orchestrate immunity responses using high resolution long read sequencing. Ultimately, given that various plant pathogens are known to induce DNA damage in host plants during infection, this study investigates the involvement of these CHRs in DDR and plant immunity, aiming to improve crop resilience against soilborne pathogens and mycotoxin - related stresses.

ECPP 2026 Oral Abstract 2

Plant pathogens degrade TIR-derived signals to suppress plant immunity

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Small molecules produced by TIR (Toll-interleukin-1 receptor) domains are essential for plant immune signalling. A central TIR-derived signal is 2'cADPR, an isomer of cyclic ADP-ribose (ADPR) that is generated by plant TIR-domain proteins upon sensing pathogen infection. Here we show that XopQ, a virulence protein widespread in plant pathogenic bacteria, cleaves 2'cADPR and converts it into an inactive, linear ADPR molecule. Steady-state kinetic analyses revealed that XopQ is a highly efficient enzyme that hydrolyses 2'cADPR with near diffusion-limited catalytic efficiency, while displaying high specificity and no detectable activity toward closely related molecules such as 3'cADPR. We show that XopQ eliminates 2'cADPR *in planta* and promotes pathogen virulence even in the presence of an avirulence effector that triggers TIR-mediated 2'cADPR production. Furthermore, our data demonstrate that XopQ prevents *in planta* accumulation of pRib-AMP, a derivative of 2'cADPR that activates the downstream immune complex EDS1-PAD4. Finally, we show that XopQ can also inhibit type VI Thoeris, a bacterial anti-phage defense system that relies on 2'cADPR signalling, possibly explaining why XopQ and type VI Thoeris are never observed to co-occur in bacterial genomes. Our findings uncover a widespread and conserved strategy used by plant pathogens to directly target host TIR signalling.

ECPP 2026 Oral Abstract 3

Self-association allosterically configures the catalytic-site of plant NLR TIR domains

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Plant TIR domain-containing immune receptors exhibit NADase activity upon pathogen effector recognition, creating small molecules that activate defense via EDS1 and its associated proteins. Arabidopsis RPS4 and RRS1 comprise a TIR-NLR immune receptor pair that recognizes multiple effector proteins including AvrRps4 and PopP2. Overexpression of RPS4 leads to stunted growth, with increased defense gene expression, which are signatures of autoimmunity in Arabidopsis, which can be suppressed by RRS1. Upon transient expression in *Nicotiana tabacum*, RPS4 expression alone leads to HR (hypersensitive response). Previous studies showed that the AE interface of TIR domains is required for repression of RPS4 by RRS1. We designed constructs that tandemly express RPS4 wild-type with AE interface mutant of RRS1. Expressing this construct in *N. tabacum* led to lack of HR in the presence or absence of effector. Blue-native PAGE results from *N. benthamiana eds1*-infiltrated samples also showed dissociation of the RRS1/RPS4 complex when RRS1-R AE interface mutant was co-expressed with RPS4 wild-type. However, when this construct was transformed into Arabidopsis, we observed stunted growth and reduced germination. This discrepancy in immune response using the same construct in two different species *N. tabacum* and Arabidopsis suggest that RPS4 proteins may be more stable or may be able to form a more stable homomeric complex in Arabidopsis. We suggest there are additional mechanisms in Arabidopsis that enhances RPS4 protein/complex stability. This also implies the necessity for more stringent regulation of RRS1 to repress RPS4 in Arabidopsis.

ECPP 2026 Oral Abstract 4

One Motif, Two Pathways: A Molecular Switch in RXLR Effector Secretion

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Phytophthora infestans, the causal agent of potato late blight, secretes a suite of RXLR effectors into host plant cells to suppress immunity, whereas apoplastic effectors function extracellularly. Although the RXLR–EER motif is essential for host translocation and undergoes proteolytic cleavage prior to secretion, the significance of this processing is unclear. Previous studies suggested that RXLR effectors utilize an unconventional secretion pathway, prompting investigation into whether the RXLR–EER motif influences secretion route selection. Using genetic, molecular, and cell biology approaches, we examined the secretion pathway of RXLR effectors. Our findings demonstrate that these effectors are translated into the endoplasmic reticulum (ER) before proteolytic processing and secretion. Confocal microscopy revealed that RXLR and apoplastic effectors are trafficked via distinct motile vesicular compartments within cultured hyphae. Fusion of the Golgi recycling signal KDEL to RXLR effectors did not impair their secretion, whereas apoplastic effectors were recycled to the ER, indicating that RXLR effectors bypass the canonical ER-to-Golgi pathway. RXLR effectors localised to Rab7-associated vesicles prior to secretion but not to those marked by the trans-Golgi network-linked vacuolar sorting receptor BP80 or the autophagy marker ATG8. Rab7 activity was required for RXLR secretion and successful host infection, yet dispensable for apoplastic effector secretion. Notably, mutation of the RXLR–EER motif redirected effectors to the canonical secretion pathway and prevented translocation into host cells. Moreover, addition of the RXLR-EER motif to the N-terminus of a conventionally secreted protein redirected to the unconventional secretion pathway. Collectively, these results demonstrate that the RXLR–EER motif governs sorting into a Rab7-associated unconventional secretion pathway, providing new insights into effector trafficking in *P. infestans*.

ECPP 2026 Oral Abstract 5

Lineage-Specific Expansion and Diversification of Cathepsin B Effectors in Aphids

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Aphids are highly successful sap-feeding hemipterans that colonise a wide range of vascular plants. Their success depends, in part, on their ability to evade and suppress host defences by manipulating plant signalling pathways and establishing a cellular environment that supports feeding and reproduction. During feeding, aphids use their stylets to penetrate plant tissues and deliver effector molecules into plant cells, where these proteins modulate host responses. When successful, aphids establish long-term feeding sites in the vasculature, particularly the phloem.

We previously found that in the peach-potato aphid/green peach aphid *Myzus persicae*, a group of effectors belonging to a recently expanded clade of the Cathepsin B (CathB) protein family was identified in oral secretions. These CathB effectors recruit the key immunity hub protein EDS1 and its partners to processing bodies, resulting in suppression of immune responses in *Arabidopsis thaliana*. CathB effector genes are upregulated when *M. persicae* feeds on *A. thaliana* and other Brassicaceae, but downregulated on *Nicotiana benthamiana* and other Solanaceae, suggesting that CathB activity may be host-specific.

To explore this further, we analysed the evolution of the CathB protein family among aphid species with diverse host-plant preferences across the superfamily Aphidoidea. We found that the branch leading to CathB expansion in *M. persicae* is also expanded in other aphid species examined. The expanded CathB clade has undergone independent, lineage-specific expansions across aphids, with copy number and subclade membership varying among aphid lineages.

Together with evidence that CathB genes are subject to positive selection, these findings indicate that CathB effector evolution is dynamic in aphids. This is consistent with functional diversification, from venom-like roles in soldier aphids to immune suppression in plant-feeding aphids.

ECPP 2026 Oral Abstract 6

Pseudomonas syringae inhibits the plant glycosidase PR3 to promote infection

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Hydrolytic enzymes in the apoplast often act as the first line of defence against many invading pathogens. In response, pathogens secrete proteins to suppress the activity of hydrolases. Pathogenesis Related 3 (PR3) is a chitinase-like glycosyl hydrolase of unknown function that is upregulated during pathogen infection. Activity-based protein profiling (ABPP) has shown that PR3 is suppressed in *N. benthamiana* during *Pseudomonas syringae* pv tomato DC3000 HopQ infection (Sueldo et al., 2023). Here, we identified an inhibitor of PR3 through an AlphaFold Multimer screen between PR3 and 268 small secreted proteins (SSPs) from *Pseudomonas syringae* pv tomato DC3000 (*Pto*). The predicted inhibitor of *Nb*PR3 blocks the active site of the hydrolase, and the interaction was confirmed *in vitro* using co-immunoprecipitation. Knockouts of the inhibitor in both *Pto* HopQ and *Pto* were generated and showed decreased virulence in WT *N. benthamiana* and *Arabidopsis thaliana* respectively but not in *pr3* null mutants, further confirming that the virulence function of the inhibitor is dependent on PR3. Also, the effect of the inhibitor is lost in *N. benthamiana cerk1* null mutants indicating that the inhibitor prevents the release of a glycan which gets perceived by CERK1. Interestingly, the inhibitor is present on the surface of outer-membrane vesicles (OMVs) of *Pto* which suggests that the inhibitor functions at a distance from the bacterial cell surface.

ECPP 2026 Oral Abstract 7

Intracellular Trafficking as a Target of Oomycete Virulence: Functional Characterisation of the REX3 Effector

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Pathogenic microbes secrete effector proteins that enter host cells and reprogram cellular processes to promote infection and suppress host immunity. These effectors target key regulatory pathways within the host and provide important insights into the molecular mechanisms underpinning plant–pathogen interactions. The oomycete *Phytophthora palmivora*, a broad-host-range pathogen of economically important tropical crops, represents a valuable system for understanding how intracellular host processes are manipulated during disease.

Here, we investigate the *P. palmivora* effector REX3 and its role in modulating host trafficking pathways. We show that REX3 inhibits secretion in plant cells and interacts with a host Rab GTPase, a central regulator of intracellular vesicle trafficking. Co-immunoprecipitation assays identified critical amino acid residues within REX3 required for this interaction, while complementary computational structural analyses revealed corresponding residues in the Rab GTPase that support a specific molecular interface between effector and host target. Structural modelling and cellular secretion reporter experiments suggested that truncated REX3 variants may retain the capacity to bind the Rab GTPase.

Together, these findings provide mechanistic insight into how REX3 manipulates host secretion pathways during infection and highlight intracellular trafficking as a key target of oomycete pathogen effectors. This work advances our understanding of the molecular strategies used by *Phytophthora* pathogens to subvert host cellular processes and promote disease.

ECPP 2026 Oral Abstract 8

Epigenetic regulation of effectors secreted by Fusarium graminearum

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Fusarium graminearum (*Fg*) is a highly destructive fungal pathogen of wheat, responsible for annual losses of 28 million tonnes of wheat grain globally [1]. A key factor in its pathogenicity lies in the action of effectors; small, secreted proteins that suppress host plant immune responses and facilitate infection. Advancing our understanding of effector expression and function is critical for developing effective and sustainable control strategies.

To investigate the regulation of effector genes during infection on epigenetic level, we generated a Cleavage Under Targets and Tagmentation (CUT&Tag) dataset for *Fg* during wheat infection; the first such dataset for any plant–pathogen interaction. Our time-course analysis revealed that effector loci are enriched for H3K27me3, a transcriptionally repressive mark, and exhibit dynamic epigenetic changes during infection. Specifically, a subset of effectors exhibited early and late lack of H3K27me3 but were enriched in the repressive mark mid-infection, suggesting histone modifications modulate infection dynamics. These findings align with transcriptomic evidence of a conserved two-wave effector expression programme [2].

Subsequent experimental characterisation of these effectors revealed that five out of twelve epigenetically regulated effectors are able to modulate plant reactive oxygen species (ROS) burst response though either suppression or induction of a chitin induced ROS burst in *Nicotiana benthamiana*. This further verifies that this histone modification has strong influence on virulence associated genes. Together, this has enabled selection of a strong list of effectors for further analysis by gene deletion to determine role(s) in *Fg* virulence.

In summary, this study reveals key insights into the epigenetic control of fungal effectors and establishes CUT&Tag as a powerful tool to study chromatin dynamics during plant–pathogen interactions.

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ECPP 2026 Oral Abstract 9

The phytocytokine CAPE9 and its receptor CAPER1 function on plant systemic stomatal immunity

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In plants, stomata are specialised pore structures, bounded by a pair of guard cells, mediate gas flux of leaves for enhancing photosynthesis and water use efficiency. However, stomata provide natural entries for the invasion of pathogens. To restrict future invasions, plants have evolved a specific mechanism to trigger stomatal closure in infected sites by sensing conserved pathogen-associated molecular patterns (PAMPs) from pathogens. This response is also reported to be a systemic process, yet how plants activate and propagate the stomatal signal systemically is still unclear. Recently, our discovery indicates that the *Arabidopsis* CAPE9 peptide derived from the systemic acquired resistance (SAR) marker protein PR1 is essential for promoting local and systemic resistance against a foliar pathogen *Pseudomonas syringae* pv. *tomato* DC3000 (*Pst* DC3000), which mainly invades plants from open stomata, suggesting CAPE9 may be involved in regulating the stomatal closure when perceiving PAMPs. Here, we show the exogenous application of CAPE9 peptide in local leaves triggers stomatal closure and reduces the early bacterial entry of *Pst* DC3000 in not only local but also systemic leaves. By application of affinity purification-mass spectrometry and phenotypic screening, the CAPE9-perception receptor is identified and named AtCAPE receptor 1 (AtCAPER1). The direct perception of CAPE9 by CAPER1 in guard cells leads to stomatal closure depending on ABA and RBOHD-dependent ROS production. Grafting assays elucidate CAPE9 is a mobile signal transferred from local sites to systemic tissues, contributing to stomatal closure systemically. Collectively, the CAPE9-CAPER1 module achieves plant local and systemic stomatal immunity.

PH Gregory Prize Abstract 1

Reading the Host: How Host Signals Coordinate Effector Expression in the Beet Cyst Nematode

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All pathogens must recognise arrival at their host, as the developmental and transcriptional programmes required for infection are energetically costly and therefore cannot be mistimed. In the beet cyst nematode *Heterodera schachtii*, two master transcriptional regulators are induced in response to macerated root extract: SUGR-1 controls early-stage effectors required for destructive migration through the root cortex, whereas DGR-1 regulates later-stage effectors associated with feeding site establishment within the vascular cylinder. However, how *H. schachtii* coordinates these sequential transcriptional waves during invasion remained unclear. Here, we show that diffusates from the *Arabidopsis thaliana* Casparian strip mutant *myb36 sgn3-1*, enriched in vascular-derived signals, specifically upregulates *dgr-1*, but not *sugr-1*, relative to *Col-0*. These findings indicate that *H. schachtii* senses spatially compartmentalised host cues, such that induction of biotrophic effectors occurs only upon entry into the vascular cylinder. We next investigated how these host-derived signals are perceived. Our data supported a role for the nematode amphids, paired anterior sensory organs, in host cue perception. Externally detected signals must subsequently be relayed to the pharyngeal gland cells, where effector expression is regulated by SUGR-1 and DGR-1. Pharmacological perturbation of neuronal signalling pathways revealed that basal expression and extract-induced upregulation of *sugr-1*, and to a lesser extent *dgr-1,* are gated by glutamatergic signalling. Ongoing work aims to identify the plant-derived signals, nematode sensory receptors, and neuronal pathways linking host perception to gland cell activation. Together, this work introduces components of plant and nematode biology indispensable for host recognition and subsequent parasitism.

PH Gregory Prize Abstract 2

Identification and Characterisation of Novel Barley Resistance to Aphids

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Aphids are major pests of barley, causing direct yield losses and transmitting Barley yellow dwarf virus (BYDV). However, both the genetic basis of aphid resistance and efficient approaches for resistance phenotyping remain poorly understood. Here, we combined genomic and phenotypic approaches to investigate aphid resistance in barley.

Using pangenome and pan-transcriptome resources, we characterized the barley thionin gene family, a group of cysteine-rich defense peptides previously proposed as candidate genes involved in aphid resistance. Thionin genes exhibited pronounced chromosomal clustering, extensive tandem duplication, and substantial copy number variation among genotypes. Aphid infestation strongly induced thionin expression, particularly during poor-host interactions, and induction tended to increase with thionin gene copy number, suggesting a role in genotype-dependent aphid defense. To support resistance evaluation, we developed a multidimensional phenotyping framework based on aphid growth, population expansion, and population stability across three generations. These traits were integrated into a composite Aphid Resistance Index (ARI), enabling quantitative comparisons of resistance among barley genotypes.

Together, our findings identify thionins as promising candidate genes associated with aphid defense and provide a practical framework for resistance phenotyping, supporting the discovery of resistant germplasm and future barley breeding.

PH Gregory Prize Abstract 3

Oxidative stress tolerance in the plant pathogen Pseudomonas syringae

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During host colonisation, the plant-associated bacterium *Pseudomonas syringae* encounters reactive oxygen species (ROS), such as hydrogen peroxide (H2O2), released by the host, as well as endogenous ROS generated in response to environmental stressors. To proliferate, *P. syringae* must either suppress the release of or tolerate this ROS as these compounds cause damaging oxidative stress to the pathogen by reacting with bacterial biomolecules. *P. syringae* strains from diverse phylogroups exhibit significant varying abilities to tolerate ROS, but the causes are not fully understood. Upon exposure to H2O2, the transcriptional regulator OxyR plays a vital role by regulating genes involved in the response to H2O2. By predicting the OxyR regulon for strains with varying H2O2 tolerances and correlating this with RNA-seq data containing gene expression changes in two model strains under H2O2 treatment, we have identified candidate genes that may contribute to the differences in ROS tolerance. One candidate is an operon encoding an alternative methionine biosynthesis pathway that is present in higher tolerance strains, potentially providing an alternative way to synthesise methionine, especially under oxidative stress. Deletion of this operon reduces H2O2 tolerance *in vitro* and impacts survival in early plant infection. Deletion of *oxyR* in different strains significantly reduces H2O2 tolerance and alters colony morphology *in vitro*. However, its contribution to survival *in planta* varies according to the specific strain and host plant combination tested. Further characterisation will help us to further understand of how the synthesis and metabolism of key metabolites, in combination with the role of canonical oxidative stress regulators, contributes to bacterial stress tolerance and infection outcomes.

PH Gregory Prize Abstract 4

Engineering immune activation from immune suppression using pathogen effectors as synthetic biology parts

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The plant immune system uses nucleotide-binding leucine-rich repeat receptors (NLRs) to recognise pathogen-secreted effectors inside host cells and trigger immune signalling. Certain effectors suppress this response by degrading or inhibiting NLR signalling components. The *Globodera* nematode effector SPRYSEC15, for example, blocks NRC helper NLR oligomerisation, preventing immune activation. Engineering new immune responses that turn such suppression mechanisms against the pathogen requires tools beyond conventional NLR modification. Using standard plant synthetic biology parts, we constructed a genetic circuit that converts effector-mediated immune suppression into NRC-dependent immune activation. The circuit uses the phytoplasma effector SAP05 to target SPRYSEC15 for ubiquitin-independent proteasomal degradation, releasing NRC2 and NRC3 from suppression and triggering their oligomerisation and downstream signalling. This de-repression logic activates immunity without modifying the helper NLR itself. This proof-of-concept demonstrates that pathogen effectors can serve as modular parts for engineering NLR-mediated resistance through circuit design rather than receptor mutation. We are now establishing this logic for other pathosystems in which the effector degrades its host target.

PH Gregory Prize Abstract 5

Caught Red Handed: Phytophthora infestans targets red light signalling to suppress systemic acquired resistance

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Plants perceive light through photoreceptors that detect its wavelength, irradiance, photoperiod and direction - driving adaptive physiological and biochemical responses. However, during infection of potato by the devastating late blight pathogen *Phytophthora infestans,* several effector proteins target light-signalling components to promote virulence and exploit light's supportive role in plant immunity. We have shown that one such effector – Pi06099 – targets the red-light photoreceptor Phytochrome B. Our results demonstrate that stable silencing of Pi06099 significantly reduces infection, making it an essential effector for pathogenicity. We have identified key residues which mediate interaction between the effector and its target, as well as the conformational states of Phytochrome B targeted by Pi06099. Our forthcoming results, which I will discuss, reveal the function behind the targeting of Phytochrome B in suppressing systemic acquired resistance at a molecular level through attenuation of the master defence regulator NPR1. Using this information, we aim to break this interaction, achieved either by integration of target variance *in planta*, or through external modulation of plant immunity using light treatments - providing alternative and novel strategies for disease control.

PH Gregory Prize Abstract 6

From AlphaFold prediction to experimental validation of plant protein interactions at scale

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Protein–protein interactions (PPIs) underpin host–pathogen crosstalk and shape infection outcomes. Tools such as AlphaFold-Multimer now predict PPIs at proteome scale, but experimental validation remains a bottleneck: predicted interaction spaces vastly exceed the capacity of current assays, which are low-throughput, costly, or prone to artefacts.

Here, we present an optimised split-*GAL4* system for rapid and scalable PPI detection in plant cells, building on a yeast two-hybrid-based assay previously adapted to *Nicotiana benthamiana*. We introduce two advances. First, we replace the original RUBY pigmentation reporter with a quantitative readout that requires no exogenous substrate and enables rapid, non-destructive, image-based scoring. Second, we design a self-validating experimental workflow with built-in controls that distinguish genuine PPIs from common technical artefacts, including reporter autoactivation and expression failure, eliminating the need for secondary validation. We demonstrate the system on known interacting protein pairs, recovering a clear signal against negative controls. By pairing this system with recent advances in tobacco BY-2 cell packs, we scale the assay to a multiwell format for parallel screening of candidate interactions.

These rapid interaction screens are particularly relevant for host–pathogen biology, where co-evolution generates numerous allelic variants on both sides and experimental validation of genuine interactors is essential.

PH Gregory Prize Abstract 7

Simultaneous spatial visualisation of host gene expression and bacterial colonisation in plant roots using PHYTOMap

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Understanding plant-pathogen and plant-microbiome interactions requires resolving two processes that occur in the same tissue at the same time: where microbes colonise, and how nearby host cells transcriptionally respond. Conventional approaches often measure microbial distribution and plant gene expression separately or in bulk, losing the spatial coupling between a colonising microbe and the cells reacting to it — precisely the information needed to understand host-microbe conflict at the scale where it occurs.

Here, we present a dual-visualisation framework for mapping microbial colonisation and host transcriptional responses simultaneously in intact Arabidopsis roots. We combine PHYTOMap, a multiplexed 3D spatial gene-expression platform, with FISH-based bacterial detection to image bacterial cells and plant transcripts within preserved root architecture. Using a synthetic microbial community, we show that this framework co-detects bacterial colonisation and spatially resolved host gene expression in the same sample, enabling direct identification of which plant cells respond, and how, in relation to nearby microbes.

Using this framework, we find that *Agrobacterium* and *Pseudomonas* establish distinct spatial colonisation patterns along the root. Critically, by co-detecting bacteria and host transcripts in the same sample, we observe spatial association between *Pseudomonas* colonisation and host cells expressing the defence-associated gene *CYP71A12*. This directly links sites of bacterial establishment to the host cells mounting a local transcriptional response.

This co-localisation demonstrates the central strength of the approach: connecting microbial localisation to host transcriptional state in a single assay. For the plant pathology community, this framework offers a powerful new lens on plant–pathogen and plant–microbiome interactions, resolving host defence at the precise cells where bacteria establish and laying the groundwork for mapping microbe-specific response patterns across diverse colonisers.

PH Gregory Prize Abstract 8

Phytophthora infestans suppresses host immune responses by targeting two unrelated helper NLRs

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Pathogens deploy effector proteins to manipulate host processes and suppress immunity. However, the host pathways co-opted by pathogen effectors to suppress NLR-mediated immunity remain poorly defined. We previously identified the *Phytophthora infestans* RXLR-(L)WY effector, Pi82, as a suppressor of cell death mediated by two phylogenetically distinct potato helper NLRs, StNRC1 and StNRC4e. Truncation mutant analyses suggest that distinct Pi82 (L)WY motifs contribute to the suppression of each helper NLR, pointing to a modular mechanism of immune suppression. Since Pi82 did not associate with StNRC1 or StNRC4e in *in planta* CoIP assays, we employed IP-MS to identify potential host targets and identified a protein family with diverse roles in plant development, vesicle trafficking and mycorrhizal symbiosis, which we named Target of *Phytophthora* Effector (ToPE). Pi82-ToPE interactions were validated *in planta* by CoIP. Furthermore, RNAi-mediated knockdown of ToPEs enhanced StNRC1- and StNRC4e-mediated cell death, and compromised Pi82-mediated suppression. In contrast, ToPE overexpression did not suppress NRC-mediated cell death, suggesting that ToPE abundance alone is insufficient to regulate this immune pathway. These results suggest that Pi82 exploits ToPE proteins to suppress specific branches of the NRC-network, revealing a previously uncharacterised host pathway linked to helper NLR-mediated immunity.

PH Gregory Prize Abstract 9

Endomembrane trafficking disruption suppresses NLR-mediated hypersensitive response via ER stress

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Endomembrane trafficking plays fundamental roles in plant development and responses to abiotic and biotic factors. In plant immunity, the role of membrane trafficking pathways during pattern-triggered immunity has been well documented and accumulating evidence also indicates a link between these cellular processes and effector-triggered immunity mediated by nucleotide-binding leucine-rich repeat receptors (NLRs). For example, we recently showed that the barley powdery mildew fungus secretes several effectors to temporarily block the vacuolar trafficking pathway of the host cell, thereby suppressing MLA-mediated hypersensitive response (HR). However, why disruptions in membrane trafficking affect NLR-mediated HR remains unclear. Here, we show that stopping vacuolar trafficking prior to activation of the NLR RPM1 inhibits HR and reduces cytosolic calcium influx in *Nicotiana benthamiana*. Surprisingly, disrupting this pathway also diminishes protein accumulation of multiple immune components, including WRKY transcription factors, NPR1, and MAPKs. We expanded our analysis to other pathways and show that blocking endocytosis, recycling, and autophagy also leads to the inhibition of NLR-mediated HR. Notably, disruption of all tested pathways induces endoplasmic reticulum (ER) stress and activates the unfolded protein response (UPR). We further show that inducing mild ER stress inhibits HR mediated by a broad range of NLR classes. We propose a model in which disruptions in membrane trafficking lead to accumulation of misfolded proteins in the ER, triggering ER stress and a pro-survival UPR that attenuates NLR-mediated HR, and that some pathogens exploit this mechanism to suppress ETI during infection.

Main Meeting Abstract 1

Profiling substrates of ADP-ribosylating pathogen effectors by proteomics – novel modification types and targets

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Most plant pathogens employ host-targeted effector proteins with ADP-ribosyltransferase activity to establish disease. Understanding how these ADP-ribosylating effectors suppress plant immunity or trigger activation of NLRs requires identification of their target proteins and the respective ADP-ribosylation sites. We have established a proteomics workflow that facilitates detection of ADP-ribosylated peptides and in many cases allows mapping the modification site (Kaur *et al*., 2025).

We applied our method to a set of *Pseudomonas syringae* type 3 effectors with ADP-ribosyltransferase activity and found that one of these effectors catalyses a novel type of ADP-ribosylation on several substrates from *Arabidopsis thaliana*. We could confirm known targets of the type 3 effectors HopU1 and AvrRpm1. In addition to the previously established AvrRpm1 targets RIN4 and NOIs, our method identified three additional Arabidopsis proteins that are ADP-ribosylated by AvrRpm1. At least one of these proteins appears to function as susceptibility factor for *P. syringae*. We will report on the role of the additional AvrRpm1 substrates for immunity against *P. syringae* and AvrRpm1's virulence function.

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Main Meeting Abstract 2

Tissue-Specific Experimental Evolution Reveals Adaptive Trade-Offs in the Plant Vascular Pathogen Clavibacter michiganensis

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The plant pathogenic bacterium *Clavibacter michiganensis* (Cm) is a systemic vascular pathogen that colonizes both xylem vessels and the intracellular apoplast during different stages of infection. To identify traits and loci associated with adaptation to these distinct host microenvironments, we conducted tissue-specific experimental evolution. Twenty independent Cm lineages were repeatedly passaged in either tomato stems or leaves to promote adaptation to vascular or apoplastic lifestyles, respectively. After fifteen passages, adapted clones were characterized for virulence and virulence-related traits. These characterizations demonstrated clear differential associations of virulence-associated traits with the adapted tissue. The majority of vascular-adapted clones displayed enhanced surface attachment, reduced cellulase activity, reduced exopolysaccharide (EPS) production, and attenuated virulence on tomato compared to the parent clone. In contrast, apoplast-adapted clones displayed reduced biofilm formation, enhanced EPS production and retained their virulence on tomato. Whole-genome sequencing of all adapted clones revealed candidate loci linked to tissue adaptation. Six of ten vascular-adapted clones carried two independent mutations in *CMM_1284*, a putative HipB/XRE-type transcriptional regulator. A *CMM_1284* marker exchange mutant displayed phenotypes similar to vascular-adapted clones, suggesting a role for this regulator in vascular colonization. Together, these findings highlight the role of phenotypic plasticity in tissue adaptation of plant pathogens, showing that tissue-specific adaptation involves modulation of surface attachment, EPS production, and cell wall–degrading enzymes and suggest a trade-off between vascular persistence, supported by strong surface attachment, and systemic virulence, which depends on bacterial dispersal and migration.

Main Meeting Abstract 3

Disabling Susceptibility (S) Genes: A Novel Strategy for Broad-Spectrum Disease Resistance in Canola when two pathogens coinfecting shapes disease dynamics

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Canola (*Brassica napus*) is the major oilseed crop in Canada. It is grown in 22 million acres. It is also the most economically important crop in Canada. Blackleg, caused by *Leptosphaeria maculans* (Lm), has been a mainstay on Canadian farms for four decades. It has been fairly well managed with resistance (R) genes. Use of multiple R-genes and R-gene rotations introduced since 2017 is working to mitigate the disease. However, a new pathogen, *Verticillium longisporum* (Vl), causing verticillium stripe disease, was first identified in Manitoba in 2014, marking its first appearance in North America on canola. The predominant lineage is A1/D1 in Canada (Zou et al, 2020). Since then, Vl has been spreading rapidly to new areas. The advent of co-infection by Lm and Vl has been observed in several canola fields, with a potential 'breakdown' of R-gene resistance due to Vl. Our research has shown how avirulent and R-gene interactions in blackleg are compromised by the presence of Verticillium. In addition, priority effects of co-infection determine how initial exposure to pathogens shapes disease dynamics. Stunting of canola plants is observed in the presence of Vl. Transcriptomic studies have revealed the upregulation or downregulation of key genes in the host plant. The Verticillium stripe disease has no known management strategies. R-gene resistance is not available for managing Vl. Therefore, our lab embarked on a novel strategy by knocking out susceptibility (S) genes to see if we could control both blackleg and Verticillium. A TILLING (Targeting Induced Local Lesions in Genomes) population with mutations (achieved through functional disruption of susceptible (S) genes) from a canola cultivar, and its mutant lines showing single resistance to a pathogen or dual resistance to both pathogens, have been observed. These mutant lines were sequenced to identify key S-genes that work against Lm, and Vl, and S-genes that work against both pathogens. These genes will now be targeted through CRISPR gene editing to be knocked out in canola genotypes to validate how resistance can be achieved through the knocking out of S-genes, particularly being useful when there's no known single gene resistance to Vl, or when R-genes against Lm are compromised in the presence of Verticillium on the same plant. qPCR probes to detect both pathogens simultaneously were developed (Heting et al, 2024) and are helping us look at the future of the canola crop in Canada with promise. These latest findings, mainly from genetics, and approaches to mitigating blackleg and verticillium diseases through understanding host-pathogen interactions, using spatial-scale studies in the field are giving promising results to manage the new disease (Vl) and our old foe (Lm) at the same time.

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Main Meeting Abstract 4

Starship-mediated evolution of virulence and effector mobility in tan spot (Pyrenophora tritici-repentis)

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Starships are novel superfamily of transposable elements discovered recently in eukaryotes. They are defined by their large size up to 700 Kb, and by carrying combinations of cargo genes, including a tyrosine recombinase known as the captain gene, which is responsible for mediating their movement within and between species. Starships play a significant role in organismal evolution by promoting adaptation through gene duplication, disruption, and gain or loss of function. In this research, we have used comparative analyses of long-read assembled genomes of the tan spot pathogen to demonstrate the involvement of starship elements in mobilizing virulence traits within this species. We provide evidence that *ToxA*, a necrosis-encoding effector, can be mobilized on different types of starships containing an intact tyrosine recombinase in various strains. Furthermore, we present novel evidence supporting the ancient mobilization of *ToxB*, a chlorosis-inducing effector, via starships that appear to be degraded, lacking the tyrosine recombinase yet still retaining other defining features of starships. These findings challenge the previous belief that *ToxB* was vertically inherited and instead highlight starships as powerful agents driving genome anatomy, pathogen adaptation, ecological flexibility, and the evolution of virulence in the tan spot pathogen, a major threat to wheat production worldwide

Main Meeting Abstract 5

Dissecting the structural mechanisms of plant invasion by fungal pathogens with Cryogenic Electron Tomography

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Fungal pathogens pose a significant threat to global agriculture, and understanding their virulence mechanisms is essential for developing durable disease control strategies. Many of the most destructive plant infecting fungi form specialized infection cells called appressoria. Appressoria develops on the host leaf surface, undergo rapid cytoskeletal reorganisation, and generate enormous turgor pressure that breaches the plant cell wall and enable pathogen penetration. Disruption of appressorium development either by genetic mutation or by chemical inhibition disrupts pathogenicity, making this process an attractive target for innovative crop protection approaches. However, the specialized and highly dynamic nature of appressoria prevented resolving their underlying mechanisms using conventional structural biology approaches. We developed a method to germinate fungal spores and induce appressoria formation directly on cryo-EM grids. Appressoria formed on grids display normal cytoskeletal rearrangements and turgor generation, effectively recapitulating their invasion mechanism and exerting forces on the grid film. This breakthrough allows us, for the first time, to use techniques such as focused ion beam (FIB) milling, volumetric EM and Electron Tomography in cryogenic conditions to study the cellular architecture of appressoria and the establishment of fungal disease at unprecedented resolution. These findings offer a robust methodology for resolving the biological processes driving appressorium-mediated infection, including repolarization events that initiate host penetration. Furthermore, this approach could lead to the development of novel strategies to combat some of the most devastating plant diseases in agriculture.

Main Meeting Abstract 6

Effector-driven defence repression by IAA de-activation

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We previously showed that the *Hyaloperonospora arabidopsidis* (*Hpa*) effector RxL21 interacts, through its EAR motif, with the Arabidopsis transcriptional corepressors TOPLESS (TPL) and TOPLESS-RELATED1 (TPR1). We also demonstrated that *Arabidopsis* transgenic plants expressing the *RxL21* gene are more susceptible, in an EAR-dependent manner, to the biotrophic *Hpa* pathogen as well as to the necrotrophic *Botrytis cinerea* (*Bc*). Now we have found that RxL21 induces expression of a subset of *Arabidopsis* auxin-responsive *GRETCHEN HAGEN 3* (*GH3*) genes. The enzymes encoded by these genes catalyse the conjugation of indole-3-acetic acid (IAA) to aspartate and glutamate, leading to IAA inactivation. RxL21 achieves the *GH3s* upregulation by hindering the interaction of TPL/TPR1 with IAA3, a key regulator of IAA signalling. Reduced association between TPL and IAA3 allows ARF7/ARF19-driven expression of *GH3s*. We have shown that RxL21 reduces flg22-triggered accumulation of reactive oxygen species (ROS), which are required for mounting resistance against pathogens. Importantly, we have also determined that flg22-triggered ROS burst is GH3-dependent and that *GH3* deficient plants are more resistant to both *Hpa* and *Bc.*

Main Meeting Abstract 7

Conserved rust fungal pathogen ligands trigger non-host disease resistance in cereal crops

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Non-host resistance, the immunity of an entire species to all isolates of a potential pathogen, represents one of the most durable forms of disease resistance in nature[1,2,3]. In the crop plant barley, both domesticated and wild species deploy cell surface-localized lectin receptor kinases (LecRKs) to mediate non-host resistance against leaf rusts, a major group of fungal pathogens[4]. Here, we identify a conserved class of leaf rust glycoside hydrolases as ligands for these barley LecRKs and demonstrate their direct binding. Adapted leaf rust pathogens evolved glycoside hydrolase variants that escape recognition. We show that this perception mechanism is conserved across cereal species and can be functionally transferred between them. Moreover, we identify previously uncharacterized recognition specificities in distinct LecRKs, broadening the repertoire of rust pathogen detection. Our findings reveal a conserved mechanism underlying non-host resistance and provide a basis for engineering broad-spectrum resistance across diverse crop-pathogen systems.

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Main Meeting Abstract 8

Beyond local cell death: emerging roles of plant TIR-domain proteins.

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Plants rely on cell surface-localized pattern-recognition receptors (PRRs) and intracellular nucleotide-binding leucine-rich repeat receptors (NLRs) to detect pathogens. Toll/interleukin-1 receptor/resistance (TIR)-domain proteins constitute a class of NLRs known as TNLs. Many TNLs, as well as TIR-only proteins, function as NAD^+ hydrolysing enzymes that generate bioactive signalling molecules upon immune activation, often leading to host cell death. These molecules define the engagement of enhanced disease susceptibility 1 (EDS1)-family heterodimers, namely EDS1–PAD4 and EDS1–SAG101, together with co-functioning “helper” NLRs to activate and amplify immune responses. In Arabidopsis, the EDS1–PAD4 signalling branch restricts pathogen growth by reinforcing defence pathways activated by both PRRs and NLRs.

In this work, we identified a truncated TIR-domain protein, TIR-NBS 3 (TN3), that specifically interacts with PAD4 in a TIR-derived molecule-dependent manner. Genetic analyses revealed that TN3 contributes to enhance pathogen resistance in distal/systemic tissues following local infection by sensing mobile immune signals. Notably, disruption of the putative TN3 catalytic activity compromises the establishment of effective systemic resistance. Preliminary observations further suggest that the TN3–PAD4 complex functionally cooperates with additional immune-related proteins in both local and systemic responses. At the local level, this “resistance network” appears to be required not only for PRR-triggered resistance against bacterial pathogens, but also for the sensing of cell wall damage, indicating a convergence point between surface and intracellular immune signalling pathways.

Together, our findings reveal a broader role for TIR-domain proteins beyond the induction of local cell death, extending to the restriction of pathogen spread and growth in distal tissues. The evolutionary conservation of these components highlights their potential relevance for translational applications in crop protection.

Main Meeting Abstract 9

The role of the type II secretion system in Xanthomonas virulence

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Xanthomonas bacteria colonise and proliferate within the plant apoplast, where they must acquire nutrients, remodel the extracellular environment, and evade host defences to establish disease. Central to this is the type II secretion system (T2SS), which delivers effector proteins directly into this extracellular niche[1]. Despite its documented role in virulence accross damaging bacterial genera[2-4], T2SS-secreted effector (T2E) repertoires deployed during active infection have remained undefined, in part because these proteins cannot be reliably predicted bioinformatically.

Through *in planta* comparative proteomics, we have defined the T2E repertoire of *Xanthomonas euvesicatoria* (*Xe*) during active infection of tomato, uncovering a diverse suite of cell wall-degrading enzymes and proteases predicted to target a broad range of host substrates. We further found that type III-secreted effectors (T3Es) suppress intracellular immune recognition triggered by T2E activity, revealing functional cooperation between the T2SS and T3SS during apoplastic infection.

However, not all xanthomonads rely on this partnership. Several highly pathogenic species lack the T3SS entirely, raising the question of how these bacteria achieve successful apoplast colonisation in its absence. By leveraging the natural diversity of the *Xanthomonas* genus, we identified distinct virulence strategies and T2E functional specialisations that may have evolved to support survival and proliferation within the plant apoplast and shape pathogen lifestyles.

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Main Meeting Abstract 10

A conserved structural logic underlies sensor–helper NLR communication in the NRC immune receptor network

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NLR immune receptor networks consist of expanded disease resistance proteins (sensor NLRs) that signal via core executors of immunity known as helper NLRs. Although some sensor NLRs are thought to activate their cognate helpers via an activation-and-release mechanism, the structural basis of sensor-helper communication remains poorly understood. Here, we identify and validate sensor-helper NLR interfaces that are critical for immune activation in the NRC network of coiled-coil NLR immune receptors. Using AlphaFold 3 we predicted a high confidence model between the virus resistance protein Rx and its helper NLR NRC2. We validated the interfaces by loss and gain-of-function mutagenesis, including reconstituting a critical salt bridge through reciprocal mutations. We showed that these interfaces are conserved across the NRC network of asterid plants despite over 120 million years of divergence and validated the sensor-NRC interfaces within the common lettuce network. Structure-guided bioengineering of a lettuce sensor NLR enabled expansion of its NRC helper compatibility profile. These results are consistent with the activation-and-release model and point to bioengineering sensor-helper specificity in economically important crop species.

Main Meeting Abstract 11

Re-wiring defence networks to engineer disease resistant crops

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Resistance against the fungal pathogens *Botrytis cinerea* and *Sclerotinia sclerotiorum* is quantitative, governed by multiple small-medium impact loci, with plant responses involving large-scale transcriptional reprogramming. We aim to identify transcriptional regulators of the lettuce defence response against these pathogens, elucidate key regulatory interactions between them and engineer defence networks to develop cultivars with reduced susceptibility.

We have taken a systems biology approach to predict regulators and understand the complex networks in which they function. We have combined times series transcriptome profiling after infection of lettuce with *B. cinerea* and *S. sclerotiorum*, to capture the dynamics of the response, along with single time point data from diverse lettuce accessions with varying levels of pathogen susceptibility.

We inferred a gene regulatory network (GRN) underlying the lettuce defence response to these pathogens and validated specific regulatory predictions, identifying positive and negative regulators of defence against *B. cinerea*, and their downstream target genes. We are now re-wiring this network to enhance lettuce disease resistance in a highly targeted manner.

Main Meeting Abstract 12

Integrating EvoMPMI and Effectoromics for Durable Disease Resistance in Potato

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The global field crop potato (Solanum tuberosum) is threatened by numerous diseases. The causal pathogens range from old enemies, such as the devastating oomycete Phytophthora infestans, widely spread fungi such as Verticillium dahliae and Alternaria solani, to emerging phloem-limited bacteria such as Candidatus Liberibacter solanacearum and Candidatus Phytoplasma solani, which cause Zebra chip disease and Stolbur, respectively. Wild tuber-bearing Solanum species have accumulated diverse resistance traits over time, and we study how these plants respond to these pathogens. In particular, we seek to understand the dynamic interactions between pathogen effectors and (co-)evolved immune receptors. For P. infestans, effectoromics screens have led to the identification of several immune receptors, and we aim to enhance receptor-mediated immunity by integrating co-evolutionary analyses with artificial intelligence (AI)-guided protein structure predictions. For Ca. Phytoplasma solani and Ca. Liberibacter solanacearum, effectoromics screens are combined with bacterial grafting assays, targeting the identification of immune receptors that recognize these bacteria. Collectively, insights gained from studying the diverse disease resistance mechanisms across Solanum species will inform the development of more effective disease resistance strategies in potato.

