Rothamsted PhD Symposium

1st & 2nd March 2022

Fowden Hall,

Rothamsted Conference Centre

Photo Credit Dan Blumgart

Handbook

This in-person event is open for all staff and visitors to attend

and support our students

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Colour Key

Year 1 – Presenting Posters
Year 2 – 2 Minute Poster Introduction and Presenting Posters
Year 3 – 5 Minute Poster Introduction and Presenting Posters
Final Year – 15 Minute Talks

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Welcome

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 2021/2022. We are delighted that this event is now able to take place in person, but we also realise that the “virtual” form of working is still in place for some, so you have the option to attend in person or view the event via Starleaf. We hope that through using these 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.

The Symposium provides our students with both the opportunity to showcase their research to their 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. My advice to our students would be to 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 event will be both rewarding and enjoyable!

Andrew Mead

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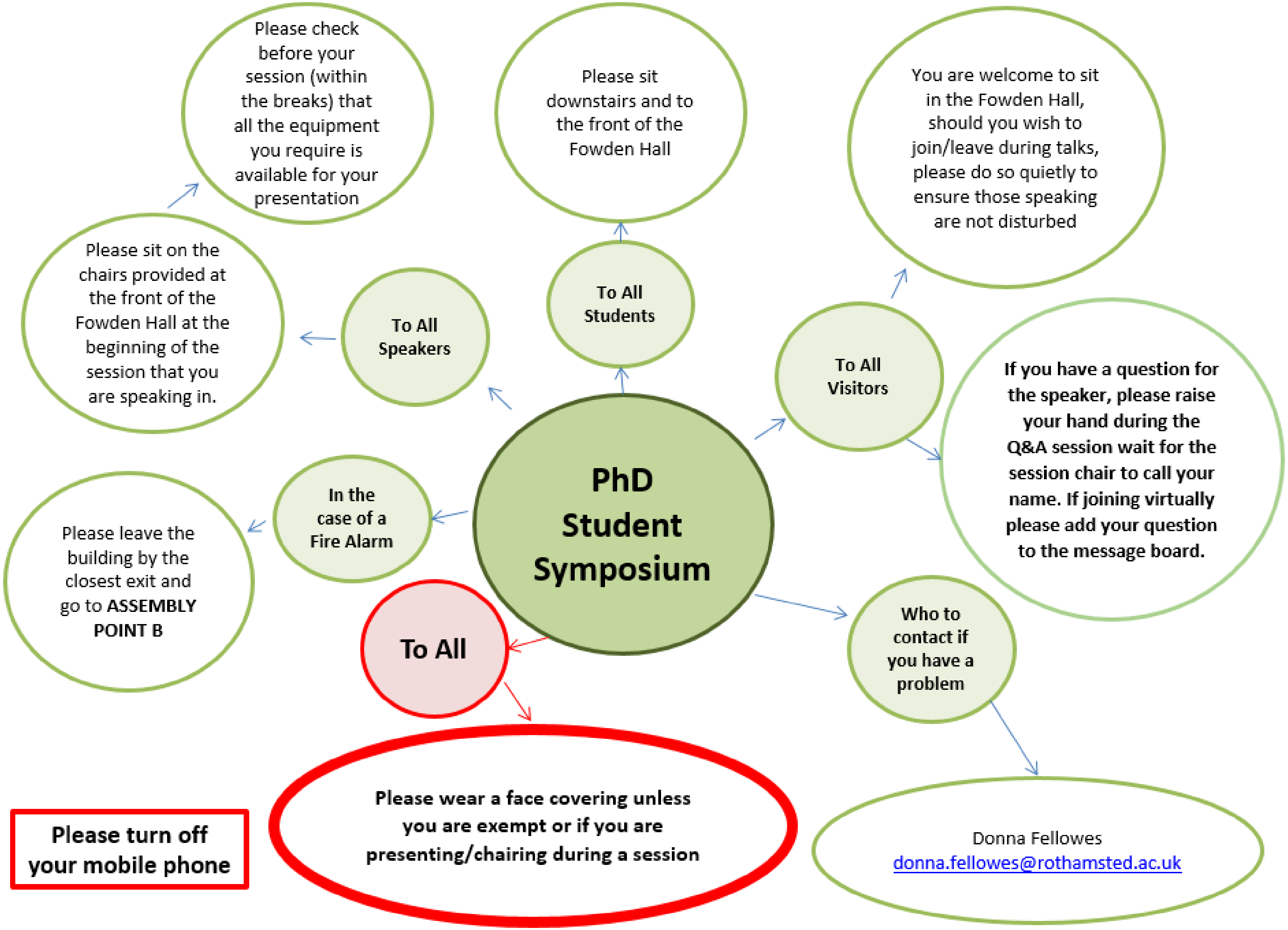

