

Rothamsted PhD Symposium

22nd - 26th February 2021



Handbook



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Welcome



As I start my second year as Chair of the Postgraduate Committee (PGC), it gives me great pleasure to welcome you all to the annual Rothamsted Research Postgraduate Student Symposium for academic year 2020/2021. As you should be aware by now, in what has been a rather unusual year for research interactions and working environments, the Symposium is also taking a rather unusual “virtual” form. We hope that through using several different technologies we will be able to support the range of different interactions among students, and between students, supervisors (both those at Rothamsted and at our University partners), mentors and other members of staff, that have contributed to the success of previous Student Symposia. By spreading the Symposium over the whole week, we also hope that we will limit the impacts of “Teams” fatigue, so that those presenting their research at the end of the week will benefit from this opportunity as much as those presenting at the start of the week.

The Symposium provides you with both the opportunity to showcase your research to your peers and the wider Rothamsted Research community, and time to learn about the wide range of exciting research that the Rothamsted student community is engaged in. Take advantage of this time for discussions with both your fellow students and other researchers across different departments and disciplines – hopefully you will hear of ideas that you can implement in your own research, and that will help you in presenting your research to different audiences in the future.

One of the strengths of this Symposium, over those that you might participate in at your University or within your DTP/CDT, is the breadth of disciplines and range of applications that are covered, mirroring the institute research portfolio. Don’t forget about this breadth and range when presenting your work and remember that not all those listening will have the background knowledge underpinning your particular research.

I hope that the week will be both rewarding and enjoyable.

Andrew Mead



ROTHAMSTED RESEARCH

Session information

Each of our sessions have a separate Teams meeting link (10 links in total).

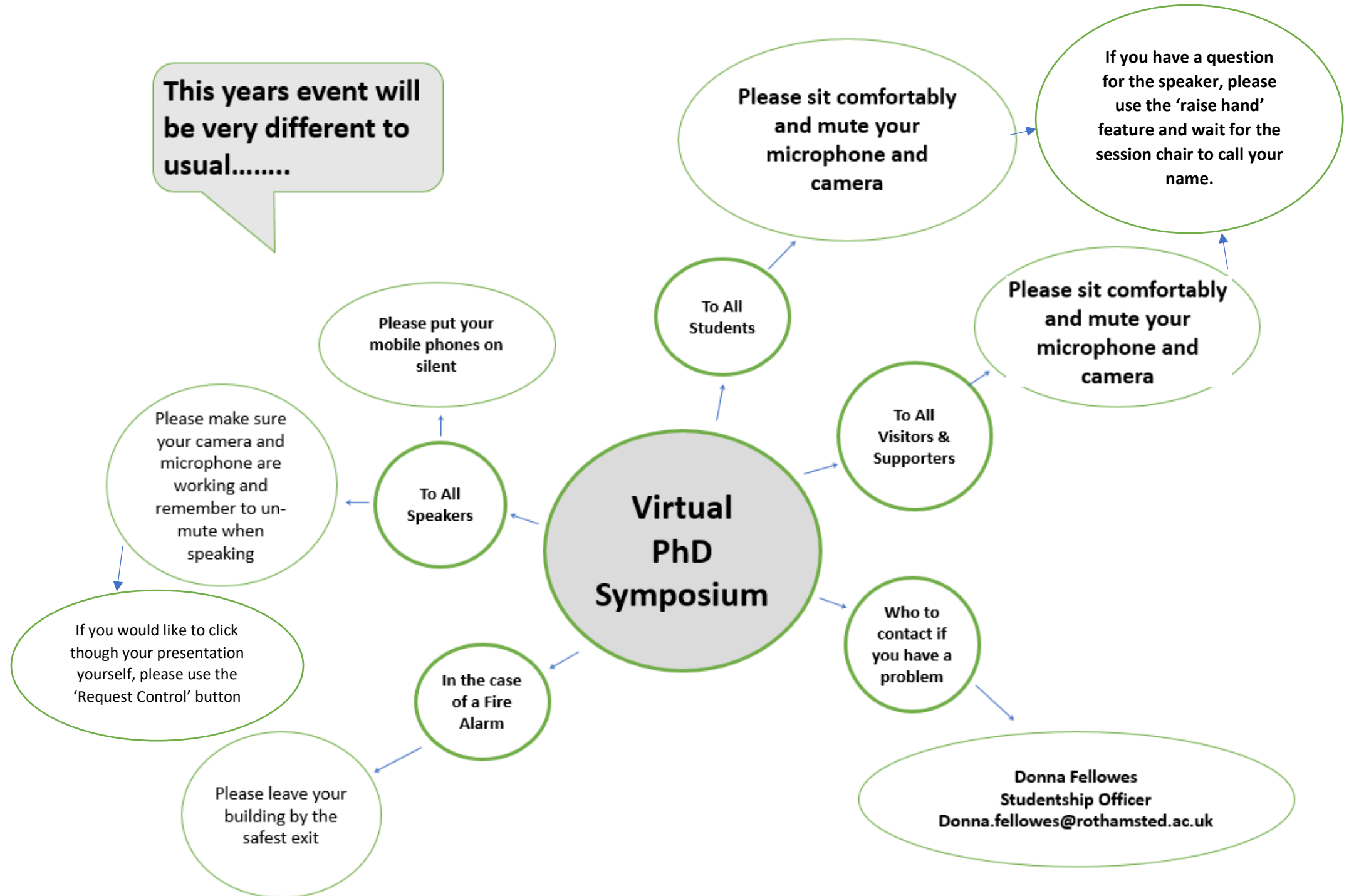
Please make sure you join each session with your camera and microphone turned off. These can be turned on when you are advised to do so either for your talk or if you are asking a question.

You can join/leave whenever you need to by using the correct link for that particular session.

All links can be found on the attached programme.

All sessions will be recorded and will be accessible from the PhD Intranet pages and will also be posted to Yammer.

This years event will be very different to usual.....



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If you have a question for the speaker, please use the 'raise hand' feature and wait for the session chair to call your name.

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Virtual PhD Symposium

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Donna.fellowes@rothamsted.ac.uk**

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Virtual Rothamsted PhD Symposium

22nd to 26th February 2021

Event Programme



Day 1 – Monday, 22nd February 2021	
11:15am	SESSION 1 - Welcome by Angela Karp and new student introductions - Click here to join the meeting Chaired by Luca Steel
11:40am	Chris Stephens (BCP) - Understanding the molecular basis of disease resistance against <i>Septoria Tritici</i> blotch in wheat
12:10am	Harry Barrat (SAS-NW) - Hot moments and warming gases: Why is so much N ₂ O released from a dry soil when it is rewetted?
12:30pm	Lunch Break – Click here to enter the Gather Town space
13:45pm	SESSION 2 - Poster introductions – 2min talks - Click here to join the meeting Chaired by Maiara Piovesana 1. Alina Igna (BCP) - Deciphering mechanisms of nonhost resistance against <i>Zymoseptoria Tritici</i> in model plant species 2. Rohan Richard (PS) - MILLERS, SAVING YOU TIME AND MONEY! creating wheat varieties with consistent and high breadmaking quality 3. Alex Borg (BCP)- Elucidating the mechanisms of aphid resistance in wheat 4. Jemima Ramarolahy (PS) – Novel phosphate fertilizer formulation for African agriculture 5. Rahul Nitnavare (PS) - Identifying novel variation in Nitrogen Use Efficiency (NUE) and its physiological and genetic basis in wheat
14:00pm	Guest Speaker – Simon Willcock - Senior Lecturer at Bangor University – Me, Myself and I
14:45pm	Tania Chancellor (BCP) - Exploiting the family feud: A fungal endophyte for the control of take-all disease in wheat
15:05pm	Comfort Break
15:20pm	2 nd Year Poster Session for Alina Igna, Rohan Richard, Alex Borg, Jemima Ramarolahy, Rahul Nitnavare - Click here to enter the Gather Town space
16:20pm	Close of day 1
19:30	Symposium Virtual Games Evening

Second year talks and poster sessions are coloured in green. Third year multi-media talks and posters are coloured in orange. Final year 15-minute presentations are coloured in blue.

Poster sessions will be held in separate areas of the GatherTown space limited to FIVE visitors at a time. All posters are displayed in the handbook, to help you choose the posters you would like to see, and they can be found in the GatherTown area which corresponds to the number beside each presenter in the programme above. There are three 20-minute sessions per poster session.

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Day 2 - Tuesday, 23 rd February 2021	
10:00am	SESSION 3 - Welcome and multi-media poster introductions - Click here to join the meeting Chaired by Chris Stephens 1. Claire Kanja (BCP)- Functional characterisation of candidate <i>Fusarium Graminearum</i> effectors 2. Jesus Castillo (SAS-H)- The nitrogen economy of rice-pasture-livestock systems in Uruguay 3. Mandy Kao (SAS-NW)- Influence of supplement source (organic vs. inorganic) of selenium, copper, zinc and manganese on micronutrient excretion and partitioning between urine and faeces in sheep
10:30am	Emma Bailey (CAS) - Beneficial predators for integrated pest management - a genomics approach
10:50am	Tessa Reid (SAS-H)- Has plant breeding decoupled beneficial plant-microbiome interactions in wheat?
11:10am	Timo Breure (SAS-H) - A loss function approach to soil sensing
11:30am	Comfort Break
11:45am	3 rd Year Poster Session - Claire Kanja, Jesus Castillo, Mandy Kao - Click here to enter the Gather Town space
12:45pm	Lunch Break - Click here to enter the Gather Town space
13:45pm	SESSION 4 - Poster introductions – 2min talks - Click here to join the meeting – Chaired by Tanya Chancellor 1. Tadesse Gashaw Asrat (SAS-H) - Soil spectroscopy and crop modelling for precise fertilizer application 2. Luca Steel (BCP) - Unmasking a cereal killer: what triggers 3lysm effector expression in a fungal wheat pathogen? 3. Sophia Bahddou (SAS-H) - Technical and practical innovations to reduce soil and water losses by improving soil physical properties 4. James Brett (PS) – Identification of novel QTIs and genes for high fibre in wheat landraces 5. Ika Nurziah (BCP)- Plant-based vaccines for prevention of poultry viral diseases: Newcastle Disease
14:00pm	Andy Jones (SAS-NW) - Redefining key performance indicators for livestock production systems: What is the value of information
14:20pm	Amy Withers (BCP) - How does the expression of three Toll-pathway immune response genes change following flight in fall armyworm (<i>Spodoptera frugiperda</i>) challenged with SfMNPV?
14:40pm	Emily Masters-Clark (SAS-H) - Exploiting mycorrhizal selection of beneficial rhizosphere bacteria from the soil microbiome
15:00pm	Comfort Break
15:15pm	2 nd Year Poster Session for Tadesse Gashaw Asrat, Luca Steel, Sophia Bahddou, James Brett, Ika Nurziah - Click here to enter the Gather Town space
16:15pm	Close of day 2

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Virtual Rothamsted PhD Symposium

23rd to 27th November 2020

Event Programme



ROTHAMSTED
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Day 3 - Wednesday, 24 th February 2021	
10:00am	SESSION 5 - Welcome and multi-media poster introductions - Click here to join the meeting Chaired by Hannah McGrath 1. Manpartik Gill (PS) - Novel brassinosteroid dwarfing genes as alternatives for improving wheat grain yields 2. Anastasia Sokolidi (BCP) - Smart detection of airborne diseases in tomato production 3. Petros Sigalas (PS) - Transcriptomic data and SL-deficient mutant to provide new insights into tillering control in response to nitrogen supply 4. Henry Tidd (BCP) - Characterisation of major genes mediating resistance to <i>Septoria Tritici</i> blotch disease in wheat
10:30am	Patricia Ortega Ramos (BCP) - New heroes to defeat cabbage stem flea beetle (<i>Psylliodes Chrysocephala</i>)
10:50am	Nikolaos Vavlas (SAS-H) - Providing satellite-based soil and crop productivity indicators to display meteorological, pedological and farm management effects
11:10am	Hannah Blyth (BCP) - Spotting the difference: a mutagenomic dissection of virulence and avirulence in <i>zymoseptoria tritici</i>
11:30am	Comfort Break
11:45am	3 rd Year Poster Session for Manpartik Gill, Anastasia Sokolidi, Petros Sigalas, Henry Tidd - Click here to enter the Gather Town space
12:45pm	Lunch Break - Click here to enter the Gather Town space
13:45pm	SESSION 6- Poster introductions – 2min talks - Click here to join the meeting Chaired by Joe Oddy 1. William Rickard (SAS-H) - The Why of soil measurement 2. Munisath Khandoker (SAS-H) - Soil health metrics for sustainable agricultural systems 3. Musa Kisiriko (CAS) - Agricultural bioproducts from medicinal and aromatic plants 4. Paul Rous (SIEP) – An innovation ecosystem approach to the agricultural sector – Exploring innovation and co-creation of value in the context of UK ecosystem 5. Gavers Oppong (PS) - Understanding the mechanisms of hypoxia tolerance in rice: Assessing the effect of different imbibition conditions on anaerobic germination of rice seeds- a role for ethylene priming? 6. Mahassine Arhazzal (SAS-H) – Exploitation of beneficial root-associated bacteria in grain cereal-based cropping systems
14:05pm	Maiara Piovesana (PS) - A gain-of-function allele of <i>CRK10</i> causes collapsed xylem vessels and enhanced resistance to a root-infecting vascular pathogen in arabidopsis
14:25pm	Xavier Albano (SAS-H) - Effect of organic amendments and inorganic fertiliser application on nitrogen use efficiency and denitrification in controlled and field conditions
14:45pm	Anchen Kehler (SAS-NW) - The utilisation of Aminomethylphosphonic acid (AMPA) by micro-organisms as a phosphorus source in soil systems
15:05pm	Comfort Break
15:20pm	2 nd Year Poster Session for William Rickard, Munisath Khandoker, Musa Kisiriko, Paul Rous, Gavers Oppong, Mahassine Arhazzal - Click here to enter the Gather Town space
16:20pm	Close of day 3

Virtual Rothamsted PhD Symposium

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Day 4 - Thursday, 25 th February 2021	
10:00am	SESSION 7 - Welcome and multi-media poster introductions - Click here to join the meeting Chaired by Anastasia Sokolidi 1. Tom Oliver (CAS) - Using drones to track bees 2. Mesfin Kebede Desta (SAS-H) - Zinc Adsorption - Desorption studies on typical soils from different landscape positions in Amhara regional state, Ethiopia 3. Mollie Langdon (PS) - Unlocking the potential of the pod
10:30am	Amber Manley (SAS-NW) - Comparing extraction methods for biomarker steroid characterisation from soil and slurry
10:50am	Dion Garrett (BCP) - Journey to the centre of the lettuce: An aphid odyssey
11:10am	Dimitra Angelopoulou (BCP) - The role of photoprotection in disease resistance to <i>Septoria Tritici</i> blotch in wheat
11:30am	Comfort Break
11:45am	3 rd Year Poster Session for Tom Oliver, Mesfin Kebede Desta, Mollie Langdon - Click here to enter the Gather Town space
12:45pm	Lunch Break - Click here to enter the Gather Town space
13:45pm	SESSION 8 Poster introductions – 2min talks - Click here to join the meeting Chaired by Hannah McGrath 1. Owen Thornton (SAS-H) - Bio-prospecting for plant-growth-promoting microbes In Broadbalk soils 2. Daniel Cudjoe (PS) - Phenotyping the nutritional status of crops using remote sensing technologies 3. Ruth Carter (BCP) - Competition between an invasive and endemic species of armyworm in Africa 4. Marieme Drame (SAS-NW) – Enhanced nitrogen use efficiency (nue) of urea fertilisers for sub-saharan africa 5. Joseph Oddy (PS) - Characterising a natural deletion of the B genome ASN2 homoeolog in wheat
14:00pm	Mandy Stoker (SAS-H) - Adding evidence regarding the use of cover crops
14:20pm	Darwin Hickman (BCP) - Getting to the roots of the black-grass problem: allelopathic control of <i>Alopecurus Myosuroides</i>
14:40pm	Rest Break
15:00pm	2 nd Year Poster Session for Owen Thornton, Daniel Cudjoe, Ruth Carter, Marieme Drame, Joseph Oddy - Click here to enter the Gather Town space
16:00pm	Close of day 4

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Day 5 - Friday, 26 th February 2021	
10:00am	SESSION 9 - Welcome and Poster introductions – 2min talks - Click here to join the meeting Chaired by Mollie Langdon 1. Ishbel Hayes (BCP) - Flight-to-light and the decline of British moths 2. Frank Okyere (PS) - Digital image analysis for highthroughput phenotyping of quinoa plants in a glasshouse 3. Beth Roberts (SAS-H) - Quantifying the true costs of farming systems 4. Imane El Fartassi (SAS-H) – Agent based modelling of crop production 5. Isabel Corkley (BCP) – Managing concurrent evolution of resistance to fungicides 6. Bader Oulaid (SAS-H) - The economic and environmental value of agricultural model-based decision support tools for wheat crops in Morocco
10:20am	Hannah McGrath (SAS-H) - Bespoke field margins for delivering multiple services to fresh produce
10:40am	Jonah Prout (SAS-H) - Soil organic carbon indexing and measurement system
11:00am	Caitlin Willis (BCP) - Investigating insecticide resistance in UK populations of cabbage stem flea beetle <i>Psylliodes Chrysocephala</i>
11:20am	Comfort Break
11:35am	2 nd Year Poster Session for Ishbel Hayes, Frank Okyere, Beth Roberts, Imane El Fartassi, Isabel Corkley, Bader Oulaid Click here to enter the Gather Town space
12:35pm	Lunch Break - Click here to enter the Gather Town space
14:00pm	SESSION 10 - Click here to join the meeting Chaired by Kim Hammond-Kosack Guest Speaker – Helen Brewer – Policy Advisor-Market Access at DEFRA - From Plant Pathology to Ice Cream Exports
14:45pm	Conference Wrap-up

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The poster sessions will be organised in to 20 minute sessions – There will be a message sent in the board in the right hand side of your screen to let you know when it is time to move on to the next poster.