Main Meeting Abstract 13

Tradition and Innovation: Integrated Research and Breeding for Sugar Beet Pest and Disease Resistance

Olaf Czarnecki, Abigail Barker, Nina Behnke, Maria Gabriela Ronquillo Lopez, Katia Schuetze, Ullrich Dubiella, Maik Gertz, Gabor Gyetvai, Friedrich Kopisch-Obuch, Enzo Neu, David Wurbs

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Increasing pest and disease pressure, combined with evolving regulatory and agronomic constraints, is driving a transformation in sugar beet (*Beta vulgaris*) breeding. Traditionally, genetic improvement has relied on trait-specific backcrossing, recurrent selection, and exploitation of natural variation. While these approaches have delivered substantial breeding progress, the growing complexity of target traits requires a more integrated use of classical and modern breeding technologies, including marker-assisted selection, genomic tools, and genome editing.

The evolution of herbicide resistance breeding illustrates this transition, ranging from species specific natural tolerance over naturally engineered resistance (CONVISO®) and transgenic solutions (Roundup® Ready), and now towards novel resistances aligned with changing regulatory landscapes. For Cercospora leaf spot, long-term recurrent selection has generated high resistance levels; however, sustainability concerns and pathogen adaptation necessitate continuous innovation supported by deep biological insight. In virus yellows, natural variation provides partial tolerance, complemented by targeted genetic approaches that enhance resistance levels. Conversely, emerging diseases such as rubbery taproot highlight cases where conventional breeding may reach its limits, and advanced biotechnological solutions become critical.

These examples underscore the complexity of translating trait discovery into commercially viable varieties, requiring coordinated integration of diverse breeding methods. Success depends not only on scientific and technological advances but also on navigating regulatory frameworks and societal acceptance. The future of sugar beet improvement lies in combining the strengths of traditional breeding with cutting-edge innovations to deliver sustainable and resilient crop production systems.

Main Meeting Abstract 14

Toward understanding rice NLRome, its functional diversity and evolution

Ryohei Terauchi(1,2), Takumi Takeda(2), Motoki Shimizu(2)

Kyoto University, Japan

Iwate Biotechnology Research Center, Japan

A typical genome of rice (*Oryza sativa*) encodes ~400 genes for nucleotide-binding leucine-rice repeat (NLR) receptors. Yet, their function and evolution are largely unknown. In this paper, I will overview our findings on the paired-NLRs including Pia/Pias, Pik and Pii, all consisting of helper and sensor NLRs. The sensor NLRs contain integrated domain (ID), possibly recombined from host protein domains that are targeted by pathogen effectors. I will highlight this non-homologous recombination-mediated “domain bricolage” as a prevalent mechanism in the evolution of immune receptors in plant. Next, I will share our large-scale forward genetics approach to explore and functionally characterize pathogen avirulence effectors and cognate NLRs from rice.

Main Meeting Abstract 15

From Recognition to Response in Plant Immunity

Tianrun Li[1,2], Jie Zhu[1,3], Alba Moreno-Pérez[1], Daniil Prigozhin[4], Gitta Coaker[1]

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[2]University of Oxford, UK

[3]University of Missouri, USA

[4]Lawrence Berkeley National Laboratory, Berkeley, CA, USA.

Plants rely on kinases to drive receptor activation, immune signaling, and defense. At the cell surface, receptor kinases perceive pathogen-associated cues that initiate immune responses. We have identified key structural features that underlie receptor specificity and have used this knowledge to engineer synthetic flagellin receptors with expanded detection of important bacterial pathogens. We further combine spatial mapping and live-cell imaging to reveal when and where immune recognition and effector delivery occurs within plant tissues. Together, these findings show how mechanistic insight into immune recognition and signaling can be translated into strategies for enhancing disease resistance.

Main Meeting Abstract 16

Decoding Immune Recognition and Pathogen Evasion in Plants

King F[1], Ibrahim TE[1], Yuen E[1], Vuolo C[1]; Wang Y[1], Eilman N[1], Jenkins S[1], Kourelis J[1].
(1) Imperial College London, London, UK.

Plant pathogens secrete effector proteins that reprogramme host cellular processes and weaken immune responses. Plants counter these attacks with intracellular immune receptors that detect pathogen activity and trigger defence. This talk will examine the molecular arms race between pathogen effectors and plant immunity, with a focus on the strategies that effectors use to evade or suppress plant defenses. I will highlight how cell biology, structural modelling and AI-guided protein design can reveal plant-pathogen interactions and support new approaches to engineer disease-resistant crops.

Main Meeting Abstract 17

Resurrect Bio: Helping crops defeat disease

Cian Duggan

Resurrect Bio, UK

Plant pathogens frequently evolve mechanisms to suppress or evade recognition by plant immune receptors (NLRs), leading to the breakdown of disease resistance in crops. Resurrect Bio has developed an approach to identify NLRs that have been functionally suppressed by pathogen effectors, and to design targeted gene edits that overcome this suppression and restore receptor function.

This is enabled by FloraFold, an AI-based discovery tool, combined with high-throughput in planta screening, allowing systematic identification of plant-pathogen interactions. This integrated computational and experimental laboratory approach supports rapid identification of candidate edits with restored immune activity.

Our platform is crop agnostic and applicable across a broad range of pathogens and

pests, offering a generalisable strategy for restoring resistance across diverse

crop-pathogen systems.

Resurrect Bio is working in partnership with seed companies to translate these findings into commercial breeding pipelines, accelerating the delivery of disease resistant varieties. The company is a spinout from the Sainsbury Laboratory, now based in West London.

Main Meeting Abstract 18

Leveraging untapped diversity in ancient landraces to tackle a major breakdown of yellow rust resistance in the UK

Diane G.O. Saunders[1], *Yr15*-breakdown project partners[2,3]

[1]John Innes Centre, Norwich Research Park, Norwich, UK; [2]Niab, Park Farm, Villa Road, Histon, Cambridge, UK; [3]Rothamsted Research, Harpenden, Hertfordshire, UK.

Breakdown of the widely deployed yellow rust resistance gene (*Yr15*) in 2025 immediately placed 50% of UK wheat acreage vulnerable to infection. Wheat yellow rust – caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) – is the most damaging of the three wheat rusts in Europe. In response to this plant health emergency, the UK wheat research community galvanised to develop a rapid response plan and safeguard UK wheat yields. At JIC, this focused on leveraging the vast untapped genetic potential of the A.E. Watkins bread wheat landrace collection, that was recently unlocked through whole genome resequencing, to identify and validate novel sources of *Pst* resistance that could be immediately utilised within UK wheat breeding. As the Watkins landrace collection of 827 lines had already been screened for susceptibility to the preceding “Warrior” type *Pst* isolates we focused on a subset of 33 landraces that had displayed resistance. We subsequently confirmed that 32 of these Watkins lines remained resistant to *Yr15*-breaking *Pst* isolates. Utilising existing mapping populations, we are now defining the resistance sources within these lines for mobilisation into modern breeding pipelines. As 60% of the genetic diversity in the Watkins landraces is not contained in modern cultivars, exploring this has high potential to uncover multiple novel resistance loci (and associated markers) that would substantially diversify the UK resistance gene catalogue. In parallel we are examining the current diversity of known resistance genes in UK wheat varieties and developing tools for breeders to enhance resistance gene stewardship. This project will importantly contribute to the longer-term goal of broadening the genetic diversity urgently needed within the UK’s wheat resistance breeding programme to reduce the future risk of similar catastrophic single-gene breakdowns.

Main Meeting Abstract 19

Connecting the Dots: Pan-genome graph reveals structural variation underlying disease resistance in pea

Sanu Arora (1), Kumar Gaurav (1), Nicolas Trenk (1), Samuel Bruty (1), Eman Salama (2), Marcus Samuel (2)

(1) *John Innes Centre, UK;* (2) *University of Calgary, Canada*

Pea (*Pisum sativum*), the organism in which Mendel first uncovered the principles of inheritance, is one of our oldest domesticated crops and an important grain legume for sustainable agriculture. Its productivity, however, is constrained by multiple diseases, including soil-borne root rots and foliar pathogens. Many of the resistance traits available to breeders were shaped by historical domestication and selection, yet the genetic variants underlying them are often difficult to resolve with a single linear reference genome because of extensive structural variation in *Pisum* species. My group uses *k*-mer-based association genetics, pan-genome graphs, skim-sequencing imputation, and experimental validation to uncover the hidden genetic variation that controls disease resistance and its associated agronomic trade-offs.

Using these approaches, we have resolved long-standing questions in pea pathology and breeding. First, I will describe the molecular identification of the classical *Fw* locus, which confers resistance to *Fusarium oxysporum* f. sp. *pisi* (Fop) race 1 and has underpinned pea breeding for nearly a century. By combining *k*-mer GWAS with transcriptomic, and transformation-based functional analyses, we mapped *Fw* to a presence/absence structural variant largely invisible to conventional SNP-based analysis and harbouring a previously unannotated transcript.

In parallel, our analysis of resistance to *Fusarium solani* revealed an unexpected interplay between root rot resistance, the rhizosphere microbiome, and flower colour. White-flowered varieties, historically favoured by breeders and consumers, are generally susceptible to root rot, whereas purple-flowered lines show greater resistance. Using recombinant inbred populations, high-throughput root disease phenotyping, qPCR-based quantification of the dominant rhizosphere fungus, and a novel imputation strategy based on mapping skim-sequencing data to biparental graph genome, we fine-mapped a resistance locus on chromosome 6 that colocalises with a locus governing recruitment of this fungus. Crucially, we genetically separated this resistance from the flower-colour locus, the classical Mendelian *A* gene governing flower colour and seed pigmentation. This separation offers a route to combine desirable flower colour with improved *Fusarium* resistance and a beneficial rhizosphere microbiome, breaking a trade-off long entrenched by breeding.

Together, these studies show how pan-genome approaches reveal structural variants missed by reference-based analyses and expose the hidden trade-offs that classical breeding has left in the pea genome. More broadly, this work provides a framework for translating genomic discoveries into markers and diagnostic tools for durable, low-input disease management in pea.

Main Meeting Abstract 20

Tomato brown rugose fruit virus: What is the biological relevance of your detection?

Adrian Fox(1), Mary Mynett(1), George Lawrence(1), Yue Lin Loh(1,2), Aimee Fowkes(1,2), Anna Skelton(1)

Fera Science Ltd, United Kingdom

Newcastle University, United Kingdom

In 2014/15 a novel *Tobamovirus*, tomato brown rugose fruit virus, was discovered in Jordan and Israel. As the virus can overcome the resistance genes to other tomato infecting tobamoviruses, it presents a major constraint to tomato production. The virus is seed-borne and contact transmissible and primarily controlled through biosecurity and phytosanitary regulation. Despite these controls, the virus has rapidly spread around the globe, and now affects every continent where tomatoes are grown.

Once a crop is infected the virus can spread rapidly through a glasshouse by normal working procedures. Work conducted at Fera has shown the virus to be environmentally stable for at least six months on a range of glasshouse surfaces. However, the virus remains detectable by real-time RT-PCR even following disinfection (Skelton et al, 2023a). International collaborative working has shown that during an outbreak the virus can be released from plants into the wider environment through pollen, dust, and irrigation water. This can lead to the presence of environmental residues of the virus which may (or may not) present an onward infection risk (Giesbers et al, 2024). Work conducted to look at optimal surveillance strategies has indicated these residues may also confound result interpretation based on standard molecular and biological diagnostic approaches (Skelton et al, 2023b). The high proportion of imported tomato fruit carrying the virus (Skelton et al, 2023c), as well as the presence in environmental sampling, mean the potential for contamination leading to false positives is a real diagnostic risk. With the introduction of resistant varieties, which can suppress but not prevent viral replication, standard diagnostic approaches are again being challenged. Current work on understanding changing risk pathways, mitigating these risks, and adapting diagnostic approaches to meet these evolving challenges will be discussed.

Giesbers, A.K.J., et al. (2024) *Plant Pathology*, 73, 2071–2083

Skelton, A., et al. (2023a) *Viruses*, 15(10)

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Skelton, A., et al (2023c) *Journal of Plant Pathology*, 105, 1327–1333

Main Meeting Abstract 21

Breaking and Entering- The Biology of Plant Infection by the Blast Fungus

Nicholas J Talbot

The Sainsbury Laboratory, Norwich Research Park, University of East Anglia, Norwich, NR47UH, United Kingdom,

The process of plant infection by fungal pathogens is remarkable. Many pathogens elaborate specialised infection structures called appressoria that can physically break the tough outer cuticle of plants, while others seek out stomata or rupture the plant cell wall using secreted enzymes. Each of these infection strategies involves specific developmental biology and understanding the underlying mechanisms of plant infection is fundamental to disease control. My laboratory studies plant infection by the devastating blast fungus *Magnaporthe oryzae*, causal agent of rice and wheat blast diseases, which are of significant economic concern. *M. oryzae* forms a melanin-pigmented appressorium, which develops enormous turgor to generate protrusive force which can breach the plant cuticle using a rigid penetration peg. The appressorium forms in response to the hydrophobic leaf surface and requires a specific MAP kinase phosphorelay signalling pathway, coupled to cell cycle control and autophagic cell death of the fungal spore. These signals collectively lead to appressorium morphogenesis, which involves almost 50% of the genes in the *M. oryzae* genome to be differentially expressed. We are studying the mechanisms that control appressorium development and function. We have, for example, begun to determine how autophagy is spatially regulated in each cell of the fungal conidium as the appressorium develops and have characterised the biochemical process that leads to turgor generation, and its regulation by sensor kinase, which is responsible for controlling septin-dependent re-polarisation and plant infection. As well as molecular genetic and genomic approaches, we have developed mechanosensory methods to directly measure turgor generated during plant infection and investigate its genetic regulation. I will discuss recent progress into understanding the mechanisms of rice infection by this fungal pathogen, the biology of appressorium development, the role of septins and effector proteins in invasive growth, and the live cell imaging, phosphoproteomic and mechanobiology procedures we have developed to understand the infection biology of the blast fungus.

Main Meeting Abstract 22

Fungal endophytes for disease control in cereals

David B. Collinge[1], Arianna Petrucci[1, 2], Alfia Khairullina[1,3], Sabrina Sarrocco[2], Hans J.L. Jørgensen[1] and Birgit Jensen[1]

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2 Department of Agriculture, Food and Environment, University of Pisa, Italy

3 Dept of Biology, University of Lund, Sweden

Plant diseases and pests are responsible for significant crop losses worldwide both in terms of yield and quality. Conservative estimates lie at 20-40%. These losses are caused not only by direct inhibition of plant growth but also by insidious factors such as toxic metabolites (mycotoxins), which result in reduced quality and safety of the products. Although diseases are managed through a combination of technologies, ranging from farmer skills, the use of pesticides, disease resistance and biological control, there are many diseases for which effective methods for management are yet to be developed.

The use of beneficial microorganisms as a mean of controlling plant diseases, and particularly the potential of endophytic fungi for biological disease control has been explored. Our studies have focussed on cereal diseases, especially Fusarium head blight and Septoria tritici blotch. Both of these cause losses in cereals, with Fusarium head blight further resulting in the accumulation of several mycotoxins in the grain. An ecological approach was used for identifying and isolating endophytic fungi in cereal crops, specifically in plants subject to disease pressure that do not show disease symptoms. The chief rationale is that an organism isolated from a particular environment is likely to be a successful competitor with other microorganisms – including pathogens – in that environment. Therefore, it may represent an efficient means of identifying fungi which can be used as biological control agents (BCAs). A reason for concentrating on endophytic fungi is that, once they have successfully colonised the host tissues, they are less affected by external environmental conditions than phyllosphere or rhizosphere microbes and this may lead to increased stability in fluctuating environments.

The focus on biological control of Fusarium head blight is to determine whether this can lead to a reduction in mycotoxin levels in the harvested grain. We have studied this in barley, wheat and oats, primarily with an effective rhizosphere BCA, *Clonostachys rosea* IK726, and have shown that this organism can stimulate detoxification of trichothecene mycotoxins such as deoxynivalenol. A commercially successful biological control strategy is associated with the ability of the BCA to colonise the host tissue and outcompete pathogens, but induction of defence-related plant responses is also highly important. In the case of *Fusarium* diseases in cereals, several microorganisms have individually been shown to control disease under different conditions. We have demonstrated more effective control by combining BCAs in greenhouse and field conditions.

Main Meeting Abstract 23

Establishment of functional symbioses between *Epichloë* endophytes and hexaploid wheat (*Triticum aestivum*).

Richard D Johnson (1), Wayne R. Simpson (1), Hisashi Tsujimoto (2), Lisa Wood (3), Alison J Popay (1), Sarah C Finch (1), Wade J Mace (1), Stuart J Roy (4), Joanne Drummond (5), Rainer Hofmann (6), David E Hume (1)

(1) Bioeconomy Science Institute, New Zealand; (2) Tottori University, Japan; (3) Grasslanz Technology Limited, New Zealand; (4) Adelaide University, Australia; (5) Foundation for Arable Research, New Zealand; (6) Lincoln University, New Zealand

Asexual *Epichloë* endophytes have been used successfully in pastoral systems to enhance the agronomic performance of important temperate grasses such as perennial ryegrass (*Lolium perenne*) and tall fescue (*Festuca arundinacea*) via improved tolerance to biotic and abiotic stresses.

Modern cereals such as wheat (*Triticum aestivum*) and rye (*Secale cereale*) within tribe Hordeae (Triticeae) do not naturally host *Epichloë*, but some wild relatives (e.g., *Elymus* spp.) have been shown to be infected with *Epichloë bromicola.* Inoculation of *E. bromicola* into both rye and wheat has shown that successful symbiosis depends on the genetics of both the host and the endophyte strain deployed. Endophyte compatibility in rye has been improved through recurrent selection of desirable phenotypes, which is possible due to its outcrossing nature and broad population based genetic variation. However, wheat is a selfing species and populations are genetically narrow, making recurrent selection for improved phenotype impractical. Until recently the phenotypes of *Epichloë* – wheat associations have been compromised, including host death and stunting. We have overcome this barrier by utilising experimental wheat lines containing alien chromosome additions or substitutions from wild species and have identified symbioses whereby infected wheat plants are improved towards uninfected controls. These plants completed their full lifecycle including the transmission of *Epichloë* into the next generation of grain.

Progress in crossing these experimental lines to modern cultivars has improved plant phenotype, and assessment of *Epichloë* infected wheat has demonstrated increased resistance to both insect pests and fungal diseases.

Main Meeting Abstract 24

EndoReg: drawing consensus on future governance of UK endophyte-enabled crops

Lorena I Rangel[1], Damian Bienkowski[2], Niamh Mahon[3]

[1]*Cell and Molecular Sciences, James Hutton Institute, UK*

[2]*Information and Computational Sciences, James Hutton Institute, UK*

[3]*Social, Economic and Geographical Sciences, James Hutton Institute, UK*

Vertically transmitted endophytes (VTEs) are plant-associated fungi, bacteria, or yeasts that are inherited through seed and maintained within plant tissues across generations. These intimate plant–microbe associations have potential to support more sustainable agriculture by improving crop resilience, stress tolerance, and resistance to pests and diseases. However, because VTEs are neither conventional plant varieties nor externally applied microbial inputs, they challenge existing UK regulatory frameworks that were not designed for biologically integrated, self-propagating technologies.

This Plant Health Centre-funded project examined how VTE-containing crops may be classified and regulated in Scotland and the wider UK. Building on previous Scottish Government-funded work on *Epichloë*-infected grasses, we used semi-structured stakeholder interviews with regulators, policy teams, industry representatives, and scientific experts to explore how VTEs might intersect with plant variety registration, plant protection product legislation, biostimulant and fertiliser frameworks, environmental release, plant health, and food and feed safety. Four hypothetical VTE case studies were used to prompt discussion across different crop types, endophyte taxa, product claims, and organism origins.

The heritable, plant-embedded nature of VTEs complicates conventional distinctions between crop varieties, microbial products, and biological inputs. We considered how regulatory ambiguity could affect innovation, safety assessment, commercialisation, and adoption of endophyte-based technologies in UK agriculture. More broadly, this work asked how existing systems can adapt to emerging plant–microbe technologies without over-regulating beneficial innovation or overlooking meaningful environmental, animal, or human health risks.

Main Meeting Abstract 25

Enriching pathogens: development of a commercial diagnostic for Fusarium basal rot risk assessment and management in onion

John Clarkson[1], Sascha Jenkins[1], Matt Combes[1] and Ben Maddison[2]

[1]University of Warwick, UK; [2]RSK-ADAS, UK

The UK produces approximately 450,000 tonnes of bulb onions annually, with a market value of £150 million. However, production is increasingly threatened by Fusarium basal rot (FBR), caused by the soilborne fungus *Fusarium oxysporum* f. sp. *cepae* (Foc). In 2025, record crop losses of up to 40% were reported, costing the industry more than £25 million. Foc can infect onions at all growth stages, leading to seedling blight, premature plant death, and bulb rot. Postharvest losses are also significant, as infected bulbs rapidly deteriorate following drying and storage; when disease levels exceed 10%, entire stores may be lost.

Current management strategies rely primarily on extended crop rotations (>6 years), as fungicides are generally ineffective and only moderate host resistance is available in commercial cultivars. To optimise rotation planning and reduce FBR risk, growers require a reliable diagnostic tool to quantify Foc inoculum levels in soil and identify high-risk fields prior to planting.

Building on previous work identifying putative pathogenicity genes from the Foc genome as diagnostic targets (Taylor et al., 2016), we developed a specific quantitative PCR (qPCR) assay for Foc detection. Initial testing using DNA extracted directly from onion-growing soils produced highly variable results, with reliable detection only at very high Foc inoculum levels. To overcome this limitation, we incorporated an enrichment step (Mestdagh et al., 2023), in which soil samples are incubated in a semi-selective liquid medium for *Fusarium* spp. prior to DNA extraction and qPCR analysis.

Optimisation of this enrichment-qPCR method enabled sensitive and reproducible quantification of Foc DNA in field soils across two growing seasons. Crucially, a robust relationship was also established between Foc DNA levels and FBR incidence in commercial onion crops. This work has resulted in the development of a practical diagnostic tool, now offered as a commercial testing service by RSK-ADAS, to support improved FBR management and decision-making in onion production.

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Main Meeting Abstract 26

How the UK Seed Potato Industry is Responding to a Changing Potato Leaf Roll Virus Challenge

Kyran Maloney(1), Kerry Leslie(1), Heather Bruce(1), Verena Schmidt(1), Gavin Prentice(1)

(1)SAC Consulting (Part of SRUC), United Kingdom

Seed potato production is a highly specialised and regulated segment of the potato production cycle. Yield and quality of ware (processing and table potatoes) is heavily dependent on the quality of input seed. Seed potatoes produced in GB are internationally recognized as of high health status, particularly those produced from the Yorkshire Wolds and Scotland, the latter being designated as a high health status region.

In recent years the industry has been faced with a re-emergence challenge from the persistently transmitted virus Potato Leaf Roll Virus (PLRV). Although Scottish seed potatoes remain of very high health status, incidence of PLRV infected material has increased, as has the number of downgrades and fails within the seed potato classification scheme. This has already led to economic implications for some seed and ware potato producers.

Fortunately, potato growers are responding rapidly to adapt their production systems to reduce risk from aphid vectored viruses such as PLRV, and supporting researchers are investigating the drivers behind the resurgence of potato leaf roll disease and the most appropriate responses to it (Ryabov *et al.* 2026).

Conventional measures at controlling aphid vectored viruses in potato crops have involved routine applications of insecticides. Limited access to plant protection products, issues with insecticide resistance amongst key target aphid species, and unintended impacts on nontarget insects have led growers to reconsider the most appropriate management strategy.

The PLRV-potato pathosystem is a strong example where Integrated Pest Management (IPM) offers pathways to effective management (Skelsey, 2024). Only by improving surveillance and warning systems; making use of cultural measures such as barrier netting, ground covering mulches, and intercropping; by deploying non-chemical measures, and finally by appropriately timing applications of plant protection products can a reduction in incidence of PLRV in potato crops be achieved.

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Main Meeting Abstract 27

Wild Bio: Evolving seeds for a changing planet.

Ross Hendron & the Wild Bio team (1)

(1) Wild Bioscience Ltd, UK

Evolution has been solving hard problems in the wild for hundreds of millions of years. Wild Bio was founded to put those solutions to work in crops, using gene editing to translate evolutionary innovations into new crop varieties that can meet the challenges of a changing planet.

Since spinning out of the University of Oxford in 2021, Wild Bio has raised $80M and grown to a 45-person team operating an end-to-end trait discovery and development pipeline in Oxford. We have progressed multi-species crop improvement programs in four countries both independently and in collaboration with major seed businesses, spanning yield improvement, resource use efficiency, and carbon capture.

More yield, fewer resources, carbon sinks, not sources. If that sounds like your kind of problem, we’d like to meet you – .

Main Meeting Abstract 28

GetGenome: A mission-driven venture enabling global research capacity

James Canham(1,2), Sophien Kamoun(2)

(1) GetGenome, UK; (2) The Sainsbury Laboratory, UK

Founded in 2022, GetGenome is a UK-based non-profit created to improve equitable access to genomics technologies, training and collaboration for research communities worldwide (Canham et al., 2024). Since its launch, GetGenome has supported over 150 researchers across 20+ countries remove barriers to access and transition to the post-genomics stages of their work where they innovate, discover and engage in international collaborations on a more equal footing. The presentation will reflect on the realities of launching a mission-driven scientific venture: building partnerships, establishing credibility, balancing impact with scale and creating opportunities for researchers who may otherwise be excluded from utilising transformative technologies. Through the lessons learned from GetGenome, the talk aims to encourage early-career scientists to think beyond traditional academic pathways and consider how community-led initiatives or non-profits can create meaningful and scalable impact.

Canham J, Win J, GetGenome Network, Kamoun S (2024) GetGenome: Overcoming inequalities in access to genomics technology. PLoS Biology 22(8): e3002804.

Main Meeting Abstract 30

Novel approaches to oilseed rape protection – moving reduced susceptibility and targeted pest control and from lab to field

Laura Gimenez-Molina (1), Jessica Hughes (2), Ajisa Muthayil-Ali (1), Madeleine Workman (2), Emmanuel Solomon (2), Ryan E. Brock (2), Heather Fell (1), Catherine Chinoy (2), Yongju Huang (2), Steven Penfield (2), Henrik Stotz (1), Rachel Wells (2).

1: University of Hertfordshire, U.K. 2: John Innes Centre, U.K.

Historically, crop production has been heavily reliant on chemical control, however, there has been a steady decline of active substances (AS), with a loss of 95 of the 502 AS between 2018 and 2022[1]. Combined with a push towards sustainable agriculture and initiatives, such as the now withdrawn European Union 'Farm to Fork' strategy which aimed to cut pesticide use by 50% by 2030[2], novel approaches to crop protection are urgently required.

Oilseed rape (*Brassica napus*; OSR) is a major break crop in the UK yet, despite its economic value, cropping areas have declined by over 60% since 2013. Rising pest pressure from the Cabbage Stem Flea Beetle (*Psylliodes Chrysocephala*; CSFB) since the 2018 EU ban on neonicotinoid insecticides, and CSFB resistance to pyrethroid alternatives, have resulted in OSR being an increasingly challenging crop for farmers to grow. Additionally, with disease pressure from *Pyrenopeziza brassicae*, a pathogenic fungus responsible for light leaf spot (LLS) disease, one of the most important diseases of winter oilseed rape, there is a serious threat to the viability of the UK OSR supply chain.

Utilising associative transcriptomic approaches[3] on a diverse population of *B. napus* for both CSFB palatability and LLS disease incidence, we have identified novel loci associated with host susceptibility[4,5]. These represent excellent targets for mutation breeding or gene editing, to develop germplasm with reduced susceptibility. Behavioural and transcriptomic studies are being used to identify the mechanisms underlying variation in susceptibility. In addition, pest genetic and gene expression studies are being exploited to develop targeted RNAi based controls. These approaches will provide support the development of integrated pest management in OSR.

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Main Meeting Abstract 31

Paracidovorax citrulli employs multiple effectors to suppress NbPtr1-triggered cell death in *Nicotiana benthamiana*

Boyoung Kim[1,2], Yubin Jeon[3], Chang-Sik Oh[1,2,3,4,5]

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Plant pathogens deploy effector proteins to facilitate host colonization, whereas plant intracellular nucleotide-binding leucine-rich repeat (NLR) receptors recognize effectors and activate effector-triggered immunity (ETI), often culminating in localized programmed cell death known as the hypersensitive response (HR). To evade ETI, pathogens have evolved ETI suppressor effectors. *Paracidovorax citrulli*, the causal agent of bacterial fruit blotch (BFB), causes significant losses in cucurbit crops. Its pathogenicity relies on a type III secretion system that delivers effectors into host cells. Given that no genetic resistance to BFB has been identified to date, we hypothesized that *P. citrulli* encodes ETI suppressor. Using the solanaceous plant *Nicotiana benthamiana* as a surrogate host, we screened 64 predicted effectors by transient expression and identified six effectors that induced cell death. Genetic analyses revealed the involvement of coiled-coil NLRs (CNLs) in their recognition. To identify the responsible CNL, we silenced five *N. benthamiana* NLR genes previously reported to recognize effectors from diverse bacterial pathogens. HR induced by one effector was abolished in *NbPtr1* (*Pseudomonas syringae* pv. *tomato* race 1 resistance)-silenced plants, indicating recognition by NbPtr1. Notably, several *P. citrulli* effectors suppressed or attenuated NbPtr1-mediated cell death, suggesting that they function as ETI suppressors. We are generating deletion mutants lacking individual or multiple ETI suppressors and will examine whether these deletions affect the virulence ability of *P. citrulli* in host plants. Collectively, these findings advance our understanding of the virulence mechanisms by which *P. citrulli* overcomes ETI and provide insight on the molecular arms race between the pathogen and its host.

Surveillance Session Abstract 1

PhytoBacExplorer: A Genomic Platform for Plant Pathogen Population Genomics, Surveillance and Diagnostic Development

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The rapid growth of publicly available bacterial sequencing data presents unprecedented opportunities to investigate the evolution, epidemiology and diversity of plant pathogens. However, differences in data quality, assembly methods and analytical workflows can hinder large-scale comparative analyses and the development of robust diagnostic tools.

We present PhytoBacExplorer, a web-based genomic platform for the analysis of major plant pathogenic bacteria. Built upon the EnteroBase framework, PhytoBacExplorer currently contains over 10,000 genomes from the Xanthomonas/Xylella, Pseudomonas and Ralstonia species complexes. To ensure consistency across datasets, raw sequencing reads are retrieved from public repositories and processed through standardised assembly, annotation and typing pipelines, enabling reliable comparison between isolates generated by different studies and laboratories.

In addition to providing access to curated public datasets, PhytoBacExplorer allows users to upload their own sequencing data for automated assembly, annotation and genomic characterisation. New isolates can be rapidly placed within a global population context, facilitating species identification, lineage assignment and comparative analysis.

As part of the project, over 500 strains from the Warwick HRI (WHRI) and National Collection of Plant Pathogenic Bacteria (NCPPB) collections have been sequenced and incorporated into the resource. These include historically important isolates spanning more than 100 years, creating opportunities to investigate long-term pathogen evolution, lineage persistence and the emergence of economically important disease-causing populations.

The platform has also enabled the development of DiPPER2 (Diagnostic Primer Picking and Evaluation Pipeline for Reproducibility and Reliability), which identifies unique diagnostic targets from large genome collections, designs conventional and quantitative PCR assays, evaluates their specificity and sensitivity in silico, and generates comprehensive reports to support assay development.

By integrating large-scale comparative genomics, historical collections, user-submitted sequence analysis and diagnostic assay development within a single framework, PhytoBacExplorer provides a valuable resource for plant pathology research, surveillance, diagnostics and biosecurity. Ongoing development is extending the platform beyond genome typing to include annotation and comparative analysis of pathogen-associated features, including effector repertoires, mobile genetic elements and other determinants relevant to virulence, host adaptation and disease emergence.

Surveillance Session Abstract 2

Gene expression polymorphism linked to virulence diversification in wheat yellow rust

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Puccinia striiformis f. sp. *tritici* (*Pst*), the causal agent of wheat yellow rust, is the most damaging wheat rust pathogen in Europe. Recently, three distinct *Pst* races (termed Kalmar, Amboise, and Benchmark) emerged and became prevalent across Europe. Named after the wheat varieties where they were first detected, these three *Pst* races differ in virulence profiles, notably with Kalmar and Amboise *Pst* isolates virulent on the three wheat varieties and Benchmark *Pst* isolates virulent only on Benchmark. To investigate the molecular basis of virulence diversification among these *Pst* races, we first combined comparative genomics and pathology-based race profiling, revealing that these races emerged through diversification within the *PstS10/Warrior(–)* lineage, which was first reported in Europe in 2014. Next, we searched for gene sequence variation between the *Pst* races and found that no specific gene isoforms could explain the differences in virulence profiles. However, analysis of gene expression profiles revealed that all Kalmar and Amboise *Pst* isolates lacked expression of a single gene, *PST130_P495001*, whereas all Benchmark *Pst* isolates retained high levels of expression. Further characterisation of *PST130_P495001* demonstrated that it possesses classical effector features: it is short, is highly expressed in haustoria and has a functional signal peptide that was confirmed in a Yeast Signal Trap assay. To further examine the relationship between *PST130_P495001* expression and *Pst* virulence, Host-Induced Gene Silencing (HIGS) was performed using a Benchmark-derived *Pst* isolate that normally expresses *PST130_P495001* and is avirulent on the wheat variety Kalmar. Silencing *PST130_P495001* significantly increased fungal biomass of the Benchmark *Pst* isolate during Kalmar infection. Additional analysis of *Pst* field isolates also found that those with low *PST130_P495001* expression were only found on wheat varieties with shared parentage, which also exhibited high infection levels with a Kalmar-derived *Pst* isolate lacking *PST130_P495001* expression. These findings support *PST130_P495001* as a candidate avirulence effector, with the corresponding resistance gene likely within this shared host lineage. Together, these results suggest that loss of *PST130_P495001* expression may have contributed to recent virulence gains within the *PstS10* lineage. Thus, highlighting the important role of expression polymorphisms in facilitating potential virulence gains for the wheat rust pathogens.

Surveillance Session Abstract 3

Genetic analysis of potato late blight R genes in differential sets

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Potato late blight, caused by *Phytophthora infestans*, remains a major threat to global potato production. In the 1950s, the Black and Mastenbroek differential sets were developed in Scotland and the Netherlands to standardise the nomenclature and virulence classification of *P. infestans* populations. These differential lines were generated by introgressing late blight resistance (*R*) genes from *Solanum demissum* into cultivated potato, *Solanum tuberosum*, producing plants thought to contain single resistance genes, designated *R1–R11*. However, increasing evidence has shown that many of these differential plants possess multiple *R* genes, complicating their use in accurately characterising *P. infestans* pathogenicity profiles and potato breeding.

This study uses resistance gene enrichment sequencing (RenSeq) to investigate the genetic composition of *R* genes within the Black and Mastenbroek differential sets.

Amongst the differential set, there are still unidentified resistance genes, such as *Rpi-R4*, which contributes to the recognition of Avr4 in the MasR4 differential plant. Furthermore, virulence towards the R5 differential plant remains relatively rare within the *P. infestans* population, suggesting the presence of additional resistance genes within the differential lines. Through independent RenSeq-based association genetic studies, this work addresses these questions by identifying candidate genes corresponding to *Rpi-R4* and *Rpi-R5,* which could be identical to *Rpi-Smira1*. The identification of *Rpi-Smira1* represents a novel finding within the differential sets and further highlights the genetic complexity underlying these historically important differential lines.

Surveillance Session Abstract 4

Detection of Acute Oak Decline-associated bacteria in declining cork oak trees in Sardinia (Italy)

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Cork oak (*Quercus suber* L.) is an emblematic tree species of major ecological importance across the western Mediterranean, especially in Sardinia, where it is a key component of forest and silvo-pastoral systems and an important resource for the regional economy. In recent decades, cork oak forests have been increasingly affected by decline phenomena driven by interacting biotic and abiotic agents. In Mediterranean regions, these events are generally consistent with the Chronic Oak Decline (COD) pattern, characterised by slow disease progression and associated with environmental stressors, root-rot pathogens, canker-causing fungi and insect pests. In contrast, Acute Oak Decline (AOD), a rapid decline syndrome associated with stem bleeding and a bacterial complex, has been well documented in the UK and across Europe in temperate oak species, whereas evidence of AOD-associated bacteria in Mediterranean oaks remains scarce. Nevertheless, recent findings suggest the occurrence of this syndrome in Mediterranean oak ecosystems, particularly affecting holm oak, while its presence on cork oak is currently restricted to a single report from Portugal. Given the limited records of AOD in Italy, a survey was conducted in declining oak stands in Sardinia, including a cork oak-dominated woodland, to investigate the occurrence of bacterial agents associated with the disease. Exudates from stem bleeds were sampled from recently debarked trees showing sudden crown wilting and dieback using sterile swabs. Bark and inner bark tissues were also collected from surrounding necrotic areas. Swab and tissue samples were screened for AOD-associated bacteria using a multiplex real-time PCR assay. Positive samples were subsequently used for bacterial isolation. Resulting colonies were morphologically characterised, and representative isolates identified through real-time PCR. The identity of selected isolates was further confirmed by sequencing the 16S and gyrB loci. In parallel, small fragments of necrotic tissues beneath weeping patches were used for fungal isolation. Identification of fungal isolates was confirmed by ITS rDNA sequencing. *Brenneria goodwinii* and *Gibbsiella quercinecans,* as well as *Diplodia corticola,* were consistently detected. In addition, exit holes and adults of the wood-boring beetle *Platypus cylindrus* were observed, suggesting a possible role of multiple interacting biotic agents in symptom development. Inoculation assays were performed on freshly cut cork oak logs to assess the pathogenicity of AOD-associated bacteria and *D. corticola* and to evaluate potential synergistic interactions. Results of the field survey and inoculation trials will be presented.

Surveillance Session Abstract 5

Genomes of the pathotypes of Plasmodiophora brassicae causing clubroot on winter oilseed rape in Poland

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Genome sequencing of five *Plasmodiophora brassicae* isolates representing different pathotypes was performed using the Illumina MiSeq platform. Root galls were propagated using the single-club isolate method. To obtain the *P. brassicae* spore suspension for DNA sequencing, a modified methodology according to Mehrabi et al. (www.bio-protocol.org/e2864) was employed. Subsequently, DNA extraction was performed from the spores of individual *P. brassicae* pathotypes. In the initial stage of DNA isolation, the material was ground in liquid nitrogen using a porcelain mortar. DNA was isolated using the semi-automated Maxwell® 16 FFS Nucleic Acid Extraction System (Promega GmbH, Madison, WI) according to the manufacturer's protocol. DNA quality was verified on a 1% (w/v) agarose gel stained with 0.5 µg/ml ethidium bromide. The concentration and purity of the DNA samples were assessed spectrophotometrically and fluorometrically. For genome sequencing, appropriate genomic DNA libraries of the pathogen were prepared using the Nextera XT DNA Library Preparation Kit (Illumina Inc., San Diego, CA). The libraries were sequenced on the Illumina MiSeq platform with 250 bp paired-end reads using the MiSeq Reagent Kit v3 (Illumina Inc.). Sequencing encompassed both the mitochondrial and nuclear genomes. The quality of the obtained raw reads was evaluated using the FastQC tool. The raw reads were trimmed (removing reads with a PHRED score <20), and the clean *P. brassicae* reads were subsequently mapped to the reference sequence PRJEB24736 (GenBank, NCBI) using the default medium-low sensitivity parameters of Geneious Prime software (v.22.1.1). The mapped regions of coding sequences (CDS) were extracted and re-mapped against the *P. brassicae* reads with high sensitivity (minimum overlap >50 bp and minimum overlap identity >96%). Bioinformatic analyses were performed according to the protocols described by Pszczółkowska et al. (2016).

The genomes were composed of 20 chromosomes with total length 25,246,849 bp. The analysis used 9,230 protein coding genes. Each isolate mapped with ~99% quality. Most of genetic variables was the SNP type. The analysis evaluated the most critical locations within the gene structure, including coding sequences (CDS) and intron regions. The highest number of identified variables in CDS regions had a synonymous effect on translation. The number of significant changes with a missense effect was relatively low but existent. A consistent trend of the above was observed in each comparison of the five *P. brassicae* isolates.

Surveillance Session Abstract 6

Powdery mildews everywhere: Where do all the new species come from?

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Powdery mildews – obligate biotrophic pathogens infecting more than 10,000 dicot and monocot species – are seldom regarded as highly invasive fungi, despite historical examples including the rapid spread of grapevine and gooseberry powdery mildews across Europe in the 19th century; and many recent reports of diverse species appearing in new regions worldwide [1]. Across Europe, including the UK, the emergence of powdery mildews on horse chestnut and *Catalpa* trees planted as ornamentals in urban areas have been clear examples of the invasiveness of two species apparently introduced from North America. In contrast, tomato powdery mildew appears to have been introduced to North America from Europe. Population genetic studies are still needed to test these assumptions.

The global spread of powdery mildews is best documented for *Blumeria graminis* infecting wheat, supported by analyses of 172 genomes [2]. Hybridisation events may have contributed to the invasiveness of several powdery mildew species; the most prominent example is the emergence of triticale powdery mildew, a hybrid between wheat-pathogenic and rye-pathogenic *Blumeria* lineages [3].

Host range expansions appear to underlie many recent records of powdery mildews on plants not previously reported as hosts, either within their known distribution ranges or in newly colonised geographic areas. *Podosphaera xanthii*, a species primarily associated with cucurbits, and *Erysiphe quercicola*, mostly known from woody hosts, are two examples of powdery mildews that have been recently reported from a wide range of new, sometimes unrelated hosts worldwide.

Australia likely represents an entire continent that remained free of powdery mildews until European colonisation began in 1788. All species, including those infecting native Australian plants, appear to have been introduced only recently, with some now capable of infecting native species encountered in their new environments [4]. Therefore, the Australian continent may offer a special environment to study the rapid evolutionary processes of powdery mildew populations in the field. Further experimental and genome-level studies are needed to decipher the mechanisms of host range expansions in this highly successful group of plant pathogens.

Reference:

1. Thines *et al.* (2023) *In:* S Pöggeler & T James (Eds.) Evolution of Fungi and Fungal-Like Organisms, The Mycota 14, pp. 123-148.