PhD Student Symposium

To All Speakers

- Please sit on the chairs provided at the front of the Fowden Hall at the beginning of the session that you are speaking in.
- Please check before your session (within the breaks) that all the equipment you require is available for your presentation

To All Students

- Please sit downstairs and to the front of the Fowden Hall

To All Visitors

- You are welcome to sit in the Fowden Hall, should you wish to join/leave during talks, please do so quietly to ensure those speaking are not disturbed
- **If you have a question for the speaker, please raise your hand during the Q&A session wait for the session chair to call your name. If joining virtually please add your question to the message board.**

Who to contact if you have a problem

- Donna Fellowes
  donna.fellowes@rothamsted.ac.uk

In the case of a Fire Alarm

- Please leave the building by the closest exit and go to **ASSEMBLY POINT B**

To All

- **Please wear a face covering unless you are exempt or if you are presenting/chairing during a session**

Please turn off your mobile phone

Rothamsted PhD Symposium

1st & 2nd March 2022

Event Programme

Click here to join the PhD Symposium - Meeting ID: 444 064 6523 - More ways to join your meeting

Please feel free to ask questions to our Final Year Students and Guest Speakers here

Day 1 – Tuesday, 1st March 2022	
09:30am	**Registration/Coffee** – Conference Centre Plaza
10:00am	**Welcome from Andrew Mead Chair of PGC** – Fowden Hall
SESSION 1 – Chaired by Mollie Langdon – Fowden Hall	
10:10am	**2-minute Poster Introductions** 7. **Victoria Armer** (BCP) **-** Unlocking the door: how *Fusarium graminearum* exploits plasmodesmata during host-tissue colonisation 9. **Erika Kroll** (BCP) - Using network analysis to investigate host-pathogen interactions between wheat and *Fusarium graminearum*
10:15am	**5-minute Poster Introductions** 11. **Mahassine Arhazzal** (SAS-H) - Does wheat select for beneficial soil microbiome when grown under abiotic stresses? 13. **Tadesse Gashaw Asrat** (SAS-H) - Comparison of portable and bench-top soil scanning instruments and calibrations: for fertilizer decision making perspective 15. **Frank Gyan Okyere** (PS) – A neural network based segmentation method for high throughput plant phenotyping 17. **Bader Oulaid** (SAS-H) – Global sensitivity analysis for the calibration of AquaCrop for wheat crops in semi-arid regions
10:35am	**Photo Call for all PhD students outside the Centenary Building**
10:45am	**Poster session and coffee** – Fowden Hall and Plaza 1. **Izayana Sandoval-Carvajal** (BCP) - Assessing the genetic diversity of UK strains of barley yellow dwarf virus (BYDV) 3. **Lisa Humbert** (BCP) - Fungal sex factors as novel antifungal compounds for control of plant disease 5. **Sandra Lucia Cortes Patiño** (BCP) - Herbivore-plant-soil microbe interactions: who is helping whom 7. **Victoria Armer** (BCP) **-** Unlocking the door: how *Fusarium graminearum* exploits plasmodesmata during host-tissue colonisation 9. **Erika Kroll** (BCP) - Using network analysis to investigate host-pathogen interactions between wheat and *Fusarium graminearum* 11. **Mahassine Arhazzal** (SAS-H) - Does wheat select for beneficial soil microbiome when grown under abiotic stresses? 13. **Tadesse Gashaw Asrat** (SAS-H) - Comparison of portable and bench-top soil scanning instruments and calibrations: for fertilizer decision making perspective 15. **Frank Gyan Okyere** (PS) – A neural network based segmentation method for high throughput plant phenotyping 17. **Bader Oulaid** (SAS-H) – Global sensitivity analysis for the calibration of AquaCrop for wheat crops in semi-arid regions
SESSION 2 – Chaired by Dr Sarah Raffan – Fowden Hall	
	Final Year Talks – **Ask questions here**
11:15am	**27. Anastasia Sokolidi** (BCP) - SMART Detection of airborne pathogens for improved disease management in the UK tomato industry
11:35am	**29. Henry Tidd** (BCP) - Characterisation of major genes mediating resistance to *Septoria Tritici* blotch disease in wheat
11:55am	**31. Manpartik S. Gill** (PS) - Regulation of canopy architecture in wheat by modulating brassinosteroid pathway genes