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**ROTHAMSTED
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Session One
Monday, 22nd
February
2021

Chaired by Luca Steel

UNDERSTANDING THE MOLECULAR BASIS OF DISEASE RESISTANCE AGAINST SEPTORIA TRITICI BLOTCH IN WHEAT

CHRIS STEPHENS¹, RUMIANA RAY², JASON RUDD¹, KOSTYA KANYUKA¹

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, UNIVERSITY OF NOTTINGHAM, NOTTINGHAM

The recently cloned wheat gene *Stb6* confers genetic resistance against the pathogenic fungus *Zymoseptoria tritici*, the causal agent of *Septoria tritici* blotch. *Stb6* encodes a wall-associated kinase (WAK)-like protein and stimulates an immune response against strains of *Z. tritici* expressing the cognate *AvrStb6* gene, in a gene-for-gene interaction. However, the nature of the putative interaction between *Stb6* and *AvrStb6*, as well as the mechanism by which *Stb6* confers resistance, is currently unknown. The aim of this project is therefore to begin to elucidate these mechanisms, to better understand the functioning of *Stb6* and other WAKs in plant immunity. We have demonstrated the localisation of *Stb6*, when transiently expressed in the tobacco plant *Nicotiana benthamiana*, to the cell membrane. Furthermore, we show that expression of a functional *Stb6* allele stimulates a pronounced cell death phenotype in tobacco. We aim to use this finding to identify interactors with *Stb6* during expression in tobacco, to provide candidate interactors in the wheat resistance response. Finally, we carried out an analysis of the global population genetics of *AvrStb6*, which revealed the modern extinction of “original” allele found to be avirulent on *Stb6* wheat. This project aims to provide the basis for a greater understanding of the resistance mechanism conferred by *Stb6*. As the only *Stb* resistance gene currently cloned, findings from this project may provide a model for the function of other *Stb* genes, as well as WAK resistance genes in other pathosystems, enhancing our understanding of genetic resistance to crop pathogens and helping with the creation of resistant crop varieties in the future.

HOT MOMENTS AND WARMING GASES: WHY IS SO MUCH N₂O RELEASED FROM A DRY SOIL WHEN IT IS REWETTED?

HARRY BARRAT¹, LAURA CARDENAS¹, IAN CLARK¹, ANDY NEAL¹, MAIDER ABADIE¹ AND DAVE CHADWICK¹

¹, ROTHAMSTED RESEARCH, HARPENDEN.

My PhD has tried to understand how a soils past affects its function and its health. I've looked at two main factors, the impact of management over many decades by studying the soil on Broadbalk, and the impact of weather, by taking soil into the lab and changing its drying and wetting history. My presentation is going to focus on the impacts of drying and wetting, as currently that's the part of my PhD that I've made the largest progress with.

If you rewet a dry soil it produces a large pulse in N₂O which can be 40 times above the background level. When I started my PhD there wasn't a unified understanding of why this could be the case, and there was a limited number of lab studies trying to explain the mechanism behind it. In this presentation I go through the first meta analysis of this phenomenon, which we managed to get published in the European Journal of Soil Science, and two other lab experiments that are currently unpublished, but shed further light onto what might be happening.





**ROTHAMSTED
RESEARCH**

Session Two
Monday, 22nd
February
2021

Chaired by Maiara Piovesana

DECIPHERING MECHANISMS OF NON-HOST RESISTANCE IN MODEL PLANT SPECIES TO AN IMPORTANT FUNGAL PATHOGEN OF WHEAT

ALINA A IGNA¹, JASON RUDD¹, CYRIL ZIPFEL²⁻³, RUMIANA RAY⁴ AND KOSTYA KANYUKA¹

1, ROTHAMSTED RESEARCH, HARPENDEN, UK. 2, THE SAINSBURY LABORATORY, NORWICH RESEARCH PARK, UK. 3, ZURICH-BASEL PLANT SCIENCE CENTER, UNIVERSITY OF ZURICH, SWITZERLAND.
4, FACULTY OF SCIENCE, UNIVERSITY OF NOTTINGHAM, UK

Non-host resistance (NHR) is a durable form of resistance exhibited by an entire plant species to a specific pathogen. Studies of this phenomenon often use biotrophic pathogens that penetrate plant cells and form intracellular feeding structures. In contrast, *Zymoseptoria tritici* - the causal agent of the foliar disease Septoria tritici blotch (STB) of wheat - is a hemibiotroph that invades the host through stomata and remains extracellular during its entire life cycle. While the molecular nature of *Z. tritici* virulence has been investigated on its natural host (wheat), NHR against *Z. tritici* remains poorly understood.

A previous study by Kettles *et al.* (2017) at Rothamsted have identified fourteen *Z. tritici* secreted effector proteins, which triggered cell-death defence response when transiently expressed in the non-host tobacco species *Nicotiana benthamiana*. Interestingly, cell death induced by the three of the investigated effectors was shown to be dependent on BAK1 and SOBIR1, which are well-known co-receptors for many plant cell surface immune receptors (CSIRs). This suggests that the recognition of *Z. tritici* effectors in a non-host *N. benthamiana* plant occurs at the plasma membrane-apoplast interface and is likely to be mediated by CSIRs. However, the specific CSIRs involved in *Z. tritici* effector recognition remain unknown.

The main aim of this PhD project is to identify the CSIRs that recognise *Z. tritici* effectors in *N. benthamiana*. Using a novel biochemistry/proteomics approach, a GFP-tagged BAK1 will be used as a bait to capture and identify BAK1-CSIR complexes formed only in the presence of specific *Z. tritici* effectors (i.e. presumed CSIR ligands). These complexes will be identified through liquid chromatography-mass spectrometry following co-immunoprecipitation with anti-GFP tag antibodies. Next, potential candidate CSIRs will be functionally characterised using a rapid functional genomics tool - Virus-Induced Gene Silencing (VIGS). Silencing of the *bona fide* receptor in *N. benthamiana* is expected to result in the loss of defence (i.e. no cell death) in response to specific *Z. tritici* effector. Lastly, the cumulative contribution of effectors-receptors interaction to NHR will be tested by simultaneously silencing the group of identified CSIRs. This approach will give insights into the overall CSIRs contribution to the NHR phenomenon.

These findings will provide fundamental insights into NHR mechanism to extracellular pathogens, and also pave the way for development of novel, more efficient disease resistance strategies against STB in wheat.

Kettles G. J., Bayon C., Canning G., Rudd J. J., and Kanyuka K. [2017] *Apoplasmic recognition of multiple candidate effectors from the wheat pathogen Zymoseptoria tritici in the nonhost plant Nicotiana benthamiana*. *New Phytologist* 213: 338-350

TITLE: MILLERS, SAVING YOU TIME AND MONEY! CREATING WHEAT VARIETIES WITH CONSISTENT AND HIGH BREADMAKING QUALITY

ROHAN RICHARD¹, LUZIE WINGEN², MERVIN POOLE³, PAOLA TOSI⁴, SIMON GRIFFITHS², ALISON LOVEGROVE¹, AND PETER SHEWRY¹

¹ ROTHAMSTED RESEARCH, HARPENDEN, AL5 2JQ, UK; ² JOHN INNES CENTRE, NORWICH, NR4 7UH, UK; ³ HEYGATES LTD, NORTHAMPTON, NN7 3QH, UK;

⁴ UNIVERSITY OF READING, READING, RG6 6AH, UK

A good quality flour is essential for breadmaking. Flour quality is related to protein content – a minimum of 13% for the UK breadmaking industry – and composition and proportion of gluten proteins. However, currently, a high protein content is only achieved with high nitrogen input, which can have severe detrimental effects on the environment. In order to optimize the use of nitrogen, it is of great importance to know more about its use inside the plant. With this aim, the project will be looking at the genetic architecture of grain protein deviation (GPD). which is related to the ability of certain cultivars to make a better use of nitrogen – concentrate more nitrogen in their grain - than others. GPD has been reported to be a complex trait involving various gene loci across the wheat genome and to be influenced by environmental variations. Therefore, a study of a population of two UK breadmaking cultivars under three environments (year x location) is underway to identify suitable stable lines with show high GPD. An emphasis will also be on the breadmaking quality of these lines to match end users' expectation. This will be done by studying intrinsic grain components, namely the amount and composition of gluten protein, and by performing baking tests.

ELUCIDATING THE MECHANISMS OF APHID RESISTANCE IN WHEAT

ALEXANDER BORG, DR. MIKE BIRKETT, DR. JOHN CAULFIELD, DR. JOZSEF VUTS, DR. JOHN FOULKES
ROTHAMSTED RESEARCH, HARPENDEN, UK - UNIVERSITY OF NOTTINGHAM, NOTTINGHAM, UK

Aphids are a major agricultural pest of wheat, inducing significant damage by reducing nutrient availability, photosynthesis rate due to aphid honeydew enabling saprophytic fungal growth on leaves and by viral transmission. Resistance to insecticides, initial and re-registration costs of insecticides and the banning of working insecticides by the European Union gives farmers less options to tackle aphid infestations. Identifying plants naturally resistant to aphids, understanding their mechanisms of resistance and engineering this resistance into modern elite wheat is a possible alternative to the use of insecticides.

As modern wheat has a low genetic diversity, resulting in a lack of aphid resistance genes, studies have screened ancient wheat and related *Aegilops* species for aphid resistance. Multiple aphid resistant varieties have been isolated that show different mechanisms of resistance. These mechanisms are not yet fully understood but suggest pre-alighting cues and phloem occlusion through callose deposition as prominent mechanisms of resistance. Interestingly, these resistant varieties lack benzoaxinoids (BXs), the secondary metabolites (SMs) attributed to aphid resistance in maize and *Aegilops speltoides*, indicating other SMs may be contributing to this resistance.

Additionally, abiotic stresses also effect aphid resistance, with elevated temperatures, drought, elevated CO₂, high salinity and nitrogen limitation inducing an increased aphid resistance by priming the plants defence response. No studies have yet investigated the effects of abiotic stress on ancient wheat resistant to aphids and whether this priming effect enhances or diminishes this resistance.

In this project, SM chemistry produced by aphid-resistant *Triticum monococcum* and *Aegilops longissima* lines at varying aphid densities and aphid feeding times will be investigated. Compounds that may be attributed to this resistance will be isolated and identified, and a further understanding of the aphid resistance mechanisms will be generated. Furthermore, the project will explore how a combination of abiotic stresses effects the above aphid resistance mechanisms, highlighting links between the abiotic stress response and aphid resistance mechanisms and observing how a change in abiotic factors due to climate change and soil nutrient depletion will affect the aphid resistance in these plant lines.

- Aradottir, G. I. et al. (2017) 'Searching for wheat resistance to aphids and wheat bulb fly in the historical Watkins and Gediflux wheat collections', *Annals of Applied Biology*, 170(2), pp. 179–188. doi: 10.1111/aab.12326.
- Elek, H. et al. (2009) 'APHID RESISTANCE IN WHEAT VARIETIES', *Communications in agricultural and applied biological sciences*, pp. 233–241.
- Elek, H. et al. (2013) 'Hydroxamic acids in *Aegilops* species and effects on *Rhopalosiphum padi* behaviour and fecundity', *Bulletin of Insectology*, 66(2), pp. 213–220.
- Foyer, C. H. et al. (2016) 'Cross-Tolerance to biotic and abiotic stresses in plants: A focus on resistance to aphid infestation', *Journal of Experimental Botany*, 67(7), pp. 2025–2037. doi: 10.1093/jxb/erw079.
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- Greenslade, A. F. C. et al. (2016) 'Triticum monococcum lines with distinct metabolic phenotypes and phloem-based partial resistance to the bird cherry-oat aphid *Rhopalosiphum padi*', *Annals of Applied Biology*, 168(3), pp. 435–449. doi: 10.1111/aab.12274.
- Migui, S. M. and Lamb, R. J. (2003) 'Patterns of resistance to three cereal aphids among wheats in the genus *Triticum* (Poaceae)', *Bulletin of Entomological Research*. University of Nottingham, 93(4), pp. 323–333. doi: 10.1079/ber2003246.
- Pickett, J. A. (2013) 'Food security: Intensification of agriculture is essential, for which current tools must be defended and new sustainable technologies invented', *Food and Energy Security*, 2(3), pp. 167–173. doi: 10.1002/fes3.32.
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NOVEL PHOSPHATE FERTILIZER FORMULATION FOR AFRICAN AGRICULTURE

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Soil phosphorus (P) deficiency is a major constraint for agriculture in sub-Saharan Africa where soils are highly weathered and extremely low in available P, and fertilizer inputs are often far less than replacement values. P use efficiency depends on both internal plant mechanisms, allowing greater growth for a given amount of P in the plant, and external mechanisms, allowing greater P uptake. External mechanisms include root geometry and hair effects, mycorrhizal effects, and solubilisation effects due to root-induced changes in the soil affecting P solubility. Each of these differ between crop genotypes and can be manipulated by the combination of compounds in the fertilizer, and the placement of the fertilizer. In this project we are looking at how P efficiency mechanisms in crops in highly-weathered low-P soils can be exploited by manipulating the admixture of nitrogen and potassium fertilizers added with P fertilizers. This will be done using upland rice genotypes differing in P uptake efficiency and through a combination of controlled-environment experiments, mathematical modelling and field experiments. Based on understanding of the processes controlling P use efficiency, we will draw conclusions for developing fertilizer formulation and management technologies for sub-Saharan African agriculture.