2. Menardo *et al.* (2016) Nature Genetics 48: 201-205.

3. Sotiropoulos *et al.* (2022) Nature Communications 13: 1-14.

4. Kiss *et al.* (2020) Frontiers in Microbiology

Surveillance Session Abstract 7

Targeted intact whole genome sequencing as a diagnostic tool to indicate virus viability

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Tomato brown rugose fruit virus (ToBRFV) is a member of the genus *Tobamovirus*. Since emerging in Israel and Jordan in 2014/2015, it now affects tomato production around the globe and is a focus for regulatory phytosanitary controls. ToBRFV is highly stable, readily transmissible by contact and through seed-borne-transmission. Viral RNA is still detectable by real-time RT-PCR from seed samples and contaminated surfaces even after heat or chemical treatments have inactivated the virus (Davino et al., 2020; Skelton et al., 2023). Currently, bioassay using a local lesion indicator host plant is the standard method to verify the viability of the virus (ISF, 2024). This method lacks reliable sensitivity, requires skill, and takes up to 21 days to obtain a result making it unsuitable as a routine test.

In this study, targeted whole genome sequencing by combining long range PCR using the Flongle (Oxford Nanopore Technologies) has been developed to detect the intact whole genome of ToBRFV. This technique has been compared to RT-PCR, real-time RT-PCR, ELISA and bioassay. The suite of detection methods has then been used to investigate the difference between the detection of heat treated (non-viable and partially viable) and untreated (viable) virus samples to allow inferences to be made regarding the viability of detected virus.

The results indicated that intact whole genome sequencing could be used as a proxy diagnostic tool in indicating the virus viability in diagnostic samples allowing inferences of biological relevance directly from the diagnostic test. The latest results and potential applications of this approach will be discussed.

References:

Davino et al. 2020. Plants 9(11):1615.

Skelton et al. 2023. Viruses 15(10):2076

Surveillance Session Abstract 8

Fungal Antimicrobial resistance; the very low hanging fruit

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Our knowledge of the global extent of fungicide resistance (or antifungal resistance if we are referring to clinical fungal pathogens) is very patchily distributed across the world. We know from FAO data that fungicide use is found in nearly every country. Recent modelling studies have highlighted risk factors for resistance, related to fungicide class, pathogen characteristics and use patterns. We can therefore predict in which regions, on which crops, which pathogens are likely to be impacted by resistance. There is a large discrepancy between the prediction and demonstration of resistance. This is important as the continued use of fungicides where resistance has occurred is wasteful and environmentally damaging.

To address this gap, we have conducted a systematic review of studies of fungicide resistance and surveyed experts in all parts of the world. The results show that collection of data on fungicide resistance is very limited. Of particular concern is the almost complete absence of data from many low and middle income countries. We have identified two cases where molecular diagnostic kits could be deployed for easily detected target site mutations; G143A for Qoi and E198X for MBC fungicides.

Resistant pathogens are not only a major threat to a particular region but are capable of spreading from one region to another. A key message is to call upon the appropriate authorities to redouble efforts to ascertain patterns of pesticide use and focus particularly on areas where these patterns have been shown to lead inexorably to resistance.

Surveillance Session Abstract 9

A Likelihood Framework for Estimating Infection Efficiency in Inoculation Experiments

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Inoculation experiments are fundamental in studying plant-pathogen interactions, providing critical insights into the efficacy of chemical control, mechanisms underlying disease resistance/susceptibility, and responses to environmental change. However, conventional analyses based on aggregated disease incidence or severity can obscure underlying infection dynamics, particularly when high inoculum doses cause symptom masking. We present a likelihood framework to estimate infection efficiency from paired measurements of inoculum dose rates and disease incidence, without the requirement of counting infection points. The likelihood of formulation naturally yields principled estimation of uncertainties; this enables the derivation of formulae for the optimal inoculum dose rate and lower bounds on sample sizes required for a given level of precision. The methodology is validated using controlled-environment data for septoria tritici blotch [1], which serves as an illustrative example of application. Although developed for foliar diseases, the framework is applicable, in principle, to infectious diseases affecting any plant organs. The approach is well suited both to high-throughput experiments, using imaging and computer vision for disease measurement, as well as smaller scale experiments relying on visual disease measurements.

Reference:

[1] Karisto, P., Dora, S. and Mikaberidze, A. (2019), Measurement of infection efficiency of a major wheat pathogen using time-resolved imaging of disease progress. Plant Pathology, 68: 163-172.

Surveillance Session Abstract 10

Rapid Seedling-Based Screening of Fusarium Root Rot Resistance in Wheat Using Automated Imaging

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Fusarium species are globally distributed soil-borne pathogens that reduce wheat production and contaminate grain with mycotoxins, posing risks to human and animal health. Reliable assessment of *Fusarium* root rot resistance remains challenging due to strong environmental effects, uneven soil inoculum distribution, and the labour-intensive nature of destructive scoring. To address this bottleneck, we developed an automated high-throughput phenotyping system based on the Macrobot platform for quantitative image-based assessment of *Fusarium* root rot in wheat seedlings. A panel of 40 winter wheat genotypes was inoculated with *F. culmorum* and *F. graminearum* under controlled conditions, and disease progression was imaged daily from 1 to 4 days post-infection. The resulting image series were used to quantify root rot development in a standardised and reproducible manner and lesion area was quantified based on lesion length and brown discolouration intensity. Fungal colonisation and infection dynamics in roots were confirmed by confocal and light-sheet microscopy. This study presents the development of a rapid screening system for root rot resistance and evaluates the relationship between seedling root rot responses and field-derived Fusarium head blight scores.

Surveillance Session Abstract 11

Airborne cereal pathogen surveillance using AirSeq

Jade van Wijk[1], Darren Heavens[1], Charlotte Hayes[2], Diane Saunders[3], Paul Nicholson[3], Matt D. Clark[4], Richard M. Leggett[1]

Earlham Institute, UK [2]Elsoms Wheat, UK [3]John Innes Centre, UK [4]Natural History Museum, UK

Wheat provides roughly 20% of caloric intake worldwide, making it vitally important to protect. Some of the biggest threats to wheat production include the cereal rusts *Puccinia striiformis* f. sp*. tritici (Pst)* and *P. triticina (Pt),* which cause yellow rust and brown rust respectively. Pst alone is known to cause yield losses of up to 5.5 million tonnes annually worldwide (Beddow *et al*., 2015). The obligate biotrophic nature of these pathogens also makes them impossible to culture and therefore difficult to study pre-infection. Here, we apply AirSeq, a novel sequencing-based approach for studying environmental bioaerosols, to monitor rust and other cereal pathogens on farms.

Using AirSeq, we have asked: (i) Can fungi be detected in the air before crop infection occurs? (ii) How long before infection occurs? (iii) How does weather and other environmental conditions affect the air microbiome and fungi within it? (iv) How can AirSeq insights be utilised within Integrated Pest Management strategies (IPM) to prevent unnecessary fungicide applications to crops, reduce costs and improve sustainable farming practices?

Here we present surveillance data taken from multiple commercial UK wheat breeding sites and from a research farm at regular intervals across seasons (Spring to Winter). This data was collected over several years for robust comparisons. Infected leaf samples were also collected at the same time as air, along with meteorological data and field disease scoring observations. We demonstrate AirSeq’s ability to act as an early warning system for cereal rust pathogens, with air-detected pathogen levels rising in advance of leaf detected infections. We also show the influence the weather has on disease spread.

Surveillance Session Abstract 12

Using bees as surveillance sentinels for pollen-transmitted viruses: detection of a novel nepovirus isolated from Tilia in hive debris and pollen

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A key obligation of any country seeking to control imports for the purposes of plant health is to prove absence from a given pathogen. Such proof requires laborious monitoring and surveillance efforts, often involving costly field work and extensive lab testing. Surveillance sentinels, such as pollinators, present a promising alternative to this by gathering pollen from within their foraging area as part of their ecological role and depositing them where humans may collect them. Bees are a good example of this as they are also present over an extensive network of hives and beekeepers that can be found at national level. Pollen may be sampled either from the hive, where it is stored in cells, or from the debris beneath the hive containing fragments of bees, comb, shed pollen etc. To investigate the potential usage of bees as natural samplers for pollen-transmitted viruses, Tilia nepovirus 1 (TiNV1) was chosen as the focus of this work due to being recently described with limited knowledge regarding its distribution in the UK.

Paired samples of pollen (n=23), hive debris (n=24) and *Tilia* leaf tissue (n=63 from n=33 trees located near the sampled hives) were sourced from 28 beehives in York and the surrounding countryside. An extraction method was developed to obtain high-quality RNA from these matrices which contain wax that can present a challenge for amplification. We used the Nucleospin RNA Plant Mini Kit with a modified protocol using a melting step and a grinding step for the hive debris and pollen samples respectively. Two qRT-PCR assays, designed to detect RNA1 and RNA2 respectively, were then employed. TiNV1 was detected in 16/28 (~60%) of hives and 19/33 (~57%) of trees. 9 hives (~32%) tested positive only for pollen and 2 hives (~7%) tested positive only for hive debris, suggesting that both have diagnostic utility when combined. This case study indicates the promise of bees as natural samplers for pollen-transmitted viruses utilising local beekeepers to assist in plant health monitoring.

Surveillance Session Abstract 13

Microfluidic Biosensors for the Detection of Motile Plant Zoospores

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Zoospores are central to the dispersal and infection cycles of many devastating plant pathogens, making their early detection critical for effective disease management. However, current diagnostic approaches rely on labour-intensive sampling and laboratory assays that lack real-time, in-field capability. To address this gap, we developed an innovative microfluidic zoospore-sensing platform that combines chemotactic enrichment with impedance-based single-particle detection. The device integrates a microfluidic sampling module, a microfluidic cytometer, and a controlled chemical gradient that selectively guides motile spores into a detection channel. Zoospores of *Phytophthora cactorum* were shown to actively swim up the attractant gradient and traverse a pair of microelectrodes, producing measurable transient impedance shifts. Single-zoospore detection was achieved with signal-to-noise ratios of ~17 under carrying flow and ~5.9 when spores entered solely through chemotaxis. This work demonstrates a selective, sensitive, and real-time detection strategy for motile zoospores and provides a promising foundation for future development of portable, remotely addressable, low-cost biosensing systems for field-based pathogen surveillance. In this presentation, I will review emerging sensor-based technologies for plant pathogen detection and discuss their potential to enhance early disease detection, surveillance, and response strategies.

Reference:

Zhang, P., Williams, D. E., Stephens, L., Helps, R., Pushparajah, I. P. S., Travas-Sejdic, J., & Wood, M**.** (2025). Microfluidic Biosensors for the Detection of Motile Plant Zoospores. *Biosensors*, *15*(3), 131. https://doi.org/10.3390/bios15030131

Endophyte Session Abstract 1

Utilising Native Endophytes for Pathogen Inhibition in Barley

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As climate change alters plant pathogen range and the growing occurrence of fungicide resistance in agricultural systems increases, growers are in desperate need for alternative methods to manage pathogens. Fungal endophytes are a commensal to mutualistic polyphyletic group of organisms that grow within the tissues of nearly all plants. They have shown to cause a variety of different effects on their hosts plants, one of these being plant pathogen through a diverse range of mechanisms. Specifically, fungi within the genus *Epichloë* form intimate, long-lasting endophytic interactions with grasses in the subfamily *Pooideae*. Although native to Europe, these fungi were introduced and are currently used within the pasture grass industry in the Americas and New Zealand towards pest deterrence. Some *Epichloë* spp. have shown promising results in reducing disease in their native host grasses, however, little work has been done on agriculturally important cereal crops and associated plant pathogens. Barley (*Hordeum vulgare*) is one of the most widely grown crops in the UK and is heavily infected by many fungal pathogens. Establishing a stable, compatible symbiosis between *Epichloë* endophytes and barley, and determining whether these endophytes suppress common barley pathogens, could provide a novel strategy to improve grain yield and plant health while reducing the reliance of fungicides.

Endophyte Session Abstract 2

Festulolium–Epichloë symbiosis: Suppressing stubby root nematodes and delivering nematotoxic plant metabolites

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This study investigated the potential of utilising cool season grasses naturally associated with *Epichloë* endophytic fungi for the management of plant-parasitic stubby root nematodes (*Trichodorus* spp. and *Paratrichodorus* spp.). Stubby root nematodes are economically important in East England where they cause docking disorder in sugar beet, resulting in up to 50% root yield reduction. The limited availability of chemical nematicides due to environmental concerns warrants more eco-friendly measures. *Epichloë* fungal endophytes confer protection from herbivory to their cool-season grass hosts via production of alkaloids. Several species produce loline alkaloids, known for insecticidal, insect-deterrent, and nematode-inhibiting properties, affecting mobility, egg hatching, and mortality.

In this study, *Festulolium loliaceum* and *Epichloë uncinata* were investigated for suppressing stubby root nematodes. In a field experiment in Docking, Norfolk, endophyte-infected grasses reduced nematode reproduction seven times more compared to endophyte-free grasses. Laboratory experiments showed that extracts from shoots and roots immobilized nematodes. Age, source, and concentration of the grass significantly affected nematicidal activity. Extracts from younger grasses were more potent; shoot extracts from 8-week-old endophyte-infected plants had six times lower LD50 values than 20-week-old plants. In contrast, root extracts from older plants were more potent than extracts from younger plants, although overall they had lower potency compared to shoot extracts. Overall, the results suggest that endophyte-infected grasses could serve as a potential cultural management strategy for stubby root nematodes in a sugar beet crop rotation system, with scope for optimisation to support nematode suppression under field conditions.

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Endophyte Session Abstract 3

Genetic links between rice immunity, phyllosphere microbiome assembly and bacterial blight resistance

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Plant disease outcomes are shaped not only by host immune genes and pathogen virulence factors, but also by the microbial communities that occupy plant tissues. In rice, the leaf microbiome represents a potential interface between genetic resistance and pathogen establishment, yet the host mechanisms that structure these communities and their contribution to bacterial blight (BB) resistance remain unclear. We investigated whether rice genes involved in disease resistance and microbiome assembly act through shared biological pathways that influence interactions with *Xanthomonas oryzae* pv. *oryzae* (*Xoo*).

Using rice near-isogenic lines carrying different BB resistance genes, we compared leaf microbial community responses before and after *Xoo* inoculation. These analyses showed that resistance-gene backgrounds were associated with distinct shifts in the leaf microbiome following pathogen challenge, suggesting that host immune genotype contributes to microbiome restructuring during infection. In parallel, we characterized OsCatA, a catalase gene identified through a leaf microbiome genome-wide association study as a determinant of core phyllosphere microbiota. Loss of OsCatA function altered the interaction between rice and *Xoo* and enhanced resistance to *Xoo* isolates with low catalase activity. These findings implicate host redox regulation as a mechanism connecting microbiome assembly, pathogen oxidative-stress tolerance and bacterial blight outcome.

Together, our results support a model in which rice immune genes and microbiome-regulatory genes jointly shape the phyllosphere environment encountered by invading pathogens. This work provides a genetic and mechanistic basis for developing microbiome-informed approaches to improve BB resistance of rice.

Endophyte Session Abstract 4

Invisible Defenders: Harnessing Endophytes for Sustainable Plant Protection

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The discovery of *Epichloë* fungal endophytes in cool-season grasses fundamentally reshaped our understanding of plant–microbe interactions in agriculture. Early observations of vertically transmitted endophytes in grasses were followed by pivotal discoveries linking Epichloë infections in tall fescue to livestock toxicosis. While these findings initially highlighted a major agricultural challenge, they also sparked decades of research revealing the profound ecological roles these symbionts play in plant health and productivity. Subsequent studies demonstrated that *Epichloë* endophytes can enhance host fitness by improving tolerance to drought, insect herbivory, and environmental stress. Advances in endophyte biology and grass breeding have led to the development of novel endophyte cultivars that retain plant protection while minimizing livestock toxicity, illustrating how fundamental discoveries can be translated into practical solutions for sustainable pasture systems. These benefits are often associated with a diverse array of bioactive alkaloids and other secondary metabolites produced by the endophyte. Increasingly, genomic analyses are revealing how the organization and evolution of these biosynthetic pathways contribute to the chemical diversity that shapes plant–insect and plant–microbe interactions.

Building on this foundation in forage grasses, emerging research suggests that *Epichloë* endophytes may also provide novel disease protection in cereal crops. Experimental work with wheat indicates that plants colonized by *Epichloë* exhibit reduced severity of powdery mildew caused by *Blumeria graminis* f. sp. *tritici*. Early infection-stage observations suggest the presence of the endophyte limits pathogen penetration, pointing to new mechanisms of disease suppression. Together, these advances highlight the potential of endophytes as microbial tools for sustainable crop protection, expanding their role from pasture symbionts to promising biological solutions for managing plant disease and strengthening future food security.

ECPP Poster Abstract 1

AVR2-like effectors from diverse fungal pathogens are recognised by the tomato immune receptor Cf-2

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The tomato receptor-like protein (RLP) Cf-2 detects the *Cladosporium fulvum* effector AVR2 indirectly: AVR2 inhibits the apoplastic protease Rcr3, and Cf-2 monitors Rcr3 perturbation to trigger cell death. We searched for AVR2-related sequences across fungal genomes and identified unannotated homologs in pathogens of non-Solanaceous crops. Co-expression of several AVR2-like proteins with SlCf-2 and SlRcr3 in *Nicotiana benthamiana* triggered cell death, confirming recognition by the Cf-2/Rcr3 surveillance system. Structural modelling predicts that these homologs, like AVR2, act as protease inhibitors of Rcr3, indicating a conserved mechanism of action across the family. That these effectors were absent from existing annotations suggests functionally important secreted proteins remain hidden in fungal genomes, and that effector conservation across pathosystems is more widespread than currently appreciated. We are now testing natural Rcr3 alleles from diverse Solanaceae species to determine whether allelic variation expands recognition to additional AVR2-like proteins, and using the structural models to predict which effector–allele combinations will be recognised. Transferring functional Cf-2/Rcr3 combinations into new crop backgrounds through receptor engineering is the long-term goal.

ECPP Poster Abstract 2

Contrasting physiological and transcriptomic responses highlight cultivar-specific tolerance to Peronospora variabilis in cañahua and quinoa

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Cañahua (*Chenopodium pallidicaule*), the closest domesticated diploid relative of quinoa (*C. quinoa*), provides a valuable system to investigate plant–pathogen interactions due to its simpler genome and resilience to environmental stress. Downy mildew, caused by *Peronospora variabilis*, represents a major constraint for quinoa production, and biocontrol strategies such as *Trichoderma* spp. offer promising alternatives. However, the molecular mechanisms underlying host responses and *Trichoderma*-mediated modulation remain poorly understood.

Here, we investigated the physiological and transcriptomic responses of quinoa and cañahua cultivars during infection with *P. variabilis*, in the presence or absence of *Trichoderma* strains T-22 and Bol12QD. Disease progression was quantified using image-based analysis and qPCR, while RNA-seq was used on cañahua plants to characterize host responses.

The cañahua cultivar Lasta exhibited enhanced resistance compared to Illimani and quinoa cultivars. Reduced chlorosis and lower pathogen colonization were observed on Lasta cultivar; in contrast, Illimani displayed pronounced disease symptoms and higher susceptibility. Gene ontology enrichment analysis revealed distinct response strategies between cultivars. The Lasta cultivar was associated with metabolic reprogramming and activation of stress-related pathways, including autophagy. In contrast, Illimani showed enrichment of extensive catabolic processes, including cell wall degradation, pigment breakdown, and nitrogen starvation, consistent with induced tissue damage.

Distinct transcriptional responses we also observed in the presence of *Trichoderma*, indicating a modulatory effect of this biocontrol agent on host defence pathways. Together, these findings suggest that tolerance against *P. variabilis* is linked to coordinated metabolic and stress responses, whereas susceptibility is associated with widespread cellular degradation. This work provides new insights into host–pathogen interactions and highlights potential targets for improving disease resilience in quinoa and its relatives.

ECPP Poster Abstract 3

Where is FHB resistance in Oats? An exploratory study with Fusarium culmorum

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Fusarium head blight (FHB) is one of the most devastating diseases affecting cereal crops. The main causal agents of FHB are several species within the Fusarium genus, including *Fusarium culmorum*. Although FHB poses a global threat to food security, only a limited number of genes have been clearly associated with effective resistance. However, these genes do not confer effective resistance to the pathogen. Instead, currently known resistance QTLs alter spikelet architecture or delay flowering time, thereby reducing the probability of infection.

The situation is even more challenging in oats, where no resistance genes against FHB have been identified, and disease symptoms are more difficult to detect than in other cereals. As oats are a major source of carbohydrates for animal feed and an important crop in northern and western European countries, identifying new sources of resistance to FHB is essential for the sector.

Here, we developed a screening pipeline for an oat diversity panel using an AI-aided image analysis approach. The screening can be completed within a few months, and we propose it has the potential of identifying stable and broad-spectrum resistance against FHB. Indeed, this pipeline allowed the identification of several novel QTLs and target genes that could lead to effective resistance against FHB in oats.

ECPP Poster Abstract 4

The Protective Role of Silicon in Grasses Against Fungal Pathogens Depends on Infection Mechanism

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Pathogen infection drives plant community structure and constrains global agricultural productivity. Silicon improves resistance to abiotic and herbivory stress, particularly in grasses, but relatively little attention has addressed silicon-mediated resistance to pathogens, nor has it tested how this varies according to the type of plant and pathogen or how it is altered by environmental factors.

We performed a meta-analysis to quantify the effect of silicon on pathogen disease severity and test the factors underpinning any positive outcomes. We identified 114 studies across 14 grass species and 31 pathogens, although most studies were on rice and wheat and the most common pathogens were rice blast and wheat rust. We tested how the beneficial effects of silicon on disease severity, crop biomass, and yield were affected by the mode of infection of the pathogen and environmental factors.

We found that pathogen infection significantly increased silicon accumulation. Application of silicon fertiliser decreased disease severity by 43% and increased biomass of infected plants by 35%. Soil application was more effective than foliar spraying. The disease suppressive effect of silicon was greater for pathogens producing appressoria, a structure involved in cell wall penetration and effector release, but lower against pathogens entering through stomata. Furthermore, silicon was more effective against pathogens that produce haustoria or infection hyphae, which are involved in nutrient acquisition.

Overall, our meta-analysis provides new insights into the positive effects of silicon at reducing disease severity and improving crop yield and demonstrates the crop-pathogen interactions where silicon treatment will be most effective in preventing crop losses to pathogen attack.

ECPP Poster Abstract 5

The desert thorn apple (Datura discolor) genome reveals an unexpected contraction of the NRC immune receptor network

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Members of the nightshade family (Solanaceae) have remarkable immune signalling pathways that include a complex network of sensor NLRs and helper NRC (NLR required for cell death) proteins. These expanded families of immune receptors has functionally diversified to confer resistance to diverse pathogens. Most Solanaceous plants possess 100s of NLR genes – including dozens of NRCs – yet the recently sequenced desert thorn apple (*Datura discolor*) has been found to have a substantially reduced immune receptor network. Comparative analyses suggest that this reduction is not species-specific and is shared amongst the *Datura* genus. Furthermore, many Datura NLRs are strikingly diverged and do not belong to known NLR subfamilies. These findings have revealed important gaps in our understanding of the of plant immune responses, laid the foundation for future research into the functional roles of NLR diversity, and point towards the importance of non-crop species for generating fundamental knowledge regarding the processes governing plant-pathogen interactions.

ECPP Poster Abstract 6

Towards structural and functional characterisation of lectins from the twayblade orchid (Neottia ovata)

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Lectins are carbohydrate binding proteins which are involved in a large range of biological processes such as plant defence and cell recognition. This project focuses on the Twayblade orchid (*Neottia ovata*, formerly *Listera ovata*) lectins which specifically bind to mannose. We have identified and cloned four lectins from the Twayblade orchid, this included three sequences previously described on the NCBI database as well as a fourth novel lectin. The aim of this project was to perform functional analysis and to characterise these lectin clones both individually and together. As well as antifeedant properties, lectins are also known to cause allergic-like responses in humans and, depending on the type of lectin, can cause human erythrocytes to agglutinate.

Sequence and structural analysis (AlphaFold) of the four lectins has identified highly conserved regions whilst suggesting that two structural forms of the lectin exist. By expressing the lectin genes in heterologous systems, we are undertaking experiments to determine how the identified structural and conserved domains of the lectins may be related to the lectin functions.

ECPP Poster Abstract 7

Bacterial hormone mimicry in potato blackleg disease

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Plants under attack rapidly fortify themselves. Defence hormones surge, antimicrobial environments are created and entry points such as stomata are sealed shut to restrict pathogen invasion. One step ahead, some pathogens can subvert these defences through molecular mimicry, secreting compounds that imitate plant hormones to redirect the immune response in their favour.

The jasmonate mimic coronatine is a well characterised example of this strategy in *Pseudomonas*, consisting of coronafacic acid (CFA) conjugated to coronamic acid (CMA). However, not all bacterial pathogens are equipped with the biosynthetic machinery required to produce coronatine. One example is *Pectobacterium atrosepticum* (*Pba*), a major driver of potato blackleg causing devastating losses to the UK potato industry, for which no effective control measures are available. *Pba* lacks the genes required for CMA production despite possessing conserved gene clusters associated with CFA synthesis and instead produces different CFA-conjugates predicted to act as jasmonate mimics during plant infection. The biological role and regulation of these compounds during potato infection remains poorly understood.

Our work investigates the regulation of CFA biosynthesis in *Pba*. Using transcriptional reporter assays and bacterial genetics, we are examining factors that influence expression of the CFA biosynthetic cluster. Understanding how bacterial jasmonate mimics are regulated during infection will provide new insight into potato–pathogen interactions and may support the development of future crop protection strategies.

ECPP Poster Abstract 8

Spatiotemporal dynamics of NRG1-mediated cytoplasmic and nuclear calcium signaling in TNL-ETI

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Toll/Interleukin-1 receptor (TIR)-domain NLRs (TNLs) are intracellular immune receptors that promote plant defense by producing signaling molecules (SMs) upon pathogen recognition. TNL signaling proceeds via SM-bound EDS1-family dimers and downstream CC^{HeLo}-domain helper NLRs, including ADR1s and NRG1s, which have been proposed to function as calcium-permeable channels. Although TNL activation is associated with characteristic calcium changes, how these signals are encoded and decoded remains poorly understood.

Here, we utilized GECO-based calcium sensors in transgenic *Arabidopsis thaliana* EDS1 pathway mutants to resolve the *in vivo* spatiotemporal dynamics of cytoplasmic and nuclear calcium signaling at single-cell level during TNL activation. Calcium levels in both compartments began to rise at ~1.5 h post pathogen challenging. Functional analyses demonstrate that NRG1s, but not ADR1s, act as the primary mediators of calcium influx in TNL immunity. Moreover, NRG1-dependent calcium elevation is required for robust host cell death and timely transcriptional reprogramming. Together, these findings provide *in vivo* evidence linking helper NLR function to calcium influx and identify compartment-specific calcium signatures as key regulators of TNL immune outputs.

ECPP Poster Abstract 9

Identification of MARVELlous Protein Markers for Phytophthora infestans Extracellular Vesicles

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Extracellular vesicles (EVs) are released from cells by unconventional secretion, but little is known about the biogenesis routes, composition or cargoes of EVs from fungal or oomycete plant pathogens. We investigated the proteome of EV-associated proteins secreted by the oomycete *Phytophthora infestans*, cause of potato late blight disease. We found that vesicle-associated proteins, transmembrane proteins and RXLR effectors, which are delivered into host cells to suppress immunity, were enriched in the EV proteome. By contrast, the EV-independent secreted proteome was enriched in cell wall modifying enzymes and apoplastic effectors which act outside plant cells. Two proteins each containing two tetraspanning MARVEL domains, PiMDP1 and PiMDP2, were associated with *P. infestans* EVs. PiMDP1 and PiMDP2 were co-buoyant with RXLR effectors in sucrose density fractions containing EVs and co-localised frequently with each other and with RXLRs at vesicles within pathogen hyphae grown in vitro and during infection. Interestingly, PiMDP2, which is up-regulated during the early biotrophic phase of infection, accumulates at the haustorial interface, a major site of effector secretion during infection. We argue that PiMDP1 and PiMDP2 are molecular markers that will facilitate studies of the biogenesis and secretion of infection-associated *P. infestans* EVs.

ECPP Poster Abstract 10

Engineered bacterial effector allows for ubiquitin-independent degradation of custom targets

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Protein degradation is a fundamental cellular process. In eukaryotes, one of the most important pathways for protein degradation is the ubiquitin–proteasome system, in which proteins are post-translationally modified by conjugation with ubiquitin chains. This pathway is exploited by several pathogens to promote or evade degradation of host proteins. Previously, we showed that SAP05, an effector from phytoplasmas (obligate intracellular plant–insect pathogens) can mediate the degradation of two families of transcription factors by directly recruiting them to the proteasome in a ubiquitin-independent manner. Here, by exploiting the natural diversity of SAP05-like domains and using a combination of biochemical, crystallographic, and artificial intelligence-based approaches, we engineered SAP05 to degrade new and unrelated targets in plants. This has significant potential as a tool for researching protein function, and for engineering biology approaches.

ECPP Poster Abstract 11

Decoding Peronospora viciae: Do repeats and genome size drive virulence?

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Pea is one of the most important legumes in European agricultural systems as it represents an excellent source of plant-based protein and improves soil health due to their interaction with *Rhizobium* bacteria. This reduces the fertiliser requirements and offers a more sustainable alternative to animal protein due to its lower carbon footprint [1]. However, pea production face significant challenges, with prevalence of diseases being one of the major constraints [2].

Pea downy mildew, caused by the oomycete pathogen *Peronospora viciae* f. sp. *pisi* (Pvp), is one of the most widespread and destructive disease of pea crops, particularly in temperate and cool, humid climates such as the UK. It can infect plants systemically through seedlings or locally on leaves and pods, leading to symptoms such as chlorotic lesions, stunted growth, and pod deformation. DM can cause losses of up to 75 % reported in severe outbreaks [3]. Effective management relies on a combination of resistant cultivars, crop rotation or sanitation.

To date, the Pvp genome has not been made available, drastically limiting our understanding of the plant-pathogen interactions taking place during infection, hence impacting our chances of successfully developing resistant pea lines. In this project, we have isolated a set of geographically distinct Pvp isolates, evaluated their *in planta* virulence, performed PacBio sequencing, and assembled their genomes to a near-chromosome level.

Here, we present the first two fully assembled and annotated Pvp genomes: one from the UK and one from Germany. Our preliminary findings showed that non-UK isolates exhibited overall higher virulence, potentially matching a larger genome size enriched in repetitive elements. Between the two genomes sequenced, orthogroup (OG) analyses showed that the German Pvp contained a higher proportion of species-specific OGs, reinforcing the hypothesis that those regions might be linked to higher number of virulence-associated genes. Effector annotation identified over 100 proteins in each isolate, with a slightly higher proportion found in the highly repetitive genome.

Future steps include the addition of more isolates to the dataset to build a pangenomic view of the Pvp population. By characterising these genomes, we aim to identify key virulence factors that contribute to disease management strategies that exploit both host and pathogen genetics.

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ECPP Poster Abstract 12

Investigating Histone Acetylation Dynamics During Plant Immune Responses

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Upon pathogen invasion, plant cells must rapidly translate elicitor perception into an appropriate cell-fate response by selectively reprogramming gene expression. A key mechanism controlling this targeted transcriptional response is local chromatin remodelling, which modulates chromatin accessibility. This process is mediated by covalent histone modifications, ATP-dependent chromatin remodelling complexes and DNA methylation.

Previous work from our lab has implicated the histone acetyltransferase GCN5 in disease resistance through the regulation of histone H3 lysines' 9 and 14 acetylation (H3K9ac and H3K14ac) levels at target genes[1]. GCN5 is recruited to target loci through interactions between its co-activator ADA2b with transcription factors. However, the transcription factors that recruit ADA2b remain unknown, and the role of the GCN5 complex in plant immunity is not yet fully understood.

This project investigates the dynamics of H3K9ac, an activating chromatin mark primarily deposited by GCN5, during plant immune responses. Using GFP-tagged mintbodies against H3K9ac[2,3], ChIP-seq, transcriptomics, and mutant analysis in *Arabidopsis thaliana*, we aim to track the H3K9ac fluctuation following pathogen perception and correlate it with active transcription. The overall goal is to uncover chromatin-based mechanisms of plant immunity.

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ECPP Poster Abstract 13

Insights into insect vectors and SBR-associated pathogens in Swiss sugar beet and potential reservoir crops

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Syndrome des Basses Richesses (SBR) is an emerging problem in European sugar beet production. Its spread is driven by interactions between infected plants, the SBR-associated pathogens *Candidatus* Arsenophonus phytopathogenicus (Ap) and *Candidatus* Phytoplasma solani-related strain (stolbur), and their vectors. In 2025, within the SBR programme coordinated by the Schweizerische Fachstelle für Zuckerrübenbau (SFZ-CBS) in collaboration with Agroscope, we conducted insect monitoring to document the distribution and abundance of *Pentastiridius leporinus* in Switzerland and to identify other insect species carrying SBR-associated pathogens. Insects were collected from commercial fields, with a focus on leafhoppers. A DNA extraction and detection workflow was established and validated using a multiplex qPCR assay targeting Ap and stolbur.

The 2025 monitoring confirmed presence of *P. leporinus* in several Swiss sugar beet fields, as well as in potato and carrot fields, and provided an overview of its seasonal dynamics. The monitoring in sugar beet was carried out in Eastern Switzerland, which had previously been free of infestation. The first, very few, positive plants were recorded in 2023 on individual sugar beets showing SBR-associated symptoms. In sugar beet, 35 out of 377 insects (9%) tested positive for Ap, including 30 *P. leporinus*, 3 *Laodelphax striatella*, 1 *Aphrophora* sp., and 1 *Reptalus artemisiae*. Two of the Ap-positive *P. leporinus* individuals in sugar beet were also positive for stolbur (group 16SrXII-P).

To assess pathogen carriage in alternative vegetable crops, 37 *P. leporinus* individuals from commercial potato fields and 32 from carrot fields were analyzed. In potatoes, 30 of the 37 individuals (81%) were positive for Ap, while none tested positive for stolbur. In carrots, 2 of the 32 individuals (6%) were positive for Ap and 1 for stolbur. No individuals from alternative crops carried both pathogens simultaneously.

Overall, the 2025 survey provides a first overview of *P. leporinus* populations in Swiss sugar beet and alternative crops, highlights a limited set of insect species carrying SBR-associated pathogens, and underscores the importance of continued monitoring, particularly given the detection of a stolbur-positive *P. leporinus* individual in carrots, suggesting potential reservoir roles of alternative crops.

ECPP Poster Abstract 14

RNP-Based CRISPR/Cpf1 Gene Editing Platform for Rapid Isolation and Characterisation of Fusarium oxysporum Mutants

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Fusarium oxysporum, a soil-borne fungal pathogen with a broad host range, poses significant challenges to global agriculture due to limited control strategies. This necessitates innovative approaches to elucidate its molecular mechanisms of virulence. We developed an RNP-based CRISPR/Cpf1(Cas12a) gene-editing system that delivers pre-assembled Cpf1 ribonucleoprotein complexes directly into *F. oxysporum* protoplasts. This approach achieves high editing efficiency while minimising exogenous DNA background by designing homologous recombination arms. We also developed a comprehensive pathogenicity assessment platform to evaluate RNP-edited *Fusarium* strains, showing that editing the *ura5*-EGFP strain results in significantly lower virulence than in wild-type strains. Fluorescence microscopy revealed dynamic colonisation within Arabidopsis roots, confirming the functionality of the edited strains for studying virulence genes. Additionally, microfluidic chip technology enables efficient single-cell isolation of edited protoplasts to facilitate mutant recovery, whilst whole-genome sequencing of *F. oxysporum* f. sp. *conglutinans* establishes a genomic database for systematic identification of virulence genes. This RNP-based workflow offers an efficient approach for gene editing and screening in *F. oxysporum*. It can be adapted to other *Fusarium* species, improving understanding of fungal pathogenicity and aiding the development of sustainable biocontrol strategies for crop resilience.

Keywords: *Fusarium oxysporum*, RNP-based CRISPR/Cpf1, protoplast isolation, pathogenicity assessment, microfluidic chip, whole genome sequence

ECPP Poster Abstract 15

Investigating the role of the Myzus persicae effector complex Mp1-Mp58 in targeting host cellular trafficking

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Aphids are phloem-feeding insects that cause significant crop loss worldwide. Understanding molecular plant-aphid interactions is important to underpin the development of new protection strategies. During infestation, aphids secrete effector molecules into host cells. Individual aphid effectors have been found to interact with host proteins to enhance susceptibility, but if and how they work together is largely unknown. We previously identified that the effector pair Mp1 and Mp58 from the aphid *Myzus persicae*, as well as orthologous pairs in other aphid species, form an effector complex. The Mp1-Mp58 complex targets the cellular trafficking protein VPS52 (a member of the Golgi-Associated Retrograde Protein (GARP) complex) at vesicle-like structures, pointing to targeting of cellular trafficking. Through co-immunoprecipitation combined with mass spectrometry (Co-IP-MS), we have since found that Mp1 and Mp58 interact with several components that mediate cellular trafficking in *N. benthamiana*, including the retromer complex, which facilitates endosome-to-Golgi trafficking. In addition, we have identified that specific components of the retromer complex interact with VPS52 upon transient expression in *N. benthamiana*. This finding links two highly conserved cellular trafficking complexes in plants, which had previously only been demonstrated in fungi. We are using a combination of biochemical approaches and functional characterisation assays to further determine the link between the GARP and retromer complexes in plants and whether the Mp1-Mp58 complex may be targeting cellular trafficking to promote susceptibility to aphids. Together, our work highlights important cellular trafficking mechanisms that may be altered by aphids, providing new insight into aphid effector-mediated targeting of host proteins.

ECPP Poster Abstract 16

Leveraging molecular mimicry of a pathogen virulence target to engineer multiple disease resistance by an NLR

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Plants and animals respond to pathogen attack by mounting innate immune responses that require intracellular nucleotide binding leucine-rich repeat (NLR) proteins. These immune receptors detect pathogen infection by sensing virulence effector proteins. However, the mechanisms by which receptors evolve new recognition specificities remain poorly understood. Here we report that a plant NLR has evolved the capacity to bind to a pathogen effector by acting as a molecular mimic of a virulence target of the effector, thereby triggering an immune response. The barley NLR Mildew Locus A 3 (MLA3) confers resistance to the blast fungus *Magnaporthe oryzae* by recognizing the effector Pwl2. Using structural analysis, we show that MLA3 has acquired the capacity to bind and respond to Pwl2 through molecular mimicry of the effector host target HIPP43. We demonstrate that the amino acids at the binding interface of MLA3 and Pwl2 are highly conserved in interface of HIPP43 with Pwl2, and are required to trigger an immune response. We used this discovery to bioengineer SR50—an MLA ortholog in rye that confers resistance to wheat stem rust—by introducing the Pwl2 binding interface of MLA3. The resulting chimeric receptor has dual recognition activities, conferring disease resistance to wheat stem rust and blast in barley transgenic lines. Collectively, these results provide evidence that plant immune receptors have evolved sophisticated mimicry strategies to counteract pathogen attack, and this knowledge can be leveraged to engineer multiple disease resistance by NLRs.

ECPP Poster Abstract 17

Identification and validation of candidate genes for resistance to mildew diseases in pea

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Pea (*Pisum* sativum) is an economically important crop valued for its nitrogen-fixing capabilities and high protein content. However, pea production suffers from several biotic stresses, including downy mildew, caused by *Peronospora viciae*, and powdery mildew, caused by *Erysiphe pisi*. These diseases can cause yield losses of up to 75%[1] and 80%[2], respectively, making genetic resistance an important strategy for sustainable disease management. While several genes conferring downy mildew resistance have been identified in other crops such as lettuce[3] and grapevine[4], in pea only one resistance locus, *Rpv*[5], has been mapped to date. For powdery mildew, resistance genes including *er1, er2,* and *Er3*[2] have been described, but additional sources of resistance are needed to broaden the genetic basis of disease control. The aims of this study are to identify loci conferring resistance to both downy mildew and powdery mildew through *k*-mer GWAS and to validate candidate genes using virus-induced gene silencing and transient expression. We phenotyped over 200 genetically diverse *Pisum spp.* lines separately for response to downy mildew and powdery mildew infection and identified two regions significantly associated with resistance to each disease. For downy mildew resistance, we identified a 2 Mb region on chromosome 5 which contains three CC-type NLRs that are more highly expressed in resistant lines. For powdery mildew, we identified a novel resistance locus on chromosome 7 that spans 0.6 Mb. Markers for these loci have been developed for use in breeding programmes. Ongoing functional validation of the prioritised candidate genes will help elucidate the molecular basis to resistance and guide gene-editing strategies to improve resistance against these important mildew diseases in pea.

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ECPP Poster Abstract 18

An AlphaFold3-predicted rhizobia-legume interactome identifies new factors required for symbiotic accommodation

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While many host genetic determinants governing nodulation have been characterized, our knowledge of the molecular interactions between rhizobia and legume proteins inside nodules remains very limited.

In this study, we employed AlphaFold3 to construct the first cross-kingdom interactome for *Medicago truncatula* and its symbiont *Sinorhizobium meliloti*. Screening over 217,000 protein pairs yielded 7,137 high confident interactions - an unparalleled resource for the broad symbiosis community (). We leveraged this rich interactome resource to functionally investigate two uncharacterized Secreted Rhizobial Proteins (SRPs), SRP86 and SRP485, and confirmed their predicted interaction with DEFECTIVE IN NITROGEN FIXATION 2 (DNF2), a host protein required for rhizobial persistence. Knockout of *SRP86* and *SRP485* led to the development of a large number of white nitrogen-fixation-deficient nodules containing symbiosomes with abnormal morphology. Moreover, we found that DNF2 localizes to the peribacteroid space where it associates with SRPs, likely serving as a key hub for endosymbiotic communication.

Collectively, our interactome resource and the functional analysis of the DNF2-SRP module provide novel insights into the molecular mechanism governing symbiotic nitrogen fixation, exemplifying an AI-driven framework to decode plant-microbe interactions for sustainable crop production.