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12:15pm	**Guest Speaker – Chaired by Claire Kanja** – Fowden Hall - **Ask questions here** **Julian Smith – Science Director, Rothamsted Research - Science, partnerships and careers – my time in international development**
13:00pm	Lunch Break
SESSION 3 – Chaired by Dr Maria Oszvald – Fowden Hall	
14:00pm	**5-minute Poster Introductions** **19. James Brett** (PS) - A major QTL for high fibre in wheat **21. Gavers Oppong** (PS) - A comparative cross-omics analysis of anaerobic germination tolerance in rice **23. William Rickard** (SAS-H) - Structural and hydraulic properties of the extended soil phenotypes on highfield **25. Munisath Khandoker** (SAS-H) – Can smartphone applications revolutionise how we measure soil health?
	Final Year Talks - Ask questions here
14:20pm	**33. Mesfin Kebede Desta** (PS) **-** Linking adsorption – desorption characteristics with grain Zn concentrations and uptake by teff, wheat and maize in different landscape positions in Ethiopia
14:40pm	**35. Petros Sigalas** (PS) - Wheat tillering control in response to n supply: the case of strigolactones
15:00pm	**37. Rohan Richard** (PS) - Exploiting variation in grain protein content and quality to determine effects of environment on processing quality
15:20pm	**Poster session and coffee** – Fowden Hall and Plaza **1. Izayana Sandoval-Carvajal** (BCP) - Assessing the genetic diversity of UK strains of barley yellow dwarf virus (BYDV) **3. Lisa Humbert** (BCP) - Fungal sex factors as novel antifungal compounds for control of plant disease **5. Sandra Lucia Cortes Patiño** (BCP) - Herbivore-plant-soil microbe interactions: who is helping whom **19. James Brett** (PS) - A major QTL for high fibre in wheat **21. Gavers Oppong** (PS) - A comparative cross-omics analysis of anaerobic germination tolerance in rice **23. William Rickard** (SAS-H) - Structural and hydraulic properties of the extended soil phenotypes on highfield **25. Munisath Khandoker** (SAS-H) – Can smartphone applications revolutionise how we measure soil health?
15:50pm	**Session 4 – Training Session for students with Leanne Gunn -** Fowden Hall
17:20pm	Close of day 1