IDENTIFYING NOVEL VARIATION IN NITROGEN USE EFFICIENCY (NUE) AND ITS PHYSIOLOGICAL AND GENETIC BASIS IN WHEAT

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Nitrogen (N)-use efficiency can be defined as the grain yield per unit of nitrogen supplied (from N fertilizer and other sources including the soil) and is dependent on the two key components, N-uptake efficiency (NUpE) and N-utilization efficiency (NUtE). The excess use of N fertilisers causes serious environmental impacts including nitrate leaching into ground water, eutrophication of water bodies, and global warming. Therefore, a key breeding target in wheat cultivation is enhancing NUE. In wheat, there is relatively small genetic variation in NUpE and NUtE within adapted elite germplasm. This study aims to identify novel variation for NUE by screening wheat germplasm derived from diverse genetic material for NUE and associated traits. The BBSRC Designing Future Wheat (DFW) Breeder's Diversity Toolkit of hexaploid wheat lines, including near-isogenic lines (NILs) derived from landraces backcrossed to Paragon, were screened in three replicates at two sites. The subset NILs were selected for QTLs for NUE and related traits. These NILs are being used for extensive phenotyping studies and will subsequently be subjected to mutational studies with identified genes candidates through in-silico studies and transcriptome analysis. In screening experiment, NILs incorporating QTLs related to the NUE traits: Normalised Difference Vegetative Index (NDVI), aboveground DM (AGDM), straw DM and grain filling thermal time (GFPTT) were phenotyped. Initial data indicates that alleles from Watkins landraces had NDVI significantly above Paragon, suggesting greater N accumulation, which also correlates to higher yields. The grain yield at Rothamsted site was higher (1-1.8 t/ha) as compared to the Nottingham site.

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Guest Speaker

Dr Simon Willcock

Senior Lecturer at Bangor University

‘Me, Myself and I’

Dr Simon Willcock (Senior Lecturer in Environmental Geography, Bangor University) is an interdisciplinary researcher that focuses on global challenges and sustainable development. Being 34, he can (just) remember what it was like to be a PhD student and a post-doc in the seemingly endless pursuit of a career in academia. He will talk through his career progression, from a naïve student who accidentally drank a bottle of kerosene in the field to achieving the pinnacle of science – being quoted in the Daily Mail – in the hope that you can learn from the things he accidentally got right and avoid some of his mistakes.

EXPLOITING THE FAMILY FEUD: A FUNGAL ENDOPHYTE FOR THE CONTROL OF TAKE-ALL DISEASE IN WHEAT

TANIA CHANCELLOR, KIM HAMMOND-KOSACK, JAVIER PALMA-GUERRERO

1. ROTHAMSTED RESEARCH, HARPENDEN. 2. UNIVERSITY OF NOTTINGHAM

Take-all disease, caused by the soil-borne ascomycete fungus *Gaeumannomyces tritici*, is the most economically important root disease of wheat in the UK and worldwide. Yield losses of up to 60% have been reported in the UK but are typically in the range of 5-20%¹. The fungus invades the roots and destroys the vascular tissue, hindering the plants ability to uptake water and nutrients from the soil. Current control methods include crop rotation, later sowing of crops at risk and the use of partially effective seed dressings or foliar fungicide sprays². Closely related species in the Magnaporthaceae family, such as *G. hyphopodioides*, occur naturally in arable and grassland soils and have considerable potential to suppress take-all disease³. However, the infection mechanism and subsequent wheat response to colonisation by beneficial Magnaporthaceae species remains poorly characterised. Furthermore, the mechanism of take-all control by these species is unknown.

Detailed microscopy analyses have revealed a strong lignification response in roots colonised by *G. hyphopodioides*. In addition, *G. hyphopodioides* has been found to produce chlamyospore-like structures, thought to act as fungal resistance structures produced in response to upregulated plant defences. A co-inoculation bioassay demonstrated that effective take-all control was only achieved when *G. hyphopodioides* colonised the root system first, further strengthening the hypothesis that *G. hyphopodioides* induces a plant defence response, thereby preventing future infection by *G. tritici*. An RNA sequencing experiment is underway to investigate plant transcriptional changes in response to *G. hyphopodioides* colonisation and *G. tritici* infection. In addition, a virus-induced silencing (VIGS) system is being developed for wheat roots, providing a method to investigate candidate wheat genes involved in the *Gaeumannomyces*-wheat interaction.

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³Osborne, S. J., McMillan, V. E., White, R., & Hammond-Kosack, K. E. (2018). Elite UK winter wheat cultivars differ in their ability to support the colonization of beneficial root-infecting fungi. *Journal of Experimental Botany*, 69(12), 3103–3115. <https://doi.org/10.1093/jxb/ery136>



**ROTHAMSTED
RESEARCH**

Poster Session

Alina Igna
Rohan Richard
Alex Borg
Jemima Ramarolahy
Rahul Nitnavare



**ROTHAMSTED
RESEARCH**

Close of
day one

Symposium
Virtual Games
Evening



**ROTHAMSTED
RESEARCH**

Session Three
Tuesday, 23rd
February
2021

Chaired by Chris Stephens

FUNCTIONAL CHARACTERISATION OF CANDIDATE *FUSARIUM GRAMINEARUM* EFFECTORS

CLAIRE KANJA^{1,2}, ANA MACHADO WOOD¹, KAREN IRAWAN³, MATT DICKENSON² & KIM HAMMOND-KOSACK¹

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3. IMPERIAL COLLEGE LONDON, LONDON, UK

The effector repertoire of plant pathogens is a key determinant of the success of pathogen-host interactions and could mean the difference between a compromised or a successful crop harvest. One notorious pathogen, the fungus *Fusarium graminearum* is the causal agent of fusarium head blight, one of the most destructive diseases threatening wheat production worldwide¹

A main challenge facing *F. graminearum* effector characterisation is pinpointing high quality effector candidates from the predicted proteome. Despite the publication of the refined *F. graminearum* secretome in 2012², finding candidates suitable for functional studies from a pool of almost 300 secreted proteins with unknown functions remains problematic³.

Previously, we had adopted in silico bioinformatic pipelines that consider transcriptional (RNA-seq and microarray), proteomic, taxonomic distribution analysis and the genome location of candidates for effector discovery. This has proven to be successful in finding clusters of candidate effectors in multiple filamentous phytopathogens⁴. Using this approach, we have identified two putative effectors in *F. graminearum*; FgSSP34 and FgSSP53.

For the functional characterisation of these candidates we have taken a two-pronged approach. This includes *Agrobacterium*-mediated overexpression in the non-host *Nicotiana benthamiana* and the using the BSMV-VOX system to overexpress candidates in the wheat host in combination with *Fusarium* inoculations. Different types of plant responses to *Fusarium* effectors will be presented and discussed.

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THE NITROGEN ECONOMY OF RICE-PASTURE-LIVESTOCK SYSTEMS IN URUGUAY

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In Uruguay, rice rotates with perennial pastures for cattle production and country productivity has stabilised 8 Mg ha⁻¹ with the application of only 75-80 kg N ha⁻¹. It is believed that this rice-pasture rotation has allowed rice farmers to minimise the use of N through the preservation of soil quality. On average, about 100 kg grain per kg N added are obtained (Pittelkow et al. 2015), which at least doubles reported values for the major producer countries (Lahda et al. 2005). But although research efforts have sought to quantify the responses and efficiencies of N use in the rice crop, little is known about the N use efficiency (NUE) in the full rice-pasture-cattle system as well as the N dynamics through all the stages of the rotation. The aim of the study was to quantify the country-level Full Chain NUE (EU Nitrogen Expert Panel, 2015) and the N balance (inputs-outputs) of the rice-pasture-livestock system of Uruguay, based on an N budget approach. A national scale database for the last 16 years was constructed and analysed for this purpose. On average, main N inputs (123 kg ha⁻¹) for the rice system were fertilisers (55%) and direct animal deposition (38%), while for the livestock sector (13 kg ha⁻¹), 41, 46 and 13% corresponded with biological N fixation, atmospheric depositions and rice bran, respectively. Main output in the rice system was the N retained in the grain (86%). Of 11.5 kg ha⁻¹ as N livestock output, 78 and 14% corresponded with environmental losses and N in animal products, respectively. Full Chain NUE was 74, 12 and 23% for the rice, livestock and complete system respectively for the entire period. These values were higher (rice), and similar compared with international published information but with less N addition in both systems, possibly, because a high direct total N recycling (61%) in the entire chain.

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INFLUENCE OF SUPPLEMENT SOURCE (ORGANIC VS. INORGANIC) OF SELENIUM, COPPER, ZINC AND MANGANESE ON MICRONUTRIENT EXCRETION AND PARTITIONING BETWEEN URINE AND FAECES IN SHEEP

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In the framework of sustainable ruminant systems, grazed pasture and forage is the most important feed due to its low unit cost, widespread global availability, rumen and animal health benefits and reduced competition for human-edible feed (Lee et al., 2018). Being the major feed for ruminants in the UK (Wilkinson, 2011), forage plays a key role in ruminant nutrition and the quality of animal-products. However, frequently forages lack sufficient micro-minerals for ruminant requirements. To improve ruminant nutrition, direct mineral supplementation to the diet of ruminants is commonly adopted, with minerals often offered in excess of requirements.

The excessive minerals taken in by the animal, as well as endogenous waste, will be excreted mostly through urine and faeces (Lee et al., 2018; Minson, 1990). A previous study reported that the ratios of micronutrient concentrations in manure : dietary feed ranged from 1.4-6.5 in cattle (Sheppard and Sanipelli, 2012). Through their direct deposition by livestock and via application as fertilizers, manures become a major source of micronutrients in pasture systems (Kao et al., 2020). However, a survey at North Wyke Farm Platform (NWFP) reported an average concentration of 0.041, 30.0, 7.4 mg kg⁻¹ DM of selenium (Se), zinc (Zn) and copper (Cu), respectively, in forages which are lower than those required by sheep, of 0.2, 33, and 11 mg kg⁻¹ DM, respectively (Lee et al., 2018). This suggests that, apart from total micronutrient input, other factors, such as composition of manures, forage-soil interaction, and soil-climate interaction, might also have effects on forage micronutrient concentrations.

The aim of my PhD is to study the critical factors affecting micronutrients' flux and their availability to forages in pasture systems. We started from feeding sheep with silage supplemented with Se, Cu, Zn and Mn of different forms (inorganic versus organic) and of different supplementary levels under NRC (National Research Council, US) mineral supplementation regulation, and collecting separated urine and faeces for analysis. We hypothesize that the intake form and level of micronutrients influence their excretion and partitioning between urine and faeces by going through different metabolic routes in sheep, which in turn affects their availability to forages post manure application.

The results from the sheep experiment showed that both the supplementation level and the chemical form of mineral supplements had no significant impact on micronutrient partitioning between urine and faeces. Over 90% of the Cu, Zn and Mn intake were excreted via faeces, which is aligned with the literature. However, although there was no difference in Se partitioning across treatments in the current study, the literature suggests that Se partitioning between urine and faeces can be different when a higher dose is supplied (>0.4 mg-Se/day). The supplementary levels adopted in the current study are, however, both under the NRC regulated level (<0.23 mg-Se/day) which is the level that industry should follow.

The different amounts of Se and sulphur (S) excreted in faeces and urine after the supplementation, although not significantly different across treatments, result in significant higher ratios (w/w) of Se : S (mg) in faeces over urine (6.5-8.0 times higher). Se uptake by plants are known to be affected by the S input in soil from fertilisers or atmospheric deposition (Cartes et al., 2006; Fan et al., 2008), which may be due to the shared transporters between SO₄²⁻ and SeO₄²⁻ in plants or due to the acidity provided by the elemental S from fertilizers. Therefore, whether Se from different excreta sources (urine vs. faeces) can affect Se uptake by grass and Se movement in soil due to the sulphur effect will be studied together with other important factors, including different soil organic matter contents, different excreta sources and excreta from sheep fed with different forms of supplements.

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BENEFICIAL PREDATORS FOR INTEGRATED PEST MANAGEMENT - A GENOMICS APPROACH

KEYWAN HASSANI-PAK, CHRIS RAWLINGS, FADY MOHAREB, (BAYER & SYNGENTA)

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Pests such as aphids, thrips and whiteflies can devastate crops, hugely impacting yields. In order to tackle the global food shortage crisis, measures are needed to control these pest populations and increase yields. Beneficial predators (natural enemies of pest species) have a crucial role to play in this, however, with pests often being the focus of research, the genomic information currently available for beneficial predators is limited.

Integrated Pest Management (IPM) strategies aim to control pests in an effective and sustainable way. IPM methods include the use of beneficial predators, disrupting pest habitats, using pest resistant crop varieties and monitoring pest populations to ensure insecticides are only applied when necessary. IPM strategies aim to choose insecticides which minimise the harm to nontarget organisms, i.e. beneficial predators. However, beneficial predators often exhibit far lower insecticide resistance levels than pest species. This can result in beneficial predators being virtually eradicated following insecticide application, leaving the resistant pest population free to rapidly grow. To avoid this, it would be advantageous if we can understand the differing mechanisms for insecticide resistance in pests versus beneficial predators.

Previously there has been no genomic information available for many of the beneficial predator species being incorporated into IPM strategies. This project has therefore involved the sequencing, assembly and annotation of beneficial predator genomes including pirate bug (*Orius laevigatus*), green lacewing (*Chrysoperla carnea*), hoverfly (*Sphaerophoria rueppellii*) and a parasitoid wasp (*Microtonus brassicae*). These genomes are subsequently being used for comparative genomics analysis against their target pest genomes (which are already widely available). The focus is on genes involved in insecticide resistance, this includes detoxification genes such as cytochrome P450s, ABC transporters and Carboxylesterases, as well as genes involved in insecticide target-site resistance such as Acetylcholinesterases and Sodium channels.

The knowledge gained from this project should help us understand how insecticide resistance mechanisms differ between pests and beneficial predators and therefore aid in the selection of insecticides when developing effective future IPM strategies.

HAS PLANT BREEDING DECOUPLED BENEFICIAL PLANT-MICROBIOME INTERACTIONS IN WHEAT?

TESSA REID^{1,2}, IAN CLARK¹, MARK PAWLETT², JIM HARRIS² AND TIM MAUCLINE¹

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The development of dwarf wheat cultivars combined with high levels of agrochemical inputs during the green revolution resulted in high yielding cropping systems. However, changes in wheat cultivars were made without considering impacts on beneficial plant and soil microbe interactions.

This project aims to investigate whether plant-microbiome co-evolution in wheat has been hindered by domestication, by assessing both genotypic and treatment effects through experimental work. This will be achieved by using both culture -independent (Illumina sequencing of total rhizobacterial DNA) and -dependent methods (isolation using growth media and functional bioassays).

To date, we have shown that nitrogen-potassium-phosphorous (NPK) fertilizer addition decreased the proportion of beneficial bacteria isolated from rhizocompartments in a commercial wheat variety (Cadenza). Additionally, microbial community analysis revealed significant differences in community composition between treatments (non-fertilized vs fertilized) and between plant genetic groups (diploid, tetraploid and hexaploid wheat varieties). Furthermore, a range of wheat hormone signalling mutants have been selected to test whether the introduction of semidwarfing genes, which confer dwarfism through decreased responsiveness to the phytohormone gibberellin, may have reduced selection for beneficial rhizobacteria in wheat.

Together, these findings increase our understanding of the importance of microbial soil health and wheat cultivar in shaping the root microbiome and this knowledge will facilitate the exploitation of plant-microbe interactions for the development of novel microbial inoculants.

A LOSS FUNCTION APPROACH TO SOIL SENSING

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Advances in sensor technology and agricultural equipment should enable farmers to improve the precision management of nutrients, water and adjust crop density appropriately, but the decision of when to use what sensor is still ad hoc. Uncertainty of predictions change amongst other things as a function of sampling, calibration and the decision which sensors are deployed. The aim of this project is to quantify the effect of sampling and sensor configuration on the estimates of soil properties that are important for agronomic production.

To investigate this, we considered four case study fields in the Cambridgeshire fens (UK) that were planted with lettuce. We sampled at 697 locations across the fields and made visible near-infrared, mid-infrared and X-ray fluorescence spectral measurements. A subset of the soil samples was analysed for C, N, Mg, P, S, Ca, K, pH, and their particle size fractions.