Key words: legume-rhizobia symbiosis, *Medicago trunculata*, root nodule, nitrogen fixation, effector, AlphaFold3, structural modeling

ECPP Poster Abstract 19

A BDBBX21–BDSK1 regulatory module connects shikimate-derived metabolism with salicylic acid-associated immunity in bamboo

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Bamboo shoot blight, caused by *Apiospora sphaerosperma*, is an important disease affecting bamboo production, but the regulatory mechanisms underlying bamboo disease resistance remain poorly understood. In this study, we identified a B-box transcription factor, *BDBBX21*, as a positive regulator of disease resistance in *Bambusa pervariabilis* × *grandis*. Overexpression of *BDBBX21* enhanced resistance to *A. sphaerosperma*, whereas RNA interference plants showed increased disease susceptibility. DNA affinity purification sequencing indicated that BDBBX21 binds to multiple genomic regions, and integrative analysis with transcriptomic data identified *BDSK1*, encoding a putative shikimate kinase, as a candidate direct downstream target. Yeast one-hybrid, electrophoretic mobility shift and dual-luciferase assays showed that BDBBX21 binds to a G-box element in the *BDSK1* promoter and activates its expression. Functional analyses further showed that *BDSK1* overexpression enhanced disease resistance, increased callose deposition and promoted the accumulation of defense-related phenolic and flavonoid compounds, whereas *BDSK1* silencing compromised these responses. Hormone measurements and gene expression analyses indicated that *BDSK1* was associated with increased salicylic acid accumulation and enhanced expression of SA-related genes, including *PAL*, *ICS1*, *NPR1* and *PR1*. By contrast, jasmonic acid-related marker genes showed a time-dependent response, suggesting dynamic modulation of SA- and JA-associated outputs during infection. Together, these results support a model in which BDBBX21 directly activates *BDSK1* to connect shikimate-derived metabolism with SA-associated immunity and bamboo shoot blight resistance. This work provides new insight into transcriptional regulation of disease resistance in a non-model woody monocot.

ECPP Poster Abstract 20

Structure and Mechanism of a Conserved Aphid Effector Complex

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Similar to plant pathogens, phloem-feeding insects such as aphids deliver effector proteins inside their hosts that act to promote host susceptibility, enable feeding and infestation. Despite exciting progress toward identifying and characterizing effector proteins from these insects, their mechanisms of action remain largely unknown. *Myzus persicae* (green peach aphid) is a globally important crop pest with an exceptionally broad host range, which may be used as a model to understand evolution of protein-protein interactions between insect pest and plant host. Previously, a computational study predicted the structure, functional and interactive properties of the *M. persicae* salivary effector repertoire (Waksman *et al.*, 2024). The results suggested that many effector proteins have unpredictable structure and function, perhaps being intrinsically disordered or oligomeric. Subsequently, a conserved effector complex consisting of two co-expressed proteins was characterized in detail, using *M. persicae* and *R. padi* orthologous complexes (Mp1/Mp58, Rp1/Rp58).

Proteins were expressed in *E. coli*, purified and analyzed using size exclusion chromatography with multi-angle light scattering (SEC-MALS) to determine oligomerization states. This resulted in high-confidence AlphaFold models of the effector complex, supported by a high-resolution crystal structure. This reveals a novel oligomeric structure, with no matches found in any database using Foldseek multimer, that may have exceptional physical properties. Our data show evolution of different oligomerization states among orthologues of this effector complex, as well as dissociation of the oligomers under some conditions. These dynamics are related to function, including how Mp1/Mp58 interact with separate domains of their shared target (*Arabidopsis thaliana* vacuolar protein sorting protein 52). Electrophoretic mobility analysis of native proteins reveals stabilization of Mp58 by Mp1 *in planta*, suggesting strong interdependence and co-operation between the two proteins. In addition, an innovative synthetic rigid enlargement method has been applied to protein complex samples – this may improve outcomes in cryo-electron microscopy (cryoEM) analysis of effector-target complexes, which have low structure prediction confidence and crystallization potential. Application of cryoEM, mass spectrometry and molecular dynamics simulations may lead to successful engineering of these protein interactions for agricultural applications in the future.

Reference:

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ECPP Poster Abstract 21

Proteogenomic insights into transposable elements of Blumeria hordei

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Blumeria hordei (*Bh*) is a filamentous obligate biotrophic fungus and the causal agent of powdery mildew disease on barley. Due to the proliferation of transposable elements (TEs), it has a large genome size and a high proportion of approximately 75% TEs. We used *Bh* as a model to understand the landscape of TE-associated RNA and protein expression in a fungal plant pathogen. To investigate this, we applied long-read genome sequencing to generate two near-telomere-to-telomere genome assemblies from *Bh* isolates TUM1 and AUS1 originating from Germany and Australia. After combining these assemblies with multi-omic resources, we completed new gene and TE annotations based on TUM1. With long-read RNA sequencing technology, we identified novel splice variants of genes as well as many chimeric transcripts of genes and TEs. We also detected transcripts produced from intergenic space and many of them derive from TEs. Additionally, we evidenced gene and TE products by mass spectrometry proteomics. This revealed that highly abundant TEs give rise to not only novel transcripts but also proteins in *Bh*.

ECPP Poster Abstract 22

Mutation of Sucrose: Fructan 6-fructosyltransferase (6-SFT) in Hexaploid Wheat Reduces Susceptibility to Fungal Disease without Compromising Growth or Yield

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Fructans serve as key reserve carbohydrates in many grasses, including wheat, and are synthesised from sucrose through the coordinated action of the enzymes 6-SFT, 1-SST, and 1-FFT. Fructans accumulate primarily in stem tissues and are later mobilised to support spike and grain development following anthesis. Previous work has suggested that fructans may function as host susceptibility factors, potentially enhancing the severity of Fusarium head blight (FHB).

To investigate this, genome-edited (GE) 6-SFT knock-out lines were generated in the wheat cultivar Cadenza. Mutations consisting of 61–70 bp deletions were identified across the three homoeologous loci located on chromosomes 4AL, 7AS, and 7DS. These deletions resulted in frameshifts and premature stop codons. Phenotypic evaluation of T1–T3 triple homozygous lines under controlled environmental conditions showed that most edited lines were comparable to control plants in terms of growth, grain morphology, and yield components. Notably, one of the six lines produced a significantly increased thousand grain weight (TGW). Biochemical analyses revealed that fructan levels in grains of T1–T3 edited lines were significantly reduced relative to non-GE and wildtype Cadenza plants, while starch content remained consistent across T2 GE and control lines.

A major focus of this study was the assessment of disease responses in the GE lines. T2 homozygous seedling inoculation assays revealed altered responses to biotrophic pathogens: five lines displayed moderate resistance to yellow rust, and one line showed moderate resistance to powdery mildew. Importantly, FHB phenotyping of T3 adult plant demonstrated that two independent lines consistently exhibited reduced disease severity, with lower infection levels observed between 7 and 14 days post-inoculation.

These findings support the hypothesis that fructan metabolism can influence host–pathogen interactions. The 6-SFT knock-out lines therefore provide a valuable genetic resource for dissecting the role of carbohydrate partitioning in disease development and for breeding wheat varieties with improved resistance to multiple fungal pathogens.

ECPP Poster Abstract 23

Physical barrier formation to protect the root vasculature from pathogen entry

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Successful colonialisation of plants by pathogenic microbes requires strategies to overcome both the plant's innate immune system and the plant's physical barriers. Among these, the vascular system presents a dual challenge for the plant: while it needs to facilitate efficient nutrient uptake, transport, and distribution, it also needs to be protected by robust structural defences. The endodermis, a specialized layer surrounding the root vasculature, forms a strict barrier through the deposition of suberin. This hydrophobic biopolymer seals the cell walls, effectively restricting pathogen entry. Despite its central role in plant defence, suberised tissues are difficult to characterise due to their resistance to standard cellular isolation methods. In particular, suberin impedes protoplasting, preventing access to these cells in single-cell transcriptomic studies and leaving their molecular dynamics largely unexplored.

To address this challenge, I have utilised a single nuclei RNA sequencing (snRNA-seq) strategy. This approach enables high-resolution transcriptional profiling of targeted cell populations, uncovering dynamic developmental trajectories and key regulatory networks governing endodermal barrier formation such as suberin biosynthesis.

ECPP Poster Abstract 24

Exploiting Wheat-Wild Relative Introgression Lines as a Source of Barley Yellow Dwarf Virus (BYDV) Resistance

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Barley Yellow Dwarf Virus (BYDV) is the most damaging virus of wheat in the UK. Controlling its aphid vectors, *Rhopalosiphum padi* and *Sitobion avenae*, is cited by 93% of farmers as the primary reason for using pesticides on wheat crops. Additionally, the class of insecticide used, pyrethroids, are becoming less effective as aphids become resistant to them. Therefore, a genetic resistance to BYDV would allow for more effective and more environmentally friendly BYDV control.

The only current resistance to BYDV in wheat is the gene *bdv2* which was introgressed from the wheat wild relative *Thinopyrum intermedium*. To complement *bdv2*, this study exploits the genetic diversity found in wheat wild relatives to identify novel sources of resistance. We screened introgression lines derived from *Aegilops speltoides*, *Aegilops mutica*, *Triticum timopheevii*, *Aegilops caudata*, *Thinopyrum bessarabicum*, and *Thinopyrum elongatum* in growth room and field trial experiments. These results were used to select two lines, L368 and L369, that exhibit both reduced viral accumulation in growth room screens and less severe symptoms in the field, compared to susceptible controls.

All the lines used in this study have been characterised with a suite of genotyping tools, including KASP markers, genomic *in situ* hybridization (GISH), and skim-sequencing, enabling introgressed wild segments to be physically mapped within a bread wheat background. L368 and L369 have overlapping introgressions from 7T of *Ae. mutica* into 7D of wheat, and so offer a promising genetic resource for breeding programs aiming to restore BYDV resilience in elite wheat cultivars.

ECPP Poster Abstract 25

Heat mobilises the fungal accessory genome and remodels lipid metabolism in the wheat–Zymoseptoria tritici interaction

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Zymoseptoria tritici causes septoria tritici blotch, the most economically damaging foliar disease of wheat (Triticum aestivum) in the UK and Europe. As temperatures rise, wheat will increasingly face heatwaves during *Z. tritici* infection, yet how the combined stress reshapes this interaction remains poorly understood. We profiled the transcriptome and lipidome of the reference isolate IPO323 in culture across three temperatures, and across the wheat–*Z. tritici* interaction at ambient and elevated temperatures through the infection cycle. To test whether the culture response generalised across isolates, we also profiled the transcriptome of a second European field isolate, Zt116, from the Chen et al. (2023) pangenome collection, in culture.

In culture, heat raised the expression of accessory genes relative to core in both isolates. The fungal lipidome contracted in membrane phospholipids, expanded in triacylglycerols and ceramides, and shifted towards saturation. Comparing *in vitro* and *in planta* data identified a subset of fungal genes whose heat response *in planta* differed from their response in culture, enriched for cell-wall-degrading enzymes, sterol biosynthesis, drug-efflux pumps, and putative secreted effectors.

In the host, expression of defence-associated genes was higher under heat early in infection and lower at the later timepoints, while the wheat plastidial galactolipids were progressively depleted as infection advanced. Joint transcriptome–lipidome analysis recovered a host phenylpropanoid defence axis that scaled with fungal abundance, alongside a distinct axis specific to the heat–infection combination that separated host cell-wall biosynthesis from chitinase expression. Across both organisms, the heat response concentrated in two parts of the system: the fungal accessory genome and a host programme specific to combined heat and infection.

Reference:

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ECPP Poster Abstract 26

Nutritional warfare: effector targeting of nutrient deficiency pathways in plants

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Phytoplasmas are among the few bacteria capable of colonizing both plants and insects, thriving inside plant phloem cells and systemically spreading throughout the insect body. These pathogens deploy a diverse array of effectors that destabilize transcription factor families responsible for regulating plant development. This disruption causes dramatic phenotypic aberrations, including stem and leaf proliferations, the emergence of leaf-like flowers, and prolonged juvenile stages. Notably, these effectors induce direct proteasomal degradation of target proteins in a ubiquitin-independent manner. Despite this, the mechanisms underpinning robust cytoplasmic colonization of plant and insect cells without triggering autophagic clearance remains enigmatic. In this study, we identified and isolated a phytoplasma protein, likely functioning as an effector, and hypothesize that it shields the pathogen from host ubiquitylation machinery. Analysis of its enzymatic activity suggests that this protein enables phytoplasmas to rapidly evade ubiquitin-mediated defenses in the plant and insect cells. Collectively, our findings reveal that phytoplasmas not only deploy effectors to circumvent the ubiquitin-proteasome pathway but likely also do so to directly counteract host innate immune response, thereby ensuring persistence in diverse intracellular environments.

ECPP Poster Abstract 27

Comparative genomics and cross-pathogenicity in brassica-infecting Fusarium oxysporum strains

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Cruciferous crops of the Brassicaceae (brassicas) such as cabbage, radish, and wild rocket are globally important sources of nutrition, fibre, and glucosinolates with anti-cancer properties.

However, brassica production can be severely constrained by the soil-borne fungal pathogen *Fusarium oxysporum* (Fo), which causes vascular wilt disease characterised by yellowing, stunting, and plant death. Fo is an increasing concern, as warming climates favour the pathogen, and new strains with increased virulence or altered pathogenicity profiles continue to emerge. As Fo can persist in soil for over a decade, chemical and cultural control strategies are largely ineffective; planting resistant cultivars is therefore the most effective control approach, but research on identifying resistance in some brassicas remains sparse.

Although Fo has a broad host range, individual strains are generally host-specific, infecting a single plant species. This specificity has led to their classification into *formae speciales* (f.spp.) according to host species and races according to cultivar-level specialisation. Within the brassicas, distinct f.spp. infect cole crops (*Brassica oleracea;* f.sp*. conglutinans,* Focn races 1 and 2), radish (*Raphanus sativus;* f.sp*. raphani*, Forpi), wild rocket (*Diplotaxis tenuifolia;* f.sp*.* undescribed*, Fodip)*, salad rocket (*Eruca sativa;* f.sp. undescribed*, Foruc*), field mustard (*Brassica rapa;* f.sp. *rapae, Forpe*), and stock (*Matthiola incana;* f.sp. *matthiolae, Fom*).

Pathogenicity assays testing several brassica-infecting Fo (Focn races 1 and 2, Forpi, Fodip, Foruc, Fom) against both their primary (homologous) and non-primary (non-homologous) hosts revealed substantial cross-pathogenicity for some isolates. For instance, Forpi infected not only radish but also wild rocket. This suggests that these isolates may share overlapping effector repertoires, potentially mediated by horizontal gene transfer. To test this hypothesis, we integrated phenotypic data with several newly generated long-read MinION assemblies and existing high-quality public genomes for different brassica-infecting Fo. This revealed both shared and isolate-specific genomic regions, alongside putative effectors that may be required to infect a given host or set of hosts. Subsequent RNA-seq will determine which of these putative effectors are expressed during infection, prioritising the genomic regions and effectors most likely to determine host range.

ECPP Poster Abstract 28

Resolving the century-old mystery of Fusarium wilt resistance in pea

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Pea (*Pisum sativum*) is an important pulse crop, but its production is constrained by soil-borne root diseases, including Fusarium wilt caused by *Fusarium oxysporum* f. sp. *pisi* (Fop). A single dominant resistance locus, *Fw*, conferring resistance to Fop race 1, was first reported nearly a century ago and remains a priority trait in modern pea breeding. Yet the molecular identity of the causal genetic element has remained unresolved, limiting mechanistic understanding of durable wilt resistance and constraining the development of precise markers for breeding. Here, we combine *k*-mer-based genome-wide association mapping with transformation-based functional validation to molecularly resolve *Fw*. Screening of 336 diverse pea accessions revealed strong phenotypic variation for wilt resistance, and *k*-mer-based Genome-Wide Association Mapping (GWAS) mapped the trait to a 700-kb interval on chromosome 5, refining the known *Fw* locus. Further sequence, structural and transcriptomic analyses localised resistance to a previously unannotated transcript. This genetic factor is poorly captured by conventional SNP-based analysis, highlighting the value of *k*-mer-based approaches for causal variant discovery. Hairy-root and stable transformation of susceptible pea genotypes with *Fw* conferred whole-plant resistance to Fop race 1, demonstrating that *Fw* alone is sufficient for Fusarium wilt resistance and, to our knowledge, providing the first transformation-based functional validation of a disease resistance determinant in pea. Evolutionary analyses indicate that *Fw* has a recent origin within *P. sativum* and that related sequences are undergoing retrotransposon-mediated dispersal. Together, these findings molecularly resolve a century-old resistance locus and reveal unusual evolutionary dynamics at the *Fw* locus and provide precise markers for deploying Fusarium wilt resistance in pea breeding.

ECPP Poster Abstract 29

AI-guided discovery of plant resistance genes

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Plant diseases pose a clear and present threat to global food security. While durable genetic resistance is the most sustainable management approach, traditional methods to identify and deploy resistance genes (R-genes) remain slow, labour-intensive, and frequently outpaced by rapidly evolving pathogens. Thousands of valuable, unidentified R-genes lie within the germplasm of crop plants and their wild relatives. Our project exploits AlphaFold 3 (AF3) at an unprecedented scale to predict novel interactions between major crop pathogen effectors and a specific class of plant immune receptors called nucleotide-binding leucine-rich repeats with integrated domains (NLR-IDs). These receptors carry non-canonical domains that act as molecular decoys for effectors. Our goal is to dramatically accelerate the identification of functionally relevant NLR–effector pairs.

We assembled a curated dataset comprising thousands of NLR-ID sequences from hundreds of plant species and hundreds of effector sequences from major pathogens, including oomycetes, nematodes, aphids, and viruses. Using this dataset, we executed approximately 750,000 pairwise AF3 structural predictions, saving months, if not years, of traditional experimental screening. Interface confidence scoring was used to prioritize high-confidence candidate pairs, which we are currently validating through a combination of in vitro and in planta protein-protein interaction assays, alongside cell death and pathogenicity assays. Ultimately, our work provides a scalable, AI-driven pipeline for uncovering NLR–effector interactions. This enables the rapid development of disease-resistant crop varieties, reduces reliance on chemical pesticides, and enhances global food security.

ECPP Poster Abstract 30

Identifying drivers of bud rot disease incidence in oil palm: a work in progress

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The world's vegetable oil supply largely depends on oil palm. However, oil yields are being negatively affected by several biotic stressors. Among them, *Phytophthora palmivora*, causing 'bud rot' disease, has been the most destructive pathogen in Latin American palm oil production. To identify key environmental and agronomic factors in bud rot disease incidence, we collected and integrated different datasets for a plantation in the region of Santander, Colombia, for the years 2009 to 2025. These datasets contain information on disease incidence, nutrient content in frond tissue, soil properties, weather variables, pest insect populations, and agronomic management, such as cultivar choice, fertilization, and pesticide application. We will apply structural equation modelling to estimate the relative contribution towards incidence of each of these explanatory variables. For the year 2021, the dataset consists of 36 observational plots and 24 explanatory variables. Preliminary analyses of this dataset indicate that around 80% of disease incidence (%) variability is explained by the cultivar choice. Follow-up analyses will include comparisons of results among different years, and use of landscape information to infer microclimate differences as additional explanatory variables. These analyses will shed light on the relative contribution of each environmental and agronomic factor, which will inform growers about which aspects of their management can potentially prevent severe outbreaks.

ECPP Poster Abstract 31

From mechanism to symptoms: effector-mediated reprogramming of development turns plants into zombies

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Phytoplasmas are obligate bacterial parasites that infect most vascular plant species and are transmitted by sap-feeding insects that feed predominantly from the phloem. Phytoplasmas secrete small effector proteins into the cytoplasm of phloem sieve cells and these effectors then migrate to other cells where they disrupt various developmental pathways, such as extended vegetative growth phase and delayed flowering, as well as affecting plant immunity leading to enhanced vector attraction and fecundity. These effector actions are likely to have a positive impact on phytoplasma spread by insects.

Secreted effectors of Aster Yellows strain Witch's Broom phytoplasma proteins (SAPs) induce changes in plant development by mediating the degradation of multiple key plant transcription factor (TF) families. These include TCPs, MADS-box, SPLs, and GATAs. SAP11-mediated degradation of TCPs leads to crinkled leaves and stem proliferations, SAP54-mediated degradation of MADS-box TFs leads to the formation of leaf-like flowers, and SAP05-mediated degradation of both SPLs and GATAs promote vegetative growth, stem proliferation and longevity. All SAPs also promote the attraction and/or the fecundity of phytoplasma leafhopper vectors. These phenotypes are also apparent in AY-WB-infected plants. We have uncovered the actions of several other SAPs.

Studying phytoplasma effectors has not only revealed strategies to enhance plant resistance to phytoplasma infection, but also uncovered new cellular processes, including ubiquitin-independent degradation mechanisms.

ECPP Poster Abstract 32

Future climate conditions increase severity of soilborne diseases in table beets

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With climate change, the nature and intensity of crop diseases are likely to change[1]. In Switzerland, wetter springs and hotter and drier summers are suspected to have led to a higher incidence of soilborne diseases in table beets (*Beta vulgaris*)[2]. However, knowledge of how different soilborne pathogens respond to climate change is scarce. To investigate climatic effects on fungal community dynamics and plant health, beets were grown in six naturally disease-infested agricultural soils in phytotrons under end-of-century climate projections (RCP 4.5 and RCP 8.5) compared with a past control climate. Beet disease development was monitored over an entire growing season and during six months of storage. Climate effects on disease outcome were especially severe in the first half of the growing period, represented by increased post-emergence damping-off in the majority of soils under future climatic conditions. Fungal community profiling of beet seedling roots showed that while overall community composition changed minimally under future climate treatments (~5% of variation explained), the increase in post-emergence damping-off was associated with an increased abundance of a *Fusarium* spp. At harvest, a yield reduction of 25-60% was observed under future climate conditions. Abiotic stressors, including heat and drought, were the main drivers of biomass reduction under future climate conditions, while pathogens played a secondary role in further reducing beetroot weight. Future work will focus on assessing the role of oomycetes in climate-driven disease development and disentangling whether warming-associated increases in post-emergence damping-off reflect enhanced pathogen virulence and growth or reduced plant immunity.

References:

[1] Delgado-Baquerizo et al. The proportion of soil-borne pathogens increases with warming at the global scale. Nat. Clim. Change 10, 550–554 (2020).

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ECPP Poster Abstract 33

Mapping the proteome of rare PRIMER cells in plant immunity

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During pathogen infection, individual plant cells of the same cell type can mount heterogeneous immune responses[1]. Using single-nucleus multiomics (RNA-seq and ATAC-seq), our lab recently identified a molecularly distinct cell state in plant immunity, which we termed PRIMER cells[2]. Although these cells are presumed to be in direct contact with invading pathogens, spatial evidence is lacking, and their functional contribution to immunity remains unknown. To investigate the role of PRIMER cells, we developed *Arabidopsis* reporter lines expressing nuclear-localised mNeonGreen under the control of newly identified PRIMER cell-specific promoters. Using these lines, we demonstrate that PRIMER marker gene activation spatially coincides with bacterial microcolonies in the leaf, linking PRIMER cell identity to sites of infection. Since protein abundance is more directly linked to cellular function than transcript levels alone, acquiring proteomes from PRIMER cells offers critical insight into the molecular mechanisms through which this immune cell state contributes to defence. Building on our spatially validated markers, we aim to generate a proteome map of PRIMER cells using two complementary enrichment strategies. First, FACS-based sorting of protoplasts derived from PRIMER marker lines will enable direct isolation of PRIMER cells for downstream proteomics. Second, *pPRIMER:TurboID* lines will allow proximity-based biotinylation to enrich for proteins accumulating in PRIMER cells. By integrating these two orthogonal methods, this work aims to establish the first proteomic signature of a rare immune cell state in plants.

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1 Nobori, T. Immune cell states: Critical building blocks of the plant immune system. *Cell Host Microbe* **33**, 1227–1232 (2025).

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ECPP Poster Abstract 34

NLRome characterisation of potato cv. Spunta reveals an expanded NRC4 helper clade

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NRC (NLR-Required for Cell Death) proteins are helper nucleotide-binding and leucine-rich repeat (NLR) immune receptors that form a massively expanded network in the Solanaceae, acting downstream of multiple sensor NLRs to trigger immunity against diverse pathogens. However, the diversity of NRC helpers in cultivated potato (*Solanum tuberosum*) and how they are transcriptionally deployed during infection remains unknown. Here, we combined time-resolved transcriptomics with AI-based genome re-annotation and state-of-the-art NLR annotation pipelines to characterise the NRC network of the commercial cultivar Spunta during a compatible interaction with PiNSL-19, an Argentine isolate of *Phytophthora infestans*, the late blight pathogen. We identified 2,479 putative NLR genes, including 58 NRC helpers structured into eight clades, among which the NRC4 clade is markedly expanded relative to other Solanaceae. Phylogenomic analysis resolved three subclades (NRC4a, NRC4b, NRC4t) evolving under purifying selection. By mapping sequence conservation onto the cryo-EM structure of *Nb*NRC4 resistosome with ConSurf, we revealed subclade-specific diversification at distinct molecular surfaces. NRC4 expression was sustained throughout infection, indicating that Spunta retains the helper infrastructure required to support NRC4-dependent sensor NLRs. Together, these results define the helper NLR repertoire of an elite potato cultivar and lay the groundwork for NLR-ome–guided stacking of sensor NLRs to engineer durable late-blight resistance.

ECPP Poster Abstract 35

Developing an experimental system to study Starship Transposon-Mediated Horizontal Gene Transfer in Fungal Wheat Pathogens

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Horizontal gene transfer (HGT) drives fungal evolution, yet the underlying mechanisms remain poorly understood. One well-characterised pathogenicity gene that has been horizontally transferred up to three times between four different fungal wheat pathogens is the necrotrophic effector *ToxA*. This gene is an important virulence factor identified in four fungal wheat pathogens (*Pyrenophora tritici-repentis*, *Bipolaris sorokiniana*, *Parastagonospora nodorum, and Alternaria ventricosa*). Comparative genomic analyses revealed that in all four species, *ToxA* is embedded within a class II transposon named ToxTA. This transposon is found nested within two different giant Starship transposons (Sanctuary/Frontier and Horizon). Starships are a newly described superfamily of giant transposons that encode a conserved tyrosine recombinase transposase ("Captain"), as well as accessory genes. Sanctuary is mobile in *B. sorokiniana,* as evidenced by variable chromosomal positions in different isolates, whereas Horizon in *P. nodorum* and *P. tritici-repentis* is RIP-inactivated. Starships, like other tyrosine-recombinase transposons, are predicted to mobilise via the formation of circular intermediates. This project pursues two objectives: A) To characterise the movement of Sanctuary within the genome by measuring Captain gene expression under different growth conditions and to test the hypothesis that Starships move via circularisation by attempting to amplify circular junctions under the conditions when the Captain gene is most highly expressed B) To develop an experimental system for studying inter-species transfer using a hygromycin resistance-tagged Sanctuary (*Hyg*R-Sanctuary) in *B. sorokiniana* (Donor). This donor is paired with an acceptor *P. nodorum* strain with phleomycin resistance (*BleR-Acceptor*). Preliminary qRT-PCR results demonstrate that antibiotic stress significantly increases Captain expression in *B. sorokiniana*. Successful amplification of Sanctuary circular junctions from fungal cultures also supports the circular intermediate hypothesis. Through fungal donor-acceptor pairing experiments *in planta* and *in vitro*, we have recovered *BleR-Acceptor* colonies that grow under double selection and are PCR-positive for the Sanctuary Captain; whole-genome sequencing validation is ongoing to confirm *the presence of HygR-Sanctuary* DNA in these candidate transfer strains. These tools provide a foundation for functional validation of Starship-mediated HGT, enabling mechanistic studies of mobile element-driven fungal adaptation and pathogenicity.

ECPP Poster Abstract 36

Testing the efficacy and accuracy of the MinION sequencing device in forestry pathogen detection

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Quick and accurate pathogen detection is critical in being able to enact appropriate pathogen response programmes to contain or mitigate the spread of the infection. Current methods of pathogen detection in forestry involve culturing the pathogens from collected infected plant material on selection media through multiple rounds, to isolate the pathogens from other microbes that may be present in the sample. DNA extraction followed by PCR is performed and the PCR product sequenced by Sanger sequencing to potentially identify the pathogens. This workflow is time-consuming, taking an order of magnitude of weeks to identify the pathogens present in the sample. Moreover, this method only works on those pathogens that are culturable, which some are not. Hence an alternative method is needed to fully characterise, quickly and accurately, the pathobiome of an infected sample and tree. The work described in this poster makes use of direct sample DNA extraction and high throughtput sequencing, specifically Oxford Nanopore's MinION sequencing device, to accelerate accurate detection of the pathogens present in the tested samples, bringing the timeframe down to a matter of days. The workflow and results obtained from this analysis will be presented.

ECPP Poster Abstract 37

Silencing the Rust: Virus-Induced Gene Silencing (VIGS) for functional genetic studies in Asian Soybean Rust

Abstract withdrawn at the request of the author.

ECPP Poster Abstract 38

The Entomology and Insectary Platform at the John Innes Centre: Advancing Research on Plant–Invertebrate–Pathogen Interactions

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John Innes Centre

The Entomology and Insectary Platform supports world-leading research in entomology and plant health at the John Innes Centre, and fosters collaborations with academic and industrial partners nationally and internationally. The platform team manages a purpose-built containment insectary operating under rigorous quarantine standards and holds a Defra licence that permits the importation, rearing, and study a wide range of regulated invertebrates and plant pathogens.

Our team has extensive experience in establishing and maintaining colonies of diverse herbivorous invertebrate species, particularly crop pests, disease vectors and other agriculturally important taxa. We specialise in developing bespoke experimental designs and standardised protocols to support highly controlled, reproducible research. The platform provides expertise across a range of applications, including screening of plant varieties for resistance to pests and pathogens, vector biology, pathogen transmission, or the evaluation of novel pest control treatments.

A major focus of the platform is the study of plant–invertebrate and plant–pathogen–invertebrate interactions that underpin crop health, disease emergence and pathogen spread. By combining expertise in entomology, plant pathology and multi omics approaches, we support research into the biology of agricultural pests and vectors, mechanisms of pathogen transmission, host adaptation and the ecological and evolutionary processes shaping disease dynamics. The platform also enables research on symbiotic interactions involving insects and their associated microbiota, providing insights into how these relationships influence nutrition, adaptation, vector competence and interactions with plants and pathogens.

We invite conference participants to visit our poster to learn more about the platform's facilities, capabilities and ongoing research activities. We welcome discussions on plant–invertebrate, plant–pathogen and symbiotic interactions, and are keen to explore opportunities for new collaborative projects with researchers and stakeholders interested in advancing innovative approaches to understanding and managing pests, vectors and plant diseases.

ECPP Poster Abstract 39

HMAking Sense of Tandem Kinase Proteins as Plant Immune Receptors

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Tandem kinase proteins (TKPs) are an emerging family of intracellular immune receptors in the Triticeae tribe of grasses, which includes major crops such as barley and wheat.[1] To date, four cloned TKPs have been identified to have an N-terminal heavy metal associated (HMA)-like domain, alongside a central pseudokinase domain and a C-terminal kinase domain.[2,3] This includes the barley TKP Rmo2, which confers resistance to *Magnaporthe oryzae*. Its HMA-like domain is an effector-binding sensor domain that dictates the recognition profile of the receptor.[2,4] How the effector-HMA interaction confers activation of the receptor and consequently the downstream immune response is unclear. Using wheat protoplast cell death assays, we demonstrate that HMA-like domain truncation in Rmo2 drives constitutive activity of the protein, suggesting that the HMA-like domain represses signalling in the absence of recognised effectors. Further, fusion of Rmo2 tandem kinase domains with HMA domains from other plant proteins fails to restore repression of the resting state, indicating specificity between the coupling of the HMA-like domains and tandem kinase domains. Mutants in predicted kinase catalytic residues abolish cell death signalling, whilst expression of the kinase domain alone fails to elicit cell death, suggesting an intramolecular regulatory role of phosphorylation. These insights into the mechanism of Rmo2 suggest that the protein functions through a novel mechanism of effector-triggered immunity. Going forwards, this may guide the use of TKPs with HMA-like integrated domains in the bioengineering of novel disease resistance.

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2. Asuke, S. et al. (2025). bioRxiv.

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ECPP Poster Abstract 40

Fungal Endogenous Ethylene Signalling Machinery Plays a Key Role in Pathogenesis in the Cereal Blast Fungus

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Magnaporthe oryzae causes devastating cereal blast disease, threatening global food security. While ethylene regulates immunity and developmental transitions in plants, the functional role of endogenous ethylene signalling (and/or perception) in a fungal pathogen remains unexplored. In the blast fungal pathogen, we identified a two-component based ethylene signalling machinery (MoETR/MoRPFC) that regulates pathogenic development and successful host-invasion. We found that disruption of ethylene signalling triggers programmed cell death (PCD), followed by re-initiation of appressorial development in 30-40% of *Moetr-rpfc*ΔΔ conidia. Our multi-omics, biochemical and *in silico* interaction studies shed light on the role of endogenous ET signalling in fungal pathogenesis and help in understanding a likely co-evolution between the plant host and its fungal pathogen.

ECPP Poster Abstract 41

NOSH-A, a multicomponent signalling donor, primes systemic acquired resistance in potato against Phytophthora infestans

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The need for sustainable methods of crop protection drives the search for new compounds capable of enhancing plant immunity. In this study we analysed the effects of NOSH-aspirin (NOSH-A; [4-(5-sulfanylidenedithiol-3-yl)phenyl] 2-(4-nitrooxybutanoyloxy)benzoate) – a donor of nitric oxide (NO), hydrogen sulfide (H2S) and salicylic acid (SA) – on the establishment of systemic acquired resistance (SAR) in potato (*Solanum tuberosum* L.) against the globally significant pathogen (*Phytophthora infestans* (Mont.) de Bary), the cause of late blight disease. All three of the released compounds are known to play important roles in plant immune responses, acting as components of interconnected signalling pathways. The aim of this study is therefore to determine whether the multicomponent donor can effectively trigger systemic defence responses in plants. The experiments were conducted using the potato cultivar Bintje, which is highly susceptible to *P. infestans* due to the lack of resistance (R) genes protecting against the oomycete pathogen. Lower leaves of potato plants were sprayed with 100 µM NOSH-A and left for 48 hours to allow immune priming. Subsequently, both treated and distal leaves were detached, transferred to growth chambers, and inoculated with a *P. infestans* spore suspension. Samples were collected subsequently at 6, 24, 48 and 72 hours post inoculation (*hpi*) and were later used for RNA extraction, reverse transcription and qPCR. The effectiveness of SAR acquisition was evaluated through the measurement of the expression of *Pathogenesis Related 1 (PR1), PR2, PR3* and *Nonexpressor of Pathogenesis-Related Genes (NPR1)* genes. Moreover, disease progression was evaluated by monitoring the expression of the pathogen *PiTEF* gene and by assessing phenotypic symptoms in the inoculated leaves. In addition, since NO is a key signalling molecule in plant immune responses, its levels in plant tissue were measured at 24 *hpi* using a Chemiluminescence Nitric Oxide Analyzer. The study included a negative control treated with water and a positive control inoculated with *P. infestans* without prior NOSH-A treatment. Preliminary data from the ongoing experiments indicate that NOSH-A treatment may restrict pathogen development while promoting the expression of SAR-associated marker genes. Moreover, NOSH-A mediated priming enhanced NO accumulation in the leaves measured at the time of pathogen inoculation, but the response declined by 24 *hpi* in comparison with the positive control, highlighting the importance of temporal dynamics in NO-dependent defence signalling. In conclusion, these findings support the potential of multicomponent gasotransmitter-releasing donors as innovative priming agents for SAR and as a basis for developing novel crop protection strategies. They also underscore the need for deeper investigation into the role of NO, H2S and SA in plant immune responses.

ECPP Poster Abstract 42

A singleton integrated-domain NLR scaffold enables modular plant immune receptor design

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Plants use intracellular immune receptors called nucleotide-binding leucine-rich repeat proteins (NLRs) to detect pathogen-secreted effectors. Upon activation, these receptors can assemble into oligomeric complexes called resistosomes, which promote immune signalling and cell death. Some NLRs function as singletons, whereas others function in pairs or networks. Plant NLRs with integrated domains (NLR-IDs) are generally regarded as sensor NLRs that require partner helper NLRs to trigger immunity. Among such paired NLRs, the rice Pik system has provided a powerful platform for engineering novel immune receptors by replacing its integrated HMA domain with effector-binding modules. However, whether some NLR-IDs function as singletons remains unclear. Here, we used AlphaFold 3 to model resistosome structures for 296 NLR-IDs from 180 diverse plant species and identified a singleton NLR-ID (sNLR-ID) clade in Poaceae (the grass family) based on high-confidence structural predictions. The NLR-IDs in this clade triggered cell death in autoactive mutant backgrounds upon agroinfiltration in *Nicotiana benthamiana*. Intriguingly, they carry diverse C-terminal IDs, including DUF761, NUDIX, and HMA, suggesting recurrent natural domain shuffling. Using an *Aegilops tauschii* sNLR-ID carrying a DUF761 domain as a scaffold, we replaced the native integrated domain region with either HIPP43, which binds the *Magnaporthe oryzae* effector PWL2, or the GFP-binding nanobody Enhancer. In transient expression assays in *N. benthamiana*, these engineered receptors showed elicitor-dependent cell-death. Our results identify a naturally modular and engineerable singleton NLR-ID scaffold, expanding immune receptor design from paired sensor-helper systems to self-contained modular receptors.

ECPP Poster Abstract 43

The Effect of Temperature on Xanthomonas ROS Tolerance

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Understanding the effect of temperature on plant-pathogen interactions is essential to engineering climate-resilient disease resistance and food security. Bacterial spot disease of pepper and tomato, caused by *Xanthomonas* spp., provides a model pathosystem with temperature-dependent disease outcomes. For instance, experimental assays and field prevalences suggest that *X. perforans* is more virulent at higher temperatures and *X. gardneri* at lower temperatures. Given that plant pathogens must overcome both endogenous oxidative stress and oxidative stress imposed by reactive oxygen species (ROS) produced in the plant immune response, temperature-dependent ROS tolerance may contribute to temperature-dependent disease outcomes. Here, we investigate whether and how temperature affects the ROS tolerance of bacterial spot-causing *Xanthomonas* spp.

In vitro fitness following H2O2 treatment was assessed at 24°C and 36°C for *X. euvesicatoria* 85-10 (Xe85-10), *X. gardneri* 963 (Xg963), *X. perforans* AL65 (XpAL65), and *X. vesicatoria* 1111 (Xv1111). Over 24 hours in liquid culture, XpAL65 exhibited greater growth at 36°C than 24°C at 0.25-2 mM H2O2, but not at 0 mM H2O2. Following 30 minute exposure to 1 mM H2O2 at 24°C or 36°C: XpAL65 and Xe85-10 exhibited greater survival at 36°C; Xg963 at 24°C. These findings broadly agree with previously characterised temperature-dependences.

We are currently working to assess the molecular mechanisms underlying these temperature-dependent differences in ROS tolerance, focussing on specific ROS tolerance mechanisms and separating transcriptional from protein-level effects. Orthogroups were predicted across strains of interest to search for candidate genetic presence/absence differences which correlate with phenotypic differences. No clear candidate differences were noted. *oxyR* is conserved across the strains as the master transcriptional regulator of the oxidative stress response. Assays in *oxyR* mutants will identify how the overall *oxyR*-dependent response varies with temperature, whilst *lux* reporters will single out the *oxyR*-mediated transcriptional response. Finally, preliminary assays suggest superior H2O2 scavenging at 36°C than 24°C for XpAL65. Upcoming cell lysate scavenging assays and RT-qPCR of scavenging enzymes aim to distinguish between transcriptional and non-transcriptional effects.

In conclusion, temperature affects ROS tolerance of bacterial spot pathogens in a species-specific manner, potentially contributing to temperature-dependent disease outcomes. Underlying mechanisms may include temperature-dependent ROS scavenging and are under further study.

ECPP Poster Abstract 44

Cell-state-specific cis-regulatory logic of pattern-triggered immunity with csRNA-seq and snMultiome

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Plant immune responses are tightly regulated, generating transcriptional programs that differ by cell type and state, yet the cis-regulatory elements and transcription factor (TF) networks underlying these cell-state-specific responses remain poorly defined. To address this, we paired two complementary genome-wide assays across a matched flg22 (a flagellin-derived elicitor of pattern-triggered immunity, PTI) time-series in Arabidopsis seedlings. Capped small RNA sequencing (csRNA-seq) mapped active enhancers genome-wide, identifying thousands induced by flg22. Single-nucleus multiome profiling (joint snRNA-seq and snATAC-seq) of the same response resolved tens of thousands of nuclei spanning ten cell types. Comparing the 30-minute and 3-hour samples captured successive waves of activation, with distinct early and later transcriptional programs apparent across both assays. Integrating the two datasets indicates that immune activation is partitioned across the cellular landscape, with cell type-specific enhancer activation. Linking enhancers to their target genes further points to combinatorial TF logic that varies by cell type. Together these observations begin to assemble a cell-state-resolved framework for the cis-regulatory code of plant immunity.

ECPP Poster Abstract 45

From gene to field: accelerating crop trait discovery and validation, illustrated by Wild Bioscience's WB-01 soybean trait

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At Wild Bioscience, an Oxford University spinout, we discover and engineer yield-enhancing traits in major crops. To do this, our platform integrates evolutionary insight with phenotype-linked omics data and AI/ML-driven gene discovery to identify the genes controlling agronomically valuable traits. We have also developed a plant cell (protoplast) screening system that allows us to validate gene function rapidly before committing to stable transformation. Here we use one of our flagship traits, WB-01, to illustrate this discovery-to-validation pipeline.

To develop WB-01, which targets starch metabolism in soybean, we identified a previously uncharacterised native gene predicted by our platform to control this trait. Using protoplasts, we confirmed the gene's function and resolved the precise starch-biosynthesis step it targets, providing rapid functional validation ahead of transformation. Now implemented in a high-performing soybean variety (Illini3025N), WB-01 is yielding promising results: a significant increase in chloroplast-containing starch per cell and significant improvement in yield components in field trials across multiple US locations. WB-01 is one example of a growing pipeline of traits discovered and validated through this platform. By coupling ML-driven discovery with fast, scalable functional screening, we are shortening the path from candidate gene to field-validated trait across multiple crops.

Beyond WB-01, the cell screen is a powerful tool for prioritising candidate genes early, before resources are committed to transformation. Across our screens it clearly distinguishes high-impact candidates from those with little or no measurable effect. We will discuss how this early triage de-risks the pipeline and focuses downstream effort where it counts.