First, we assessed different modelling approaches to predict crop data to evaluate soil spectra for crop management decisions. Secondly, we contrasted model prediction errors from spectra taken under different sample conditions and spectra from a wider geographical range. Third, we mapped the variation in each soil property and the associated uncertainty by kriging. Fourth, we use our findings to formulate loss functions to quantify the effect of management decisions that are based on uncertain information.



**ROTHAMSTED
RESEARCH**

Poster Session

Claire Kanja
Jesus Castillo
Mandy Kao



**ROTHAMSTED
RESEARCH**

Session Four
Tuesday, 23rd
February
2021

Chaired by Tania Chancellor

SOIL SPECTROSCOPY AND CROP MODELLING FOR PRECISE FERTILIZER APPLICATION

¹TADESSE GASHAW ASRAT, ¹DR RUBEN SAKRABANI, ¹PROF RON CORSTANJE, ²PROF FASSIL KEBEDE, ³DR STEPHAN M. HAEFELE, ³DR KIRSTY HASSALL

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Fine resolution soil information is a necessary basis for precision agriculture. This can be achieved with qualitative and quantitative determination of spatial and temporal variability of soil properties. However, chemical testing of soils has shortcomings such as costs and timing, limiting the feasible number of sampling points. In addition, results of different laboratories are often difficult to compare due to the wide array of different methods employed worldwide. An alternative option is to develop novel, non-destructive, low cost and rapid spectral sensing methods. Promising spectral sensing techniques in predicting soil variables include visible and near-infrared (vis-NIR), mid-infrared (MIR) and x-ray fluorescence (XRF). The comparison between spectral analysis and conventional chemical testing methods will confirm the validity of the former technique which is quicker and easier to deploy in field conditions. Once the validity of the spectra calibration is established, the respective nutrient values can be incorporated into suitable crop models that can predict crop requirements (e.g. QUEFTS model) and thus predict fertilizer rates to meet crop demand. There could also be an opportunity to directly relate soil spectral measurements to crop requirements/traits. However, proper calibration remains an essential component, together with the estimation of nutrient availability, crop response and knowledge of the scale-dependent spectra interpretation. Spectral sensors give best results if locally calibrated using wet chemistry analysis. This restricts their use as it adds cost and complexity but can be addressed by developing soil spectral libraries covering a wide variety of spectra from which the bests are then selected for calibration based on suitable statistical models. The effect of soil and environmental conditions on in-situ spectral measurements is another challenge.

Hence, this project is devised to achieve four objectives: (1) to apply and test dry spectral methods to identify crop available nutrients economically and quickly; (2) to develop models that use dry spectral soil (and plant) data to determine fertilizer recommendations; (3) to evaluate handheld vis-NIR tool for in-field soil analysis and determine the most reliable characteristics that can be determined; and (4) to develop an analytical framework for the best use of spectral libraries for prediction of soil variables at a range of scales. The project will generate primary data from diverse soils and environments in Morocco through 1) controlled on-station experimentation on NPK fertilization, 2) on-farm wheat production assessment and use of hand-held vis-NIR to capture wider soil/environmental variations and 3) pot experimentation using identified soils to determine specific rates for macro and micronutrients in greenhouse facilities. The test crop will be wheat, which is the dominant cereal crop being grown in Morocco. Other environmental and auxiliary datasets will be obtained from different institutions and online sources which will be processed to fit the research domain and coverage. The outputs of the project will be integration of spectral sensing techniques into fertilizer decision tools and development of frameworks for utilizing the soil spectral libraries.

Keywords: Spectral sensing technique, spectral library, framework

UNMASKING A CEREAL KILLER: WHAT TRIGGERS 3LYSM EFFECTOR EXPRESSION IN A FUNGAL WHEAT PATHOGEN?

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

An effector protein essential for *Z. tritici* virulence on wheat, Zt3LysM, may be useful in developing future control strategies. Zt3LysM sequesters chitin fragments, preventing their recognition by wheat immune receptors and 'masking' the pathogen. Little is known about how *Zt3LysM* expression is controlled. This project aims to investigate what triggers the expression of *Zt3LysM* and how this is regulated.

Preliminary experiments were conducted *in planta* and *in vitro* using *Z. tritici* strains expressing GFP under the control of the *Zt3LysM* promoter. We found GFP expression was affected by nutrient source (nutrient-rich, nutrient-poor or plant-derived) and changed temporally during wheat leaf infection. GFP intensity was also affected by *Zt3LysM* promoter length, adding evidence for the existence of an upstream regulatory sequence. Future work will verify these observations, and use a yeast one-hybrid approach to identify proteins involved in Zt3LysM regulation.

An understanding of how Zt3LysM expression is controlled could lead to new disease management strategies blocking the secretion of this important effector. This would allow wheat to mount a full immune response to *Z. tritici*, preventing Septoria Leaf Blotch disease and associated yield losses.

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TECHNICAL AND PRACTICAL INNOVATIONS TO REDUCE SOIL AND WATER LOSSES BY IMPROVING SOIL PHYSICAL PROPERTIES

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Soil erosion is one of the most serious environmental problems in the world in general and in North Africa in particular where soil losses are the highest among selected countries worldwide. In Morocco, erosion is a serious agro-environmental threat, considered as major constraint to plant and crop productivity, because it removes the fertile part of the soils and reduces the effective depth to be exploited by plant roots. Erosion affects over 40 percent of the territory and causes around 100 million tonnes yr⁻¹ of soil loss and a decrease in the capacity of reservoirs, caused by sedimentation estimated at 75 million m³ yr⁻¹. Soil erosion is a result of a combination of natural and anthropogenic factors such as the slope of the land, increased population putting pressure on limited land resources by removing vegetation which makes the topsoil vulnerable to wind and flowing water, leading to soil erosion. Inappropriate land management, mainly intensive tillage practices also disturbs and exposes bare soil, making it prone to degradation. These factors enhance the erodibility of the soil as well as the erosivity of the eroding agents such as rainfall and wind.

Soil erosion is a three-phase process consisting of the detachment, transport and deposition of individual soil particles and small aggregates from the soil mass by erosive agents such as water and wind. In most studies, water and wind erosion have been studied separately. Thus, one of the contributions to knowledge of the current project is to understand the simultaneous interactions between wind and water (especially their kinetic energies available for erosion) and their effect on arable soil erosion rates. This will require use of a combined wind tunnel and rainfall simulation facility that will simulate, in a laboratory-based experiments, combinations of variable wind speeds and rainfall intensities over different durations that reflect current and future conditions, using predicted climate change scenarios.

The reduction of soil degradation caused by erosion needs the application of strategies for soil and water conservation which include covering the soil to protect it from raindrop impact; increasing the infiltration capacity of the soil to reduce runoff; improving the aggregate stability of the soil; and increasing surface roughness to reduce the velocity of runoff and wind. Moreover, the role of crops and notably roots to improve soil physical conditions and reduce erosion will be explored in the laboratory. Field trials will be conducted to test selected soil / crop / water scenarios for local conditions, considering existing agronomic practices, local climate and soil conditions.

The laboratory-based experiments, along with the field experiments will help understanding the erosion processes and the techniques to help solve the problem by improving both environmental protection through improved soil structure and reduced soil erosion, and crop yield with securing an economic return to farmers, which will then contribute to sustainable agriculture.

Keywords: Water erosion, wind erosion, soil physical properties, roots traits

IDENTIFICATION OF NOVEL QTLS AND GENES FOR HIGH FIBRE IN WHEAT LANDRACES

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Wheat is one of the most important food crops in the world and as well as providing calories it is also an important source of dietary fibre in our diets. Wheat provides up to 20% of our dietary fibre (DF) intake. Including fibre in our diets has been shown to help manage chronic diseases such as type II diabetes, cardiovascular disease, obesity and some types of cancer. Despite this, only around 20% of people eat the recommended level (30g/day) of DF every day. This deficit has been termed the 'Fibre Gap'.

Refined wheat products are particularly popular in the western diet, though these are typically deficient in fibre when compared to the wholemeal alternatives. Between 60-70% of the bread bought in the UK is white, which likely contributes to the fibre gap. Since wheat- and bread- are staple foods, increasing the DF content of wheat, particularly in the endosperm tissues from which white flour is produced, is an attractive target to improve human health.

Arabinoxylan (AX) is the major cell wall component that makes up 70% of the Non-Starch Polysaccharides in wheat endosperm. The pathway for AX synthesis is well known. However, the control of its synthesis is not fully understood. QTLs for high AX have been identified in a Chinese wheat cultivar, Yumai-34, and crosses made with it. However, it is clear that other sources of variation in AX content exist.

My project aims to discover more QTLs in the Watkins landrace collection of wheat, some of which have been shown to have AX levels as high or higher than Yumai-34. Using 5 mapping populations, grown in field trials for 3 successive years I hope to identify novel QTLs for use in future

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**PLANT-BASED VACCINES FOR PREVENTION OF POULTRY VIRAL DISEASES:
NEWCASTLE DISEASE**

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²BIOINTERACTIONS AND CROP PROTECTION, ROTHAMSTED RESEARCH, HARPENDEN, UNITED KINGDOM

The development of plant virus-based transient expression systems has enabled the production of complex polypeptides in plants. The system provides a robust tool to generate a high yield of recombinant proteins with superior speed while managing to achieve cost-efficient production. Thereby, the system is amenable for responding to emerging infectious diseases, including Newcastle disease (ND). ND has been a constant threat for domestically reared birds. ND affects economic livelihoods by causing major severe losses in poultry industries and poses a risk to global food security. The current prevention of Newcastle disease virus (NDV) infections is based on live-attenuated and inactive vaccines. The commercialised live-attenuated vaccine has been used for almost 60 years but elicits several drawbacks. The live-attenuated vaccine is known to be genetically unstable and can revert to virulence. The live-attenuated vaccine may undergo recombination with wild strains generating new variants of viruses and another outbreak. Moreover, the inactive vaccine is reported to only show mild immunological protection against some field viruses. Several studies suggested Virus-Like Particle (VLP) as a vaccine candidate. VLPs are known to induce strong humoral and cellular immune responses. This study demonstrates the development of VLPs as a vaccine candidate against NDV infections. Here NDV VLP will be assembled from F (fusion), HN (haemagglutinin-neuraminidase), and M (matrix) proteins originated from velogenic ZJ1 strain. The NDV VLP will be transiently expressed and produced in *Nicotiana benthamiana* using pEAQ-HT “hypertranslational” expression vector. Following the transient expression in *N. benthamiana*, the downstream cellular trafficking of protein, protein isolation, purification, and biochemical characterisations will also be conducted in order to ensure the production of stable and correctly folding NDV VLP.

Keywords: newcastle disease virus, plant-based vaccines, transient, virus-like particles

REDEFINING KEY PERFORMANCE INDICATORS FOR LIVESTOCK PRODUCTION SYSTEMS: WHAT IS THE VALUE OF INFORMATION

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The use of key performance indicators (KPIs) to assist on-farm decision making has long been seen as a promising strategy to improve operational efficiency (Franks and Collis, 2003). The potential benefit of KPIs, however, is heavily dependent on the economic relevance of metrics used (Fleming et al., 2006), and therefore an overabundance of ambiguously defined KPIs in the livestock industry has disincentivised many farmers to collect information beyond a minimum requirement. Using high-resolution sheep production data from the North Wyke Farm Platform, a system-scale grazing trial in southwest United Kingdom (Orr et al., 2019), this study proposes a novel framework to quantify the information values of industry recommended KPIs, with the higher level objectives of ranking them according to their usefulness and then compiling a list of variables to measure and not to measure. The results demonstrated a substantial financial benefit associated with a careful selection of metrics, with top-ranked variables exhibiting up to 3.5 times the information value of those randomly chosen. When individual metrics were used in isolation, ewe weight at lambing had the greatest ability to predict the subsequent lamb value at slaughter, surpassing all mid-season measures of the lamb's own performance. When information from multiple metrics was combined to inform on-farm decisions, the peak benefit was observed under four metrics, with inclusion of variables beyond this point shown to be detrimental to farm profitability regardless of the combination selected. The developed framework is readily extendable to other livestock species, and with minimal modifications to arable and mixed agriculture as well.

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HOW DOES THE EXPRESSION OF THREE TOLL-PATHWAY IMMUNE RESPONSE GENES CHANGE FOLLOWING FLIGHT IN FALL ARMYWORM (SPODOPTERA FRUGIPERDA) CHALLENGED WITH SFMNPV?

AMY WITHERS, AISLINN PEARSON, PHILIP DONKERSLEY, CHRIS M. JONES, KEN WILSON

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The fall armyworm (*Spodoptera frugiperda*) is a highly invasive crop pest, it is native to the Americas and has spread throughout Africa, Asia and Australasia. One mechanism driving this rapid spread is its ability to undergo long distance flights. Due to the presence of *Spodoptera frugiperda* nucleopolyhedrovirus (SfMNPV) naturally, and the potential for it to be sprayed as biocontrol, this work aimed to determine how SfMNPV changes expression of the Toll-pathway immune response following flight. Adult FAW were flown experimentally on a tethered flight mill system, RNA was extracted and qPCR used to determine gene expression changes in three Toll-pathway genes (cactus, defensin and MYD88) following experiments to determine suitable reference genes. There were differences in Toll-pathway response to SfMNPV between the sexes. Males had higher baseline expression of the Toll-pathway genes that decreased following flight, whereas females had lower baseline expression of the genes and increased expression following flight. This differential investment in immunity was visible in flight behaviour, with females flying longer distances than males. This study provides a novel insight into how FAW males and females change Toll-pathway expression differently in response to SfMNPV and flight, and that these differences in expression are reflected in flight behaviour.

EXPLOITING MYCORRHIZAL SELECTION OF BENEFICIAL RHIZOSPHERE BACTERIA FROM THE SOIL MICROBIOME

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Novel and optimised alternatives to artificial fertilisers, which can be deleterious to the environment, are required to achieve sustainable intensification of agriculture. Plant growth promoting microbes found at the root-soil interface – part of the root microbiome – have an underexploited arsenal of capabilities that can improve plant health, growth and nutrient status. The network of interactions between microbial partners and the host plant is complex and not well understood. Many different bacterial groups are associated with plant health, but the major beneficial plant-fungal interaction is with arbuscular mycorrhizal fungi (AMF), which boosts plant growth by extending root systems and supplying nutrients, especially P. An important, but poorly understood aspect of AMF is their interaction with other microbes in the mycorrhizosphere. We propose that AMF are an important conduit, bridging soil pores and facilitating plant-beneficial bacteria to gain access to roots, either on hyphal surfaces or within hyphae. Manipulative experiments and amplicon sequencing have been used to study the impact of mycorrhizal influence on rhizosphere communities. Split root microcosm pot experiments were used to reveal the long-distance transport of bacteria via fungal hyphae through soil to access plant roots. This project aims to better understand the tri-trophic interactions between exemplar host-plants, AMF, the wider soil microbiome, soil fertility and physical structure.