ECPP Poster Abstract 46

Chromatin regulation during plant immune responses

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Plants mount complex defence responses upon pathogen attack, involving large-scale transcriptional reprogramming. In the model plant Arabidopsis thaliana, chromatin modifications such as DNA methylation and histone marks, play key roles in regulating immune responses. However, the mechanisms by which chromatin dynamics control immune responses is poorly understood.

Our work indicates that many chromatin regulators are induced upon bacterial infection and control key immune gene targets. Using capped-small RNA sequencing (csRNA-seq), we identify immune-specific cis-regulatory elements associated with gene-activating chromatin marks.

We will systematically map modifications that govern dynamic immune responses and, controlling dynamic immune responses and, using a targeted epigenome-editing approach, directly manipulate chromatin states at immune loci to test their causative effects on gene regulation. We will extend this framework to resolve cell type- and cell state-specific immune responses by integrating single-cell and spatial omics technologies.

Ultimately, our goal is to provide mechanistic insights into how chromatin-based regulation shape plant immune responses at cellular resolution.

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ECPP Poster Abstract 47

A buttery smell makes plants strong: Volatile-Mediated Priming of Resistance against Root Pathogens

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Plants defend themselves against biotic stress through complex immune mechanisms, including induced systemic resistance (ISR) triggered by plant growth-promoting rhizobacteria (PGPR). While microbial volatile organic compounds (VOCs) are recognised as major signalling molecules in this priming process, the precise contributions of individual volatiles remain poorly understood. In this study, we investigated acetoin, the primary VOC produced by the PGPR *Bacillus velezensis* K165, as an elicitor of immune responses in *Arabidopsis thaliana* against pathogens with different infection strategies. Our findings demonstrate that root-applied acetoin, at concentrations naturally produced by the bacterium, significantly reduces disease symptoms caused by the soil-borne vascular wilt pathogens *Fusarium oxysporum* and *Verticillium dahliae* whereas no significant effect was observed against the foliar pathogen *Pseudomonas syringae* pv*. tomato* DC3000, indicating a preferential enhancement of resistance against soil-borne vascular pathogens. Ongoing and future research will determine whether this acetoin-mediated defence involves pathogen-specific epigenetic reprogramming and whether these changes can be inherited. As soil-borne vascular pathogens are notoriously difficult to mitigate due to their endophytic lifestyle, wide host range and lack of effective pesticides, these insights are essential for developing innovative priming strategies and sustainable agricultural practices to protect crops from root diseases.

ECPP Poster Abstract 48

Non-host resistance genes – new sources for durable rust resistance?

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The tight co-evolution between cereal crops and rust fungi has led to a pronounced host specialization, with one rust species generally only infecting one cereal host. Understanding the molecular principles that govern these non-host resistance mechanisms may provide new sources of durable resistance across cereal species.

Previously, we had identified orthologous lectin receptor kinases (LecRKs) from domesticated and wild barley that mediate non-host resistance to leaf rust. Through biochemical, proteomic, and structural analyses, we show these receptors interact with a highly conserved class of rust-derived glycoside hydrolases (GHs), triggering a cell death response.

Notably, we found that some rice LecRKs perceive stem rust-derived GHs, indicating that this molecular perception mechanism is conserved across cereal species. Transgenic expression of one rice LecRK in the wheat cultivar Fielder enhanced resistance to wheat stem rust, demonstrating the feasibility of transferring non-host immune receptors across cereal species to improve wheat disease resistance.

Together, these findings reveal previously uncharacterized recognition specificities within cereal LecRKs. The successful transfer of rice LecRK-mediated immunity into wheat highlights the potential of exploring naturally occurring receptor variants to possibly engineer durable and broad-spectrum resistance in wheat and other crops.

ECPP Poster Abstract 49

Thermal modulation of virulence in the Xanthomonas-pepper interaction

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Rising global temperatures threaten agricultural production by perturbing all three factors of the disease triangle (host, pathogen and environment), leading to unpredictable outcomes of plant-pathogen interactions

Some pathogens can adapt to small changes in temperature, a capacity that reflects physiological flexibility, which allows the pathogens to cope with a warmer environment. Understanding how pathogens respond and adapt to elevated temperatures is instrumental in developing adaptive disease management strategies and resistant crop varieties.

Bacterial spot of pepper, caused by *Xanthomonas spp*., offers a suitable model for this purpose. Pepper lines carrying well-established resistance genes are available, and the four species of *Xanthomonas* responsible for the disease differ in their relative abundance across warmer and colder agricultural contexts. How temperature affects *Xanthomonas* virulence is not known, and neither is how this could favour or break disease resistance in pepper. The project investigates the effect of elevated temperatures on *Xanthomonas* virulence by analysing the major virulence factors, with a particular focus on the type III secretion system (T3SS), motility and biofilm production. High temperature inhibits bacterial growth and, accordingly, reduces motility and biofilm production without abolishing them entirely. How temperature affects the T3SS is being investigated by monitoring the activity of four promoters of the T3SS genes, using a reporter system based on the *lux* operon. The project also examines the thermotolerance of plant immunity, focusing on the molecular mechanisms shaping pattern-triggered immunity (PTI) and the hypersensitive response (HR). A ROS (reactive oxygen species) burst assay was employed as a proxy for flagellin-induced PTI at different temperatures. Results showed a more pronounced but less prolonged response at high temperatures than at lower ones.

ECPP Poster Abstract 50

Visualising Plant-Microbiome interactions at single-cell resolution using PHYTOMap

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Plant immune responses are tightly regulated, generating transcriptional programs that differ by cell type and state, yet the cis-regulatory elements and transcription factor (TF) networks underlying these cell-state-specific responses remain poorly defined. To address this, we paired two complementary genome-wide assays across a matched flg22 (a flagellin-derived elicitor of pattern-triggered immunity, PTI) time-series in Arabidopsis seedlings. Capped small RNA sequencing (csRNA-seq) mapped active enhancers genome-wide, identifying thousands induced by flg22. Single-nucleus multiome profiling (joint snRNA-seq and snATAC-seq) of the same response resolved tens of thousands of nuclei spanning ten cell types. Comparing the 30-minute and 3-hour samples captured successive waves of activation, with distinct early and later transcriptional programs apparent across both assays. Integrating the two datasets indicates that immune activation is partitioned across the cellular landscape, with cell type-specific enhancer activation. Linking enhancers to their target genes further points to combinatorial TF logic that varies by cell type. Together these observations begin to assemble a cell-state-resolved framework for the cis-regulatory code of plant immunity.

ECPP Poster Abstract 51

Bacterial community profiles associated with Kimchi cabbage cultivated in South Korea

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Plants selectively recruit specific microbes from surrounding environment for their growth and health. The microbial community in the rhizosphere is particularly influenced by plant root exudates shaping beneficial microbes. In this study, we investigated the bacterial diversity associated with Kimchi cabbage from three regions (Pyeongchang, Taebaek, and Yeongyang) that are major Kimchi cabbage cultivating area in South Korea. In addition, we investigated the bacterial diversity after growing the same cultivar of Kimchi cabbage in soil originated from three regions, but kept in the same controlled smart greenhouse. Each plant sample (n = 9 for each region) was divided into three different compartments (bulk soil, rhizosphere soil, and endosphere). The bacteriome was analyzed by sequencing the V3–V4 region of 16S rRNA gene using an Illumina MiSeq platform (2 × 300 bp paired-end reads). Soil chemical analysis revealed that Yeongyang and Pyeongchang soils contained higher EC, available phosphorus, and nitrate-N levels than Taebaek soil. Accordingly, Kimchi cabbage cultivated in Taebaek soil exhibited reduced shoot growth but enhanced root development. Alpha diversity analysis showed that the bacterial richness generally declined toward the endosphere probably as a result of plant selection effects. Under controlled greenhouse conditions, rhizosphere bacterial richness was significantly higher in Taebaek region compared to Pyeongchang and Yeongyang regions. Beta diversity analysis based on Principal Coordinate Analysis showed that the bacterial dissimilarity among the three regions was primarily determined by both soil origin and plant compartment. Relative abundance analysis at order level suggested that bacterial composition varied more in the rhizosphere and bulk soil than in the endosphere, while the endosphere remained relatively conserved across the three regions. These results suggest that soil characteristics are important variables influencing the bacterial community associated with Kimchi cabbage. However, the differences in bacterial communities observed between field and greenhouse conditions indicate that not only soil characteristics, but also cultivation environment are important for bacterial community composition. Therefore, understanding the bacteriome associated with Kimchi cabbage requires identifying the key bacterial taxa responsible for the bacterial community patterns observed across regions and cultivation conditions, as well as their potential roles in plant-soil-microbe interactions.

ECPP Poster Abstract 52

Rapid response to major yellow rust resistance breakdown in UK wheat

Faci I[1], Saunders DGO[1], Yr15 breakdown rapid response partners

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In May 2025, *Puccinia striiformis* f. sp. *tritici* (*Pst*) isolates were identified that had overcome resistance to the widely deployed yellow rust resistance gene *Yr15.* First reported in the UK by the UK Cereal Pathogen Virulence Survey, these *Yr15*-breaking *Pst* isolates were rapidly detected across multiple countries in Europe. Because *Yr15* had been extensively deployed in European varieties, nearly 50% of the UK national wheat area was potentially vulnerable, underscoring the risks associated with reliance on single resistance genes. In June 2025, we conducted rapid genetic analyses at the John Innes Centre and confirmed that the *Yr15*-virulent *Pst* isolates emerged from within the existing 'Warrior' *Pst* race group rather than through an exotic introduction. Fortunately, prior screening of the A.E. Watkins heritage landrace collection had identified 33 lines resistant to the 'Warrior' group, and we rapidly confirmed that 32 of these lines retained resistance to the *Yr15*-breaking *Pst* isolates. Using existing mapping populations derived from resistant Watkins lines, we have now applied bulk segregant analysis (BSA) to identify the underlying resistance loci, alongside *k*-mer GWAS as an alternative approach. This has also included the generation of new genome assemblies for three of the resistant Watkins lines that contain unique resistance sources not present in modern wheat. In parallel, we are characterising resistance diversity in current UK wheat varieties to help generate reliable markers to better track prevalent resistance gene diversity in the UK breeding pipeline and limit single-gene reliance in future. Together, these efforts aim to address current vulnerabilities in UK wheat and offer a model for responding quickly to future virulence shifts in crop diseases.

ECPP Poster Abstract 53

Paracidovorax citrulli employs multiple effectors to suppress NbPtr1-triggered cell death in Nicotiana benthamiana

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Plant pathogens deploy effector proteins to facilitate host colonization, whereas plant intracellular nucleotide-binding leucine-rich repeat (NLR) receptors recognize effectors and activate effector-triggered immunity (ETI), often culminating in localized programmed cell death known as the hypersensitive response (HR). To evade ETI, pathogens have evolved ETI suppressor effectors. *Paracidovorax citrulli*, the causal agent of bacterial fruit blotch (BFB), causes significant losses in cucurbit crops. Its pathogenicity relies on a type III secretion system that delivers effectors into host cells. Given that no genetic resistance to BFB has been identified to date, we hypothesized that *P. citrulli* encodes ETI suppressor. Using the solanaceous plant *Nicotiana benthamiana* as a surrogate host, we screened 64 predicted effectors by transient expression and identified six effectors that induced cell death. Genetic analyses revealed the involvement of coiled-coil NLRs (CNLs) in their recognition. To identify the responsible CNL, we silenced five *N. benthamiana* NLR genes previously reported to recognize effectors from diverse bacterial pathogens. HR induced by one effector was abolished in *NbPtr1* (*Pseudomonas syringae* pv. *tomato* race 1 resistance)-silenced plants, indicating recognition by NbPtr1. Notably, several *P. citrulli* effectors suppressed or attenuated NbPtr1-mediated cell death, suggesting that they function as ETI suppressors. We are generating deletion mutants lacking individual or multiple ETI suppressors and will examine whether these deletions affect the virulence ability of *P. citrulli* in host plants. Collectively, these findings advance our understanding of the virulence mechanisms by which *P. citrulli* overcomes ETI and provide insight on the molecular arms race between the pathogen and its host.

ECPP Poster Abstract 54

Characterisation of quantitative Verticillium wilt resistance in hop using GWAS

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Verticillium wilt is the most important disease in UK hop production. Progressive forms of the pathogen can cause dieback of entire hop gardens. This soil-borne disease is particularly problematic because there are no curative or protective products available to remove the pathogen once established. As such, growers must embrace disease resistant varieties in order to protect hop production. All new hop varieties released for UK production must be resistant to Verticillium wilt. There are two distinct sources of Verticillium resistance that are present in the Wye College genotypes Y90 and AA7; Y90 progeny have shown an additive mode of inheritance whilst AA7 progeny have shown an undiluted transmission of resistance between generations. Both have been introgressed into high quality varieties as part of the UK hop breeding programme. However, the identity of alleles controlling these resistances have eluded the community to date. Here we provide the first report of genetic markers associated with Verticillium wilt disease resistance in hop. Through implementing a Genome Wide Association Study (GWAS) analysis, we have identified a single region on chromosome 5 associated with Verticillium wilt resistance. A large proportion of the variation was controlled by genetic factors with a H2 of 90%. The resulting genetic markers have been identified across a diverse population of hops including from both sources of resistance meaning that they hold high relevance across both UK and international breeding germplasm. These results represent a game changing resource that will enable marker assisted breeding of Verticillium wilt resistance into high quality hop varieties.

ECPP Poster Abstract 55

Harnessing compost microbes for new crop protection products against foliar diseases

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Plant diseases threaten sustainable crop production, highlighting the need for effective, environmentally friendly crop protection solutions. Composts and compost-derived extracts have been shown to suppress plant diseases, yet the microbial determinants underlying this activity remain poorly understood. Given that composts are largely produced from decomposed plant material, including leaves, we hypothesized that they may contain microorganisms originating from the phyllosphere and thus represent an underexplored source of potential biocontrol agents against foliar diseases. We focus on two major foliar diseases: tomato early blight, caused by *Alternaria solani*, and grapevine downy mildew, caused by *Plasmopara viticola*.

To identify microorganisms associated with disease suppression, compost extracts are prepared and applied as foliar sprays to tomato and grapevine plants in bioassays. Microorganisms that successfully establish on leaf surfaces are recovered and characterized using comparative metabarcoding to identify taxa associated with disease suppression. In parallel, microbial isolates obtained from suppressive composts are screened for antagonistic activity through *in vitro* assays evaluating *A. solani* spore germination and *P. viticola* zoospore motility.

Preliminary results show that a selection of compost-derived microbial extracts can suppress *A. solani* infection in tomato. In addition, several microbial isolates recovered from suppressive composts showed inhibitory activity against *P. viticola in vitro*. These findings support compost-derived microorganisms as a promising source of novel biocontrol agents against foliar diseases. Ongoing work focuses on identifying the microorganisms and mechanisms responsible for disease suppression, including antimicrobial metabolite production and induction of plant defenses, to support the development of sustainable crop protection strategies.

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ECPP Poster Abstract 56

Fungal pathogens causing saffron corm rot in the UK: identification, pathogenicity and sustainable management using biocides and biocontrol agents

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Saffron (*Crocus sativus* L.) is a high-value crop with growing interest in the UK but symptoms of yellowing, poor emergence, and corm rot were recently observed in a commercial field in Cheshire. The aetiology of saffron corm rot under UK conditions is poorly understood, and no fungicides are currently approved for its control. This study aimed to identify the fungal pathogens associated with saffron corm rot, confirm their pathogenicity, and assess the potential of biocontrol agents and biocides for disease management. Fungal isolation and molecular identification revealed the presence of *Stromatinia gladioli*, *Fusarium culmorum*, *F. equiseti*, and *F. oxysporum*. Pathogenicity was confirmed for all these species through fulfilling Koch's postulates, but virulence was much greater for *S. gladioli*. Four registered biocontrol agents, *Coniothyrium minitans*, *Clonostachys rosea*, *Trichoderma asperellum*, and *T. harzianum*, were evaluated for their ability to degrade *S. gladioli* sclerotia in soil over eight weeks and suppress germination of recovered sclerotia on agar. *C. minitans* degraded up to 90% of sclerotia, while *C. rosea* completely inhibited the germination of recovered sclerotia. Biocontrol products were also assessed for their ability to reduce *Fusarium* spp., infection in saffron under controlled conditions over three months but none of the tested agents significantly reduced infection in daughter corms compared with the untreated control. Additionally, plants inoculated with *Fusarium* spp., with or without biocontrol treatment, exhibited reduced root dry weight compared with uninoculated controls. Biocide products were also evaluated for their effect on *Fusarium* spp. chlamydospores *in vitro*. Hydrogen peroxide reduced chlamydospore viability by more than 75% at 6000 ppm after 60 min of exposure, while hypochlorous acid applied at 3 mL L^{-1} for 15 min resulted in approximately 90% reduction in chlamydospore viability. These findings represent the first report of *S. gladioli* and *Fusarium* spp. as causal agents of saffron corm rot in the UK. Furthermore, *C. minitans*, *C. rosea*, hydrogen peroxide, and hypochlorous acid demonstrated potential for inclusion in environmentally sustainable integrated disease management programmes for saffron production.

J Colhoun Prize Poster Abstract 1

Investigating the role of DNA methylation in regulating plant resistance to pests.

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There is gathering evidence that DNA methylation plays an important role in regulating the expression of environmentally responsive genes in plants including those involved in defence against pathogens. For example, transient activation of the DNA demethylase REPRESSOR OF SILENCING 1 (AtROS1) in *Arabidopsis thaliana* (Arabidopsis) results in increased expression of immunity-related genes and enhanced resistance to pathogens (1). What remains less clear, is the role of DNA methylation in regulating resistance against pests such as chewing insect herbivores, and in plants beyond Arabidopsis. Here, we are utilising an estradiol inducible system to transiently activate AtROS1 (*XVE:ROS1-YFP*) in Arabidopsis and tomato (*Solanum lycopersicum*) and explore the impact on resistance to the generalist chewing herbivore *Mamestra brassicae*.

Initial experiments using single estradiol treatments, which are sufficient to transcriptionally activate *AtROS1*, have found no impact on resistance to *M. brassicae* in either tomato or Arabidopsis. Consistent with these phenotypes, jasmonic acid-inducible herbivore defence genes showed no upregulation post-estradiol treatment. Ongoing work is investigating the effectiveness of multiple estradiol treatments, which have been shown to elicit stronger resistance against pathogens in Arabidopsis (1). In parallel, whole genome bisulfite sequencing and confocal microscopy are being used to characterise AtROS1-induced methylation changes and AtROS1 localisation in tomato.

Collectively, this work characterises inducible *XVE:ROS1-YFP* tomato lines and advances understanding of how AtROS1-mediated DNA demethylation influences plant defence against chewing herbivores, providing insight into epigenetic regulation in immunity and its application in crop protection strategies.

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J Colhoun Prize Poster Abstract 2

Decoding and rewiring sensor–helper communication in plant NLR immune receptor networks

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Plants deploy intracellular immune receptors called NLRs to detect pathogens and mount defence responses. NLRs can function as multifunctional “singletons”, or in complex pairs and networks of functionally specialized receptors. In the NRC network, "sensor" NLRs recognise pathogen effectors and activate downstream "helper" NLRs that execute immune signaling and cell death. Although sensor–helper communication is central to disease resistance in many crops, the structural basis of signal transduction in the NRC network has remained elusive, in part due to the transient nature of sensor-helper interactions. We used AlphaFold 3 to study activation in this network, using the sensor Rx and its helper NRC2a as a system. Modeling of the Rx-NRC2a complex, revealed a previously uncharacterized interface mediated by the sensor's NB and the helper's NB and LRR domains. To test whether this predicted interface is functionally relevant, we designed structure-guided point mutations in both Rx and NRC2a and characterised them using cell death assays in *Nicotiana benthamiana*. We identified residues on both sides of the interface that are essential for helper activation and confirmed the specificity of these contacts through reciprocal charge-swap experiments that rescued a critical salt bridge. Building on the observation that this interaction logic appears structurally conserved across NRC network-encoding species, we applied structure prediction to study sensor-helper communication in the compact NRC network of lettuce. Structure-guided swaps of the NB-domain interface regions allowed us to expand the helper compatibility profile of a lettuce sensor NLR. These results provide a structural framework for understanding and engineering sensor–helper communication, with direct implications for bioengineering disease resistance in crops.

J Colhoun Prize Poster Abstract 4

Dissecting Plant-Microbe Interactions in Grapevine Trunk Disease: a genotype-focused approach

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Rapid climate change is significantly affecting the delicate equilibrium between plant and their associated microbial communities, raising the occurrence of endophytes-related diseases. Among these, ESCA syndrome is one of the most destructive grapevine trunk diseases (GTD) affecting grapevine, caused by a vast consortium of fungi. Genotype response to ESCA syndrome is variable, although not well characterized. To comprehensively characterize this aspect, we identified the resident endophytic fungal communities isolated from the propagation material of 12 distinct grapevine genotypes to establish a baseline microbial profile and evaluate ESCA pathogens occurrence. Subsequently, an inoculation with ESCA's primary etiological agents (*Phaeomoniella chlamydospora*, *Phaeocremonium aleophilum*, and *Diplodia seriata*) were performed on 16 grapevine genotypes, selected among traditional, commercially relevant, and putatively tolerant varieties. Wood samples from inoculated plants were collected for Microbiome and Transcriptome analysis. Wood's metabolomic completed our multi-omics approach applied to a vast panel of grapevine diversity. The inoculation points were sampled for staining experiments to analyze structural and compositional variations in the infected tissue.By cross-examining these multi-layered data, this study aims to shed light on the complex interactions that occur in GTDs. This holistic perspective will be critical to identify the specific genetic, metabolic, and microbial determinants associated with fungal pathogenicity, ultimately shifting the paradigm in evaluating genotype-specific susceptibility and tolerance.

J Colhoun Prize Poster Abstract 6

Enhancing Genetic Resistance to Downy Mildew in Pea

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In recent years, there has been a heightened demand for plant-based proteins due to growing concern surrounding our food's origin and environmental impact. Pea (*Pisum sativum*), is a legume valued for its high nutrient and protein content, containing all essential amino acids, whilst being low in allergens, making pea an ideal crop for protein isolation (1-2).

Biotic and abiotic stresses can severely impact pea production. Downy mildew (DM), caused by *Peronospora viciae* in pea, has been reported to cause up to 75% yield loss (3). Currently, there are no effective treatments against pea DM, therefore alternative control methods, such as genetic resistance, are needed.

Few resistance loci against pea DM have been identified. A virulent isolate has been able to overcome one of these resistances, therefore it is important to identify additional resistances that can be combined to confer durable resistance. To identify novel resistance genes against pea DM, phenotypic screening of a large Pisum diversity panel against the highly virulent isolate of DM was carried out. SNP-based Genome wide association studies (GWAS) have been carried out on the phenotype data which has led to the identification of candidate resistance genes on chromosome 1. The resistance locus identified in this study can be deployed into breeding programmes to produce plants resistant to pea DM. Computational methods are being used to further validate candidate genes before using wet lab methods for final validation.

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J Colhoun Prize Poster Abstract 7

Molecular basis of higher-order septin assembly during infection by the blast fungus Magnaporthe oryzae

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The rice blast fungus *Magnaporthe oryzae* poses a major threat to global food security by infecting over 50 grass species, including rice, finger millet, and wheat. Host invasion requires the appressorium, a specialised infection cell whose pore is cortically organised by a toroidal septin ring. This higher-order septin assembly acts as a scaffold for the F-actin network and associated penetration machinery, and serves as a diffusion barrier for polarity factors[1]. We aim to investigate the molecular basis of septin higher-order oligomerisation and ring formation.

To elucidate the structural basis of oligomer formation, we reconstituted *M. oryzae* septin higher-order assemblies *in vitro* and characterised their architecture by mass photometry and electron microscopy (TEM and cryo-EM). We observed assemblies with structural flexibility, branching, sequential and parallel interactions between filaments, and larger bundle assemblies. The C-termini of septins appear important for filament bundling and interactions with other proteins. To confirm this hypothesis, we generated septin C-terminal truncations for functional and structural analyses.

To understand how the interaction between septin C-termini may be dynamically regulated, we conducted an AlphaFold3 screen. We focused on phosphorylation as it is one mechanism suggested to regulate septin higher-order organisation[2], and *M. oryzae* C-termini were indeed reported to be phosphorylated[3]. We assessed the conservation of these phosphosites across ascomycetes. Then, we identified possible kinases from the AlphaFold3 screen that are predicted to interacts with septin C-termini, such as the mitogen-activated protein kinase (MAPK) Mst7, essential for pathogenesis. We propose that phosphorylation of the C-termini of *M. oryzae* septins regulates septin organisation during appressorium morphogenesis.

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J Colhoun Prize Poster Abstract 8

HAG5/HAM2 a tool to engineer resilient crops?

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Part of the plant response to abiotic and biotic stress is the reprogramming of gene expression. One major mechanism controlling the partial expression of the genome is acetylation of the N-terminal tails of histones by histone acetyltransferases (HATs).

Here we investigate the role of the Arabidopsis thaliana MYST-family HATs, AtHAG4/HAM1 and AtHAG5/HAM2, in abiotic and biotic stress responses. Our results show that these two HATs have distinct functions. *AtHAG4* regulates responses to root pathogens, including *Fusarium oxysporum*, whereas *AtHAG5* regulates immunity against the leaf pathogen *Pseudomonas syringae pv. tomato* and contributes to drought responses. Mutants of *HAG5* show enhanced bacterial resistance and improved drought tolerance, with better recovery after dehydration and reduced leaf water loss. HAG5 also interacts with ARIA, an ABA-signalling protein, linking chromatin regulation to hormone-mediated stress responses.

Phylogenetic analysis showed that *HAG5* is highly conserved across plant lineages, including Brassica and tomato orthologs. CRISPR/Cas9-generated *hag5* mutants in *Brassica oleracea* displayed enhanced drought tolerance and reduced leaf water loss. Together, these results highlight MYST-HAT-mediated histone acetylation as an important regulator of plant stress responses and identify HAG5 as a promising target for developing climate-resilient crops.

J Colhoun Prize Poster Abstract 9

HIPP43 interacts with immune response proteins and may be targeted to p-bodies by blast effector PWL2

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The pathogen *Magnaporthe oryzae* causes rice blast disease, destroying up to 30% of the annual rice harvest. *M. oryzae* secretes effector proteins to aid infection of its host. The effector PWL2 has previously been shown to interact with the plasmodesmata-localised heavy metal binding domain isoprenylated protein 43 (HIPP43) in rice and barley [1, 2]. When transiently expressed in *Nicotiana benthamiana*, PWL2 alters HIPP43 localisation away from the plasmodesmata, and the two proteins colocalise together in mobile bodies. These mobile bodies are reminiscent of processing bodies (p-bodies), liquid-liquid phase separated aggregations of proteins and mRNAs, thought to be sites of mRNA storage and degradation. The targeting of p-body related processes by pathogen effectors is a recently emerging theme [3, 4], but until now, whether the HIPP43-PWL2 mobile bodies are p-bodies has not been tested. To do this, we co-expressed HIPP43 and PWL2 with p-body markers and studied the localisations of the proteins by confocal microscopy. In addition, overexpression of either HIPP43 or PWL2 suppresses PAMP-induced ROS in transgenic barley and rice. We showed that HIPP43 interacts with multiple immune response-related proteins in yeast-2-hybrid assays, including an E3 ligase, two hypersensitive induced reaction proteins and one predicted metalloendopeptidase. These data suggest that PWL2 may target and sequester HIPP43, and possibly other immune-signalling components, to p-bodies and reduce immune responses during infection.

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J Colhoun Prize Poster Abstract 10

Improving crop yields through mycovirus-mediated resistance

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Phoma stem canker devastates oilseed rape (*Brassica napus*) yields worldwide and is caused by two closely related fungal species: *Leptosphaeria biglobosa* and *L. maculans*. Current control methods rely on cultivar resistance and fungicide applications. Due to changes of pathogen populations, cultivar resistance can be rendered ineffective in 2-3 years. Thus, control of phoma stem canker epidemics relies on fungicides which can have detrimental effects on the environment. Mycoviruses infect fungi and alter phenotypes such as growth, virulence and antifungal sensitivity upon infection, and are emerging as potential biocontrol agents for both clinical and agricultural diseases. This research aims to explore how *Leptosphaeria* viruses mediate host phenotypes, disease severity and oilseed rape resistance against phoma stem canker and other plant pathogens. This work will a) uncover the true ability of Leptosphaeria biglobosa quadrivirus-1 (LbQV-1)-infected strains to induce systemic resistance against *Leptosphaeria* and other plant pathogens b) explore the underlying mechanisms of LbQV-1-mediated plant resistance and c) investigate the impact of other *Leptosphaeria* mycoviruses on *in planta* virulence. *In planta* virulence and host resistance will be measured both phenotypically (lesion area of *L. maculans* challenge infections) and quantitatively (qPCR analysis of fungal DNA). Microscopy, LC-MS, and transcriptomics will be used to assess the molecular mechanisms behind LbQV-1-mediated resistance. Ultimately, this research will reveal the potential of *Leptosphaeria* mycoviruses as biocontrol agents against phoma stem canker pathogens and aid their integration into future crop protection programmes.

J Colhoun Prize Poster Abstract 11

Coordination of Xanthomonas secretion systems during plant disease

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The type-2 secretion system (T2SS) is a conserved and critical player in the virulence of many Gram-negative plant pathogens including *Xanthomonas* [1, 2], *Xylella* [3] and *Ralstonia* [4]. It delivers effectors (T2Es) into the apoplast, the site of bacterial colonization and a key battleground between plants and microbes. Proteins secreted by the T2SS include cell wall degrading enzymes (CWDEs) and proteases which are assumed to function in nutrition, but how they aid bacterial survival and contribute to disease development remains poorly understood.

To uncover the T2E repertoire of the model pathogen *X. euvesicatoria* (Xe), we employed *in planta* comparative proteomics during infection of tomato. This analysis revealed a diverse arsenal of CWDEs and proteases, with evidence that they function as a nutrient acquisition system, enabling the pathogen to scavenge nitrogen and carbon from the plant cell wall and proteins. However, beyond nutrient acquisition, T2E functions are intimately connected to type-3 secretion system (T3SS) activities. The T3SS translocates effector proteins (T3Es) into the plant cell cytosol, many of which function in the suppression of immune responses. We demonstrate how CWDE-type T2Es support T3SS functionality at the transcriptional level. Reciprocally, T3Es suppress plant immune responses triggered by T2E activities, suggesting that these secretion systems mutually support each other. We are dissecting how these secretion systems coordinate to execute a multi-pronged attack on the plant.

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J Colhoun Prize Poster Abstract 13

RootSock: A Microflidic Platform to Study Pathogen-Root Interactions

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Recent advances in microfluidic systems have enabled studies of microbial interactions in simulated soil systems[1]. However, existing root-integrated platforms are often limited by confined growth spaces, short experimental durations, and continuous nutrient flow that poorly mimic natural soil environments. The fabrication of a device that accommodates both plant roots and single fungal hyphae is highly challenging, as it lies at the interface between different fabrication technologies. Photolithography enables precise fabrication of micro- and nanoscale features while advanced 3D printing technologies can readily fabricate larger-scale compartments. Combining these approaches provides a practical strategy for integrating macro-scale root growth chambers with microscale structures for single-hypha studies within a single platform.

To address these limitations, we developed a new polydimethylsiloxane (PDMS)-based module, the RootSock, designed for integration with the existing SoilChip platform[1]. The RootSock provides an expanded root growth compartment and nutrient supply without continuous flow, enabling studies of rhizosphere interactions under more soil-like conditions. The device was fabricated by first molding the root growth compartment using a 3D stereolithography (SLA)-printed mold. After curing, the compartment was removed and placed onto a microfluidic chip master fabricated by photolithography. PDMS was then cast onto the master, integrating both micro- and macro-scale structures into a single device, enabling the fabrication of a large step transition from 10 µm microstructures to a substantially larger root growth chamber. The cured device was peeled from the master and bonded to a coverslip. The fabricated device was subsequently filled with Murashige and Skoog medium, and sterilized seedlings were introduced through the inlet.

The platform is currently being applied to investigate how the soilborne plant pathogen *Rhizoctonia solani* colonizes host roots. Through time lapse videos and automated image analysis, we are able to closely monitor spatiotemporal hyphal growth dynamics and morphological changes of the pathogen in proximity to roots and the progression of responses upon host contact. The RootSock also enables future incorporation of soil communities and biocontrol agents to study more complex rhizosphere interactions.

Reference:

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J Colhoun Prize Poster Abstract 14

AI-Guided Immune Receptor Discovery and Engineering

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Many devastating plant pathogens secrete effectors into the apoplast to promote infection. Plants detect these effectors using cell-surface leucine-rich repeat receptor-like proteins (LRR-RLPs) to trigger disease resistance. The cognate receptor for most extracellular effectors remains unknown, and the structural basis of recognition has been mapped for only a handful of pairs. With millions of possible receptor-effector combinations across crop and pathogen genomes, exhaustive experimental screening is not feasible.

AlphaFold-Multimer models known effector-RLP interactions accurately. Building on this, we developed a computational pipeline that screens apoplastic effectors from economically important pathogens against the full LRR-RLP repertoires of host plants. Candidates are ranked using custom confidence metrics combined with structural and biological insight, reducing the candidate pool by >99%. Top candidates are validated by transient expression and silencing assays in *Nicotiana benthamiana* and relevant crop species, compressing years of screening into weeks.

Beyond discovery, the same framework supports rational re-engineering of RLPs against stealthy effectors that evade recognition. Structural insights from validated pairs guide targeted substitutions, and our *in silico* confidence scoring ranks engineered variants before experimental testing. Together, this platform accelerates the discovery of natural resistance and, where none exists, provides resistance by design.

J Colhoun Prize Poster Abstract 15

Providing an Alternative Approach to Disease Management via Engineered Biocontrols

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Grey mould is a disease caused by the fungi *Botrytis cinerea* which poses a substantial threat to strawberry production by causing post-harvest losses and crown rot that ultimately leads to plant death. Conventional chemical fungicides have been utilised for decades but have several drawbacks. Firstly, the efficacy of many chemical fungicides has reduced due to increased prevalence of pathogen resistances, chemical residues have also been found on fruit, and some fungicides have been found to cause environmental damage. To provide a more sustainable and environmentally friendly control strategy we have identified a novel strain of *Bacillus velezensis* that exhibits antifungal properties against *B. cinerea*, demonstrating superior control of *B. cinerea* compared to commercial strains already on the market.

Candidate bacteria were isolated and sequenced, after which *B. velezensis* strains were selected and screened for antifungal activity through *in vitro* solid and liquid assays. Subsequently, promising candidates were screened for protective capacity through a pathogenicity assay which led us to identify an isolate with superior antifungal activity. To quantify the mechanism of action, we used a combined multi-omics approach to understand how this novel *B. velezensis* strain protects against *B. cinerea* infection. Comparative genomics and Liquid Chromatography Mass Spectrometry have been used to identify the antifungal secondary metabolites produced by our candidate biocontrol. We intend to engineer our novel strain of bacteria, via CRISPR, to increase the antimicrobials being produced and increase the efficacy of our biocontrol in combatting *B. cinerea*.

We have identified a future biocontrol product and elucidated its modes of action. The findings from these experiments will enable mechanistic informed engineering of our bacteria to better prevent *B. cinerea* infection thereby replacing widely used chemical fungicides by offering a more effective and sustainable solution.

J Colhoun Prize Poster Abstract 16

Quantifying early immune signalling at scale using BY-2 cell packs

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Plant immune signalling produces rapid calcium fluxes, reactive oxygen species (ROS) and transcriptional reprogramming within hours of pathogen perception. These early outputs carry quantitative information about immune activation, yet most assays used to measure plant immunity are low-throughput, qualitative, or restricted to late-stage readouts such as the hypersensitive cell-death response (HR). A scalable, quantitative platform for early immune signalling is lacking.

Here, we establish a *Nicotiana tabacum* Bright Yellow-2 (BY-2) plant cell pack (PCP) system for high-throughput, quantitative measurement of plant immunity. We standardised PCP preparation using settled cell volume measurements and optimised *Agrobacterium*-mediated transient expression across infiltration buffers, bacterial strains and expression parameters. We deployed two complementary reporters based on the fungal bioluminescence pathway (FBP). An immune-inducible FBP reporter detects early transcriptional activation as a gain of bioluminescence, while a constitutively expressed FBP reporter quantifies HR as a loss of bioluminescence upon cell death. For cell-surface immunity, flg22 and chitin triggered measurable responses detected by both the inducible FBP reporter and L-012-based ROS quantification. For intracellular NLR-mediated immunity, we reconstituted three receptor–effector pairs that signal through distinct NLR architectures: Cf-4/Avr4 (NRC3-dependent), Roq1/XopQ (TIR-NLR, NRG1-dependent) and Ptr1/AvrB (CC-NLR). All three triggered HR quantified as loss of constitutive bioluminescence, and the inducible reporter detected immune activation before visible cell death.

This platform enables scalable screening of immune components, biosensor-based perturbation assays and gene-silencing experiments in a multiwell format.

J Colhoun Prize Poster Abstract 17

An effector cloaked in danger – exploring potential NLP-mediated host uptake of Phytophthora infestans RXLR effectors

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Extracellular vesicles (EVs) are released from cells by unconventional secretion, but little is known about the biogenesis routes, composition or cargoes of EVs from fungal or oomycete plant pathogens. We investigated the proteome of EV-associated proteins secreted by the oomycete *Phytophthora infestans*, cause of potato late blight disease. We found that vesicle-associated proteins, transmembrane proteins and RXLR effectors, which are delivered into host cells to suppress immunity, were enriched in the EV proteome. By contrast, the EV-independent secreted proteome was enriched in cell wall modifying enzymes and apoplastic effectors which act outside plant cells. Two proteins each containing two tetraspanning MARVEL domains, PiMDP1 and PiMDP2, were associated with *P. infestans* EVs. PiMDP1 and PiMDP2 were co-buoyant with RXLR effectors in sucrose density fractions containing EVs and co-localised frequently with each other and with RXLRs at vesicles within pathogen hyphae grown in vitro and during infection. Interestingly, PiMDP2, which is up-regulated during the early biotrophic phase of infection, accumulates at the haustorial interface, a major site of effector secretion during infection. We argue that PiMDP1 and PiMDP2 are molecular markers that will facilitate studies of the biogenesis and secretion of infection-associated *P. infestans* EVs.

J Colhoun Prize Poster Abstract 18

Phytoplasma-induced pectin remodelling in sieve elements: a possible trade-off between defence and phloem mass flow

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Phytoplasmas are prokaryotic pathogens that colonize the sieve elements (SEs) of plants. They interfere with phloem functionality by inducing structural and molecular changes which severely reduce source-to-sink balance, and so sugar allocation in the host. In Micro-Tom plants infected by grafting with '*Candidatus* Phytoplasma solani', SE cell wall shows enhanced thickness and swelling, perhaps contributing to the impairment of phloem transport. SE cell wall is characterized by elasticity (van Bel *et al.*, 2026), which depends on the balance between high methyl-esterified (HM) and low methyl-esterified (LM) pectin and their distribution along the cell wall, resulting critical for maintaining phloem sap flow. Here we characterize SE cell wall modifications at molecular, biochemical and microscopic levels, to propose an interpretative model of the reduction of phloem sap flow as a possible mechanism of reduction of phytoplasma spread. Indeed, phytoplasma infected plants show altered expression of genes encoding for vasculature-associated pectin methyl-esterases (PMEs) and increased enzymatic activity of PMEs in the midrib. Although total pectin content decreases upon infection, LM pectin becomes the predominant form and accumulates mainly in SE cell wall corners, while HM pectin redistributes to the middle lamella, indicating a major shift in pectin distribution and methyl-esterification pattern. Together, these findings suggest extensive remodelling of the pectic matrix in response to phytoplasma infection. Such modifications likely may represent a plant defence strategy that restricts phytoplasma spread.

Reference:

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J Colhoun Prize Poster Abstract 19

Mendelian Mishaps: How breeding has shaped the rhizosphere microbiome and disease resistance in pea.

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Plants have formed complex and diverse relationships with soil-borne microbes, enabling tolerance of both biotic and abiotic stress and increasing nutrient availability for the plants. These relationships have developed throughout the evolution of plants and are tightly controlled through mechanisms which we are only just beginning to unravel.

There has been a recent effort to re-introduce crop genetic diversity which was lost during the breeding of modern cultivars, especially with a focus on nutritional value, climate tolerance and disease resistance. This project aims to expand that thinking to the rhizosphere microbiome of pea. When swapping rhizosphere microbiomes between wild and cultivar plants, we have shown that the wild microbiome leads to both better plant performance and reduced root rot disease severity. This demonstrates the importance of understanding microbiome recruitment and dynamics, and how these characteristics have been impacted by breeding.

To begin unpicking microbiome recruitment in pea, a panel of 10 diverse *Pisum* accessions, bridging wild relatives through to representative cultivars, had their rhizosphere microbiome sequenced using shotgun metagenomic sequencing. This data shows clear microbiome selection patterns correlated with domestication and breeding. One such pattern, the selection of the most abundant fungus in the rhizosphere, was investigated further using an advanced RIL population for genetic mapping via a qPCR phenotyping method. This mapping shows an associated QTL on LGII (chromosome 6), in close proximity to both a fungal disease resistance locus and the mendelian *A* gene. The *A* gene is a dominant gene responsible for coloured flowers and pigmented seeds, both traits which have been selected against during modern breeding. Candidate genes within this region are being screened for their ability to shift microbiome selection and provide resistance to fungal disease.

J Colhoun Prize Poster Abstract 20

Microbiome-Mediated Resistance to Cochineal Scale in Opuntia: A Shotgun Metagenomic Approach

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The rhizosphere microbiome constitutes a critical interface mediating plant nutrition, abiotic stress tolerance, and biotic defense. In Opuntia spp., microbiome-mediated processes may contribute to differential resistance against the cochineal scale insect (Dactylopius opuntiae), a pervasive pest in arid agroecosystems. We hypothesised that host resistance phenotype is associated with distinct taxonomic configurations and functional capacities of the rhizosphere microbiome.

To test this, we performed shotgun metagenomic sequencing of rhizosphere soils from resistant and susceptible Opuntia ecotypes, including bulk soil and barley rhizospheres as environmental and phylogenetically unrelated controls. A non-redundant gene catalog was constructed to support high-resolution taxonomic assignment and functional annotation against KEGG, eggNOG, and CAZy databases. Community structure analysis revealed a pronounced host genotype effect, with clear segregation of samples in beta-diversity space, indicative of deterministic assembly processes.