**ROTHAMSTED
RESEARCH**

Poster Session

Tadesse Gashaw Asrat
Luca Steel
Sophia Bahddou
James Brett
Ika Nurzijah



**ROTHAMSTED
RESEARCH**

Session Five
Wednesday,
24th February
2021

Chaired by Hannah McGrath

NOVEL BRASSINOSTEROID DWARFING GENES AS ALTERNATIVES FOR IMPROVING WHEAT GRAIN YIELDS

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Wheat is one of the leading cereals which is grown and consumed globally. Due to changing climate and increasing human population it is predicted that wheat yields will need to increase by 60% by 2050. Overwhelming evidence suggests that during grain filling wheat yield potential is sink-limited, as carbon accumulation is limited by the storage capacity of the grains. Therefore, strategies to improve grain number are one of the most important avenues in the genetic improvement of yield potential. During the last 50 years, the Rht-1 dwarfing alleles have been essential for increasing grain yields and providing lodging resistance in most wheat varieties. However, under some growing conditions Rht-1 alleles are suboptimal and can confer a yield penalty. Brassinosteroids (BRs) are phytohormones that also have an important role controlling architecture and assimilate partitioning. It is well established that lesions in the BR signalling pathway can produce beneficial traits in cereals. For example, the barley Uzu1 dwarfing alleles, containing lesions in the BR receptor (BRI1), have been widely used in breeding programs in Asia. In addition, partial suppression of the OsBRI1 gene in transgenic rice confers a beneficial erect-leaf phenotype that could provide an estimated 30% increase in grain yields. In barley, other BR signalling components, including the biosynthetic gene HvDIM, have also been demonstrated as targets for developing dwarfing alleles. This project aims to target the BR signalling pathway to develop new alleles that can increase the genetic yield potential in wheat. We have identified wheat orthologues of BRI1 and DIM, and homoeologous loss-of-function mutations have been identified by TILLING. The homoeologous alleles have been stacked and the tabri1 triple mutant demonstrated to exhibit a severe-dwarf phenotype. In contrast, the tadim triple mutant has a semi-dwarf and erect-leaf phenotype. As an alternative strategy for generating new BR alleles, we are performing a targeted forward genetics-based screen to identify tabri mutants that display an erect-leaf phenotype.

SMART DETECTION OF AIRBORNE DISEASES IN TOMATO PRODUCTION

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3. APS GROUP, ISLE OF WIGHT

Currently, there is no method that allows growers to monitor the presence of inoculum in glasshouses thereby limiting their ability to manage the application of crop protection products. The current methods used for identifying plant infections rely on inoculum collected from already infected plant tissue, therefore, they are only good for characterizing the infection present. However, precise methods for inoculum detection, such as loop-mediated isothermal amplification (LAMP) assays, can be coupled with spore traps to monitor the increase of inoculum in the glasshouse real-time. Such warning systems will allow growers to move from prophylactic spraying and apply crop protection products only when necessary. Therefore, this work focuses on identifying the limitations of different spore-trapping methods in industrial tomato glasshouses and addresses the efficiency of it being used with a LAMP assay and quantitative polymerase chain reaction assays (qPCR). The infection model used for this project is *pseudoidium neolycopersici*, the widest spread tomato powdery mildew in UK glasshouses.

TRANSCRIPTOMIC DATA AND SL-DEFICIENT MUTANT TO PROVIDE NEW INSIGHTS INTO TILLERING CONTROL IN RESPONSE TO NITROGEN SUPPLY

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Nutrient limitation is one of the main factors affecting plant growth and development. The main responses of plants to nutrient-deficient conditions includes changes in root and shoot architecture. Above ground plant architecture is highly influenced by changing tillering patterns. To facilitate this response long-distance root to shoot signals coordinate plant growth at the whole-plant level. In most cases, phytohormones are this signal. Tillering is known to be regulated by the interaction between 3 classes of phytohormones, auxin, cytokinin and strigolactones (SLs). How those hormones coordinate tiller suppression under nutrient limiting conditions is not well-understood. Our initial experiments showed that SL production is upregulated soon after N limitation in wheat roots and basal nodes, as indicated by the gene expression analysis of most of the SL biosynthetic genes. Combination of new transcriptomic and phytohormonal data provides new insights into the low nutrient-induced regulation of tillering. Low N triggered many changes in the phytohormone profile of different tissues, particularly in the basal nodes. RNA-seq also revealed that N limitation altered gene expression of more than 6000 genes involved in important signalling and metabolic pathways, locally in basal nodes. Moreover, to study further the role of SLs in controlling wheat architecture, the generation and characterization of an SL-deficient mutant was necessary. For this purpose, mutant lines from the hexaploid wheat TILLING population containing nonsense mutations in the three TaCCD7/D17 homoeologues were identified and stacked. After several rounds of crossing, a triple homozygous d17 knock-out mutant has been identified. The performance of the d17 mutant will be assessed in field trials next season, while after backcrossing it will be used for more dedicated functional studies.

CHARACTERISATION OF MAJOR GENES MEDIATING RESISTANCE TO SEPTORIA TRITICI BLOTCH DISEASE IN WHEAT.

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The fungus *Zymoseptoria tritici* is one of the most destructive wheat (*Triticum aestivum*) pathogens in Europe and worldwide, causing crop losses of up to 50% in high risk climates (Goodwin, 2007). Traditionally this disease has been controlled with widely used resistance genes and fungicides, but the high selection pressures placed on the fungi create a serious risk of these protections being overcome, particularly when heavily relied upon. Some major resistances have already been widely broken – for example, the *Stb6* resistance gene present in most European wheat cultivars is now ineffective against many *Septoria* strains in the field.

It is therefore important that new, more diverse sources of resistance be identified and utilised in elite wheat lines. These will allow us to prepare for the breaking of currently common resistances but may also extend their lifetimes – Chartrain et al. (2004) found that many wheat lines with highly durable *Septoria* resistance contain multiple resistance (*Stb*) genes, suggesting that gene pyramiding may be a viable method for enhancing the longevity of resistances in this pathosystem.

The research described here involves screening known *Stb* genes against an array of recent *Septoria* field isolates, to identify resistances still effective in the field and potentially interesting combinations of resistances that could provide protection against most or all isolates tested. KASP markers are then tested against interesting resistances to facilitate fine mapping of their locations and enable breeders to more easily integrate them into elite lines.

In light of the recent identification of the *Stb6* gene as a wall-associated receptor-like kinase (WAK) (Saintenac et al., 2018), candidate *Stb* genes identified by us and other collaborators are being investigated using Virus-Induced Gene Silencing to identify individual resistance genes, potentially providing perfect genetic markers and helping to establish the mechanisms through which these resistances function.

NEW HEROES TO DEFEAT CABBAGE STEM FLEA BEETLE (*PSYLLIODES CHRYSOCEPHALA*)

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The cabbage stem flea beetle (CSFB; *Psylliodes chrysocephala*), is a major pest of oilseed rape (OSR) in Europe¹. CSFB adults and larvae feed on the plant during autumn and winter, affecting crop establishment and plant vigour; often resulting in plant death, reductions in yield or, if the pest pressure is high, total crop failure. Since the neonicotinoid seed treatment ban in 2013, growers have been relying exclusively on one class of insecticides (pyrethroids) to control adult CSFB. However, it has been increasingly evident that the efficacy of these insecticides is declining due to a sharp increase in the extent and severity of insecticide resistance in CSFB populations across UK. As a result, there has been a 27.5% decrease in the area of OSR grown in the UK since 2013^{2, 3}.

Growing OSR in this scenario is challenging and requires new management practices to reduce crop damage and keep insecticide resistance at low frequency. The aim of this project is to better understand the ecology of CSFB and develop integrated pest management techniques, in particular the role of beneficial parasitic insects in CSFB mortality. This project involves monitoring the migration and daily activity of CSFB in the field, modelling climate and agricultural management impacts on the spatio-temporal changes in CSFB populations and assessing the potential of the parasitic wasp *Microctonus brassicae* as a biocontrol agent for CSFB.

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PROVIDING SATELLITE-BASED SOIL AND CROP PRODUCTIVITY INDICATORS TO DISPLAY METEOROLOGICAL, PEDOLOGICAL AND FARM MANAGEMENT EFFECTS

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High-frequency earth observation (EO) data have been shown to be an effective means for identifying crops and monitoring their development. For regions clouded over, like the UK, the use of Synthetic Aperture Radar (SAR) is particularly interesting to explore how these EO data can support precision farming decisions, by recording land surface variables over large areas with reasonable spatial resolution.

In my PhD Thesis we test the hypothesis that the parameters of the dynamic SAR time series during the vegetation are indicators for the performance at the end of the season (yield). The quantitative analysis was developed for winter wheat grown on Rothamsted Research farm during 2017 to 2019 and then upscaled to other farms across the UK. Average SAR backscatter from Sentinel-1 satellites were extracted for each field and a novel robust temporal analysis of the signal was developed. The calculation of the different curve parameters during the whole vegetation involved the fitting of two sigmoid curves (growth and senescence) of the SAR backscatter ratio (VH/VV). These defined Crop Productivity Indicators (CPIs) were used to relate field-specific satellite information to yield data.

The study confirmed the opportunities that lie in these high frequency SAR backscatter data in terms of quantifying crop phenological development, growth, and yield formation. The results show that the day of the year of the maximum VH/VV value was negatively correlated with yield ($r = -0.56$), and the duration of “full” vegetation was positively correlated with yield ($r = 0.61$). It will be shown how these indicators of crop performance vary in dependence of soil and meteorological conditions, and whether they are sensitive to distinguish crop productivity within and across a range of arable and mixed agricultural systems.

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SPOTTING THE DIFFERENCE: A MUTAGENOMIC DISSECTION OF VIRULENCE AND AVIRULENCE IN *ZYMOSEPTORIA TRITICI*

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Zymoseptoria tritici (previously *Mycosphaerella graminicola*) is the causal agent of Septoria tritici leaf blotch (STB), an economically important disease that significantly reduces wheat (*Triticum aestivum*) yields. Depending on nutrient availability, and temperature, *Z. tritici* can grow *in vitro* and switch between a “yeast-like” budding form or a hyphal form. The ability of this pleomorphic fungus to grow *in vitro* in a yeast-like form is unusual for filamentous fungi and enables functional genomics studies aimed at the isolation of morphogenic switching genes, which are known to contribute to fungal virulence (King *et al.*, 2017). The ability to rapidly generate strain libraries and the compact nature of its fully sequenced haploid genome (~37Mb) aids mutation discovery.

This project aimed to identify non-pathogenic *Z. tritici* in a library of 240 *HindIII* restriction enzyme-mediated integration (REMI) mutants and a random *Agrobacterium*-mediated T-DNA mutagenesis library using both *in planta* and *in vitro* screening. The development of rapid, reliable and cheaper sequencing technologies enabled easier identification of the genes affected in the mutant isolates sent for whole-genome re-sequencing. Comparison of these mutants to their respective assembled ‘parental’ *Z. tritici* genomes identified sites of interruptions and variation that was not directly associated with an integration event. Attempts to validate candidate genes were made through either independent, targeted knockout or restoring function through complementation. From a total of 21 shortlisted candidates, three have shown a reduced virulence phenotype *in planta* and restored hyphal growth in *in vitro* tests.

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**ROTHAMSTED
RESEARCH**

Poster Session

Manpartik Gill
Anastasia Sokolidi
Petros Sigalas
Henry Tidd



**ROTHAMSTED
RESEARCH**

Session Six
Wednesday,
24th February
2021

Chaired by Joe Oddy

THE WHY OF SOIL MEASUREMENT

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Soil science has historically partitioned soil into chemical, physical and biological components. Such reductionism has resulted in an abundance of observations, but no unifying theory to explain them. The myriad of processes occurring in soil do not fit neatly into these compartments. Soil processes are hierarchal, occurring at different scales and time periods. A systems approach based on theory is a necessary step to develop a measurement that integrates across this hierarchy.

Soil structure is the direct result of processes that occur between the physical, biological and land management. The extent and the connectivity of porosity control functions that are directly related to soil health such as water storage, nutrient transport, microbial habitats, gas exchange and wider ecosystem services.

X-ray computed tomography has shown that soil under different management develops different amounts of connected porosity at scales relevant to microbial activity. Soils with higher carbon inputs have a greater amount of connected porosity. The generation of this porosity is driven by soil microbes.

We have attempted to find practical, affordable methods that farmers can use to measure the micro connected porosity to track the temporal changes in their soil and to be used as a guide to understanding optimum carbon inputs.

SOIL HEALTH METRICS FOR SUSTAINABLE AGRICULTURAL SYSTEMS

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Soil is the foundation of all agricultural systems. It is a complex biophysical system of aggregated particles and pore networks that, if managed carefully, provides plants with the medium for roots to extract nutrients to produce food. In addition to agricultural production, soils provide other important functions often referred to as ecosystem services. Soils can store and transmit water, they can buffer pollutants and contaminants, store carbon, and they can support biodiversity. The ability of the soil to carry out these functions is commonly referred to as 'soil health'.

Several approaches to quantify soil health now exist, but there is no agreed standard. Variation of soil in time and space is a particular problem when trying to derive a set of meaningful metrics. The overall aim of my PhD project is to develop soil metrics that can be used to quantify and monitor soil health, as related to agricultural production and ecosystem services. This is especially important in the light of food security and climate change.

AGRICULTURAL BIOPRODUCTS FROM MEDICINAL AND AROMATIC PLANTS

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Africa has the fastest growing population in the world, and this has put a strain on its agricultural sector to produce more food. There has consequently been heavy reliance on synthetic fertilisers and pesticides to increase yields and to protect crops against pests and pathogens respectively. However, there is now more advocacy for the use of natural and more sustainable options to these synthetics [1].

Biostimulants and Bioprotectants (Bioproducts) have gained appreciable recognition over the past few decades as ecologically friendly and sustainable alternatives derived from natural sources [2]. Secondary metabolites from plants are major sources of these bioproducts, and medicinal and aromatic plants (MAPs) contain a diverse array of such compounds. MAPs are abundant in arid areas of Morocco and are suspected to have high proportions of secondary metabolites given that many of these compounds are produced in plants as a defence response to the drought stress. However, most of these plants have largely not been assessed for their bioactive potential. This project seeks to develop novel biostimulant and bioprotectant compounds and formulations from these plants growing in arid areas of Morocco for use in African agriculture.

Fifteen MAPs sourced from Morocco were selected and their extracts have been screened using NMR spectroscopy and Liquid Chromatography-Mass Spectrometry (LC-MS). Less polar components will be analysed with Gas Chromatography-Mass Spectrometry (GC-MS) later in the project. The data from the initial metabolite screening is being analysed to identify the component compounds with an aim of identifying novel molecules. Among these plants, the medicinal plant *Acacia gummifera* has been characterised for the first time. Crude plant extracts as well as purified compounds from each plant will be trialled in biostimulant and bioprotectant assays. Formulations that consist of mixtures of compounds and extracts from different plants will also be considered. In biostimulant assays, extracts and purified compounds will be applied to seeds by soaking, or to plants by foliar or soil drench application, and their effect on stimulation of physiological growth parameters will be assessed. In bioprotectant assays, the extracts and purified compounds will be tested for their effect on fungal strains relevant to Moroccan crops as well as on cochineal beetles on cactus plants.

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AN INNOVATION ECOSYSTEM APPROACH TO THE AGRICULTURAL SECTOR – EXPLORING INNOVATION AND CO-CREATION OF VALUE IN THE CONTEXT OF UK ECOSYSTEM

PAUL ROUS

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Agriculture is the oldest industry in the world and has innovated throughout history to meet the growing needs of an ever-increasing world population. Challenges such as sustainability, policy changes, increased urbanisation, and resource constraints, continue to drive the need to build ecosystems to deliver value and meaningful change within the sector. An Innovation Ecosystem approach requires multiple actors, stakeholders, activities, institutions and governments to deliver a networked approach to innovation across sectors to engage wide innovation led systems thinking. Agricultural Innovation Systems, on the other hand, tends to apply to specific country, sector or technology. Whilst the UK's technology ecosystem is recognised as being a world leader and has developed globally recognised clusters such as "Silicon Roundabout" and the "Golden Triangle", the agricultural sector seems to have been bypassed. This project aims to introduce the concept of an Agricultural Innovation Ecosystem and critically assess the UK against existing models globally.

TECHNICAL AND PRACTICAL INNOVATIONS TO REDUCE SOIL AND WATER LOSSES BY IMPROVING SOIL PHYSICAL PROPERTIES

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Rice (*Oryza sativa*) serves as a staple for more than half of the global population which makes it an important food security crop world-wide. Due to rising labour costs, water scarcity and convenience, many farmers in sub-tropical and tropical regions are adopting direct seeded rice (DSR) over the traditional method of transplanting. However, a major bottleneck to the widespread adoption of DSR is poor germination and seedling establishment especially in flood prone areas. This is because most elite rice varieties germinate poorly under flooding (sensitive to anaerobic germination; AG). Apart from genetics which is the main factor for AG tolerance, pre-sowing practices such as seed priming and pre-soaking have been identified to increase tolerance in some rice cultivars and other plant species such as Arabidopsis.