Resistant ecotypes exhibited significant enrichment of taxa commonly associated with plant growth promotion and antagonistic activity, notably Streptomyces, Bacillus, and Pseudomonas. Functionally, these communities were characterised by overrepresentation of genes involved in environmental information processing, including two-component regulatory systems, quorum sensing pathways, and ABC transporters, as well as an expanded repertoire of carbohydrate-active enzymes. In contrast, susceptible rhizospheres displayed distinct taxonomic signatures, including increased relative abundance of Rhizobium and Flavobacterium, coupled with reduced representation of interaction- and defense-related functional modules.

Collectively, these results demonstrate a coordinated taxonomic and functional restructuring of the Opuntia rhizosphere microbiome associated with resistance to D. opuntiae. The identified microbial consortia and functional traits provide a foundation for mechanistic investigations and the development of microbiome-informed strategies for sustainable pest management in arid systems.

J Colhoun Prize Poster Abstract 20

Transcriptomic profiling of the barley fungal pathogen Ramularia collo-cygni reveals virulence-associated secreted enzymes and candidate effector proteins

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Ramularia collo-cygni (*Rcc*), the causal agent of Ramularia leaf spot (RLS), poses a major threat to barley production, with yield losses reported to reach 70%. The chlorothalonil ban, increasing restrictions on fungicide use, and the absence of effective genetic resistance highlight the need for alternative control strategies. Here, we investigated the effector repertoire of *Rcc* to identify virulence-associated candidates during barley infection. We phenotypically screened 20 *Rcc* isolates on the susceptible barley cultivar RGT Planet. Disease development was quantified using combined area under disease progression stairs (AUDPS) and ImageJ-based lesion analysis, confirming Rcc02 as the most aggressive and Rcc06 as the least aggressive isolates. Dual host-pathogen RNA-seq at 2, 4, 6, 10, and 14 dpi identified 7,562 differentially expressed genes in Rcc02, of which 581 were significantly more highly expressed than in Rcc06. SignalP-6.0 and EffectorP-3.0 predicted 55 secreted effector proteins, which were further refined to 18 high-confidence candidates showing peak expression during infection. Further analysis revealed seven distinct phase-specific co-expression clusters, abundant proteases and redox-related enzymes, and candidate effectors associated with both biotrophic and necrotrophic stages of *Rcc* infection. The identification and characterisation of these fungal effectors would help in the development of RLS-resistant barley varieties.

J Colhoun Prize Poster Abstract 21

Branch invaders: Investigating the Botryosphaeriaceae in South African avocados

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Fungi of the *Botryosphaeriaceae* threaten avocado production in South Africa, causing branch cankers, dieback, and fruit rot that reduce long-term tree productivity. While these fungi are widespread on woody hosts, the species affecting avocado locally remain uncharacterised. This study aimed to determine their diversity, distribution, and pathogenicity in South African avocado nurseries and orchards.

Symptomatic and asymptomatic avocado tissues were collected from Limpopo, Mpumalanga, KwaZulu-Natal, and the Western Cape. Fungal isolates were purified, DNA extracted, and the ITS region amplified for genus-level identification, with selected isolates further analysed using *TEF-1α*, *β-tub*, and *rpb2* loci. Sequences were aligned and subjected to maximum-likelihood phylogenetic analysis, and a detached-stem assay assessed the pathogenicity of representative isolates.

A total of 248 *Botryosphaeriaceae* isolates were recovered, representing nine species across four genera: *Neofusicoccum*, *Lasiodiplodia*, *Diplodia* and *Botryosphaeria*. The dominant species were *Neofusicoccum parvum*, *Lasiodiplodia theobromae* and *Neofusicoccum australe*. *N. parvum* was most prevalent in Limpopo, Mpumalanga and KwaZulu-Natal, while *N. australe* predominated in the Western Cape. Several less common species, including *L. pseudotheobromae*, *D. pseudoseriata*, *N. cryptoaustrale* and *B. dothidea*, were also detected. *N. kwambonambiense* and *L. gonubiensis* were recorded on avocado for the first time. All tested isolates produced lesions on detached avocado stems, confirming their pathogenicity.

The *Botryosphaeriaceae* population associated with South African avocados is diverse, dominated by a few widespread species and several rare taxa that may become more significant under shifting environmental conditions. This study provides the first assessment of this fungal family on avocado, delivering crucial baseline data to improve monitoring and guide management strategies.

J Colhoun Prize Poster Abstract 22

Investigation of the Role of Cytokinin Biosynthesis and Degradation Pathways in pathogenesis of Pyrenopeziza brassicae

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Light Leaf Spot (LLS), caused by *Pyrenopeziza brassicae*, is one of the most economically important diseases affecting oilseed rape (*Brassica napus*) in the United Kingdom. Current disease management strategies rely mainly on fungicides and partially resistant cultivars, but with the increasing fungicide tolerance/resistance and the pathogen's prolonged symptomless growth phase make disease control challenging. Recent studies suggest that phytohormones, particularly cytokinin, play an important role in plant defense responses and disease development. However, the involvement of cytokinin biosynthesis and degradation pathways in LLS tolerance of oilseed rape remains poorly understood.

This project aims to investigate the role of cytokinin biosynthesis (IPT) and degradation (CKX) genes in the response of *Brassica napus* to *P. brassicae* infection. Bioinformatic analyses will be conducted to identify and characterize IPT and CKX gene homologues in the *B. napus* genome. Gene-specific primers will be designed for selected targets. In addition, whole transcriptome of resistant and susceptible oilseed rape cultivars will be analyzed under pathogen stress to evaluate differential gene expression patterns.

The expected outcome of this research is the identification of cytokinin-related genes associated with disease development and resistance in oilseed rape. The findings will improve understanding of hormone-mediated defense mechanisms and may contribute to the future development of more sustainable disease management strategies and resistant rapeseed cultivars.

J Colhoun Prize Poster Abstract 23

Opposing transcriptional programs define pre-parasitic activation and sustained parasitism in Meloidogyne enterolobii

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Root-knot nematodes (*Meloidogyne* spp.) are among the most damaging plant parasites worldwide, relying on a coordinated deployment of effectors to suppress host immunity, reprogram host tissues, and establish specialised feeding structures that sustain parasitism. Yet, the transcriptional programs governing early parasitic establishment and the transition from invasive to sedentary lifestyles remain poorly understood, particularly in the emerging resistance-breaking species *Meloidogyne enterolobii*. Here, we generated life-stage-resolved transcriptomic atlas of the *M. enterolobii*–sweet potato interaction, profiling pre-parasitic juveniles and infection stages at 36 hours post-infection and 3, 5, and 7 days post-infection. Guided by acid fuchsin staining, these timepoints captured successive stages of parasitic development, from host penetration and migration to feeding-site initiation, and early sedentary establishment. Comparative analyses revealed extensive transcriptional reprogramming across developmental stages, including dynamic, stage-specific enrichment of genes encoding secreted proteins and distinct temporal expression programs associated with host invasion and sustained parasitism. Network-based analyses uncovered opposing transcriptional clusters: sensory and signalling-associated functions dominated during pre-parasitic, invasive stages, whereas sustained parasitism clusters were enriched for genes encoding secreted proteins, extracellular remodeling enzymes, and proteolysis-related pathways. Gene Ontology and metabolic analyses further revealed modular and partially conserved biological processes distributed across transcriptional clusters, consistent with coordinated but segmented regulation of parasitic functions. Together, these findings reveal stage-specific molecular logic underlying parasitic establishment in *M. enterolobii* and provides a framework for dissecting infection strategies in this resistance breaking root-knot nematode.

J Colhoun Prize Poster Abstract 24

Do plants recognise Aphid Chitin? Functional Analysis of CERK1 and LYR4 in Medicago truncatula

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Chitin is a polysaccharide universally present in fungi and in insects such as aphids. In *Medicago truncatula* and other species, the widely conserved receptor-like kinase CHITIN ELICITOR RECEPTOR KINASE 1 (CERK1) and Lysine-Motif receptor 4 (LYR4) are associated with the recognition of fungal cell wall chitin. Chitin acts as a pathogen-associated molecular pattern (PAMP) signal to induce host immunity. As a result, chitin has been widely advocated as a sustainable alternative to chemical pesticides. However, whether aphid chitin is a herbivore-equivalent that triggers similar immune responses is poorly understood. In this study, we aim to investigate whether aphid chitin is a herbivore-associated molecular pattern (HAMP) recognised by chitin receptors CERK1 and LYR4, similarly to fungal chitin. So far, differential expression analysis in *M. truncatula* has shown that CERK1and some other Lysin-Motif receptors are significantly upregulated by aphids. Additionally, aphids survived better on *cerk1* and *lyr4* knockout plants, suggesting a role for these chitin receptors in immune activation by aphids. To probe further for HAMP-dependent immune response, we are evaluating suppression of the reactive oxygen species (ROS) burst upon chitin treatment in *cerk1* and *lyr4* plants. In addition, the attenuated induction of defence hormones such as Jasmonic acid in *cerk1* and *lyr4* plants after aphid infestation would further support the role of CERK1 and LYR4 in the aphid-induced immune response.

J Colhoun Prize Poster Abstract 25

Biocontrol activity of Pseudomonas spp. against Pseudomonas syringae pv. actinidiae is linked to novel natural product clusters.

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Pseudomonas syringae pv. *actinidiae* (Psa) is a present and ongoing threat to the kiwifruit industry as the causal agent of the disease kiwifruit bacterial canker. Psa infection leads to heavy fruit losses unless carefully managed, which can have large impacts on local and national economies. This is exemplified by the 2010 New Zealand incursion which, by 2017, had led to an economic deficit of over NZ$930 million from lost exports alone. Whilst the disease is currently controlled through antibiotics and the use of harsh copper treatments, resistant strains have been identified in orchards causing concerns about the future of Psa control. Naturally occurring pseudomonads have long been recognized as a source of natural products and so offer a potential avenue for the discovery of novel Psa treatments.

Two BCAs were identified from a screen of >1000 *Pseudomonas* strains isolated from kiwifruit vine leaves from New Zealand's North Island where Psa is highly prevalent. These strains are non-phytopathogenic and provide a level of Psa control equal to leading market competitors with further trials ongoing. Investigations into the mode of action of these BCAs led to the discovery of novel natural product clusters linked to anti-microbial activity. These strains also demonstrate wide ranging activity against plant and human pathogens. There is huge potential therefore for these strains to be developed into a new biocontrol product aimed at reducing the incidence of Psa, and these findings may additionally lead to the discovery of a new potent antimicrobial with utility in agriculture and medicine.

J Colhoun Prize Poster Abstract 26

Rachis tip dieback: a phenology-driven, multi-pathogen disease of macadamia racemes

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Rachis tip dieback (RTD) is an emerging disease of macadamia racemes associated with the flower blight complex. Affected racemes exhibit necrosis progressing from the distal to proximal end of the rachis, causing curvature and greyish black discolouration of florets, ultimately reducing flower formation. This study characterises the aetiology and epidemiology of RTD. Field surveys were conducted on 20 commercial macadamia orchards in Australia at flowering seasons in 2023 and 2024. From over 300 raceme samples, 20 fungal genera were identified using multi-locus DNA sequencing. Species of *Neopestalotiopsis* (27.5%), *Epicoccum* (20.4%), and *Diaporthe* (19.1%) were the most prevalent. Pathogenicity assays confirmed that *N. maddoxii*, *N. macadamiae*, and *E. italicum* caused severe RTD symptoms at the raceme early elongation stage, supporting RTD as a distinct but interconnected component of the flower blight complex. To resolve infection dynamics, single- and mixed-species inocula containing flower blight pathogens (*Botrytis cinerea*, *Cladosporium angustisporum*, *N. macadamiae* and *N. maddoxii*) and *E. italicum* were used to inoculate racemes at different developmental stages. The results revealed that RTD severity reduced with mixed-species inoculations compared to the mean observed across single-species. Disease severity declined when racemes were infected at more advanced maturation phases, and infection occurred exclusively at the distal rachis. These findings demonstrate that RTD incidence is governed by host phenology and multiple fungal pathogens. This understanding provides a basis for predicting disease risk and optimising the timing of management in the macadamia industry.

J Colhoun Prize Poster Abstract 27

Generation of a high-quality reference assembly for the generalist pathogen Armillaria mellea

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Armillaria mellea, commonly known as honey fungus, is a generalist root pathogen, affecting over 500 plant species worldwide and accounting for substantial agricultural and forestry losses. With rising global temperatures and increased frequency of extreme weather events, climate change is expected to increase Armillaria root rot (ARR) disease by weaking host immunity, expanding the pathogen's geographic range, and potentially enhancing its pathogenicity. Existing studies also suggest that rising temperatures and altered precipitation patterns may enhance the growth of rhizomorphs and subsequently increase the rate of spread of the disease. Increased fungal growth is not just for *A. mellea,* but also its sister species, *A. gallica,* which to-date is known primarily as an opportunistic pathogen. Despite the potential impact of these changes, significant knowledge gaps remain regarding how either species will respond to increasing temperatures. To comprehensively assess these species response to increased temperatures, high quality genomic resources are required. Current genome assemblies are fragmented and haploid, limiting crucial allele-level variation and structural diversity in this diploid pathogen. This research aims to address this knowledge gap by generating a long-read *de novo* assembly using Hi-C to scaffold and phase homologous chromosomes. This chromosome-scale assembly will be used as the foundation to support population genomic analyses of an existing collection of 150+ *A. mellea* isolates collected from a wide-range of host plants from the RHS’s diagnostic service. Our initial data for a draft genome assembly, genome and transposon annotation will be presented.

J Colhoun Prize Poster Abstract 28

Elevated CO_2 Under Climate Change Affects the Metabolite Profiles of Quercus robur Leaves.

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Climate change, driven by elevated carbon dioxide concentration (e[CO2]), is predicted to significantly impact the health of trees. Important tree species, such as *Quercus robur* (English oak), are threatened by emerging pathogens which could be exacerbated by climate stress. Trees utilise metabolites to enhance tolerance to stressors, including pathogens, by boosting defence responses and increasing resilience. However, it's hypothesised that climate change, specifically e[CO2], will cause a variation in trees metabolic profiles and microbial communities, which could lead to increasing disease susceptibility. At the Birmingham Institute for Forest Research – Free Air Carbon dioxide Enrichment facility (BIFoR-FACE) we are investigating the effects of e[CO2] on oak leaf metabolite profiles and assessing interactions between key metabolites and oak microbial communities. At BIFoR-FACE, open arrays of oak-dominant forest are exposed to elevated CO_2 (+20% e[CO_2], ~520 ppm), simulating atmospheric concentrations projected for 2050. Oak leaves from 12 trees were collected at 3 timepoints across the growing seasons of 2016, 2019, and 2024 from e[CO2] and ambient arrays. Untargeted Liquid Chromatography – Mass Spectrometry (LC-MS) was used to determine whether e[CO2] drives changes in the leaf metabolome composition. Variations in metabolite profile were beginning to emerge between the two CO2 concentrations (PERMANOVA: $p = 0.0715$), with most shifts occurring between timepoints (year $p=0.0001$, month $p=0.0113$), a trend mimicked in ITS and 16S rRNA gene microbiome analysis. Assessing variably important features highlighted an increased abundance of flavonoids in e[CO2] conditions. Further analysis identified a cluster of procyanidins enriched under e[CO2]; including procyanidin B1 and A1 (T-Test: $p = 0.022$). These compounds are associated with plant defence responses and stress. Current experiments are exploring how increased procyanidin concentration impacts the oak leaf microbiome. These investigations are crucial for predicting future tree health and developing innovative climate-change based strategies to safeguard oak trees from climate change.

J Colhoun Prize Poster Abstract 29

Engineering Gene Regulatory Networks to Design Disease Resistant Lettuce

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Lettuce is an economically significant crop, valued at over £200 million in the UK. However, fungal pathogens such as *Botrytis cinerea* and *Sclerotinia sclerotiorum* cause 20-30% lettuce yield loss. Current control methods, including fungicides, are unsustainable, and field resistance is increasing. This study aims to enhance lettuce disease resistance by rewiring the gene regulatory network (GRN) involved in its defense response. We developed a GRN model to identify transcription factor (TF)-target gene interactions linked to pathogen-induced transcriptional changes. From this, we selected a subnetwork of 18 TFs with positive and negative impacts on lettuce defense. To validate the network, we combine *in silico* promoter analysis with high-throughput protoplast assays. These include transient expression with luminescent reporters and the TARGET (Transient System for Specific TF Targets) assay coupled with RNA-seq to pinpoint direct downstream targets. Furthermore, transient TF overexpression in *Nicotiana benthamiana* combined with fungal infection assay are used to screen for enhanced fungal resistance *in planta*. Taken together, these datasets will refine the GRN model, enabling predictive simulations to guide precise network rewiring via synthetic TFs, promoter editing, or the introduction of novel regulatory elements.

J Colhoun Prize Poster Abstract 30

Frustration guided design of plant TIR domains to introduce ground up functionality.

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Plant pathogens cause approximately $200bn of crop losses globally each year. Plant immunity often relies on recognition of pathogen virulence proteins by intracellular nucleotide-binding leucine-rich repeat (NLR) receptors, which often culminates in programmed cell death, limiting the spread of infection. Toll-interleukin-1 like receptor (TIR) domains are enzymatic immune signalling domains, found in many NLRs, which hydrolyse NAD^+ into a variety of small molecules to signal pathogen recognition within the plant cell, often resulting in cell death responses. However, with high levels of structural homology across TIR domains, it is unclear how these proteins are able hydrolyse NAD+ to create the different resultant signalling molecules that affect differential immune signalling pathways.

We hypothesise that frustrated surface regions of TIR domains, where residues are in energetically unfavourable conditions to accommodate global energy minimums, may determine the specificity of metabolite production. Here, we aim to identify frustrated residues at functional sites and correlate these regions with signalling molecule production. We collected 23,465 known TIR domains sequences using the pfam identifier (PFA01582) from the AlphaFold2 prediction database. Structures were filtered for high pTM (>0.75) and high plddt across functional regions. We then developed a custom pipeline that utilises FrustratometeR to calculate per-residue frustration as well as sequence conservation. We present this combined metric as DRES to identify residues that are highly conserved and highly frustrated across the TIR family to help characterise the mechanism for each of the signalling products produced by NAD+ hydrolysis. These results will grant a better understanding of the structural and biophysical mechanisms behind TIR domain signally and guide future design of synthetic immune signalling for engineering disease resistance.

J Colhoun Prize Poster Abstract 31

A harmonized annotation resource of 305 Fusarium genomes prioritizes conserved cytoplasmic effectors for resistance breeding

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Plant pathogenic fungi secrete effector proteins that manipulate host cells and promote infection. Effector repertoires can evolve rapidly through horizontal gene transfer, accessory chromosome dynamics, genome rearrangements, and strong selection imposed by host immunity. Consequently, related effector families often show low sequence similarity and occur in phylogenetically distant lineages. In *Fusarium*, many effectors are encoded on accessory chromosomes, making it challenging to compare effector repertoires across genomes and prioritize conserved targets for resistance breeding and immune receptor bioengineering. To address this, we annotated 305 diverse *Fusarium* genomes using Helixer, a deep learning genome annotation tool, and identified 419,534 putative effectors, which were grouped into 11,447 sequence-based clusters. We further characterized these effectors using AlphaFold 3 and performed structure-based clustering. Among the prioritized candidates, we found that the ToxA-like fold effector AVRFOM2, which is recognized by the melon NLR immune receptor Fom2, is highly conserved across *F. oxysporum* f. sp. *albedinis* (Foa) isolates. Foa causes Bayoud disease of date palm, a devastating disease for which no effective resistance gene has yet been identified. We also examined KP6-like and ToxA-like fold effectors because these folds include cytoplasmic effector pairs in *F. oxysporum* that interact with each other and are genetically linked, such as SIX5/Avr2 and PSL1/SIX8. In Foa, we identified a KP6-fold PSL1 homolog that is genetically linked to a ToxA-like fold effector. However, this ToxA-like effector showed little detectable sequence similarity to SIX8 despite sharing a related protein fold, highlighting the extensive sequence diversification of ToxA-like effectors in *Fusarium*. Together, our dataset and comparative analyses prioritize conserved cytoplasmic effector candidates in Foa, including genetically linked ToxA-like and KP6-like fold effectors, as promising targets for resistance breeding and immune receptor bioengineering. Beyond these candidate effectors, this harmonized *Fusarium* genome annotation resource provides a foundation for studying *Fusarium* genome evolution and effector diversificatiosn across Foa and other *Fusarium* pathosystems.

J Colhoun Prize Poster Abstract 33

Structure-based atlas of Phytophthora effectorome reveals conserved folds and novel host-pathogen interactions

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Oomycete pathogens of the genus *Phytophthora* deploy diverse effector repertoires to manipulate host immunity, yet functional characterisation remains limited by low sequence similarity to known functional domains.

To address this, we constructed a large-scale structural resource of effectoromes from 40 *Phytophthora* species spanning major evolutionary clades, with effector candidates identified from proteomes and their structures modelled using AlphaFold3.

Structural comparisons of effector proteins enabled the reconstruction of a structure-based classification and phylogeny of the effectoromes. Structural annotation revealed conserved folds undetectable at the sequence level, supporting novel assignments of previously uncharacterised effector families and the identification of homologues across distant taxa. Through structural modelling of effector-host interactions, we identified candidate effectors with predicted host targets.

Together, this resource provides a genus-wide framework for resolving effector diversity, tracing evolutionary relationships, and prioritising candidates for functional study of *Phytophthora*-host interactions.

J Colhoun Prize Poster Abstract 34

Proposed Take-All resistance mechanisms in the Watkins collection

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Take-All disease is caused by the root infecting fungus of wheat, *Gaeummanomyces tritici*, which is present globally and can cause up to 50% yield loss in high disease years. This fungus uses hyphae to infect the steele of young wheat roots and cause necrosis, impeding the plants' ability to uptake nutrients and water. Current control mechanisms are limited to fungicidal seed dressings and crop rotation as genetic resistance to Take-All is not present in the modern wheat germplasm.

Over several years of field trials at Rothamsted Research Experimental farm in Harpenden, more than 20 lines from the Watkins collection were identified as having increased resistance to Take-All disease. This data was then used in a Genome Wide Association Study to identify two QTLs which are highly associated with TA resistance. These QTLs are present on the same arm of the same chromosome, only ~56Mb apart.

Identification of this genomic region has facilitated investigation of potential underlying genes within Chinese Spring reference genomes as well as representative genomes from other Ancestral groups present within the Watkins collection. Several of the most resistant of the Watkins lines belong to Ancestral Group 5 and so work on representative accessions has focussed on this group.

This investigation has highlighted several possible mechanisms of resistance which will be explored further during my PhD.

J Colhoun Prize Poster Abstract 35

Membrane – stressor interaction in the plant pathogen Pseudomonas syringae

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During infection *Pseudomonas syringae* must contend with multiple hostile environments, with differing stresses in different hosts and infection stages. The first layer of defence for the bacterium is its cell envelope which acts as a multi-layered barrier preventing the access of toxic molecules and providing protection against physical stresses. However, there is little understanding of what the composition of this cell envelope is, how it varies during infection, and how these changes allow the bacterium to survive in its infection cycle. Using a combination of *in vitro* wet lab biology, bioinformatic prediction, neutron reflectometry and molecular dynamics simulations, we are beginning to determine how different membrane states interact with stressor molecules. Different lipopolysaccharide (LPS) modification genes may be important under different stress conditions, and the resulting LPS species have altered bulk properties in computational simulation. We are also investigating the role of the O antigen, the long repeating polysaccharide element of LPS, in stress resistance and infection. To this end, we have prepared rough mutants lacking this element in several model *P. syringae* strains. Reflectometry experiments show reversible interactions between *P. syringae* outer membrane models and agricultural surfactants, which is of mechanistic interest in treatment of *P. syringae* and in understanding the resistance of the bacterium to its own surfactants. We have found that this interaction, and the survival of *P. syrinage* subjected to surfactants *in vitro*, are independent of O antigen presence though surfactants were found to have a solubilising effect on rough mutant aggregates. Further work will determine how these model systems interact with *in vivo* relevant plant defence molecules, and the effect of cell envelope mutants on *in planta* and *in vitro* stress resistance, to determine the mechanistic role of cell envelope variation and potentially inform treatment strategies.

J Colhoun Prize Poster Abstract 36

Stress and Hunger Drive Pathogen Survival at the Host Interface: Gene Expression and Regulation in Powdery Mildew Haustoria

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Powdery mildew fungi are obligate biotrophic plant pathogens that establish haustoria as specialised feeding structures within living host cells. Haustoria play essential roles in nutrient acquisition and the delivery of virulence factors that suppress host immunity, but the molecular regulation of haustorial function remains poorly understood.

To investigate gene expression and transcriptional regulation in haustoria, we compared *Podosphaera xanthii* haustoria and hyphae transcriptomes during powdery mildew infection of cucurbit plants. This was combined with promoter motif discovery to identify regulatory elements associated with haustoria-upregulated genes.

Many differentially expressed genes, upregulated in haustoria were identified. Their functional annotation highlighted roles in nutrient acquisition, metabolic adaptation and host–pathogen interactions, and it included homologues of virulence-associated metalloprotease-like gene (*BEC1019*), lytic polysaccharide monooxygenase 1 (*LPMO1*) and a putative maltose permease. qRT-PCR confirmed their upregulation in both *P. xanthii* and *Blumeria hordei* during infection of zucchini and barley, respectively.

To investigate the molecular mechanisms driving haustoria gene expression, gene promoter sequences of haustoria versus hyphae upregulated genes were compared for *ab initio* identification of motifs enriched in the pool of haustoria upregulated genes. Many of these were associated with transcriptional responses linked to stress adaptation, metal ion homeostasis, carbon and nitrogen metabolism, glucose and maltose regulation, and amino acid starvation pathways.

These findings support a model in which powdery mildew haustoria coordinate nutrient sensing, starvation responses and virulence-associated gene expression to promote pathogen survival and successful colonisation. The study also identifies candidate regulatory elements that may contribute to powdery mildew pathogenicity.

J Colhoun Prize Poster Abstract 37

Presymptomatic plant disease detection with PSNet: A low-cost hyperspectral imaging and RGB fusion framework

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Plant pathogens cause yield losses worldwide, threatening food security and livelihoods. Because early infection is difficult to diagnose, management often relies on prophylactic pesticide use, increasing costs and environmental impact. Here we present PSNet, a multimodal framework that fuses hyperspectral imaging with RGB information for presymptomatic plant disease detection, together with a low-cost hyperspectral camera incorporating a 3D-printed housing, costing under £500. We validate PSNet using Arabidopsis thaliana infected with the oomycete Albugo candida. Imaging at 2 and 4 days post inoculation, prior to visible symptoms, revealed spectral signatures that distinguished infected from healthy plants, while imaging at 6 days post inoculation captured the transition toward early symptom emergence. Discriminative spectral regions overlapped wavelengths associated with plant responses to biotic stress, supporting the biological plausibility of these signatures. Performance was evaluated using strict plant-level partitioning, ensuring samples from the same plant were confined to a single split. On a four-class task (healthy, 2 dpi, 4 dpi, 6 dpi), PSNet achieved 90.00% accuracy and 97.50% accuracy for binary classification. Together, these results demonstrate that presymptomatic detection is achievable using low-cost hardware combined with multimodal learning, underscoring the potential of scalable systems for early disease monitoring.

J Colhoun Prize Poster Abstract 38

CommonBean–Xanthomonas interaction: Physiological, Genetics and Environmental approaches to breeding for disease resistance

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Common bean (*Phaseolus vulgaris* L.) is a popular crop cultivated in many parts of the world and one of the most widely consumed legume in Brazil and the whole of Latin American. However, the interaction between common bean and the bacterium *Xanthomonas phaseoli* pv. *phaseoli* (Xpp) poses serious challenges to global common bean production, leading to substantial yield losses. The objective of this research is to evaluate and select common bean genotypes with resistance to common bean blight using Genetic, environment and physiological approaches after inoculation with (Xpp) isolate. Thirty common bean genotypes were obtained from the gene bank of Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF), and grown in a screenhouse. The research was laid out in a randomized complete block design with three replications, and four pots per genotype, totaling 360 experimental units. The foliar inoculation method by infiltration was performed with the Xpp isolate (139y). Disease severity was characterized daily for 7 days, starting 24h after inoculation, using visual scales and lesion diameter measurements from RGB images processed in ImageJ. ClorofiLog meter was used to evaluate the total chlorophyll content (a and b) for photosynthesis activities. Additionally, Thermal images of the inoculated leaves were captured using an infrared thermographic camera. The maximum differential temperature was calculated based on the differences between the temperatures of the diseased leaf area and the healthy leaf area.The results showed highly significant ($p < 0.05$) variation in chlorophyll content among the genotypes. The analysis revealed a coefficient of variation (CV) of 16.73% for chlorophyll a and 34.35% for chlorophyll b, indicating distinct physiological responses to the pathogen. Genotypes such as UENF2434 showed the highest photosynthetic content, suggesting superior tolerance. In contrast, genotypes UENF2430 showed the lowest levels of chlorophyll a and b, indicating higher susceptibility to the bacterial infection. The observed differences in chlorophyll content among the genotypes indicate that chlorophyll content can be used as a phenotypic marker for identifying common bean genotypes with tolerance to Xanthomonas, and represent promising genetic resources for breeding programs focused on bacterial blight resistance.

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J Colhoun Prize Poster Abstract 39

Unravelling the mechanisms of effector-triggered immunity for durable plant resistance.

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Plant immunity relies heavily on nucleotide-binding leucine-rich-repeat (NLR) proteins, that recognise pathogen-derived effectors and activate effector-triggered immunity (ETI)[1]. Following effector recognition, mitogen-activated protein kinases (MAPKs) are activated and NLR proteins oligomerise into high molecular weight complexes called resistosomes[2]. The tomato resistance complex Prf-Pto is a model system for studying NLR signalling pathways in crops. The NLR Prf is associated with the Pto kinase, which directly binds to the *Pst* DC3000 effectors AvrPto(B), and activates two distinct signalling branches. One signalling branch is initiated by Prf dissociation from the helper NLR NRC3, allowing NRC3 to form resistosomes, travel to the plasma membrane, and induce a hypersensitive response (HR). The other signalling branch involves Pto dissociation from 14-3-3 proteins, which frees MAPK cascades from repression[1]. However, it is not currently understood whether the two signalling branches interact; which is activated first; and how NRC3 resistosomes are shuttled to the plasma membrane. To explore the possible crosstalk between the pathways, an N-term deletion autoactive MAPKKKa was co-expressed with components of the Prf-NRC3 branch. Autoactive MAPKKKa was shown to induce Prf-NRC3 dissociation, and NRC3 resistosome formation, indicating a crosstalk between the two signalling branches. Using fluorescence-tagged NRC3, we have also shown that myosins enable NRC3 resistosome movement along actin filaments. We are currently further investigating the activation of the two signalling branches using ‘analog-sensitive’ MAPKKKa mutants, and TurboID constructs for proximity labelling-mass spectrometry (PL-MS) to identify potential protein interactors through biotinylation. Overall, our data elucidate the role of MAPKs-mediated crosstalk in coordinating the two branches of Prf-Pto signalling and reveal actin-myosin-dependent resistosome trafficking as a key step in ETI. Unravelling the downstream mechanisms of the Prf-Pto resistance complex, and ETI signalling more generally, can inform resistance-gene breeding and crop protection strategies.

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J Colhoun Prize Poster Abstract 40

AI-guided discovery of atypical protein assemblies

AmirAli Toghani[1], Benjamin A. Seager[1], Yu Sugihara[1], Lisa-Marie Roijen[1], Juan M. Azcue[1], Maián Garro[1], Maryam Sargolzaei[1], Ioanna Morianou[1], Adeline Harant[1], Sam Gallop[2], Jiorgos Kourelis[3], Dan MacLean[1], Mauricio P. Contreras[4,5], Sophien Kamoun[1], Daniel Lüdke[1]

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Artificial intelligence (AI) systems such as AlphaFold have transformed structural biology by enabling accurate prediction of protein structures. However, their capacity to uncover new classes of macromolecular assemblies remains largely untapped. We developed the Structural Novelty Index (SNI), a quantitative framework that combines structural modeling with prior knowledge to identify protein complexes that diverge from canonical architectures at scale. As one implementation, we applied SNI to nucleotide-binding, leucine-rich repeat immune receptors (NLRs) to identify unconventional resistosome assemblies. Our analysis led to the discovery of several atypical NLR resistosome complexes, including the undecameric (11-mer) NRC7 resistosome. Our results establish SNI as a scalable approach for discovering atypical protein complexes.

J Colhoun Prize Poster Abstract 41

HopBZ1, a novel Type III Effector Protein in Pseudomonas syringae confers virulence in plants using two enzymatic domains

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Gram-negative plant pathogens have evolved the use of the type III secretion system to deploy type III effector proteins into plant cells. Once inside the cell, the effectors carry out a range of functions that are designed to reprogramme the plant cell and create a permissive environment for pathogen survival and growth.

Pseudomonas syringae is a major plant pathogenic species complex that is widely distributed in the environment. Across the species´ pangenome, there are 5127 unique effectors belonging to 70 families, but the function of most effectors remains unknown. *Pseudomonas syringae* pv. *syringae* 9644 (*Pss* 9644), a pathogen used as a model to study cherry canker disease, harbours 16 known effector genes. However, in this study we identified an additional effector.

Pss 9644 carries a gene cluster encoding the previously characterised effector protein HopBE1 and a second downstream gene encoding a novel effector, designated HopBZ1. Both genes are enriched among *Pseudomonas syringae* isolates from sweet cherry and form an operon that was likely acquired through horizontal gene transfer from members of the *Pseudomonas fluorescens* complex.

This locus enables an otherwise avirulent *Pss* 9644 mutant to proliferate within sweet cherry leaves and allows an avirulent mutant of *Pseudomonas syringae* pv. *tomato* DC3000 to induce chlorosis in the model plant *Arabidopsis thaliana*. HopBZ1 contains two functional enzymatic domains: an N-terminal glycosyltransferase domain, homologous to toxins from human pathogens like *Clostridium difficile,* and a C-terminal P-loop kinase/NTPase domain. Mutations disrupting the catalytic activity of these domains abolished the locus-mediated chlorosis in *A. thaliana*. Furthermore, transient expression of dual fluorescently tagged HopBZ1 in *Nicotiana benthamiana* demonstrated its localisation to both the cytoplasm and chloroplasts of plant cells.

Collectively, these findings identify HopBZ1 as a novel virulence factor in *Pss* and broaden our understanding of effector diversity, evolution, and function in plant-pathogenic bacteria.

J Colhoun Prize Poster Abstract 42

Development of molecular markers for rapid identification and detection of macadamia husk rot pathogens

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Macadamia husk rot is a fungal disease affecting macadamia fruit and is associated with multiple fungal genera and species. Among these, *Diaporthe* spp. and *Colletotrichum* spp. are considered the dominant pathogens responsible for the disease. However, limited information is available regarding their epidemiology, lifestyles, and infection cycles. Both pathogens have been isolated from asymptomatic fruit during early developmental stages as well as from symptomatic fruit later in the season, suggesting the presence of a latent infection phase. Due to the lack of critical epidemiological information, continuous monitoring of these pathogens throughout the growing season is required. The aim of this study was to develop TaqMan-probe-based quantitative PCR (qPCR) molecular markers for the rapid detection and identification of the husk rot pathogens. Primers were designed targeting the translation elongation factor 1-alpha (TEF1-α) gene region for *Diaporthe nebulae*, and the *Apn2*-Mat1 intergenic spacer and partial mating type (ApMat) gene region for *Colletotrichum siamense* and *C. theobromicola*. Primer specificity was verified *in silico*, followed by *in vitro* optimisation and specificity testing using conventional PCR against target and non-target macadamia-associated pathogens. qPCR assays were subsequently conducted to evaluate primer sensitivity and specificity. The *D. nebulae* primer pair (TFD) and the *C. theobromicola* primer pair (ATCT) demonstrated high specificity during conventional PCR assays. In contrast, the *C. siamense* primer pair (ATCS) failed to amplify all C. siamense isolates, likely due to base-pair mismatches within the primer-binding region. qPCR analysis, however, revealed low amplification efficiency and poor linearity for the ATCT primer pair, limiting its application to pathogen diagnosis rather than reliable quantification. The ATCS primer pair exhibited high linearity and amplification efficiency (R^2 = 0.98 and 97.5%) and a limit of detection (LOD) of 1 pg. The TFD primer pair demonstrated high linearity (R^2 = 0.97), a low LOD of 0.1 pg, and high amplification efficiency (108.21%). qPCR assays containing *C. siamense* and *D. nebulae* DNA at 1:1 and 1:10 ng/µl ratios further demonstrated that the TFD and ATCS primer pairs produced comparable cycle threshold (Ct) values in the presence and absence of potential inhibitors, indicating stable assay performance. The developed molecular markers show strong potential as rapid diagnostic tools for macadamia husk rot pathogens, although further optimisation is required for the ATCT marker. These markers provide a rapid and cost-effective alternative to conventional multilocus identification methods and may, in the future, contribute to an improved understanding of husk rot disease epidemiology.

J Colhoun Prize Poster Abstract 43

Development of Phage therapy to treat Ash canker

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Ash canker, caused by *Pseudomonas savastanoi* pv. *fraxini* (*Psf*), poses a significant threat to *Fraxinus excelsior* across the UK. Chemical control methods show limited efficacy, and increasing environmental concerns highlight the need for sustainable alternatives. Bacteriophages (phages or viruses that infect and kill bacteria), offer a promising biocontrol strategy.

Seven phages specific to *Psf* were isolated from soil samples around ash trees. They were screened against a panel of 132 *Psf* isolates obtained from multiple UK regions. Genomic analysis of the bacterial isolates was conducted to investigate antiphage defence mechanisms, phage-associated genes, and factors influencing phage susceptibility, thereby improving our understanding of phage-host interactions and identifying potential candidate phages for biocontrol applications.

Effective biocontrol also requires understanding the potential for bacterial resistance. Therefore, phage-resistance assays were performed by exposing *Psf* to high phage titre and collecting the resistant colonies that emerged after 48 hours. Genomic analysis revealed mutations associated with phage-receptor pathways. These findings support the development of phage-based biocontrol strategies.

Main Poster Abstract 1

Ghost in the machine? The function of effector protein PME10 of 'Candidatus Phytoplasma mali' in the context of photosynthesis and proteasomal degradation.

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Apple proliferation is an economically significant disease affecting apple-growing regions across Europe. It is associated with the plant pathogen '*Candidatus* Phytoplasma mali' (P. mali). Infection results in reduced fruit quality, and disease outbreaks can lead to substantial economic losses in affected areas . Phytoplasmas secrete so called effector proteins that alter host plant metabolism and play a key role in symptom development . Elucidating the function of these effectors is essential for a deeper understanding of disease mechanisms and represents a critical step toward the development of targeted control strategies against P. mali. PME10 is a newly identified candidate effector of P. mali. It is expressed during infection and interacts with several *Malus* × *domestica* proteins, including RuBisCO activase (RCA) and E3 ubiquitin ligases as discovered by a yeast two-hybrid assay and confirmed by bimolecular fluorescence complementation *in planta*. RCA is crucial for photosynthesis, as it facilitates the activation of RuBisCO , while E3 ligases are involved in regulating proteasomal protein degradation. Western Blot analyses revealed that RCA is degraded in *Malus* × *domestica* during P. mali infection. We found no direct interaction between RCA and the E3 ligases that bind PME10. However, yeast three-hybrid (Y3H) assays demonstrated a trimeric interaction among PME10, RCA, and an E3 ligase. These findings suggest that PME10 may function as an adaptor, promoting the interaction between RCA and E3 ligases and thereby facilitating the proteasomal degradation of RCA. This leads us to the hypothesis that PME10 functions as a molecular saboteur hijacking the plant's proteasome and acting as a manipulating "ghost" in the plant "machine".

Main Poster Abstract 2

Modelling Cocoa-Phytophthora megakarya (causal agent of the black pod disease) metabolic interaction to weaken plant-host compatible relationship

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Cocoa (Theobroma cacao L.) is a major cash crop in West and Central Africa but is severely threatened by black pod disease caused by the soil-borne oomycete *Phytophthora megakarya*. Despite existing control strategies, long-term management remains challenging, and the development of resistant cultivars is a key priority. A promising approach is to better understand the metabolic interactions between the host and the pathogen, which remain poorly characterized. In particular, a quantitative description of nutrient exchanges during infection is essential for identifying potential intervention strategies for improved pathogen resistance. To address this knowledge gap, we developed a fully compartmentalized genome-scale metabolic model for *P. Megakarya* comprising 2277 reactions and 3195 metabolites. The built model was characterized by a good score on Memote and used to simulate plant-pathogen metabolic exchange fluxes by integrating genomic data and known physiological requirements such as sterol auxotrophy and specific amino acid dependencies. Our preliminary results provide insight into the metabolic processes driving the host-pathogen interaction and reveal key potential targets for disrupting this interaction. This systems biology approach aims to guide metabolic engineering and precision breeding and ultimately leads to support sustainable agricultural development strategies for cocoa resilience.

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Main Poster Abstract 3

Silent but present: do asymptomatic grapevines contribute to Flavescence dorée spread and which tissues best reveal phytoplasma infection?

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Flavescence dorée (FD) is a highly impactful grapevine yellows disease that threatens the European viticulture [1]. An increasing incidence of the disease has been observed in South Tyrol in recent years, causing considerable yield reductions [2]. Transmission of Flavescence dorée phytoplasma (FDp) occurs via the leafhopper *Scaphoideus titanus* during its feeding on grapevine phloem sap [3]. To date, control strategies rely exclusively on vector management, while plant-based resistance or tolerance mechanisms remain largely unexplored. In addition, the epidemiological role of asymptomatic infected plants is still unclear. During the first year of this study, four grapevine cultivars (Chardonnay, Pinot gris, Pinot blanc, and Lagrein) were monitored across three vineyards per cultivar in different areas of South Tyrol. Rows containing at least one symptomatic individual were selected, and leaf and root samples were collected from both symptomatic and neighboring asymptomatic plants. A total of 100 plants per vineyard was sampled. FDp presence and concentration in leaves and roots were assessed using multiplex qPCR. Less than 1% of plants were infected by FDp without showing any symptoms. Moreover, FDp detection was more consistent in leaves than in roots. Only a few plants tested positive in roots, and leaf positivity did not necessarily correspond to root infection. FDp concentrations also varied among the cultivars, although unequal sample sizes limit the reliability of the interpretation. These initial findings suggest that asymptomatic plants are currently unlikely to play a major role in FDp spread in South Tyrol and that leaf sampling is the most reliable diagnostic approach. However, the monitoring will be repeated in 2026 on different vineyards to determine whether the previous conclusions can be confirmed. Ongoing work includes FDp strain characterization (*16S rRNA* and *map* genes) to investigate whether strains originate from non-host plants like *Clematis vitalba* and *Alnus glutinosa*. In addition, a field study will be conducted in a Chardonnay vineyard, with periodic leaf and root sampling of FDp-positive plants to monitor phytoplasma dynamics within the plant and their relationship with symptom progression. Finally, in this study we will assess whether FDp loads vary among cultivars and if this correlates with differential cultivar susceptibility and symptom severity.

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Main Poster Abstract 4

RPN10 paralogs as potential resistance modulators in apple

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Apple proliferation (AP), a disease associated with the bacterial pathogen '*Candidatus* Phytoplasma mali', severely impacts apple production leading to symptoms such as witches' broom, reduced fruit quality, and decreased yield [1]. Phytoplasmas reprogram plant development using secreted effector proteins that often target key regulatory transcription factors (TFs) [1]. In *Arabidopsis thaliana*, the phytoplasma effector SAP05 has been shown to induce ubiquitin-independent proteasomal degradation of SPL and GATA TFs by hijacking the host ubiquitin receptor RPN10, revealing a new paradigm of pathogen-induced targeted protein degradation [2,3].

Malus domestica is highly susceptible to AP phytoplasma, while the crabapple species *Malus sieboldii* is a genetic key source for AP-resistance breeding [4]. However, the underlying molecular resistance mechanisms in *M. sieboldii* remain unclear. Given the central role of RPN10 in SAP05-mediated phytoplasma virulence, in this study we investigate whether *rpn10* paralog diversity contributes to resistance in *Malus spp*. Four *rpn10* paralogs in the *Malus* genome were identified, and comparative single nucleotide variation (SNV) analysis of the von Willebrand A (vWA) domain between resistant *M. sieboldii* and susceptible *M. domestica* revealed polymorphisms located either within predicted SAP05-binding sites, potentially impairing protein–protein interactions, or outside these regions at residues that may be subject to differential post-translational modifications.

To assess their functional relevance, we combine long-read Nanopore sequencing to resolve paralog haplotypes, binding assays to determine whether the paralog-encoded RPN10 differentially interact with SAP05 and associated SPL transcription factors. Furthermore, we perform transcriptional expression profiling under infected and non-infected conditions. Structural studies and protein interaction analyses further contribute to the functional interpretation of these variants.

Our work highlights *rpn10* paralog diversity as an underexplored determinant of resistance and provides a framework for exploiting natural variation from *M. sieboldii* in advanced apple breeding strategies.

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Main Poster Abstract 5

A Generic Multiplication–Dispersal Modeling Platform for Predicting Diverse Bacterial Plant Diseases

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Plant disease forecasting models are typically highly disease-specific and region-dependent, requiring substantial time and effort for development and recalibration when transferred to new environments. This limited generality constrains their scalability and practical applicability across diverse pathosystems and geographic regions. Although generic infection models have been developed and successfully applied to certain fungal diseases, a comparable framework for bacterial plant diseases remains lacking. In this study, we present a generic modelling platform for bacterial disease risk prediction by formalising the fundamental processes of pathogen multiplication and dispersal, which are shared across many bacterial pathosystems. The framework is inherently adaptable, with disease-specific characteristics incorporated through parameterisation, enabling simulation of a wide range of bacterial diseases without structural modification. To maximise generality, the platform is structured around a core module that captures universally applicable processes, complemented by optional add-on modules that can be integrated in a plug-in manner when disease-specific mechanisms or additional inputs are required. This modular architecture ensures both flexibility and scalability, effectively bridging the gap between general applicability and disease-specific fidelity. The applicability of the proposed platform was evaluated through comparative assessments against existing disease-specific forecasting models for selected bacterial diseases. The results demonstrate that the generic multiplication–dispersal modeling approach provides a scalable and efficient alternative to conventional disease-specific frameworks.

Main Poster Abstract 6

Visible effects, invisible helices: NMR Insights into SAP11CaPm

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SAP11 is a small phytoplasma effector protein that interacts with TCP (Teosinte Branched1, Cycloidea, PCF) transcription factors, leading to their proteasome-independent deactivation. This process disrupts plant hormonal balance and defence responses, contributing to characteristic disease symptoms such as shoot proliferation and leaf malformations [1]. While it is hypothesized that SAP11 targets the TCP to induce destabilization or relocation of the complex [2], experimental evidence for the specific mechanism is still lacking.

Structural models predict SAP11 to adopt a fold with three central α-helices flanked by disordered N- and C-termini. Notably, the regions of SAP11 responsible for interaction and functional effects appear to be distinct, and SAP11 from different species exhibits varying affinities and deactivation efficiencies across the highly conserved TCP domain [3].

The detailed structural investigation of the SAP11 homolog of '*Candidatus* Phytoplasma mali' (SAP11CaPm), the phytoplasma associated with Apple Proliferation disease, via ^{13}C-detected and ^{1}H,^{15}N-detected NMR experiments, enabled the assignment of approximately 50% of the sequence (40–45 residues). The observable signals correspond mainly to the disordered and flexible portions of the protein, that is the N- and C-termini and inter-helical loops. In contrast, the three predicted α-helices exhibit extremely low intensities.

This behaviour suggests transient interactions involving the helical regions that lead to NMR signal broadening. Importantly, complementary biophysical techniques (such as SEC-MALS, mass photometry, and FIDA) consistently indicate that SAP11CaPm is a monodisperse monomer in solution. This indicates that SAP11CaPm is globally monomeric yet exhibits local interaction propensity within its helical domains. Ongoing work aims to exploit a TCP as a structural chaperone, leading to the stabilisation of the complex, thus enabling its characterisation and clarifying the mechanism of TCP inactivation.

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Main Poster Abstract 7

Reducing aflatoxin contamination in maize through host induced gene silencing

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US produces about 370 million metric tons of maize annually, accounting for about 35% of worldwide maize production. However, aflatoxin contamination of maize in the southern US and other tropical and subtropical regions poses a serious health concern, due to its ability in causing liver cancer and immune suppression in human and domestic animals and the lack of resistance in commercial maize varieties. Currently, it is mainly managed through biocontrol with atoxigenic strains of *Aspergillus flavus*. However, its efficacy varies depending on the environment and the time of application. The present study explored an RNA interference-based Host Induced Gene Silencing (HIGS) approach by transforming maize lines to produce double stranded RNAs that can silence the expression of key *A. flavus* genes involved in infection (*P2c* and *Alk*) of host or biosynthesis of aflatoxins (*AflM* and *AflP*). Our homozygous transgenic maize kernels had up to 76.4% to 96.0% less aflatoxin production compared to their null controls under repeated field trials with artificial inoculations, with *Alk* being the most effective gene target. The homozygous transgenic maize kernels targeting *Alk* or *P2c* also showed significantly less fungal growth and aflatoxin contamination during simulated post-harvest infection. We are in the process of producing transgenic maize lines in elite background and preliminary studies showed that F1 crosses had up to 72.3 to 93.7% reduction in aflatoxin contamination compared to the controls. High levels of gene specific fungal dsRNAs were also detected in the transgenic leaf and kernel tissues, demonstrating that the enhanced aflatoxin resistance is due to suppression of *A. flavus* infection or toxin biosynthesis through HIGS.

Main Poster Abstract 8

Hijacking the Host: Do SAP05-RPN10 Interactions Shape Phytoplasma Susceptibility in Apple?

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'*Candidatus* Phytoplasma mali', the bacterium associated with apple proliferation (AP) disease, alters its host *Malus domestica* by secreting effector proteins that tackle key regulatory processes in the plant. Several phytoplasma effectors target plant transcription factors (TFs), promoting their degradation and leading to characteristic symptoms such as witches' broom, abnormal growth, and reduced fruit quality [1]. Among these effectors, SAP05 induces ubiquitin-independent proteasomal degradation of SPL and GATA TFs by hijacking the host 26S proteasomal subunit RPN10 [2, 3].

Effector-host interactions have been extensively studied in *Arabidopsis thaliana*, where structural advances and predictions have provided atomic-level insights into pathogen-driven cellular reprogramming [4]. These findings established a paradigm of targeted protein degradation and opened opportunities for innovative breeding strategies [5].

In this study, we focus on SAP05-mediated host manipulation across *Malus* species to elucidate the molecular basis of susceptibility and resistance, placing structural analysis of SAP05 in complex with RPN10 and SPL TFs at the core of our approach. High-resolution structures of these complexes will help resolving the atomic determinants of binding specificity and host range. Comparative analysis of SAP05 interactions with orthologous and paralogous RPN10 and TF variants across different apple species further defines the structural basis of effector specificity and links it to natural genetic diversity and resistance to phytoplasma infections.

Building on this structural framework we assess whether sequence variation in *rpn10* contributes to differential resistance between highly susceptible *Malus domestica* and partially resistant *Malus sieboldii*, a key genetic resource for resistance breeding. Single nucleotide variation (SNV) analysis of the von Willebrand A (vWA) domain across four identified *rpn10* paralogs revealed variation in predicted SAP05-interacting and regulatory regions. These data, integrated with qPCR-based expression profiling, are used to resolve paralog-specific expression patterns, infer functional diversification, and relate host variation to susceptibility or tolerance to phytoplasma infection.

By integrating structural analyses, this work provides a mechanistic basis for SAP05-driven host reprogramming in apple, revealing species-specific differences in phytoplasma susceptibility and supporting targeted strategies for disease management and resistance breeding.

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Main Poster Abstract 9

One crop disease, two causal agents, and both developing resistance to registered fungicides: Changes in mungbean powdery mildew populations in Queensland, Australia

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Mungbean (*Vigna radiata*) is a cash crop in Queensland and New South Wales, Australia, with an annual production of up to 100,000 tonnes. Powdery mildew is a widespread disease of mungbean that can result in grain yield losses of up to 40% when epidemics develop prior to flowering and are left unmanaged. It is caused by two fungal species, *Podosphaera xanthii* and *Erysiphe vignae*. Due to limited genetic resistance in Australian mungbean cultivars, disease management predominantly relies on early sowing and fungicide applications. Currently registered fungicides either contain tebuconazole alone or are formulated to contain tebuconazole and azoxystrobin. This study was prompted by our initial observations of the inconsistent efficacy of foliar fungicide applications in some fields. Molecular analyses revealed the presence of the G143A mutation in some *P. xanthii* and *E. vignae* populations collected from mungbean in Queensland from 2019 to 2024, as well as the G461S mutation in *P. xanthii* populations. Fungicide sensitivity assays with monosporic *P. xanthii* isolates demonstrated that the G461S mutation is associated with reduced sensitivity to tebuconazole. We developed droplet digital PCR assays to quantify the two powdery mildew species simultaneously and determine the allele frequencies of the G461S mutation in DNA extracted from field samples. Assay development for the G143A mutation is currently in progress. These molecular assays are effective diagnostic tools for monitoring shifts in mungbean powdery mildew populations and supporting effective management strategies wherever fungicide use remains vital.

Main Poster Abstract 10

Aphid cathepsin B effector CathB6 targets the MORF–GUN–GLK axis to suppress SA immunity and sustain photosynthetic nuclear gene expression.

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Aphids are highly specialised, plant-dependent feeders that have co-evolved with their hosts for at least ~250 million years. These insects use stylet mouthparts to probe plant tissues en route to the phloem, injecting saliva into host cells to manipulate immune signalling and establish long-term feeding sites in sieve elements. These behaviours also make aphids efficient pathogen vectors. Yet the molecular mechanisms by which aphid oral secretions reprogramme plant immunity and support sustained feeding remain unclear. We previously showed that Myzus persicae cathepsin B (CathB) effectors promote aphid colonisation, accumulate in dynamic cytoplasmic processing bodies (p-bodies), bind Arabidopsis thaliana EDS1, and recruit EDS1–PAD4–ADR1 complexes to these bodies. This localisation is opposed by the A. thaliana Hsp20 protein ACD28.9, which also interacts with the aphid CathB effectors. Here, we investigated how the M. persicae effector CathB6 alters Arabidopsis responses. CathB6-expressing lines showed transcriptomic overlap with the eds1-2 mutant, indicating that CathB6 suppresses EDS1-dependent immunity. However, CathB6 induced broader transcriptional changes beyond eds1-2. A yeast two-hybrid screen identified GLK1 and GLK2 transcription factors as well as several MORFs, regulators of chloroplast transcript editing, as CathB6 interactors. CathB6 plant transcriptomes recapitulated GLK- and MORF-regulated expression changes, including suppressing GUN1 activity, a direct MORF2 interactor, while sustaining GLK-mediated expression of photosynthesis-associated nuclear genes (PhANGs). GLKs promoted CathB6 nuclear accumulation and reduced its presence in cytoplasmic p-bodies. TurboID proximity labelling linked the aphid effector CathB6 to regulators of PhANGs, known MORF2- and GUN1-interacting proteins, p-body and SA-signalling factors, and actin–tubulin/myosin machinery, the latter consistent with highly dynamic CathB6-associated cytoplasmic p-bodies. Taken together, these data indicate that the aphid CathB6 effector interferes with the MORF–GUN–GLK signalling pathway, suppressing SA-related immunity while sustaining GLK-mediated PhANG expression to maintain homeostasis during aphid attack.

Main Poster Abstract 11

Two peas in a pod? Identification of allelic resistances to downy mildew in pea.

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Pea (*Pisum sativum*) is an increasingly economically important crop due to the rising demand for plant-based protein, and its ability to biologically fix nitrogen reduces the need for synthetic nitrogen fertilisers and promotes sustainable agriculture. However, at present, peas are an unattractive option to growers because their susceptibility to abiotic and biotic stresses causes yield instability. One of the most prevalent diseases in the UK and Europe is downy mildew, caused by the oomycete pathogen *Peronospora viciae* f. sp. *pisi* (*Pvp*). Currently, no resistance has been characterised to *Pvp*. Here, we have identified two resistances to *Pvp* in two wild accessions: one discovered through a *k*-mer-based GWAS and found in JI0015, and another rare resistance identified through bulked segregant analysis found in JI0085. The QTL sizes were reduced through a haplotyping approach and fine mapping, and candidate genes were identified by analysing the correlation between gene presence and resistance. We have shown through virus-induced gene silencing that the JI0015 resistance is caused by one of two NLRs with 97% nucleotide identity. Both the JI0015 and the JI0085 resistances are located on chromosome 2. Phylogenetic and syntenic analysis suggests that they are derived from a single ancestral NLR cluster and that they are likely alleles. Additionally, each resistance has a distinct isolate recognition pattern, demonstrating that they are able to detect different *Pvp* effectors and therefore stacking both resistances into one cultivar may provide a more durable resistance. Marker genotyping showed that neither resistance is present in tested elite cultivars or European breeding material, showing they are novel and have not yet been deployed in breeding programs and will therefore be useful to breeders. To conclude, we have discovered two allelic resistances to downy mildew in pea which are able to recognise different isolates of *Pvp*. We have reduced the number of candidate genes to two or three for each resistance and have shown that neither have yet been deployed in European breeding programs.

Main Poster Abstract 12

Microbiome responses to Soil Amendments in Potato systems

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Intensive potato production can compact the soil, reducing pore space and oxygen levels, leading to poor drainage and restricted root growth. While the physical and chemical implications of compaction is understood, less is known about the effects on the soil and plant microbiome. These microbes can play a crucial role in plant health by competing with disease-causing organisms.

Anaerobic soil conditions are conducive to potato diseases such as powdery scab (*Spongospora*) and blackleg (*Pectobacterium*), and we hypothesise that the beneficial microbes are less diverse and active in these conditions.

This study examines metabarcoding data, across three years of field trials, to determine whether soil amendments designed to improve oxygen availability can promote beneficial microbial communities in both the bulk soil and around potato roots (the rhizosphere), leading to reduced disease pressure in potato plants and tubers.

Main Poster Abstract 13

Viral manipulation of aphid behaviour: cucumber mosaic virus has differential effects on specialists versus generalist aphids

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Cucumber mosaic virus (CMV) is vectored by aphids in the non-persistent mode. Infection of *Arabidopsis thaliana* plants with CMV affects their attractiveness to aphids as well as the performance of aphids confined on these plants. These effects on plant-aphid interactions ('viral manipulation') may promote viral transmission. *Myzus persicae*, a 'generalist' aphid (i.e., it has many plant hosts), is an efficient CMV vector. *A. thaliana* is also exploited by crucifer-specialist aphids, including *Lipaphis erysimi* (an efficient CMV vector) and *Brevicoryne brassicae* (a poor CMV vector). There have been studies on the effects of CMV-infected *A. thaliana* on *M. persicae*, but its impact on crucifer-specialist aphid behaviour had not been explored.

Using settling and olfactometry assays, we found that aphids of *M. persicae* showed a significant difference in both their settling and plant volatile preference. These aphids preferred settling on non-infected over CMV-infected plants, yet strongly preferred volatiles emitted by CMV-infected *A. thaliana*. In contrast, crucifer-specialists were more likely to settle on non-infected plants were less influenced by volatile cues than *M. persicae*. However, both specialist species' settling responses were highly variable[1]. Our results suggest that CMV-induced manipulation of aphid-host interactions is more effective with the generalist *M. persicae* than on either crucifer specialist. This work in a model system may have implications for understanding aphid-mediated non-persistent virus transmission in crops.

Reference:

1. Azuma, H., *et al.* *Virol J* **23**, 42 (2026).

Main Poster Abstract 14

Cross-kingdom activity of diverse NLR immune receptor N-terminal signalling domains

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Nucleotide-binding leucine-rich repeat receptors (NLRs) are important immune components that are present across the tree of life and often share a conserved tripartite architecture, comprising a central nucleotide-binding ATPase domain, superstructure-forming C-terminal repeats, and N-terminal signalling domains with varied biochemical activities. While NLRs are critical for disease resistance in plants, they harbour only a fraction of the known diversity of the N-terminal domain identities seen in bacteria, fungi and metazoans. Since NLRs generally activate cell death through conserved cellular mechanisms, we reasoned that the full diversity of NLR N-termini could be functionally transferable to plant cells.

To address this, we explored the capacity of bacterial, fungal, and metazoan NLR-associated N-terminal domains, as well as full-length NLRs, to activate immune-related responses in plants. We screened over 100 diverse N-terminal domains for their ability to trigger cell death through transient expression assays in *Nicotiana benthamiana*. Remarkably, we identified several NLR N-terminal domains activating cell death in plants, including proteases, nucleases, and carbohydrate-associated hydrolases.

Together, our findings suggest that plant cells can integrate immune outputs generated by diverse immune receptor domains, pointing towards a deeply conserved framework of immune activation across kingdoms. Future work will focus on elucidating the molecular mechanisms underlying diverse NLR-mediated responses in plants and cross-kingdom engineering of transferable NLRs to better protect plants from harmful pathogens.

Main Poster Abstract 15

Investigating why PAMPs associate with EVs during infection

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The movement of effector proteins and RNAs from pathogens into host cells is known to occur. However, the details of the molecular mechanisms involved in this cross-kingdom exchange are still under. One possible explanation is the secretion and uptake of extracellular vesicles (EVs) between organisms.

We have isolated EVs from the devastating plant pathogen *Phytophthora infestans* with the aim of identifying oomycete EV-associated markers and understanding the cargo of these secreted bodies. We have identified many different protein classes within the proteomic data generated from these EVs including classical EV marker proteins such as Rab7, as well as a variety of transmembrane containing proteins, RxLR effectors and pathogen associate molecular patters (PAMPs). INF4 is a PAMP, identified in the EV proteome. This PAMP has sequence similarity with INF1, a well-known *P. infestans* elicitin, however unlike INF1, INF4 does not induce cell death within *N. benthamiana* leaves. I am currently investigating INF4 to determine whether it has a role in the translocation of EVs into host cells.

Main Poster Abstract 16

Challenges of screening for host resistance against the light leaf spot pathogen Pyrenopeziza brassicae in oilseed rape

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Light leaf spot is the most economically damaging disease of oilseed rape (*Brassica napus*) in the UK. The disease is caused by the fungal pathogen *Pyrenopeziza brassicae,* resulting in over £100M annual yield losses. With occurrence of fungicide insensitivity, the need for non-chemical controls like host resistance is becoming ever more important. However, using of host resistance against *P. brassicae* faces numerous challenges. Firstly, there are many different symptoms, such as sporulation, necrotic black flecking, plant stunting, leaf distortion, leaf curling and green islands on senescing leaves. Then, there is limited information on virulence of UK *P. brassicae* populations, which is crucial for effective use of host resistance. Furthermore, there is little information on genetics of host resistance (e.g. major gene resistance or quantitative resistance). Moreover, there is a long period of pathogen symptomless growth in autumn and winter after initial infection and the symptom development is affected by various factors (e.g. the age of the plant, light intensity, inoculum concentration).

Controlled environment experiments were done to investigate the effects of plant age, light intensity, inoculum type and inoculum concentration on disease development. Results suggested that four weeks old was the optimal plant age for disease development, increased light intensity promoted symptom development, 10^5 spore/ml was the optimal concentration for discriminating cultivar resistance. Although sporulation was typically observed on susceptible cultivars, while necrotic black flecking was associated with resistance, both necrotic black flecking and sporulation were observed together on some resistant cultivars. We hypothesize that black flecking without sporulation is related to major gene mediated resistance while black flecking with limited sporulation is related to quantitative resistance. To investigate the genetics of quantitative resistance, the DY (Darmor-*bzh* Yudal) DH (doubled haploid) mapping population was inoculated with two different *P. brassicae* populations in glasshouse experiments. Eight quantitative traits were measured. With composite interval mapping analysis, a total of 21 QTL were detected. Of these, QTL on linkage groups A02, A06, C01 and C02 overlapped with resistance QTL identified in previous studies using the same DYDH population for light leaf spot and phoma stem canker. Further studies are needed not only to investigate those QTL for breeding cultivars with stable quantitative resistance but also to investigate variations in *P. brassicae* virulence for effective deployment of host resistance.

Main Poster Abstract 17

Not resting on our laurels – Findings from over 10 years of surveillance for Xanthomonas arboricola pv. pruni in the UK

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Xanthomonas arboricola pv. *pruni* (Xap) is a GB quarantine listed pathogen of *Prunus* species including peach, almond, plum and apricot, as well as ornamental *Prunus* species such as *P. laurocerasus* (cherry laurel). Xap was first detected in the UK in 2013 on *P. laurocerasus* plants imported from the Netherlands. Since this initial finding Xap has been routinely found by UK Plant Health and Seed Inspectors (PHSI) on, or associated with, imported ornamental plant material by with diagnosis being carried out at Fera Science. This study was undertaken to better understand the epidemiology and pathogenicity of Xap in the UK. 453 isolates taken from samples received over the last 10 years were whole genome sequenced and analysed using both ANI and cgMLST. This analysis indicates multiple introduction events, with evidence supporting importation into the UK, rather than endemic spread of the pathogen. Genomic data also informed the development of improved molecular diagnostics, including novel real-time PCR assays capable of distinguishing true Xap strains from closely related *Xanthomonas arboricola* isolates, addressing limitations of current *gyrB*-based identification methods. In parallel, detached leaf assays have been explored as a higher-throughput approach to assess pathogenicity across *Prunus* hosts and to evaluate the potential pathogenic relevance of divergent strains. Together, these advances enhance diagnostic accuracy and speed, improve understanding of Xap epidemiology, and support more effective plant health decision making and risk management.

Main Poster Abstract 18

The extrahaustorial membrane in the barley/powdery mildew fungal interaction depends on plant lipid transfer

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Powdery mildew fungi are serious pathogens on numerous plant species. They are obligate biotrophs and hence require living host cells for disease establishment and development. Thus, they form a specialized feeding structure, called haustoria, inside the plant cell. Haustoria are dependent on and surrounded by a plant cell-generated extra-haustorial membrane (EHM), a unique membrane that separates the fungus from the host cytosol. However, little is known about how the plant cell forms the EHM. In barley attacked by the powdery mildew fungus (*Blumeria hordei*, *Bh*), it has been shown that the EHM has endoplasmic reticulum (ER)-like properties, and multiple lines of evidence indicate that the EHM forms by a membrane trafficking-independent pathway. This suggests involvement of lipid transfer from the plant ER, mediated by lipid transfer proteins (LTPs) interacting with ER-anchored VAP proteins. We found one such LTP, LTP2 to localise to the EHM and interact with two distinct barley VAP proteins, VAP7 and VAP8, via its 'FFAT' (phenylalanine-phenylalanine-acidic-tract) motif. We show that RNAi-based silencing of LTP2, VAP7 and VAP8 results in reduced haustoria formation. An untargeted yeast 2-hybrid screen with VAP7 revealed a novel, membrane-anchored **V**AP7-**I**nteracting **P**rotein (VIP), which showed a preferential localisation to the attack site at very early stages of infection. In summary, our data suggest that *Bh* hijacks the host VIP-VAP-LTP2 lipid transfer machinery for EHM formation.

Main Poster Abstract 19

Understanding patterns of Leptosphaeria maculans and Leptosphaeria biglobosa ascospore release and oilseed rape cultivar resistance

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Leptosphaeria maculans and *L. biglobosa* are the causal agents of phoma stem canker, which is a damaging fungal disease affecting oilseed rape (*Brassica napus)* production worldwide. Epidemics of the disease are initiated by ascospores. Monitoring the timing and pattern of ascospore release is crucial for understanding disease epidemiology and developing effective management strategies. This study aimed to investigate the temporal dynamics of ascospore release and differences in cultivar resistance.

To monitor ascospore release, a Burkard spore sampler was set up at Bayfordbury, Hertfordshire, and daily air samples were collected in the 2025/2026 cropping season. To distinguish *L. maculans* and *L. biglobosa* ascospores in the air samples, species-specific qPCR will be used. To investigate the differences between different cultivars in resistance against *L. maculans* and/or *L. biglobosa*, ten cultivars were grown in the field experiments at Rothamsted Research (RRes) and John Innes Centre (JIC) in the 2025/2026 season. The incidence and severity of phoma leaf spot were assessed.

Ascospore release started in September in small numbers until late October 2025. The number of ascospores released increased quickly,and reached the maximum number in November 2025. However, ascospores were continuously released in small numbers until April 2026. For field experiments, the phoma leaf spot incidence and lesion severity were substantially higher at RRes than at JIC. At RRes, the differences between cultivars were statistically significant, whereas they were not statistically significant at JIC. Infected leaves were sampled for pathogen isolation to detect pathogen virulent races.

Acknowledgements: Thanks to John Innes Centre (JIC) in Norwich and Rothamsted Research (RRes) in Harpenden for running the field experiments

Main Poster Abstract 20

Novel virulence proteins of the Gram-positive bacterium Clavibacter michiganensis responsible for symptom development in host plants

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The Gram-positive bacterium *Clavibacter michiganensis* is the causal agent of bacterial canker in tomato. Recently, *Nicotiana benthamiana* has been reported as a surrogate host plant for this bacterium, exhibiting canker in stems as well as wilting and blister-like lesions in leaves, like those observed in tomato. Previous studies have revealed that *celA* and *pat-1*, encoding cellulase and a putative serine protease respectively, are the major virulence genes responsible for wilting symptoms in tomato. However, few virulence genes responsible for blister-like lesions, which are accompanied by numerous tiny white dots in leaves, have been identified. To identify the virulence genes responsible for blister-like lesions on *N. benthamiana* leaves, we screened 2,148 mutants of the *C. michiganensis* LMG7333^T generated by random transposon mutagenesis. Consequently, fourteen mutants were selected, comprising seven with reduced blisters and seven with no blister formation. Among them, eight mutants also showed reduced wilting symptoms on tomato plants. However, no mutants had transposons in either *celA* or *pat-1* genes. We selected two mutants that had transposons in chromosomal genes, which encode putative transmembrane proteins, named *Clavibacter* virulence (*cvi*) genes, *cviB* and *cviC*. CviB and CviC, which lack signal peptides for extracellular secretion, consist of five and three transmembrane domains, respectively, without any other known functional domains. Expression of GFP-tagged CviB proteins demonstrate that they localize to the bacterial membrane. We are currently studying on the molecular functions of CviB and CviC for virulence in host plants. Overall, we found novel virulence determinants responsible for causing blister-like lesions as well as wilting symptoms in host plants. The characterization of CviB and CviC will provide novel insights into the pathogenic mechanisms of *C. michiganensis* during host-pathogen interactions.

Main Poster Abstract 21

Control of Type III effector export and disease symptom development during Pseudomonas syringae plant infections

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Pseudomonas syringae is a destructive bacterial pathogen that infects a wide variety of plants. Following apoplastic entry, *P. syringae* uses its type 3 injectisome (T3I) to secrete specialised effector proteins into plant cells. Effector secretion through the T3I is vital for successful infection, enabling bacterial proliferation, immune system suppression and plant tissue degradation. *P. syringae* strains encode dozens of highly specialised effector proteins, whose composition defines host range and strain specificity. Effective plant infection depends on the tight temporal and hierarchical control of effector delivery through the T3I. Effector secretion is driven by HrcN, an ATPase complex that interacts with the base of the T3I and is essential for plant infection. We previously showed that HrcN binds specifically to the bacterial signalling molecule cyclic-di-GMP, although the purpose of this interaction is currently unknown.

To address this, we used a combination of genetics, plant infection assays and biochemistry to investigate the role of cyclic-di-GMP binding in HrcN function and *P. syringae* plant infection. We show that mutations in the HrcN cyclic-di-GMP binding site can effectively decouple bacterial proliferation from disease symptoms during infection, producing rare asymptomatic plant infections, a phenotype linked to reduced translocation of a subset of T3I-effectors. We further show that the previously uncharacterised effector protein HopAA1-2 is particularly important for disease symptom development. We propose that cyclic-di-GMP binding represents a novel regulatory mechanism that may enable rapid control of effector secretion during *P. syringae* plant infections.

Main Poster Abstract 23

One pathogen, two paths: Genomic and metabolic distinction of Portuguese Erwinia amylovora lineages

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Erwinia amylovora, the etiological agent of fire blight, poses a severe threat to pome fruit production worldwide. Understanding the genetic structure and evolutionary history of local populations is critical for designing effective management strategies. Thus, in this study, whole-genome sequencing data were applied to investigate the genomic diversity of *E. amylovora* isolates collected in Portugal to ascertain their introduction pathways and population structure. Phylogenetic analyses of the core genome alignment disclosed that the Portuguese *E. amylovora* population is composed of at least two distinct evolutionary introductions. Two lineages were identified within the country: one aligning closely with North American strains and the other clustering with the established European lineage. This clear population separation was robustly supported by Principal Component Analysis (PCA) derived from a dataset of 794 single-nucleotide polymorphisms (SNPs), separating the isolates into two distinct clades.

Moreover, to understand the role of genomic differences in shaping phenotypic traits, a Genome-Wide Association Study (GWAS) was conducted, with a focus on Biolog metabolic profiling. As per the previous results, the same dual-clade population signal was detected in the differential metabolization profiles of two Biolog compounds: the plant-derived sugar alcohol *myo*-inositol and the anionic surfactant Niaproof-4. These phenotypic differences were significantly linked to 127 SNPs characteristic of one of the clades, suggesting that the genomic divergence between the Portuguese lineages may translate into functional, metabolic variations that can influence host adaptability or environmental survival. Overall, this work provided important insights into the epidemiology of fire blight in Portugal, highlighting the benefits of combining genomics with phenotyping to understand and then efficiently control plant-pathogenic bacteria.

Main Poster Abstract 24

An overview of rapid pest risk assessment schemes

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Pest risk assessment (PRA) often needs to be delivered rapidly, but without compromising standards of scientific rigour, robustness, and reproducibility. Rapid PRA tend to have greater uncertainties because of the lack of time to search for and generate new data. Several National Plant Protection Organisations use rapid PRA schemes, but an overview of such efforts is lacking. This contribution will provide a summary of examples of rapid PRA approaches, highlighting their common features and peculiarities. Existing rapid PRA schemes do not seem to be quantitative. But this does not imply that rapid quantitative PRA schemes are not possible; evidence gathering has to be done anyway, and expert knowledge elicitation of model parameters might not take much longer than expert discussion to agree on qualitative ratings. Some rapid PRA schemes are concise and delivered rapidly, some are rapid in name only. Both types of rapid PRA schemes follow ISPM11, which mentions that a PRA needs to be only as complex as is technically justified by the circumstances. More standardisation of rapid PRA schemes would enhance their comparability and transferability. Regularly updated systematic reviews of existing knowledge on plant pests, as well as fundamental research on e.g. pest host range, suitable/optimal environmental conditions, and spread rate, would facilitate rapid PRA delivery.

Main Poster Abstract 25

Research and Development at Kwizda Agro

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Regulatory constraints, adverse ecological effects, and the increasing development of resistances are compromising the use of conventional agrochemicals. At the same time, plant pathogens remain a major cause of economic loss in agricultural systems, with disease pressure often intensified by changing weather conditions and pathogen populations emerging in new regions. This situation increases the need for effective and safe alternatives that are suitable for integrated and organic agriculture and forestry.

Kwizda Agro, an Austrian family-owned company with a 100-year tradition, is investing in a strong research and development unit focused on novel solutions for crop protection, with an emphasis on fungicides, insecticides, nematicides and repellents. Our product development approach includes both (i) screening-oriented projects to identify novel actives and (ii) the use expansion of established actives.

As an example of a successfully registered fungicide, UPSIDE® contains a lysate derived from cells of baker's yeast (*Saccharomyces cerevisiae)*. With a dual mode of action, UPSIDE® combines the induction of plant defense responses with a direct disruption of pathogen cell walls[1,2]. In viticulture, it is positioned for use against downy (*Plasmopara viticola*), powdery mildew (*Erysiphe necator*) as well as grey mold (*Botrytis cinerea*) and can contribute to copper reduction.

Kwizda Agro aims to embrace scientific exchange and collaborative innovation. We are currently partnering with various organisations and welcome further collaboration across academia and industry.

References:

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2. Scimone, G. et al.: Unveiling the shield: decoding UPSIDE®-induced biochemical responses against *Botrytis cinerea* in grapevine. Front. Plant Sci. 2025.

Main Poster Abstract 26

Genomic Insights into Bacteriophages Infecting Erwinia amylovora and Development of Specific qPCR-Based Detection Method

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Limited effectiveness of conventional fire blight management practices has prompted the search for alternative control strategies, with bacteriophage-based approaches as promising biocontrol tools. A collection of 34 *Erwinia amylovora*-specific bacteriophages, recovered from various agricultural environments across Serbia over a 15-year period, was comprehensively characterised to support their effective application as biocontrol agents, and 11 representative strains were selected for whole-genome sequencing and analysis. Sequencing was performed using the Illumina platform, with viral DNA extracted from high-titer, purified phage lysates. Following the identification of complete or near-complete genome sequences, genome annotation was performed using Pharokka (https://github.com/gbouras13/pharokka), a software tool specialised for bacteriophage genome annotation. Comparative genomic analysis revealed a major cluster of seven phage genomes (37–40 kb), a second lineage of three genomes (53–54 kb), and a single divergent 162 kb genome. Endolysin genes were detected in all genomes, with frequent presence of holin and spanin genes, while eight genomes encoded putative exopolysaccharide depolymerases. No integrase, excisionase, repressor, recombinase, or transposase genes were identified. The obtained genome sequences were used as a resource for the development of a qPCR assay specific to selected strain ΦEa10, enabling monitoring of its persistence in natural environments. Primers targeting the endonuclease gene were first tested against a collection of phytopathogenic bacteria and saprophytic strains to verify their specificity. Subsequently, qPCR analysis using a TaqMan MGB probe was performed across all phage strains, confirming assay specificity, with amplification detected exclusively for the target strain ΦEa10. This protocol will enable phage monitoring and quantification in our trials under natural application conditions, thereby supporting and improving the potential use of bacteriophages for the control of pome fruit fire blight.

This research was supported by the Science Fund of the Republic of Serbia, GRANT No. 7421, Innovative solutions in phage-mediated biocontrol of fire blight – InnovaPhage, and by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, Contract Nos. 451-03-33/2026-03/200010 and 451-03-33/2026-03/200116.

Main Poster Abstract 27

Unravelling Toll/Interleukin-1 Receptor (TIR) Domain Functions

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Toll/Interleukin-1 Receptor (TIR) domains are conserved components of innate immunity across the tree of life, including plants and phytobacterial pathogens. TIR domains function as NADases, cleaving NAD^+ to produce cyclic ADP-ribose (cADPR) isomers. Upon pathogen recognition, plant TIR nucleotide-binding leucine-rich repeat (TNL) receptors generate 2′cADPR, which drives the hypersensitive response and pathogen containment through the Enhanced Disease Susceptibility (EDS1) complex. In contrast, the phytobacterial pathogen *Pseudomonas syringae* pv. tomato DC3000 encodes the TIR-containing effector HopAM1, which produces a structurally distinct 3′cADPR and suppresses plant immune signalling. However, how these two isomers and their derivatives differentially modulate immune signalling dynamics remains unclear. HopBY, a 2′cADPR-producing effector, triggered a rapid hypersensitive response in *Arabidopsis thaliana* (Col-0) and loss of HopAM1 accelerated this response, consistent with HopAM1 suppressing 2′cADPR-mediated plant immunity. Notably, HopAM1 also delayed immune responses in the *eds1-12* background, suggesting that suppressive modulation of HopAM1 might not be exclusively dependent on EDS1 complex signalling. To test whether these phenotypes depend on TIR enzymatic activity, we are generating catalytically inactive mutants of HopAM1 and HopBY for *in planta* analysis, alongside bacterial growth assays to link signalling dynamics to pathogen resistance. This work aims to define the differential contributions of TIR-derived metabolites to plant immune signalling dynamics and to reveal the suppressive mechanisms of HopAM1.

Main Poster Abstract 28

Pathogenicity testing and Method development for the detection of Halophytophthora spp. in seagrass (Zostera marina)

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Seagrass meadows are a crucial part of ocean ecosystems. Seagrasses are flowering plants that grow in shallow coastal waters; they support marine life, act as carbon stores, stabilise coastlines and improve water quality. Due to human activities, changes in climate and pollution, seagrass meadows are in decline, and intervention is needed to protect these vital ecosystems. Seagrass nurseries, such as those at Project Seagrass, work to cultivate plants which can then be used in restoration projects around the coast of the UK, rebuilding damaged and establishing new seagrass meadows.

In January 2026, samples of *Zostera marina* were submitted to Fera Science Limited by the Plant Health and Seeds Inspectorate of the UK, exhibiting symptoms of leaf blackening with an unknown cause. An unknown oomycete was isolated from leaf lesions and identified as *Halophytophthora* sp. IV through DNA sequencing, which was believed to be the cause of the symptoms seen. Subsequent symptomatic seeds sampled from the Project Seagrass nursery seed storage system, resulted in further findings of *Halophytophthora* sp. IV, as well as an additional species of *Halophytophthora*, identified as *Halophytophthora lusitanica*. These findings raised questions of how the pathogens are entering the systems at the nursery, how much the pathogens have spread, and what damage they are causing to the plants and seeds.

Whilst being familiar with testing for oomycete infections in terrestrial plants, the mycology team at Fera had never worked on marine species prior to these findings and current research in this area is limited. There is a gap in the knowledge regarding pathogenicity of *Halophytophthora* spp. on *Zostera marina*, most likely due to the unique growing conditions of the plant causing unique challenges with pathogenicity testing. We have explored the pathogenicity of the two isolates on various plant species and the potential to carry out water testing using bait testing methods.

Main Poster Abstract 30

Establishing Pseudomonas-Dionaea Interactions

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Carnivorous plants have evolved sophisticated mechanisms to attract, trap, and digest insect prey. This lifestyle is generally linked to the co-option of defense genes towards host-prey interactions, yet our understanding of how this impacts host-pathogen interactions remains unclear. To address this dilemma, we established a robust pathosystem between the broad host-range bacterial pathogen *Pseudomonas syringae* and the model carnivorous plant *Dionaea muscipula* (the Venus flytrap). We discovered that *P. syringae* pv*. aptata* (sugarbeet pathogen) successfully infects traps of *D. muscipula*, exhibiting disease symptoms that radiate outwards from inoculation sites. In contrast, bacterial mutants unable to secrete type-3 virulence effector proteins known to manipulate plant immunity (ΔhrcC) were unable to infect *D. muscipula*. In addition, transcriptional changes associated with trap infection and compared these against carnivory in *D. muscipula* traps or *B. vulgaris* infection in leaves. Collectively, our data begin to shed light on balancing immune function in the context of the evolutionary novelty that is botanical carnivory.

Main Poster Abstract 31

Improving Botrytis resistance in lettuce through GRN-guided genome editing

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Botrytis cinerea is a devastating fungal pathogen responsible for widespread crop losses across the world. Susceptibility in lettuce is mediated by a complex gene regulatory network (GRN) which has been previously extensively modelled to identify key transcription factors (TFs). As a tool, genome editing is effective and precise at triggering targeted mutagenesis at a specified target site, however translating mutagenesis to trait improvement remains challenging due to genetic complexity and gene redundancy. This new project focuses on perturbing critical TF nodes to rewire the network and enhance *Botrytis* resistance in lettuce through genome editing. We will also use overexpression lines of key TFs to investigate their effect on disease resistance *in planta*. Our approach to genome editing is broad, utilising both transformation and DNA-free protoplast-based techniques, dependent upon the network context of TFs. The first phase of the project utilises a polycistronic gRNA approach to brute-force gene knock-out via transformation, followed by *Botrytis* lesion analysis. The use of elite lettuce cultivars will enable straightforward commercial application of any generated germplasm with improved *Botrytis* resistance.