The effects of different imbibition conditions (imbibing seeds in a small volume of water and imbibing seeds on Petri dishes) on seedling emergence and survival were tested for two rice cultivars: Ma Zhan (AG tolerant) and IR64 (AG sensitive). Seed imbibition resulted in significantly increased emergence percentage, higher emergence rate and higher survival percentage in both cultivars, regardless of the imbibition condition tested compared to non-imbibed seeds. Survival percentage was higher in Ma Zhan seeds imbibed in small volume of water compared to those imbibed on Petri dishes, however this was not statistically significant. Conversely, IR 64 seeds imbibed on Petri dish recorded higher survival percentage compared to those imbibed in small volume of water, however this was not statistically significant. This study forms part of a base line investigation to determine whether the increase in AG tolerance after pre-soaking before planting is as a result of ethylene priming.

EXPLOITATION OF BENEFICIAL ROOT-ASSOCIATED BACTERIA IN GRAIN CEREAL-BASED CROPPING SYSTEMS

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1, ROTHAMSTED RESEARCH, HARPENDEN. 2, CRANFIELD UNIVERSITY. 3, MOHAMMED VI POLYTECHNIC UNIVERSITY

The plant microbiome plays an important role in plant growth, development, and soil health. The plant growth-promoting rhizobacteria (PGPR) are becoming a promising tool for sustainable agriculture through enhanced nutrient provision (e.g. P and K solubilization), abiotic stress tolerance (e.g. drought, high salinity), manipulation of plant hormone signalling, as well as disease suppression of foliar and root pathogens. This work aims to identify what contribution the plant microbiome can make to enhance wheat growth under a variety of abiotic stress conditions. To analyse the plant microbiome both culture independent and dependent methods will be adopted. The culture independent approach will involve next generation amplicon sequencing to assess the total microbiome. This will be done with 16S rRNA gene and Internal transcribed spacer (ITS) based primers. The culture dependent approach will involve the isolation of microbes from the root systems of plants from the experiments. These will then be functionally screened through a suite of assays for nutrient solubilization (N, P, K, Zn, Fe solubilisation), drought, heat and salt tolerance. The microbial isolates will be identified by a 16S Sanger sequencing approach.

A GAIN-OF-FUNCTION ALLELE OF *CRK10* CAUSES COLLAPSED XYLEM VESSELS AND ENHANCED RESISTANCE TO A ROOT-INFECTING VASCULAR PATHOGEN IN ARABIDOPSIS

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1, ROTHAMSTED RESEARCH, HARPENDEN. 2, UNIVERSITY OF EXETER, EXETER.

Receptor-like kinases (RLKs) comprise a large superfamily of proteins in plant genomes, and play essential roles in plant growth, development and response to biotic and abiotic stresses. Cysteine-rich receptor-like kinases (CRKs) are one of the largest subfamilies of RLKs with over 40 members in *Arabidopsis thaliana*, and although the biological role of some CRKs have been characterised, the function of many members of this family remains elusive. Here we report the characterisation of an EMS-generated mutant of the cysteine-rich receptor-like kinase 10 (*CRK10*), which contains an amino acid substitution in subdomain III of the kinase domain of the protein replacing an alanine for a threonine residue. The *CRK10* mutant is a dwarf due to the presence of collapsed xylem vessels in the roots and hypocotyl, although the vasculature of the stem develops normally. Reporter lines showed *CRK10* expression in vascular tissues in roots, hypocotyls, cotyledons and petioles, and a translational fusion with the fluorescent protein mCherry confirmed the receptor is a plasma membrane-bound protein. Analysis of the recombinant kinase domain of *CRK10* revealed that both the WT and mutant versions of the protein are active kinases capable of auto-phosphorylation, however, the mutant kinase showed hyperactivity as it displayed isoforms with increased phosphorylation levels. Moreover, liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis determined that the threonine introduced in the *CRK10* mutant kinase domain is an additional phosphorylation site, which led us to conclude this is a gain-of-function allele of *CRK10*. Furthermore, an RNA-seq experiment revealed the constitutive induction of defence-related genes in the *CRK10* mutant hypocotyl, including genes involved in the signalling pathways of the stress hormones salicylic acid (SA) and abscisic acid (ABA). Finally, to investigate if *CRK10* modulates plant defence responses as suggested by our transcriptome dataset, a root infection assay with the vascular pathogen *Fusarium oxysporum* f. sp. *conglutinans* 699 was performed, and the *CRK10* mutant displayed significantly enhanced resistance compared to WT plants.

EFFECT OF ORGANIC AMENDMENTS AND INORGANIC FERTILISER APPLICATION ON NITROGEN USE EFFICIENCY AND DENITRIFICATION IN CONTROLLED AND FIELD CONDITIONS

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The amount of bioavailable nitrogen is directly linked to anthropogenic activity (Kuypers, Marchant, & Kartal, 2018), particularly with the intensive application of synthetic nitrogen fertilisers. Although high nitrogen inputs are required to support the ever-increasing need for food production, nitrogen use efficiency is in many cases low, to the extent that even with extra nitrogen inputs over time, increases of food production are small and slow (Battye, Aneja, & Schlesinger, 2017).

It has been suggested that roughly 40% of reactive nitrogen is denitrified in the soil (Seitzinger, et al., 2006), and most of the reactive nitrogen that results from human activities is removed by denitrification, with consequent production of N₂ and N₂O. However, even if most reactive N forms are removed by denitrification, this is an indicator that N use efficiency is not at optimum levels.

A study is being conducted in field and controlled conditions, that aims to understand denitrification and nitrogen use efficiency in a long-term experiment (running continuously since 2013) at Rothamsted Research. The experiment was designed to provide a clearer look at the effect of applications of organic amendments and/or inorganic fertilisers on nitrogen dynamics and crop yields in a conventional cereal-based cropping system.

Simultaneously, using yield data from the same trial, we aim to understand a) if the application of organic amendments leads to a reduction of the nitrogen threshold for optimum yields and, by using a modelling approach, b) if the eventual higher yields obtained with organic amendment application are due to the effect of the extra nutrients contained in the amendment or to some other effect caused by the amendments.

Soil and gas samples are being collected from a) different treatments of the field experiment (four different organic amendments: anaerobic digestate, compost, farmyard manure, straw and unamended control; and different nitrogen application rates; area of each plot: 54 m²) to assess nitrogen dynamics, and b) from soil columns (height 35 cm; width 25.5 cm) placed in a controlled environment using soil collected from the same trial. Different measurements are being taken including leachate (measurements of mineralised nitrogen), microbiology and gas emissions (using a Picarro device that measures NH₃, N₂O, CO₂, CH₄, O₂, H₂O). Simultaneously, underground sensors are being used to understand moisture and temperature evolution in the soil column, while electrochemical nitrate sensors are being used to understand nitrate dynamics before and after application of organic amendments and inorganic fertilisers.

With this, we aim at having a better understanding on denitrification processes and nitrogen use efficiency issues that may occur when using a joint regime of organic amendments and inorganic fertilisers. The main objectives of the project are the validation of the effect of organic amendments in the Fosters long-term experiment and the quantification of nitrogen gas emissions with the application of organic amendments and nitrogen fertilisers.

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THE UTILISATION OF AMINOMETHYLPHOSPHONIC ACID (AMPA) BY MICRO-ORGANISMS AS A PHOSPHORUS SOURCE IN SOIL SYSTEMS

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2. LANCASTER ENVIRONMENT CENTRE, LANCASTER UNIVERSITY, UNITED KINGDOM
3. ENVIRONMENTAL SYSTEMS SCIENCE, ETH ZURICH, SWITZERLAND
4. ELEMENTAL DIGEST SYSTEMS, WINKLEIGH, UNITED KINGDOM

Our global climate continues to change, and with that comes the change of our soil climate. Reports by the IPCC indicate annual increases in prolonged rainfall events within temperate climates. For our soils, this means the development of anaerobic systems such as saturated soils from frequent flooding events as they become more common. Reducing systems like these are capable of facilitating conditions in which reduced oxidation states of P presents itself. The change of our soil climate is rarely considered when attempting to understand how phosphorus is cycled and how it might be affected in an alternative environment. Existing knowledge from the marine sector demonstrates that a low oxidation state group of P compounds known as phosphonates (+3) are successfully utilised by micro-organisms instead of phosphate (+5) as their phosphorus source; thus, demonstrating that the phosphorus biogeochemical cycle is much more complex than previously regarded. Microbial isolates from soils capable of utilising Aminomethyl phosphonic acid (AMPA) from 10 out of a total of 16 field sites tested in the United Kingdom were obtained across a range of P gradients. The isolates obtained were a mixture of bacterial and fungal colonies with the corresponding phosphonate soil concentrations analysed; with 5 out of 16 sites demonstrating detectable concentrations within the soil samples. These results reveal that soil bacteria are able to break down and use P forms in alternative oxidation states to phosphate and contribute to ecosystem P cycling.



**ROTHAMSTED
RESEARCH**

Poster Session

William Rickard
Munisath Khandoker
Musa Kisiriko
Paul Rous
Gavers Oppong
Mahassine Arhazzal



**ROTHAMSTED
RESEARCH**

Session Seven
Thursday, 25th
February
2021

Chaired by Anastasia Sokolidi

USING DRONES TO TRACK BEES

TOM OLIVER, PAUL CROSS, ANDY REYNOLDS, JAMES MAKINSON AND LARS CHITTKA

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, BANGOR UNIVERSITY, BANGOR

Insect telemetry involves the use of tracking technology to understand invertebrate movement and behaviour. Current techniques either rely on a battery powered tag which may impact the flight behaviour of the insect, or a lighter, passive tag used in tandem with a harmonic radar dish which has a tracking range of approximately 500m but is costly. Here we show how a piezoelectric tag used in conjunction with an antennae array carried by a drone can be used to track bees at a landscape scale. Through the use of the drone, it becomes possible to track bees over much greater distances compared to existing tracking techniques at a fraction of the cost. We present preliminary results using a prototype of the antennae array to track bees exposed to pesticides and discuss the wider applications of using drones in insect telemetry.

ZINC ADSORPTION - DESORPTION STUDIES ON TYPICAL SOILS FROM DIFFERENT LANDSCAPE POSITIONS IN AMHARA REGIONAL STATE, ETHIOPIA

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Zinc (Zn²⁺) is an important micronutrient for humans, contributing to the grain quality of staple food crops. However, it is also the most deficient micronutrient in many Ethiopian soils. Its availability within the soil and uptake of applied Zn fertilizer are governed by the retention and release potential of the soil, usually termed as adsorption and desorption, respectively. To determine the trends of Zinc availability across landscape positions and soil types in Ethiopia, adsorption - desorption studies were carried out in the Rothamsted Research laboratory on soil samples collected from on-farm trials conducted in Amhara, Ethiopia, during the 2018/19 cropping season. Zinc stock solutions of 0, 2, 5, 10, 15 and 30 mg L⁻¹ were used for this study. In all locations and landscape positions, adsorption and desorption increased with increasing Zn stock solutions, but the adsorption increased faster than the desorption. The rate of adsorption and desorption corresponded to the amount of clay and soil pH, which in turn correlated with the landscape positions. The Freundlich isotherm fitted both to adsorption (r² of 0.90-0.99) and to desorption (r² of 0.99), while the Langmuir isotherm only fitted desorption (r² of 0.78-0.97). Soil pH, soil organic carbon and effective cation exchange capacity were found to be the most influential soil factors contributing to the adsorption and desorption of Zn²⁺ in the studied soils. Therefore, the findings of this study have clear implications for the current soil fertility management in these locations and landscape positions. Hence, in areas where the soil has high adsorption with less desorption, they might need an application of high doses of Zn fertilizer to compensate for the adsorbed Zn²⁺ by taking into account the amount of desorbed Zn²⁺ while in low adsorbed soils with high desorption, needs low doses of Zn fertilizers to minimize the effect of toxicity and further accumulation of Zn by taking into account the amount of adsorbed Zn²⁺. The models will help to quantify the amount of adsorbed and desorbed Zn²⁺ and help to devise stratified Zinc fertilizer recommendations for these site and even landscape position.

Keywords: Adsorption, desorption, landscape position, Isotherm, zinc

INFLUENCE OF SUPPLEMENT SOURCE (ORGANIC VS. INORGANIC) OF SELENIUM, COPPER, ZINC AND MANGANESE ON MICRONUTRIENT EXCRETION AND PARTITIONING BETWEEN URINE AND FAECES IN SHEEP

MOLLIE LANGDON¹, DR LAURA SILES-SUAREZ¹, DR GUILLAUME MENARD¹, DR PETER EASTMOND¹, DR HANS-WILHELM NUETZMANN², DR JAMES DOUGHTY² AND DR SMITA KURUP¹

1 ROTHAMSTED RESEARCH, HARPENDEN, UK; 2 UNIVERSTIY OF BATH, BATH, UK

In a world facing climate change and an increasing population, sustained increases in crop yields are important. Seeds are an important agricultural commodity and optimising seed yields is a target for research. One avenue of increasing seed yield is to investigate some of the factors that control seed yield, including seed size and seed number. By altering key developmental pathways that govern seed number and seed size, it is hoped any increases will also translate into overall increased seed yields.

Seeds develop from ovules in the gynoecium (the plant female reproductive organ). Therefore, in terms of manipulating seed number, alterations that occur at the ovule level should lead to an increase in the number of seed produced. The pathways governing ovule initiation are poorly understood but are thought to be influenced by several hormones including brassinosteroids (BRs). Preliminary research has revealed that manipulating BR levels within the model plant *Arabidopsis thaliana* can affect seed number, but further work is needed to investigate the effect on seed yield. This project will examine the effects of manipulating internal BR levels in a targeted manner on *Arabidopsis* seed yields and identify hitherto unknown genes that may control ovule number using *Arabidopsis* T-DNA knockout lines.

On the other hand, seed yields can also be influenced by increasing seed size. During the development of an ovule into a seed, a tissue called the integument helps impose an upper limit of final seed size. Preliminary research in *Arabidopsis* has shown the auxin transcription factor ARF2 negatively regulates seed size by limiting cell proliferation in the integument. However, the effect of manipulating ARF2 in a crop species is still to be examined. This project will investigate the effect of truncating the ARF2 protein (through CRISPR-Cas9 and RNAi) on seed yields of crops such as *Brassica oleracea* and rice.

Overall, this PhD project aims to investigate the impact of manipulating seed number and seed size on overall seed yield in *Arabidopsis* and two crop species, rice and *Brassica*.

COMPARING EXTRACTION METHODS FOR BIOMARKER STEROID CHARACTERISATION FROM SOIL AND SLURRY

AMBER MANLEY¹²³, ADRIAN L. COLLINS¹, ADRIAN JOYNES¹, PER-ERIK MELLANDER², PHIL JORDAN³

1. ROTHAMSTED RESEARCH, 2. TEAGASC, 3. ULSTER UNIVERSITY

Clean water is a precious resource and policies/programmes are implemented worldwide to protect and/or improve water quality. Faecal pollution can be a key contributor to water quality decline causing eutrophication through nutrient enrichment and pathogenic contamination. The robust sourcing of faecal pollutants is important to be able to target the appropriate sector and to engage managers. Biomarker technology has the potential for source confirmation, by using, for example, the biomarker suite of steroids. Steroids have been used in the differentiation of human and animal faeces; however, there is no unequivocal extraction technique. Some of the methods used include: i) Soxhlet extraction, ii) Bligh and Dyer (BD) extraction, and iii) accelerated solvent extraction (ASE). The less costly and time intensive technique of ASE is particularly attractive, but a current research gap concerns further comparisons regarding ASE lipid extraction from soils/slurries compared with the more traditional Soxhlet and BD extractions. Accordingly, a randomised complete block experiment was implemented to assess differences between the three extraction methods, differences between the different sample types, and the interactions between these two factors. Following GC-MS, it was found that there was no significant difference between the results of the steroid extraction methods, regardless of the type of sample used, for the quantity of each steroid extracted. It was concluded that ASE could be used confidently instead of the more established steroid extraction methods, thereby delivering time and cost savings.

JOURNEY TO THE CENTRE OF THE LETTUCE: AN APHID ODYSSEY

DR. JAMES BELL¹, DR. RAMIRO MORALES-HOJAS¹, DR. ROSEMARY COLLIER², DR. GRAHAM TEAKLE²,
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1. ROTHAMSTED RESEARCH; 2. UNIVERISTY OF WARWICK; 3. G'S FRESH

Climate change is driving the phenology of aphids earlier, compromising crop production because younger plants are being targeted earlier in the season. During colonisation and subsequent feeding, young plants are more susceptible to virus transmission and high levels of infestation can cause stunted growth, leading to supermarket rejections.

The currant-lettuce aphid, *Nasonovia ribisnigri*, is the most damaging species of aphid on outdoor lettuce and is responsible for large economic losses. As *N. ribisnigri* preferentially feeds at the centre of the lettuce, foliar sprays are ineffective, therefore host-resistant lettuce cultivars were previously the best method to reduce outbreaks. However, insecticide-resistant biotypes and others that break host-plant resistance (resistant-breaking (Rb)) have recently been found in the UK. It is known that the resistant lettuce cultivar is underpinned by one gene (*Nasonovia-resistant* gene – *Nr*), yet little is known about how the aphid can overcome this single gene resistance in the host. In this PhD project, *N. ribisnigri* has been used as a model to examine and explore potential insect resistance mechanisms to the *Nr-gene* resistance in the host plant.

Since no previous reference genome existed for this species, this is the first reference genome of *N. ribisnigri* that has been hybrid de novo assembled using Illumina (PE 150) and MinION sequence data obtained from both susceptible and resistance-breaking (Rb) biotypes. Microsatellite markers from these genomes have been developed to explore the population structure over the past 17 years using samples obtained from the Rothamsted Insect Survey (RIS) sample archive. This 17-year range encompasses pre and post host plant resistance breakdown to study how this may have affected gene flow between the populations.

Additionally, this species is very difficult to detect with current monitoring schemes and therefore its colonisation into crop is sporadic and unpredictable. Different approaches of detection in field have been incorporated throughout this project to improve the discovery of this elusive aphid. Together, these findings increase our understanding of the importance of microbial soil health and wheat cultivar in shaping the root microbiome and this knowledge will facilitate the exploitation of plant-microbe interactions for the development of novel microbial inoculants.

THE ROLE OF PHOTOPROTECTION IN DISEASE RESISTANCE TO *SEPTORIA TRITICI* BLOTCH IN WHEAT

RUMIANA RAY¹, ERIK MURCHIE¹, KOSTYA KANYUKA²

1, UNIVERSITY OF NOTTINGHAM 2, ROTHAMSTED RESEARCH, HARPENDEN

Excessive accumulation of energy in the photosynthetic machinery can lead to the formation of reactive oxygen species (ROS), such as superoxide (O₂⁻) and hydrogen peroxide (H₂O₂), and eventually to photoinhibition. In addition, light-triggered ROS production in the chloroplast serve as signalling molecules for the initiation of defence and as regulators of cellular metabolism. Thus, plants need a highly responsive regulatory system to keep photosynthetic light reactions in balance with the needs and restrictions of the downstream metabolism. One such mechanism is termed non-photochemical quenching (NPQ), which dissipates the unused excess energy in order to protect the integrity of photosystem (PS) II and it typically modulates plant responses to environmental stresses. Dynamic changes of NPQ reflect tight regulation of energy required to drive photochemistry and to prevent permanent damage to PSII caused by reactive oxygen and free radicals. One major stress in wheat production is *Septoria tritici* blotch (STB), a fungal disease caused by *Zymoseptoria tritici*. Symptoms of chlorotic and necrotic lesions with pycnidia appear on leaves 7-14 days after infection when the disease reduces plant photosynthesis. We have been investigating whether the photoprotective mechanism of the chloroplast is involved in the early defence responses of the plants (up to 48 hours post inoculation) and whether *Stb6*, a major resistance gene, would result in contrasting changes in NPQ formation, potentially due to different levels of production and/or detoxification of ROS in the plant. RNA sequencing and transcriptomic analysis was also performed in order to elucidate the underlying molecular mechanisms and hormonal pathways involved in photoprotection.



**ROTHAMSTED
RESEARCH**

Poster Session

Tom Oliver
Mesfin Kebede Desta
Mollie Langdon



**ROTHAMSTED
RESEARCH**

Session Eight
Thursday, 25th
February
2021

Chaired by Hannah McGrath

BIO-PROSPECTING FOR PLANT-GROWTH-PROMOTING MICROBES IN BROADBALK SOILS

OWEN THORNTON^{1,2}, GLYN BARRETT², IAN CLARK¹, ROBERT JACKSON^{2,3}, TIM MAUCLINE¹

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, UNIVERSITY OF READING, READING. 3, UNIVERSITY OF BIRMINGHAM AND BIRMINGHAM INSTITUTE OF FOREST RESEARCH (BIFOR), BIRMINGHAM

Microbes are fundamental to the maintenance of life on Earth and are widely acknowledged for their role in the survival and fitness of the many higher organisms with which they associate. Interactions between plants and microbes are believed to have facilitated the conquest of land itself and to this day can profoundly affect the success of plants in both ecological and agricultural contexts. Naturally occurring soil microbes – especially the subset that can live associatively with plant's roots – offer the potential to contribute to the sustainable intensification of agriculture by suppressing plant diseases and increasing nutrient availability. However, the effects of different agricultural management practices and cropping systems on the proliferation of particular sets of microbes may determine the manifestation of these beneficial functions. The design of the Broadbalk winter wheat experiment at Rothamsted has ensured that a diverse range of biotic and abiotic selective pressures associated with different combinations of these treatments have acted continuously on resident soil microbes over the last 177 years. Moreover, as the crops are grown, plants subjected to the specific conditions in each of the different plots may promote and suppress specific members of their root-associated microbial communities accordingly, further increasing the diversity of relevant microbes that are likely to be isolated from this single field location. As such, the Broadbalk LTE represents the ideal system in which to dissect the determinants of effective microbial plant-growth-promotion and extract microbes of interest – the trials and tribulations of which are detailed in this poster.

PHENOTYPING THE NUTRITIONAL STATUS OF CROPS USING REMOTE SENSING TECHNOLOGIES

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1ROTHAMSTED RESEARCH, HARPENDEN, 2CRANFIELD UNIVERSITY, 3UM6P, MOROCCO

Low soil fertility is one of the factors most limiting agricultural production particularly in developing countries such as Africa. However, mineral fertilizers that are applied to avert this production constraint comes with an economic cost to the farmer with low income and further cause threats to human health and environmental pollution to ecosystems [1,2]. Therefore, more restricted and reasonable use of fertilizers is critically essential. Improved agronomic practices in combination with breeding (i.e., phenotyping) of more nutrient efficient crops are necessary especially in the low productive regions to achieve food security.

Remote sensing has become an important methodology for the application of agricultural monitoring and to improve precision and throughput in phenotyping [3]. It is often used to assess the nutrient status of crops, growth monitoring, yield prediction, stress detection, nutrient deficiency diagnosis, and control of plant diseases and thus inform improved agronomic decisions even for small farm holdings [4]. In the case of phenotyping, these methodologies offer the opportunity to screen large numbers of genotypes at a lower cost and faster than conventional phenotyping. Nevertheless, these technologies capable of monitoring crop performance for agronomical purposes for breeding are bottlenecks in the pathway to full exploitation. The high cost of high-throughput plant phenotyping (HTPPs) infrastructures is a major limiting factor and the limited availability of skilled personnel may also impair its implementation in African countries.

This project will address some of these existing gaps and explore drone technologies, satellite imagery, gantry scanner systems as well as low-cost portable phenotyping tools for controlled and field evaluation of crop performance in Africa, specifically in Morocco for locally important crops with a specific emphasis on optimizing the use of fertilizers. Two strategies are considered paramount in this project: (i) phenotyping to improve crop varieties for higher nutrient use efficiency, tolerance to nutrient-deficiency and other abiotic/biotic stresses (ii) and developing low-cost tools for appropriate fertilization management including precision agriculture. Currently, nutritional pot experiments are running in both Rothamsted and Cranfield to evaluate phenotypic methods to monitor growth responses of quinoa and cowpea to different levels of nitrogen and phosphorus using both “traditional” measurements and new approaches based on imaging technologies. Our preliminary results from Rothamsted show differences in nutrient treatments for growth and yield indicators as well as the nutrient status of the crops.

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COMPETITION BETWEEN AN INVASIVE AND ENDEMIC SPECIES OF ARMYWORM IN AFRICA

RUTH CARTER, DR JOHN CAULFIELD AND PROF KENNETH WILSON

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Both African Armyworm (*Spodoptera exempta*) and Fall Armyworm (*Spodoptera frugiperda*) moth threaten food security in Africa. *S. exempta* is native to Africa. Whereas *S. frugiperda* only became invasive in Africa four years ago. Both Armyworm larvae feed on staple food crops such as maize and pastureland such as Cynodon grass. Pest Control is available, however poor smallholder farmers have less access to crop protection products as these come at some expense. Biopesticides have been suggested as an alternative to broad-spectrum pesticide.

My PhD aims to answer these questions: Can a new study guide the development of biopesticides? What happens to native pest when you get a new invasive pest? Can *S. exempta* be managed in the same way? I will look at the direct competition including interspecific predation compare behaviour of *S. frugiperda* and *S. exempta* together to control. I will study plant defences by comparing volatiles of Cynodon grass (*Cynodon dactylon*), Maize (*Zea mays*) with and without larvae damage. I will investigate Indirect Exploitation competition by studying if both larvae can be controlled by the same strain of virus and fungus or if different strains are needed. I will also study if there is host plant overlap between the two moths.

Including original content, figures made by Ruth Carter

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ENHANCED NITROGEN USE EFFICIENCY (NUE) OF UREA FERTILISERS FOR SUB-SAHARAN AFRICA

MARIEME DRAME, TOM MISSELBROOK, SIGRID HEUER, ALISON CARSWELL, GUY KIRK, MARK PAWLETT

ROTHAMSTED RESEARCH, HARPENDEN, CRANFIELD UNIVERSITY, UM6P, MOROCCO

Sub-Saharan African (SSA) agriculture is low input, associated with continuous soil nutrient mining and contributing to food insecurity. With increasing food demand, there is an increasing trend in fertiliser use, particularly nitrogen (N) fertiliser accounting for ~ 90% of all fertiliser inputs in Africa. However, only 10 to 20% of the N fertiliser applied is taken up by crops under farming practices in most SSA countries, with consequent losses of reactive N (Nr) to the environment. Enhanced-efficiency N fertilisers (EEF), including urease inhibitors (UIs) and nitrification inhibitors (NIs) have been shown to reduce Nr losses and increase NUE under temperate conditions. However, few studies have tested the stability and effectiveness of UIs and NIs on N losses in highly weathered and nutrient limited soils under SSA climatic conditions, so there are uncertainties on how they may best be used in SSA agriculture. Therefore, this study will explore how the use of urea fertilisers containing UIs, NIs and combination of both UIs and NIs influences ammonia and nitrous oxide emissions across a range of temperatures (15, 25, 35°C) and soil moisture (20, 40, 60%). Additionally, using wheat and rice varieties this study will test UIs and NIs ability to enhance N use efficiency and influence plant tissues N metabolism. There are clear opportunities to help optimize fertiliser-NUE in various crop genotypes and cropping systems in SSA.

CHARACTERISING A NATURAL DELETION OF THE B GENOME ASN2 HOMOELOG IN WHEAT

JOSEPH ODDY¹, MARK WILKINSON¹, NICHOLAS CRYER², ISABEL MOREIRA DE ALMEIDA², J. STEPHEN ELMORE³, NIGEL HALFORD¹

1. ROTHAMSTED RESEARCH. 2. MONDELEZ INTERNATIONAL. 3. UNIVERSITY OF READING.

Understanding the determinants of free (non-protein) asparagine concentration in wheat grain is necessary in order to reduce levels of the processing contaminant acrylamide in certain wheat products. Asparagine synthetase 2 (ASN2) is the most highly expressed asparagine synthetase gene in wheat grain and is likely a key determinant of asparagine levels in the grain, but expression is uneven between homoeologs. Expression of the B genome homoeolog (ASN2 B) has not previously been described, likely because of its absence in many varieties, but genomic data shows that ASN2 B is present in some.

To investigate this, we analysed the gene and protein structure of ASN2 B and identified the genomic region containing ASN2 B that has been deleted in some varieties. Using this information, we screened for ASN2 B across a range of commercial wheat varieties and investigated its effect on grain asparagine concentration alongside the application of sulphur. The presence of ASN2 B is associated with higher free asparagine concentration in the grain under sulphur sufficiency, suggesting that ASN2 B negative varieties can be exploited to help mitigate the carcinogenic risk posed by acrylamide.

ADDING EVIDENCE REGARDING THE USE OF COVER CROPS

M STOKER ¹, DR I SHIELD ¹, PROF. C STEVENS ², H WILDER, BOGNOR REGIS ³

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, LANCASTER UNIVERSITY, LANCASTER, 3 BARFOOTS

Soil can provide us with one of the World's largest carbon sinks and help to mitigate climate change. Soil is also fundamental for the provision of food. Ideally we need to discover ways to have both a carbon rich soil and produce food. Cover crops, a crop grown between cash crops, may provide one simple solution.

Through the process of photosynthesis, plants remove CO₂ from the atmosphere and convert this into sugars. This food source is then used by the plant and many beneficial bacteria and fungi that form a symbiotic relationship with the plant. One of the by-products of this relationship is the production of an enzyme, glomalin which glues the carbon to form stable aggregates around the roots of plants. However, little is understood about creating the perfect environment for the optimal performance of a microbial community to sequester carbon by using a cover crop.

Here I show how the microbial community can alter as a result of different treatments and what the effect is on soil carbon content. I found that the addition of the widely used herbicide glyphosate, and a commercially available mycorrhizal inoculant (Symbio), can alter the microbial community. The results to date show that the microbial community is very sensitive to its environment and that agricultural chemicals can have an effect on the ability to control particular eco system services such as the generation of Soil Organic Carbon (SOC).

This study highlights the complexity of the roles performed by bacteria and fungi alongside a cover crop. If increased SOC is the service required, a carefully considered approach is needed including the choice of plants species and how the crop is managed.

GETTING TO THE ROOTS OF THE BLACK-GRASS PROBLEM: ALLELOPATHIC CONTROL OF *ALOPECURUS MYOSUROIDES*

D.T. HICKMAN, D.M. WITHALL, J.C. CAULFIELD, A. RASMUSSEN, K. RITZ, D. COMONT, M.A. BIRKETT, P. NEVE

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, UNIVERSITY OF NOTTINGHAM, NOTTINGHAM

Black-grass (*Alopecurus myosuroides*) is a serious weed of cereals in northern and western Europe. Reliance on synthetic herbicides for control has led to the evolution of multiple herbicide resistance in many populations. Therefore, alternative control methods are desired. Allelopathy, the interaction of plant species through inhibitory bioactive compounds, is one such method with potential. Petri-dish assays identified two allelochemical compounds which hold promise for black-grass inhibition, specifically inhibiting root growth of both herbicide-susceptible and herbicide-resistant populations. These compounds do not inhibit wheat development at these concentrations, however, which suggests that such compounds have sufficient specificity to be applied to a wheat field to inhibit black-grass without detriment to the crop. Derivatives of these compounds have been found in the crude exudates of wheat and rye roots grown in an axenic sand system through LCMS analysis. Additionally, bioassay of these crude exudates in this system has identified that they inhibit black-grass development on a level comparable with findings from the earlier Petri-dish assays of synthetic compounds. This strongly indicates that allelochemicals derived from the root exudates of cereals hold promise for black-grass control, either through direct application of synthesised compounds, or through the deployment of an allelopathic crop variety. Future work will quantify the variability of the exudation of these compounds across a range of modern wheats and landraces. It is also vital to verify the continued phytotoxicity of these compounds in biologically active media, specifically soils, as rapid degradation by the rhizospheric microbial community has been identified as a pitfall in numerous allelopathy studies.