Main Poster Abstract 32

Structure-guided insights into PRR-mediated recognition of Phytophthora infestans in potato

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Late blight, caused by the oomycete *Phytophthora infestans*, remains a persistent threat to global potato production. Resistance breeding primarily relies on the introgression of intracellular immune receptors, which are often rapidly overcome due to the pathogen's high evolutionary potential. In contrast, Pattern Recognition Receptors (PRRs) at the cell surface are expected to confer more durable resistance, because they detect conserved pathogen molecules. In this study, we focus on the PRR PERU in potato, which recognizes transglutaminase-derived Pep-13/25 peptides from *P. infestans*. Both PERU and Pep-13/25 exhibit genetic diversity in wild *Solanum* species and *P. infestans* strains, respectively, resulting in distinct recognition specificities. This natural diversity provides an opportunity to dissect key determinants of ligand perception, co-receptor interactions and potential effector-mediated suppression. Using AlphaFold3 (AF3)-based structural modelling, we identified candidate residues at the PERU-Pep-13/25 interface involved in recognition. Mutating these residues in PERU showed a strong reduction in recognition compared to wild-type PERU. By combining co-evolutionary analysis, AF3-guided structure predictions and functional assays in potato, we define the molecular determinants of Pep-13/25 perception by PERU, bringing us closer to structure-guided design of surface receptors for durable resistance against *P. infestans*.

Main Poster Abstract 33

Diplodia fraxini on Fraxinus excelsior in the UK

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Ash dieback, caused by *Hymenoscyphus fraxineus*, has had a significant impact on European ash (*Fraxinus excelsior* L.) in the United Kingdom since its first detection in 2012. Although *H. fraxineus* is recognised as the primary cause of ash dieback, recent studies from Bulgaria [7], Croatia [8], Germany [9], Italy [1,5], Poland [2], Portugal [1] and Slovenia [6] frequently isolated *Diplodia fraxini* from symptomatic ash, in some cases more frequently than *H. fraxineus*. Historically, there have been records of *Botryodiplodia fraxini* (Fr.) Sacc syn. *Diplodia fraxini* from south-east England dating back approximately 40 years [3].

In 2021, *D. fraxini* was identified from a mature declining ash tree in Norfolk as part of an undergraduate research project undertaken at the John Innes Centre. This represents the first confirmed record of *D. fraxini* in the UK supported by both morphological and molecular analysis. Preliminary phylogenetic analysis shows that several *Diplodia* isolates from ash cluster with *D.fraxini*. Forest Research (FR) have subsequently confirmed *D.fraxini* from sites across southern and central England, suggesting that the pathogen may be more widespread than previously recognised, with the earliest report dating back to 2016.

A pathogenicity study is underway to assess the susceptibility of *F. excelsior* to *D. fraxini*. Forest Research are undertaking research surveys to determine the current distribution and prevalence of *D. fraxini* in the UK. This work will improve our understanding of the distribution, host range, and significance of *D. fraxini* in British ash health and help to elucidate whether this fungus represents an emerging agent contributing to ash decline in the UK.

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Main Poster Abstract 34

Exploring resistance to Candidatus Phytoplasma solani and Candidatus Liberibacter solanacearum in potato

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Insect-transmitted, phloem-limited bacteria, such as *Candidatus* Phytoplasma solaniand *Candidatus* Liberibacter solanacearum, are an increasing problem in potato (*Solanum tuberosum*). These vector-borne diseases can be challenging to study due to their unculturable nature, prolonged incubation periods, and strict quarantine regulations. Additionally, their vector-borne nature adds a layer of complexity, often making it unclear whether observed resistance is caused by the vector or the pathogen. Our approach to studying the interaction between bacteria, plant, and insect is therefore based on a combination of grafting, effectoromics, and insect-mediated transmission assays. This allows for isolated analysis of the plant-pathogen relationship, as well as a precise dissection othe plant-pathogen-vector interaction.

We show that grafting is a highly reliable and robust method for reproducing characteristic disease symptoms for both *Ca.* P. solani and *Ca.* L. solanacearum. Notably, we observed a wide spectrum of disease severity across different potato genotypes in response to *Ca.* P. solani infection. To validate these findings under more natural conditions, we are currently developing an insect-based disease assay for comparison. By combining grafting with insect assays and effectoromics, we aim to deepen our understanding of the plant response to these pathogens. Ultimately, this will increase the efficiency of screening for plants with resistance or reduced susceptibility and help identify the underlying defense mechanisms.

Main Poster Abstract 35

Single-cell and spatial dissection reveals distinct cellular dynamics of pattern-triggered and effector-triggered immunity

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Plant immunity involves diverse cell populations with specialised roles. Previous single-cell studies revealed cellular heterogeneity during effector-triggered immunity (ETI) and effector-triggered susceptibility in *Arabidopsis* leaves (Nobori et al., 2025). However, the cellular heterogeneity underlying pattern-triggered immunity (PTI), another major mode of immunity, remains largely unknown at the single-cell level. While PTI restricts pathogen growth, the specific contributions of diverse cell populations remain largely unexplored.

To specifically study PTI responses, we employed *Pseudomonas syringae* pv. *tomato* D36E, an effectorless strain unable to suppress PTI or trigger ETI. Infection with D36E thus predominantly activates PTI, enabling its targeted analysis. We analysed D36E-infected leaves using time-resolved single-nucleus multiomics (snRNA-seq and snATAC-seq) and spatial transcriptomics (MERFISH) at 4-24 hours post-infection. Although D36E-induced PTI elicited heterogeneous and coordinated changes in gene expression and chromatin accessibility across leaf cell populations, comparative analysis revealed distinct cellular responses between PTI and ETI. Overall, D36E infection triggered weaker and more localised immune responses compared to ETI. Notably, the rare PRIMER (primary immune responder) cell state, located at the nexus of immune-active hotspots during ETI, was not prominently induced by PTI. Similarly, markers for the ETI-associated bystander state surrounding PRIMER cells were not activated during PTI.

In summary, our integrated single-cell and spatial omics analyses reveal distinct cellular features and dynamic responses underlying PTI and ETI. Our findings suggest ETI involves specialised cellular programmes and broader spatial coordination distinct from the more localised PTI response. We present further analyses comparing the cellular responses and spatial organisation across PTI and ETI, highlighting their distinct cell state coordination.

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Main Poster Abstract 36

Optimising protoplast-based transformation for high-efficiency genetic manipulation in Zymoseptoria tritici reveals strong isolate-specific variation

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Zymoseptoria tritici, the causal pathogen of Septoria tritici Blotch in wheat (Septoria leaf blotch) is a key model fungus in plant pathology with a well-developed molecular toolbox including *Agrobacterium tumefaciens*-mediated transformation (ATMT), effective promoters, selection markers and reporter lines. However, ATMT is relatively low throughput and not suited to ribonucleoprotein-based genome editing (RNP-based CRISPR). To implement effective RNP-CRISPR, which should provide a step-change in Zymoseptoria genetic approaches, a highly effective protoplast-based transformation procedure is required.

Protoplast mediated transformation is widely used in other fungal pathogens, and although *Z. tritici* protoplasting (Payne 1998) fell out of routine use following the discontinuation of a key cell wall–digesting enzyme product, our and other's recent work with commercial enzymes has proven successful to re-instate the technique as a feasible route to transformation (Michael Choi 2026, Haseena Khan 2021).

We compared multiple strains and independent IPO323 isolates and observed marked isolate-dependent differences in protoplast generation and recovery, these differences were not only observed between strains but among different clones of the reference isolate IPO323. This finding is consistent with the very high genomic plasticity of *Z. tritici* and highlights the need for robust isolate selection and maintenance protocols when implementing protoplast-based transformation pipelines in the species. This work also suggests that mutants could be developed for high efficiency protoplast transformation.

Main Poster Abstract 37

Temporal dual RNA-seq resolves Phytophthora capsici infection programs and accession-specific effector responses in pepper

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The destructive oomycete *Phytophthora capsici* relies on the timely secretion of effectors to subvert host immunity and establish infection. To resolve this dynamic molecular dialogue, we performed a high-resolution dual RNA-seq time course of susceptible pepper (*Capsicum annuum*) roots inoculated with *P. capsici*, spanning 0–72 hours post-inoculation. This analysis dissected the interaction into four distinct and highly reproducible transcriptional phases.

The *P. capsici* transcriptome shifted from an early colonization program to a pronounced transition at 24 hours, marked by extensive remodeling and the induction of carbohydrate-active enzymes, including pectate lyases. In parallel, the pepper transcriptome showed progressive disruption of defence, cell wall, and core cellular processes, consistent with advancing root colonization.

Temporal clustering identified a *P. capsici* early-infection program co-expressed with the biotrophy-associated marker PcHmp1 and significantly enriched for genes encoding secreted, non-membrane-anchored proteins. To investigate their virulence and avirulence functions, we screened 98 secreted candidate effectors across a diverse panel of resistant and susceptible pepper accessions using PVX-based agroinfection. This transient expression assay revealed distinct, accession-dependent cell death patterns: some candidates triggered cell death across all accessions, while others responded preferentially in resistant accessions, in susceptible accessions, or in strictly genotype-specific combinations.

Together, these results define the early transcriptional program of *P. capsici* during pepper root colonization and identify candidate effectors with differential recognition across pepper germplasm, providing a foundation for linking pathogen effector repertoires to pepper resistance genes and accelerating the discovery of biologically relevant resistance mechanisms against *P. capsici*.

Main Poster Abstract 38

Streptomyces sampsonii strain C4: a promising candidate for leguminous plant protection

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The application of microbial biostimulants is a promising strategy for promoting sustainable viticulture and enhancing grapevine resilience against pathogens. This study investigated the effects of compost tea (CT), a microbial consortium (MC) (*Pseudomonas chlororaphis* subsp*. aurantiaca, P. chlororaphis* subsp*. aureofaciens; P. chlororaphis* subsp*. piscis and P. putida*) and functional cover cropping on the expression of defence-related genes in *Vitis vinifera* L. cv. Aglianico under field conditions. Six treatments were evaluated: MC, compost tea from olive pomace (CT), filtered compost tea (FCT), FCT combined with MC (FCT+MC), functional cover cropping (clover), and untreated control. Leaf samples were collected at fruit set and at the beginning of veraison, and gene expression was analysed by RT-qPCR. Among the defence-related genes analysed (*NPR1*, *JAZ1.1*, *LOX-13*, *LOX-9*, *PAL*, *PR10*, and *PR14*), *PAL* (Phenylalanine ammonia-lyase*)* showed significant differential expression 48 h after treatment at fruit set. *PAL* was significantly downregulated in vines treated with FCT, CT, and functional cover cropping compared with the untreated control; no significant differences were detected for this gene at the beginning of veraison. As *PAL* encodes the first enzyme of the phenylpropanoid pathway, its downregulation suggests modulation of this pathway. This response coincided with delayed sugar accumulation during berry ripening. The absence of natural pathogen infection in the vineyard prevented the evaluation of a potential defence-priming effect. These findings suggest that compost tea treatments and functional cover cropping may influence phenylpropanoid metabolism and berry sugar accumulation under field conditions.

Main Poster Abstract 39

When Things Don’t Work Out: Optimising High Molecular Weight DNA Extraction in Stapelia leendertziae for high-quality genome assembly

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Obtaining high molecular weight (HMW) DNA of sufficient quality is essential for long-read sequencing and the generation of high-quality genome assemblies. However, DNA extraction from succulent species can be particularly challenging due to the presence of polysaccharides, secondary metabolites, and other compounds that interfere with DNA isolation and downstream applications. *Stapelia leendertziae* is a succulent species for which no optimised HMW DNA extraction protocol is currently available. We aimed to sequence its genome as part of the Xerophyte Immunity program, which investigates the immune systems of cactus-like desert plants from distinct phylogenetic lineages.

This study aimed to optimise HMW DNA extraction from *S. leendertziae* for long-read sequencing. Initial extractions were performed using a phenol-chloroform-based protocol on whole-plant tissue samples. As these attempts did not yield DNA of sufficient quality, a nuclei isolation approach adapted from a PacBio HMW DNA extraction protocol was subsequently evaluated. To further reduce the impact of potentially inhibitory metabolites, epidermal tissue was separated from internal tissues and used as the starting material for both nuclei isolation and DNA extraction. Following unsuccessful recovery of suitable nuclei and DNA using these approaches, extraction methods were further refined through the use of the NucleoBond kit. The final extraction method successfully generated high-quality HMW DNA with sufficient integrity for long-read sequencing.

Main Poster Abstract 40

An inter-genus accessory chromosome is implicated in cultivar-specific hypervirulence of the barley pathogen Pyrenophora teres f. maculata

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Accessory chromosomes are a form of structural variation found in some eukaryotic genomes. In pathogenic fungi, they often harbour virulence-related genes and can be horizontally transferred within species or between closely related species. However, to date, such genetic elements were unknown in the destructive barley pathogen *Pyrenophora teres*. A previous study identified an isolate of *P. teres* f. *maculata* (M3) that exhibits increased virulence on the barley cultivar Baudin. A chromosome-level genome assembly of M3 was generated, revealing an accessory chromosome (Chr13) enriched in genes involved in secondary metabolism. Sequence analyses revealed that Chr13 is most closely related to members of the genus *Bipolaris*, indicating a rare inter-genus horizontal transfer. Phenotypic segregation in a population between M3 and a non-M3 pathotype revealed Chr13 is responsible for cultivar-specific hypervirulence and, uniquely, is associated with highly inefficient vertical transfer, suggesting Chr13 may represent an unstable element maintained by strong selection in the asexual state. Furthermore, Chr13 is now rare in the natural *P. teres* f. *maculata* population, potentially due to relaxed selection following changes in cultivated genotypes, and may represent an evolutionary snapshot or a transient intermediate state.

Main Poster Abstract 41

Effects of TILLING mutations in P-loops of tandemly duplicated immune receptors, FocBr1 and BrSNC1, on temperature-sensitive disease resistance in Brassica rapa

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Phylogenetic and synteny analyses identified Bra012689 as the closest ortholog of *Arabidopsis thaliana SNC1* in *Brassica rapa*. An initial TILLING mutant carrying a G211R substitution in *BrSNC1* showed enhanced resistance to *L. maculans* compared with the wild-type R-o-18 background, with reduced lesions and lower pathogen DNA at 20°C and 25°C, suggesting a temperature-resilient gain-of-function. However, two BC3F2 backcross-derived lines revealed no association between *BrSNC1* genotype and disease resistance, demonstrating that the observed resistance was caused by an unlinked mutation that had segregated away. Disease development remained temperature-dependent irrespective of *BrSNC1* genotype.

Similarly, the *FocBr1* TILLING mutant did not affect resistance to *L. maculans* or the temperature sensitivity of disease progression. In contrast, functional analysis of segregating reciprocal backcrosse populations (BC1F2 and BC2F2) showed that a G245R substitution in *FocBr1* resulted in a loss-of-function phenotype, abolishing resistance to *F. oxysporum* f. sp. *rapae*. *BrSNC1* had no detectable role in fusarium yellows resistance.

These findings confirm the essential role of *FocBr1* in conferring resistance to fusarium yellows, with loss of function attributable to the introduction of a bulky residue in the conserved P-loop motif. In contrast, *BrSNC1* did not contribute to resistance against either pathogen interactions nor to temperature-dependent disease responses in *B. rapa*.

Main Poster Abstract 42

Population genomics of the root fungal pathogen causing wheat take-all disease using a global pangenome framework

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Gaeumannomyces is a globally distributed genus of root fungi associated with cereal crops and wild grasses. It is best known for the notorious pathogen *G. tritici*, causal agent of the most important root disease of wheat, take-all, responsible for average yield losses of 20%. Yet there are basic knowledge gaps regarding the distribution, spread and reproduction of this fungus. To address this, we are undertaking the first population genomics study of *G. tritici* to investigate fundamental questions about population structure, genetic diversity and fungicide resistance in this key crop pathogen.

Using PacBio HiFi sequencing we have generated chromosome-level genome assemblies for globally distributed *G. tritici* isolates to construct a reference pangenome graph. These included isolates belonging to two distinct virulence lineages, known as type A (more virulent) and B (less virulent), which also have their own genomic idiosyncrasies. Analysis of the pangenome revealed both exceptional synteny between certain geographically distant isolates, and previously undetected chromosomal rearrangements between others. We are now using this pangenome framework as a reference for population-level analyses of ~250 *G. tritici* isolates which we have short-read sequenced. By comparing the use of the pangenome reference versus a single linear reference, we have found differences in several mapping and variant identification measures. Mapping to the pangenome generally exhibited higher mean depth values and lower transition/transversion (Ts/Tv) ratios. Furthermore, reference choice impacted type A and B virulence lineages differently. The total number of quality-filtered mapped reads was significantly lower for type B isolates aligned to the single reference, while the number of single nucleotide polymorphisms (SNPs) detected was considerably higher for type A isolates aligned to the single reference. Our preliminary results demonstrate the importance of careful reference choice in population studies and the advantages of a more representative pangenome reference, especially in cases of cryptic intraspecific lineages.

Main Poster Abstract 43

Biological stability, genetic diversity, and cross-protection of a mixture of mild strains of cowpea aphid-borne mosaic virus (CABMV) in passion fruit plants

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Passion fruit woodiness, caused by the potyvirus CABMV, is a limiting disease for the cultivation of passionflower (*Passiflora edulis*), lacking effective control alternatives. Previous attempts at cross-protection with single mild strain of the virus have failed. The successful use of mild strain mixtures to protect tomato plants against the potexvirus pepino mosaic virus in Europe supports new cross-protection approaches targeting passion fruit woodiness. The genetic diversity of 14 severe CABMV isolates from different Brazilian regions and two mild strains (CABMV/SC-Af and CABMV/GO-Jf), obtained by biological methods from the severe isolates CABMV/SC and CABMV/GO, was analyzed based on nucleotide sequences of the coat protein (CP) gene. To evaluate biological stability, both mild strains were independently subjected to 10 successive passages by mechanical inoculation onto one passion fruit plant per passage. Subsequently, both mild strains from the parent sources were inoculated into 50 passion fruit plants to confirm the stability of the mild symptoms. The mild strains were then inoculated onto passion fruit and common bean (*Phaseolus vulgaris*) plants, and infection was confirmed by RT-PCR 15 days post-inoculation, for protection tests. Preimmunized plants of both species were independently challenged with homologous (same origin) and heterologous (different origin) severe isolates. A mixture of both mild strains was inoculated onto passion fruit plants, and after confirming infection, the plants were separately challenged with the severe isolates CABMV/SC and CABMV/GO. Nucleotide sequence identities among severe isolates and mild strains ranged from 83.4% to 97.5%, and the phylogenetic tree topology grouped mild strains in a single clade. The biological stability of the mild strains was confirmed after 10 successive passages, as evidenced by the prevalence of mild symptoms. Passion fruit plants preimmunized with the mild strains were protected against infection by severe homologous isolates, but not against heterologous ones. Plants preimmunized with the mild-strain mixture were protected upon challenge with the severe isolate CABMV/SC. In contrast, protection was overcome when the plants were challenged with the severe isolate CABMV/GO. New attempts to select mild strains are underway, as are the repetition of the cross-protection assays with mixture of mild stranis.

Main Poster Abstract 44

Transforming Crop Protection Through Early Fusarium Detection

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Fusarium oxysporum (*Fo*) is one of the most economically damaging fungal plant pathogens globally, with many host-specific *formae speciales* (f.spp.) causing root rots, bulb rots and vascular wilts of important UK crops such as onion (*Fo* f. sp. cepae; FOC), lettuce (*Fo* f. sp. *lactucae*; FOL) and daffodil (*Fo* f. sp. *narcissi*; FON). FOC causes Fusarium basal rot in onion and can infect the crop at any growth stage, which is very damaging for onion growers with losses of up to 40% reported. Similarly, FON causes a bulb rot in daffodil where effects on flower yield and bulb stock can also be severe. FOL was absent in the UK until a newly emerged strain (race 4) was identified in UK indoor lettuces in 2016[1]. Other FOL races from Europe also threaten production, with continually evolving strains and the emergence of new race variants[2].

Disease control of Fusarium diseases is difficult once spores are present in the soil as fungicides are generally ineffective and long-lived chlamydospores can survive in the soil for up to 10 years, requiring extended rotation periods. There is also evidence that seed transmission is potentially a major pathway for introduction, establishment and spread of Fo, as was demonstrated for FOL on lettuce seed[3]. Therefore, pathogen diagnostics and quantification in soil and seeds could play an important role in effective disease management and decision making.

We recently developed and commercialised a specific enrichment-based qPCR diagnostic tool for FOC detection and quantification in soil, which is available now for growers to enable identification of high-risk fields prior to planting. Following on from this work, we utilised the same enrichment protocol and detected FON in soil from 20 out of 21 fields growing narcissus, and FOL in polytunnel soils which had been free from disease for the past 5 years due to the deployment of resistant cultivars. A protocol was also developed to detect FOC spores on onion seeds following enrichment, with 10 out of 27 commercial seed lines testing positive with qPCR.

The use of this enrichment qPCR approach for detecting and quantifying Fo pathogens could be applied to many important crops, helping to inform growing decisions and prevent crop losses. It may also have an important role in disease prevention and in controlling transmission through seed and contaminated soil/plant material, therefore reducing the threat of emerging pathogens to UK crop production.

Reference:

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Main Poster Abstract 45

Rysto-mediated extreme resistance emerges from a primed peripheral surveillance system

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Extreme resistance (ER) is one of the most effective forms of antiviral immunity in plants, yet the mechanisms that distinguish ER from hypersensitive resistance (HR) remain poorly understood. The potato TIR-NLR receptor Rysto confers broad-spectrum ER to many potyviruses, providing an excellent system to investigate the basis of this phenomenon.

We demonstrate that Rysto-mediated ER relies on a previously unrecognized peripheral surveillance system that is established before infection and rapidly activated upon virus perception. Transcriptome profiling revealed that Rysto plants exist in a constitutively primed immune state, characterized by elevated expression of defence-associated genes, including a cluster of glycine-rich protein (GRP)- encoding transcripts. These proteins promote the formation of Rysto punctate assemblies and enhance Rysto-dependent immune responses, linking immune priming with receptor organization.

Virus recognition triggers a pronounced redistribution of Rysto towards the cell wall–plasma membrane continuum, where the receptor accumulates in punctate structures adjacent to plasmodesmata and becomes detectable in the apoplast. This spatial reorganization is accompanied by changes within a pre-activation complex containing Rysto, Hsp70, and CP-interacting cochaperonins (CPIPs), host factors that are also exploited by PVY during cell-to-cell movement. Our analyses indicate that recognition of the PVY coat protein promotes reorganization of the complex, releasing Hsp70-associated factors and enabling assembly of an activated Rysto resistosome.

Together, these findings suggest that extreme resistance emerges from a primed peripheral surveillance system that integrates transcriptional preparedness, spatial receptor redistribution, and chaperone-assisted activation. This supports a model in which ER represents an immune strategy distinct from HR, relying on pre-positioned surveillance and rapid receptor activation rather than programmed cell death.

Main Poster Abstract 46

Spore Patrol: Tracking and Tackling the Rise of Cercospora Leaf Spot in UK Sugar Beet

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Over half of the UK's sugar is produced from sugar beet grown in eastern England. While the crop is affected by a range of endemic pests and diseases, changing climatic conditions are altering the importance and distribution of several pathogens. Among these, Cercospora Leaf Spot (CLS), caused by *Cercospora beticola*, has emerged over the last decade from a sporadic disease to one of the most economically significant foliar diseases of UK sugar beet. Severe epidemics can result in substantial reductions in root yield and sugar content, and management is increasingly reliant on fungicide applications.

To improve understanding of CLS epidemiology and support disease management, research is being undertaken to monitor airborne inoculum and assess fungicide sensitivity within UK *C. beticola* populations. Airborne spores are being sampled using Spornado spore traps deployed across the sugar beet growing area. Trap samples are analysed using qPCR to detect and quantify *C. beticola* DNA, enabling temporal and spatial assessment of inoculum dynamics and their relationship with disease development in the field. These data are being integrated with environmental and disease observations to evaluate the potential for improved forecasting and decision-support systems.

In parallel, *C. beticola* isolates recovered from symptomatic sugar beet leaves are being characterised to establish baseline fungicide sensitivity and monitor the emergence of resistance. Single-spore isolates are cultured and assessed using in vitro sensitivity assays against fungicide active ingredients representing the principal modes of action currently used for CLS control. Molecular analyses are also being conducted to identify genetic variation associated with reduced fungicide sensitivity, including target-site mutations and polymorphisms previously implicated in resistance to QoI and DMI fungicides in international *C. beticola* populations.

The integration of airborne inoculum monitoring with phenotypic and genotypic characterisation of pathogen populations provides a comprehensive framework for understanding CLS epidemiology and fungicide resistance evolution in the UK. This work will establish critical baseline data for UK *C. beticola* populations and contribute to the development of sustainable disease management strategies aimed at preserving fungicide efficacy and mitigating the impact of CLS on sugar beet production.

Main Poster Abstract 47

The Role of Berry Skin Traits in Botrytis cinerea Susceptibility of Fungus-Resistant PIWI Grapevines

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Plant diseases threaten sustainable crop production, highlighting the need for effective, environmentally friendly crop protection solutions. Composts and compost-derived extracts have been shown to suppress plant diseases, yet the microbial determinants underlying this activity remain poorly understood. Given that composts are largely produced from decomposed plant material, including leaves, we hypothesized that they may contain microorganisms originating from the phyllosphere and thus represent an underexplored source of potential biocontrol agents against foliar diseases. We focus on two major foliar diseases: tomato early blight, caused by *Alternaria solani*, and grapevine downy mildew, caused by *Plasmopara viticola*.

To identify microorganisms associated with disease suppression, compost extracts are prepared and applied as foliar sprays to tomato and grapevine plants in bioassays. Microorganisms that successfully establish on leaf surfaces are recovered and characterized using comparative metabarcoding to identify taxa associated with disease suppression. In parallel, microbial isolates obtained from suppressive composts are screened for antagonistic activity through *in vitro* assays evaluating *A. solani* spore germination and *P. viticola* zoospore motility.

Preliminary results show that a selection of compost-derived microbial extracts can suppress *A. solani* infection in tomato. In addition, several microbial isolates recovered from suppressive composts showed inhibitory activity against *P. viticola in vitro*. These findings support compost-derived microorganisms as a promising source of novel biocontrol agents against foliar diseases. Ongoing work focuses on identifying the microorganisms and mechanisms responsible for disease suppression, including antimicrobial metabolite production and induction of plant defences, to support the development of sustainable crop protection strategies.

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Main Poster Abstract 48

Unlocking the diverse Sarocladium lifestyles through CRISPR-Cas9 and live imaging

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The *Sarocladium oryzae* species complex (SOSC), a causative agent of rice sheath rot, belongs to the genus *Sarocladium*, a group of filamentous fungi. Members of this complex exhibit diverse ecological strategies, including pathogenic, endophytic and antagonistic modes of interaction. What drives these contrasting lifestyles within the SOSC remains largely unknown. Comparative genomics has revealed a wealth of biosynthetic gene clusters in *Sarocladium* species, involved in the production of specialized metabolites such as helvolic acid and cerulenin. Helvolic acid is a fusidane-type terpenoid antibiotic that interferes with protein synthesis, whereas cerulenin inhibits fatty acid and sterol biosynthesis. However, the ecological functions of these compounds, and especially the interplay between metabolite production, host colonization, microbial competition, and disease development in rice, remain poorly understood.

To functionally interrogate these predictions, we established a stable GFP-labelled *Sarocladium* strain. This was achieved through PEG-mediated transformation of fungal protoplasts with a linearized plasmid harbouring a GFP gene. This GFP strain serves as a foundation for CRISPR–Cas9-mediated genome editing, allowing targeted knock-out of genes within core biosynthetic gene clusters involved in toxin production. By coupling precise genetic perturbation with live-cell imaging, we can directly assess the impact of these metabolites on fungal behaviour, host colonization, and interactions with other microorganisms. Current efforts focus on gaining a better understanding of the role of helvolic acid and cerulenin.

By linking genomic predictions to ecological function, this work aims to elucidate the role of specialized metabolites in host–microbe interactions involving *Sarocladium*. This will advance our understanding of how these compounds shape fungal behaviour within plant-associated microbiomes and contribute to disease development.

Main Poster Abstract 49

Transcriptomic profiling of early host–pathogen interactions during Fusarium stem infection in Avena sativa

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Oat (*Avena sativa* L.) production in temperate regions is increasingly affected by stem lodging associated with severe weather. Observations that fungicide applications reduce lodging severity suggest a role for fungal pathogens in compromising stem integrity. To investigate underlying mechanisms, this study integrates pathogenicity assays with temporal transcriptomic profiling of host–pathogen interactions. Greenhouse inoculation experiments confirmed that *Fusarium graminearum* and *F. sporotrichioides* cause extensive stem lesions and significantly reduce stem strength relative to mock-inoculated controls. To characterize host responses, four oat cultivars differing in tolerance (including the susceptible cv. AAC Excellence and the more tolerant cv. Kalio) were sampled at 0, 1, 3, and 7 days after inoculation (DAI) following treatment with *F. graminearum*, *F. sporotrichioides*, or a mock control. RNA sequencing (Illumina PE150; ~60 million reads per sample) was conducted to assess transcriptional dynamics. Preliminary analyses indicate robust, cultivar-specific responses, with AAC Excellence exhibiting greater susceptibility. Differential expression patterns suggest that tolerance is associated with activation of pathways related to DNA repair, oxidative stress responses, and cell wall biogenesis and remodeling, consistent with cellular stress and structural modification of stem tissues. Notably, while host responses were highly variable, *in planta* fungal transcriptomes were temporally dynamic but unaffected by host genotype; both *F. graminearum* and *F. sporotrichioides* executed highly conserved gene expression programs across all cultivars from 1 to 7 DAI. These findings suggest that pathogen-induced stress and cell wall alterations contribute to reduced stem integrity and increased lodging risk. Ongoing analyses aim to further resolve cultivar-specific defense mechanisms and identify targets for improved disease management and breeding strategies.

Main Poster Abstract 49

Spatiotemporal Characterisation of PRIMER Cell-Associated Genes Using Promoter-Reporter Lines

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Plants rely on spatially coordinated immune responses to restrict pathogen invasion, yet how distinct cellular states are established and evolve during infection remains poorly understood. Our recent single-nucleus multiomic and spatial transcriptomic analyses identified a rare population of PRIMER cells at pathogen-proximal immune hotspots, surrounded by molecularly distinct bystander cells. While single-cell and spatial transcriptomic approaches provide high-resolution molecular snapshots, they cannot capture the dynamic activation of individual genes during immune responses. To investigate the spatiotemporal dynamics of PRIMER cell-associated genes, we generated a collection of promoter-reporter lines for candidate markers identified from our single-cell datasets. Using live confocal fluorescence imaging following bacterial infection, we monitored the activation patterns of these promoters throughout the immune response. This approach enables direct visualization of the temporal and spatial activation profiles of candidate genes and reveals their spatial relationship to infection sites and surrounding tissues. By integrating promoter-reporter imaging with our single-cell and spatial transcriptomic datasets, we aim to validate candidate PRIMER cell markers, characterize the temporal progression of PRIMER cell formation, and identify genes with distinct spatial expression patterns that may contribute to local immune coordination. Together, this work provides a dynamic framework for understanding how specialized cellular states are established and organized during plant immunity.

Main Poster Abstract 50

Monitoring Plant Pathogen Emergence with CABI Distribution Data

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Plant pathogens are estimated to cause 20 to 40% of global crop losses with the economic and social impacts felt at the local, national and international levels, which threatens global food security. Outbreaks of common pathogens on major crops tend to be well documented, but detecting new and emerging plant pathogens remains a significant challenge. New approaches and reliable data sources for pest risk monitoring to detect future plant health threats are imperative.

We took a systematic approach to track first reports of pathogens in new locations and on new host plants over a period of three years (2021 to 2023) using CABI Distribution Database. This database contains over 1.75 million distribution records across 58,000 species, is actively maintained and updated, and underpins species distribution information presented in CABI Compendium datasheets. An automated query identified candidate ‘first report’ records and a manual review filtered these to a set of confirmed first reports from the scientific literature for each study year.

Results identified 197 confirmed first reports for 71 plant pathogens from the CABI Distribution Database over the three study years. Tomato brown rugose fruit virus had the highest number of first reports, followed by cucurbit chlorotic yellows virus. Hosts most affected were tomato, apple and grapevine. Geographically, larger countries tended to have the most first reports due to in-country-spread. Mexico and Slovenia had the most first reports when only spread across international borders was considered.

The approach allowed for an unbiased review of first reports in the scientific literature without *a priori* selection of host plants or pathogens of high economic importance. The use of a well-structured and actively maintained database of presence / absence data for plant pathogens allows for regular snapshots of emerging plant pathogens, and identification of trends over time. This has practical implications for risk monitoring, supporting researchers, governments and international organisations to address the ever-increasing challenges in the fields of plant health and food security.

Main Poster Abstract 52

WRKY Transcription Factors in Defence Against *Botrytis cinerea*: Functional Characterisation and Transcriptomic Analysis

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Necrotrophic pathogens such as *Botrytis cinerea* pose a major threat to crop productivity and food security, causing grey mould disease in a broad range of the hosts including lettuce (*Lactuca sativa*) . Identifying transcriptional regulators of defence remains crucial for crop protection. This study investigated the roles of lettuce and Arabidopsis WRKY transcription factors in defence against *B. cinerea* through complementary functional, genetic, and transcriptomic approaches.

Transgenic Arabidopsis lines constitutively expressing lettuce WRKY genes were generated and their resistance evaluated using detached leaf assay. Lines expressing *LsWRKY7a* consistently exhibited enhanced resistance correlating with high transgene expression, suggesting that it is a positive regulator of defence against *B. cinerea*.

As *LsWRKY7a* was identified as a candidate defence regulator in lettuce, its putative Arabidopsis orthologues, WRKY7 and WRKY15, were further investigated to determine whether their defence functions are conserved across species. Gain and loss of function approaches were used to characterise their roles during *B. cinerea* infection. While single *wrky7-1* and *wrky15-1* mutants showed no altered susceptibility compared to the wild-type, the *wrky7-1/wrky15-1* double mutant developed significantly larger lesions, demonstrating that WRKY7 and WRKY15 act redundantly as positive regulators of basal resistance to *B. cinerea*.

To dissect the molecular mechanisms underlying these contrasting resistance phenotypes, RNA-seq was performed on wild type, *LsWRKY7a* overexpression lines, and *wrky7-1/wrky15-1* double mutants during *B. cinerea* infection. Distinct transcriptional signatures were identified associated with resistance and susceptibility, providing insight into the defence related pathways regulated by Group IID WRKY transcription factors during host-pathogen interactions. Together, these finding advance understanding of WRKY mediated immune regulation and highlight their potential for use in engineering improved disease resistance in lettuce and other crops.

Reference

Main Poster Abstract 53

Fine mapping of a centromeric locus on barley chromosome 6H reveals a candidate gene underlying the net form of net blotch susceptibility

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Net form of net blotch is a significant threat to barley production worldwide. Deploying host genetic resistance represents the most cost-effective and environmentally sustainable strategy for disease control. However, the progress has been hindered by the lack of closely linked molecular markers and an incomplete understanding of major loci associated with NFNB insensitivity. Such loci have been repeatedly identified in the centromeric region of barley chromosome 6H, yet efforts to resolve their underlying genetic determinants have been constrained by recombinant suppression in this region. Here, we show that the susceptibility allele at the 6H locus exhibits incomplete dominance over the insensitivity allele. We constructed a high-resolution genetic map of a major 6H locus controlling NFNB response in the barley cultivar Baudin. Fine mapping delimited the locus to a genomic interval of less than 200 kb, enabling the identification of a leading candidate gene underlying NFNB susceptibility. These findings resolve a long-standing bottleneck in providing practical resources for improving NFNB resistance in barley breeding programmes.

Main Poster Abstract 54

Utilizing inosine to prevent phenotypic variation and stabilize cultivation of the biocontrol agent *Paenibacillus polymyxa* E681

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While the plant growth-promoting rhizobacterium (PGPR) *Paenibacillus polymyxa* E681 serves as a potent biocontrol agent, its commercial viability is often compromised by phenotypic instability during mass production. To address this limitation, this study investigated the efficacy of inosine in preserving the phenotypic integrity of strain E681, determining both its optimal concentration and strategic application timing. Microplate assays were conducted under nutrient-limiting conditions (1/10 Tryptic Soy Broth) with varying doses of inosine, where bacterial growth dynamics and viability were systematically tracked.

The control group transitioned to the F-type variant at a frequency of 63% after one week, whereas the glucose-treated negative control shifted entirely (100%). Conversely, supplementation with 1 mM and 10 mM of inosine significantly suppressed this transition, restricting variation to 32% and 0%, respectively. Subsequent experiments evaluating the timing of a 10 mM inosine treatment (introduced at 0, 1, 2, or 3 days of incubation) revealed that protective effects were sustained through day 6, yielding low variant frequencies across all treatment groups (0d: 9.38%, 1d: 6.48%, 2d: 8.49%, 3d: 0.42%). These insights establish that inosine introduction provides reliable protection against strain attenuation, offering a robust methodological foundation for securing consistent field performance of microbial biocontrol agents.

Main Poster Abstract 55

Transcriptional responses of defence-related genes to compost tea and microbial-based treatments in grapevine

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The application of microbial biostimulants is a promising strategy for promoting sustainable viticulture and enhancing grapevine resilience against pathogens. This study investigated the effects of compost tea (CT), a microbial consortium (MC) (Pseudomonas chlororaphis subsp. aurantiaca, P. chlororaphis subsp. aureofaciens; P. chlororaphis subsp. piscis and P. putida) and functional cover cropping on the expression of defense-related genes in Vitis vinifera L. cv. Aglianico under field conditions. Six treatments were evaluated: MC, compost tea from olive pomace (CT), filtered compost tea (FCT), FCT combined with MC (FCT+MC), functional cover cropping (clover), and untreated control. Leaf samples were collected at fruit set and at the beginning of veraison, and gene expression was analysed by RT-qPCR. Among the defence-related genes analysed (NPR1, JAZ1.1, LOX-13, LOX-9, PAL, PR10, and PR14), PAL (Phenylalanine ammonia-lyase) showed significant differential expression 48 h after treatment at fruit set. PAL was significantly downregulated in vines treated with FCT, CT, and functional cover cropping compared with the untreated control; no significant differences were detected for this gene at the beginning of veraison. As PAL encodes the first enzyme of the phenylpropanoid pathway, its downregulation suggests modulation of this pathway. This response coincided with delayed sugar accumulation during berry ripening. The absence of natural pathogen infection in the vineyard prevented the evaluation of a potential defence-priming effect. These findings suggest that compost tea treatments and functional cover cropping may influence phenylpropanoid metabolism and berry sugar accumulation under field conditions.

Main Poster Abstract 56

Phosphoproteomic analysis of appressorium development identifies Vts1, a novel RNA-binding protein required for pathogenicity in the blast fungus Magnaporthe oryzae

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How fungal pathogens sense their host and initiate infection-related development is still poorly understood. We have employed a quantitative phosphoproteomic approach to investigate appressorium development by the blast fungus M. oryzae. Our study has mapped 8,005 phosphopeptides on 2,062 fungal proteins, providing a detailed landscape of the phosphorylation events that orchestrate appressorium-mediated plant infection. This reveals a profound re-wiring of phosphorylation-based signalling cascades during development, shedding light on the dynamic molecular responses elicited in the fungus during appressorium morphogenesis. The Pmk1 MAP kinase is a key orchestrator of appressorium formation which prompted us to carry out comparative phosphoproteomics and parallel reaction monitoring to identify substrates of Pmk1. In this way we identified 32 putative Pmk1 MAPK targets, revealing a complex network of regulatory interactions. One of these substrates is a novel regulator, Vts1, which undergoes Pmk1-dependent phosphorylation and is required for virulence. Vts1 is a Sterile Alpha Motif (SAM) domain protein that plays an important role in appressorium morphogenesis and pathogenesis. We show that a single Pmk1-dependent phosphorylation event is necessary for Vts1 to function as a virulence determinant and that truncation of the SAM domain of Vts1 also impairs its function. Structural modelling and structure-based phylogenetic analysis provide evidence that Vts1 is an RNA-binding protein, consistent with transcriptional profiling which identified many Vts1-dependent differentially expressed genes associated with RNA-binding and processing. Using RIP-seq analysis we defined a set of Vts1-associated mRNAs many of which have been previously implicated in fungal pathogenesis. Mutation of RNA-binding residues in Vts1 prevents complementation of a Dvts1 mutant in virulence assays, consistent with RNA-binding by Vts1 being essential for its function in plant infection. Taken together our data provide an example of how quantitative phosphoproteomic analysis of fungal infection can identify novel virulence functions and help to define new signalling mechanisms required for appressorium-mediated plant infection.

Main Poster Abstract 57

Microbial Consortia Modulate Chickpea Root Microbiomes under Rhizoctonia solani Disease Pressure

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Legumes represent one of the most important cultivations due to their use as alternative protein sources and their beneficial effects on soil health. However, they are susceptible to biotic stress, including soil-borne pathogens, which remain a major constraint to grain legume production. Among these, Rhizoctonia solani is considered one of the most aggressive because of its ability to affect the crown and the roots. In this context, biological control strategies, including the use of microbial consortia, are increasingly explored as sustainable alternatives to conventional disease management. Here, we evaluated the ability of a novel microbial consortium, named 4B, composed of Pseudomonas spp., Bacillus spp. and Streptomyces sampsonii to control R. solani in chickpea. Greenhouse experiments revealed that 4B consortium was able to reduce the severity of the disease by 25% compared to the plants inoculated with R. solani alone. However, the effectiveness of microbial consortia against root pathogens may depend not only on direct antagonistic activity but also on their ability to modulate resident rhizosphere and root-associated microbial communities. Therefore, using a metagenomic approach, we investigated the effects of 4B on the rhizosphere and root microbiome of chickpea, with the final goal to understand how the consortium shapes microbial community composition and contributes to disease control. With this aim, we used 16S rRNA and ITS amplicon sequencing to profile bacterial and fungal communities in the rhizosphere and root endosphere across pathogen- and consortium-associated treatments. The microbial response was strongly compartment-dependent. Bacterial communities, particularly in the rhizosphere, showed consistent treatment-associated shifts in composition and structure, whereas fungal communities appeared comparatively more stable, with detectable but weaker responses mainly associated with root compartments. Consortium-treated plants showed enrichment of rhizobia-related taxa, especially Mesorhizobium and Rhizobium, most clearly within roots. Because this enrichment was more evident in the plant compartment than in bulk rhizosphere patterns, it suggests a host-filtered microbiome response rather than a simple increase in soil abundance. Overall, these findings support a microbiome-centred view of biological control in chickpea-Rhizoctonia solani interactions. Rather than acting solely through pathogen antagonism, microbial consortia may contribute to plant health by reorganising the root microbiome towards host-beneficial and potentially disease-suppressive configurations. This highlights microbiome assembly as a key criterion for developing next-generation biocontrol strategies against soil-borne pathogens.

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