**ROTHAMSTED
RESEARCH**

Poster Session

Owen Thornton
Daniel Cudjoe
Ruth Carter
Marieme Drame
Joseph Oddy



**ROTHAMSTED
RESEARCH**

**Session Nine
Friday, 26th
February
2021**

Chaired by Mollie Langdon

FLIGHT-TO-LIGHT AND THE DECLINE OF BRITISH MOTHS

ISHBEL HAYES^{1,2}, JAMES BELL¹, KEVIN GASTON² AND JON BENNIE²

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, UNIVERSITY OF EXETER, PENRYN

Moths, like many other insects are in decline. In the UK, there has been a 31% decline in moth abundance since the 1960s[1] across two thirds of common species [2]. This has largely been attributed to changes in habitat availability and climate[3]. However the concurrent increase in light pollution[4] has led to speculation that increases in artificial light are likely to be a contributory factor[5] as has been suggested for nocturnal insects in general[6]. Attraction to light is associated with high insect mortality and exposure to light at night can negatively impact moths both in adult and larval stages through impacts on feeding, reproduction and development[7]. Despite the correlation between declining moth populations and life history traits associated with flight-to-light behaviours[8], little research has been conducted on the impact of light pollution on Lepidoptera at a population scale. This project aims to address the uncertainty around the role of light pollution in the decline of British moths. Night-time satellite imagery and data on ambient light from Sky Quality Meters on selected traps along with the Rothamsted light-trap network data will be used to model the influence of light pollution between lit and unlit areas. Experiments will also unravel the ability of habitat to buffer light pollution and improve understanding of the differences in flight-to-light behaviour elicited by varying wavelength.

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DIGITAL IMAGE ANALYSIS FOR HIGHTHROUGHPUT PHENOTYPING OF QUINOA PLANTS IN A GLASSHOUSE

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Quinoa plants (*Chenopodium quinoa*) is a crop widely consumed for its high protein (16%) and the right balance of carbohydrate, essential amino acids, minerals and essential oil (Zurita-Silva et al, 2014). Plant phenotyping is an increasing approach to improve plants productivity. However popular methods for phenotypic trait measurement have some limitations in aspects of labour, performance, and space-time coverage. Hence in recent years computer vision-based phenotyping approaches are being implemented. To contribute to the growing research environment in improving quinoa plant yield, a computer vision-based phenotyping of quinoa plants growth dynamics and yield was conducted in a controlled greenhouse.

Four treatments; High Nitrogen-High Phosphorus (HNHP), High Nitrogen-Low Phosphorus (HNLP), Low Nitrogen-High Phosphorus (LNHP) and Low Nitrogen-Low Phosphorus (LNLP) each with five replicates were set up at a semi-controlled greenhouse facility at Rothamsted Research. The plants were watered daily with equal amount of deionized water. A phenotyping platform was set up with an RGB camera for capturing images of quinoa plants twice weekly. Phenotyping analysis was conducted on quinoa plants from its growth stage 19 to 59 as described by Sosa-Zuniga et al (2017).

Computer vision techniques including image segmentation, feature extraction, machine learning models etc is being used to develop an automated tool to phenotype quinoa plants for chlorophyll prediction, shoot height and width estimation, canopy area estimation, growth dynamics analysis and plant type classification (based on nutrient variability). Images were first segmented using the ExGR vegetation index and suitable features (colour, morphology and texture) were extracted for further analysis depending on the objective at hand.

The image analysis is still ongoing. It is hoped that a complete automated pipeline will be developed to predict the phenotyping indices as mentioned above. From preliminary analysis, HNHP plants are showing higher growth pattern as compared to the LNLP treatment. Also, a random forest classification model with an accuracy of 62% has been developed to predict plant class based on nutrient content

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QUANTIFYING THE TRUE COSTS OF FARMING SYSTEMS

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The success of agricultural systems has traditionally been measured by profitability, with demand for “cheap” food driving unsustainable farming practises causing environmental damage. However, there is a growing body of research which aims to account for these environmental costs by putting an economic value on the natural environment, termed natural capital, and the associated ecosystem services it provides, upon which agriculture is extremely dependent. This method of true cost accounting is particularly important in agricultural systems as agriculture occupies 40% of the earth’s terrestrial land surface, so is disproportionately responsible for environmental degradation and a key target for sustainable improvements (1). Through true cost accounting there is a strong consensus that “cheap” food systems are often the most expensive in terms of their environmental and societal costs, with a trade-off existing between short-term production, associated with high external inputs and yields, and long-term maintenance of natural capital and ecosystem services (1). Therefore, there is a critical need for research into understanding the interdependencies between land use, natural capital and ecosystem service delivery to know how to best maximise yield sustainably (2).

In this project I aim to identify and monitor natural capital and the associated ecosystem services in contrasting arable farming systems and offset these costs/gains against the systems conventional economic profitability. In doing this I will highlight key trade-offs as well as develop practical methods of monitoring natural capital on farms with application for widespread monitoring to allow government incentives, through farming subsidies, to improve the sustainability of arable systems in line with the governments 25-year environmental plan and agricultural bill.

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AGENT BASED MODELLING OF CROP PRODUCTION

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^AROTHAMSTED RESEARCH ^BCRANFIELD UNIVERSITY ^CMOHAMMED VI POLYTECHNIC UNIVERSITY

Farmers in Morocco are facing the daunting challenge of increasing production to feed a growing population and support livelihoods, whilst improving the sustainability and resilience of cropping systems at the same time. This Ph.D. project aims to understand how social, economic, and environmental factors affect decisions made by farming stakeholders and in turn how these decisions impact productivity and the environment. Therefore, a key ambition in this study is to develop an agent-based approach, for modelling the dynamics of farming stakeholders' behaviour, as a result of individuals' interactions and their interactions with their environment in a space-time context and explore how cooperation among them can improve the efficiency of sustainable agricultural production.

MANAGING CONCURRENT EVOLUTION OF RESISTANCE TO FUNGICIDES

ISABEL CORKLEY^{1,2,3}, ALICE MILNE¹, MICHAEL SHAW², ALEXEY MIKABERDIZE², NEIL PAVELEY³, FRANK VAN DEN BOSCH⁴

1. ROTHAMSTED RESEARCH, HARPENDEN. 2. UNIVERSITY OF READING, UK. 3. ADAS, UK.
4. CURTIN UNIVERSITY, AUSTRALIA.

The use of fungicides to control plant pathogens is threatened by the emergence of pathogen strains with resistance to fungicides. Fungicides with a mode of action (MOA) targeting a single pathogen target site are at particular risk of resistance development. Septoria leaf blotch (*Zymoseptoria tritici*), a widespread and damaging pathogen of winter wheat which can cause up to 50% yield losses, shows increasing levels of resistance to both demethylation inhibitors (DMI) and succinate dehydrogenase inhibitors (SDHI) fungicides. With the use of multi-site fungicides increasingly restricted by legislation, there is an urgent need to understand how best to combine two or more single-site MOA in a fungicide programme. Potential resistance management strategies, aimed at slowing selection for resistant strains whilst maintaining control of disease, include alternation of MOA and applying MOA in mixture. However, each option introduces trade-offs and could either increase or reduce the selection pressure overall if resistance is evolving to multiple MOA at the same time. A model of *Z. tritici* and wheat leaf area dynamics will be adapted to enable model simulations of concurrent evolution of resistance, testing a large number of possible strategies with the aim of informing and improving resistance management tactics.

THE ECONOMIC AND ENVIRONMENTAL VALUE OF AGRICULTURAL MODEL-BASED DECISION SUPPORT TOOLS FOR WHEAT CROPS IN MOROCCO

¹BADER OULAI, ²DR ALICE MILNE, ¹PROF RON CORSTANJE, ¹DR TOBY WAINE, ³DR RAFIQ EL ALAMI,
³PROF MARYAM RAFIQI

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Providing food for a growing population in Morocco and across Africa whilst promoting the sustainability and resilience of cropping systems is the main challenge farmers, advisors and policy makers are facing nowadays.

Timely and accurate model-based decision support systems (DSS) are needed to improve farmers' decisions in terms of both productivity and the environment.

To understand these complex interactions, this project aims to investigate the economic and the environmental value of agricultural decision support tools for wheat crops in Morocco. Hence it is devised to achieve four objectives: i) to review the agricultural decision support tools that are currently available; ii) to investigate the feasibility of translating them to Moroccan conditions; iii) to evaluate these tools using primary and secondary data and iv) to quantify their uncertainty and so evaluate the value of the DSS over standard practices.

To achieve these goals; several methods will be investigated and developed in order to calibrate DSSs using existing field data and remote sensed data. These methods will adjust the initial variables of crop models to the optimal through a data assimilation approach and then explain how agricultural decision making would be affected by data quality.

The project will generate primary data through controlled on-station experimentation. Other auxiliary datasets will be obtained from satellite images and many Moroccan institutions, which will be then processed to fit the project domain and coverage.

This project seeks to improve the management of agricultural landscapes by identifying area where agricultural decision making would be improved if more precise information were available.

BESPOKE FIELD MARGINS FOR DELIVERING MULTIPLE SERVICES TO FRESH PRODUCE

HANNAH MCGRATH^{1&2}, ROSEMARY COLLIER³, SAM COOK¹, SIMON POTTS², BEN MADARASI⁴ & STEPHEN SHEILDS⁴, & JONATHAN STORKEY¹
1 – ROTHAMSTED RESEARCH, HARPENDEN. 2 – UNIVERSITY OF READING, READING. 3 – UNIVERSITY OF WARWICK, COVENTRY. 4 – HUNTAPAC PRODUCE, PRESTON.

The intensification of our farming landscapes to increase yields to feed the growing population has caused unintended and unwanted effects. Consequently, this project aims to improve the sustainability of farming by enhancing and delivering targeted ecosystem services into commercial crops.

Working alongside fourth generation family-owned carrot company, Huntapac Produce, bespoke field margins are being designed and tested. These margins have the dual aim of providing a refuge for general biodiversity such as pollinators in agro-ecosystems whilst also supporting beneficial insects that may biologically control carrot pests improving crop yields.

Six different floristically enhanced margin plots have successfully been tested in a commercial carrot field to assess the insect communities present at these margins and the effect of these on the crop. The preliminary results from harvest in 2019 suggests that we have got a sampling method which can detect treatment differences. However, 2019 data reveals there are no significant differences associated with the different flowering treatments. Nevertheless, economic values have been attributed to this harvest data. Additional fieldwork this season included developing a sampling protocol to study the spatial distribution of willow carrot aphids within commercial carrot fields.

SOIL ORGANIC CARBON INDEXING AND MEASUREMENT SYSTEM

JONAH PROUT^{1,2}, KEITH SHEPHERD³, STEVE MCGRATH¹, GUY KIRK², STEPHAN HAEFELE¹

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3, WORLD AGROFORESTRY (ICRAF), NAIROBI, KENYA

Soil organic carbon (SOC) is key to numerous soil functions, however guidelines for how much SOC a soil should hold or is “good” have been difficult to define. Studies of soils in other countries in Euro-temperate climates have suggested that the relative amounts of SOC and clay content affect physical soil properties and can be used to indicate soil structure status. We assessed the use of an index of SOC/clay for soils in England and Wales using data of 3809 soils from the first survey of the National Soil Inventory of England and Wales (NSI; Prout et al., 2020). The index looked appropriate for application in mineral soils across these countries and found that whilst grassland and woodland soils would mostly be considered very good, 38% of arable soils would be considered degraded. Applying the index to a long-term experiment on sandy loam soil showed that the index also had value at low clay contents where changes in index value would result from smaller changes in SOC. The second survey of the NSI was used to compare changes in SOC/clay over time at this scale and long-term experiments were used to test the effect of clay content and soil amendments (organic and inorganic) on changes in SOC in the context of using the index at the field-scale. Application of the index requires testing and monitoring which can be labour intensive and costly. Spectral methods can help as samples can be analysed for multiple properties simultaneously and quickly, making it more cost-effective than standard wet chemistry. To aid in the implementation of these methods we have created infrared calibrations for SOC and clay content, using 1000 soil samples from the NSI, and tested them to measure the SOC/clay index directly. Being able to determine a soil’s carbon status using two routinely measured variables and improving the accessibility for high throughput testing methods will help land managers to make more informed decisions at a field scale and policy makers at national scales.

INVESTIGATING INSECTICIDE RESISTANCE IN UK POPULATIONS OF CABBAGE STEM FLEA BEETLE *PSYLLIODES CHRYSOCEPHALA*

CAITLIN WILLIS¹, EMYR DAVIES¹, MARTIN WILLIAMSON¹, STEPHEN FOSTER¹, XIANMIN CHANG², JAN ELIAS³,
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The cabbage stem flea beetle (CSFB) *Psylliodes chrysocephala*, is a major pest of winter oilseed rape (OSR) in the UK and Northern countries in mainland Europe including Germany, attacking emerging plants in the autumn and causing severe damage to the crop if left unchallenged. Prior to December 2013, control of CSFB relied on the protection of OSR seedlings by neonicotinoid seed treatments in conjunction with subsequent application of foliar pyrethroids sprays. However, the EU-imposed restriction on the use of neonicotinoids has left growers with just pyrethroids for CSFB control. The increased selection pressure, caused by a lack of alternative control agents with different modes of action, has led to the emergence of pyrethroid resistance in this pest. As CSFB resistance to pyrethroids can cause significant yield losses in OSR crops, and the continued use of these pesticides in their current format will only exacerbate this problem, there is a need to understand the mechanisms by which resistance has developed and is sustained within CSFB populations. Despite the presence of the target-site mutation *kdr* in UK populations, resistance does not completely correlate with *kdr* genotype, suggesting another mechanism of resistance is also present. The current study reports the extent and geographical spread of pyrethroid resistance in UK CSFB populations, the contribution of *kdr* (L1014F) and *super-kdr* (L925I) to this resistance phenotype and our efforts to identify the enzyme(s) involved in conferring the additional metabolic resistance component using next generation transcriptomic approaches.



**ROTHAMSTED
RESEARCH**

Poster Session

Ishbel Hayes
Frank Okyere
Beth Roberts
Imane El Fartassi
Isabel Corkley
Bader Oulaid



**ROTHAMSTED
RESEARCH**

Session Ten
Friday, 26th
February
2021

Chaired by Kim Hammond-Kosack

Guest Speaker

Dr Helen Brewer

Policy Advisor – Market Access (DEFRA)

‘From Plant Pathology to Ice Cream Exports’

Nelly Brewer was based at Rothamsted Research from 2009 to 2014, completing a PhD in Plant Pathology and graduating from the University of Exeter. She spent 3 months of her final year on placement at the Parliamentary Office of Science and Technology. Since then she's done all sorts of things, including working in the Public Engagement team, having a baby, running the BSPP twitter account, doing a Post Doc, having another baby and founding a sling library. She currently works as a Policy Officer (sort of) in the Animal and Plant Health and Welfare directorate at Defra. Her role involves facilitating exports of animals and animal products to non-EU countries, while protecting animal health and food safety. She currently works from home, in among looking after two small children, three chickens and a cat.





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Thank you for
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Special thanks to our PhD Students 20/21 Cohort



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