18:00	**'Pizza at the Pav' - Students only**

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Day 2 – Wednesday, 2nd March 2022	
09:30am	**Registration/Coffee** – Conference Centre Plaza
SESSION 5 – Chaired by Victoria Armer – Fowden Hall	
10:00am	**2-minute Poster Introductions** **8. Heike Rolker** (SAS-NW) **-** A systems perspective on food waste: identifying determinants, impacts and trade-offs in low- and middle-income countries **10. Ed Pyne** (BCP) **-** Leveraging antagonistic interactions of wood decay fungi as biocontrol of the destructive forest pathogen *Armillaria*
10:05am	**5-minute Poster Introductions** **12. Sophia Bahddou** (SAS-H) **-** Runoff and soil erosion under different soil surface roughness **14. Beth Roberts** (SAS-H) **-** Quantifying the true costs of farming systems **16. Daniel Kingsley Cudjoe** (PS) **-** Using proximal sensing parameters linked to the photosynthetic capacity to assess the nutritional status and yield potential in quinoa **18. Owen Thornton** (SAS-H) **-** Bioprospecting for plant growth promoting microbes: Rich seams in long-term agricultural field experiments?
	Final Year Talks - Ask questions here
10:25am	**28. Claire Kanja** (BCP) **-** An 'effective' way to infect your host
10:45am	**30. Jesus Castillo** (SAS-H) - Intensification of rice-livestock systems, how sustainable is it in terms of nitrogen
11:05am	**32. Mandy Kao** (SAS-NW) - is the form (organic/inorganic) of mineral supplement to sheep a significant factor to the availability of micronutrients to grass from soil applied with the sheep excreta?
11:25am	**Poster session and coffee** – Fowden Hall and Plaza **2. Hannah Romanowski** (BCP) - Is being smooth the new trend? **4. Aishwarya Shankhapal** (PS) - Mesocotyl elongation for direct seeding of rice varieties **6. Leena Sarah Farhat** (Bangor University) - Bringing big-data to social science **8. Heike Rolker** (SAS-NW) **-** A systems perspective on food waste: identifying determinants, impacts and trade-offs in low- and middle-income countries **10. Ed Pyne** (BCP) **-** Leveraging antagonistic interactions of wood decay fungi as biocontrol of the destructive forest pathogen Armillaria **12. Sophia Bahddou** (SAS-H) **-** Runoff and soil erosion under different soil surface roughness **14. Beth Roberts** (SAS-H) **-** Quantifying the true costs of farming systems **16. Daniel Kingsley Cudjoe** (PS) **-** Using proximal sensing parameters linked to the photosynthetic capacity to assess the nutritional status and yield potential in quinoa **18. Owen Thornton** (SAS-H) **-** Bioprospecting for plant growth promoting microbes: Rich seams in long-term agricultural field experiments?
11:55am	**Guest Speaker – Chaired by Mollie Langdon -** Fowden Hall - **Ask questions here** **Dr Joanna Scales - Project Lead, AgriFood Africa Connect - What's next?**
12:35pm	Lunch Break

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SESSION 6 – Chaired by Dr Guillaume Menard – Fowden Hall	
14:00am	**5-minute Poster Introductions** **20. Marieme Drame** (SAS-NW) - Inclusion of urease inhibitors with urea to effectively reduce ammonia emissions from soil at high temperatures **22. Joseph Oddy** (PS) - Genetic and environmental regulation of free asparagine in wheat grain **24. Imane El Fartassi** (SAS-H) - Agent-based modelling of crop management **26. Musa Kisiriko** (CAS) - Agricultural bioproducts from medicinal and aromatic plants
	Final Year Talks - Ask questions here
14:20pm	**34. Mollie Langdon** (PS) - Unlocking the potential of the pod: increasing seed yields by modulating seed number and seed size
14:40pm	**36. Rahul Nitnavare** (PS) - Identifying novel variation in nitrogen use efficiency and its physiological and genetic basis in wheat
15:00pm	**38. Tom Oliver** (CAS) - The impact of novel insecticides on bumblebee flight capabilities
15:20pm	**Poster session and coffee** – Fowden Hall and Plaza **2. Hannah Romanowski** (BCP) - Is being smooth the new trend? **4. Aishwarya Shankhapal** (PS) - Mesocotyl elongation for direct seeding of rice varieties **6. Leena Sarah Farhat** (Bangor University) - Bringing big-data to social science **20. Marieme Drame** (SAS-NW) - Inclusion of urease inhibitors with urea to effectively reduce ammonia emissions from soil at high temperatures **22. Joseph Oddy** (PS) - Genetic and environmental regulation of free asparagine in wheat grain **24. Imane El Fartassi** (SAS-H) - Agent-based modelling of crop management **26. Musa Kisiriko** (CAS) - Agricultural bioproducts from medicinal and aromatic plants **40. Alexander Borg** (BCP) - Elucidating the mechanisms of aphid resistance in *Triticum monococcum l.* (poaceae)
16:00pm	**VOTING OPENS – Students only, please vote for best in category here!**
16:00pm	**Feedback and close of symposium – Andrew Mead** – Fowden Hall

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Day One

Tuesday, 1st March 2022

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Session 1

Chaired by Mollie Langdon

Fowden Hall

Poster Introductions & Poster Session

Victoria Armer, BCP

UNLOCKING THE DOOR: HOW FUSARIUM GRAMINEARUM EXPLOITS PLASMODESMATA IN WHEAT CELL WALLS DURING HOST-TISSUE COLONISATION

VICTORIA ARMER[1,2], MIKE DEEKS[2] AND KIM HAMMOND-KOSACK[1]

1. DEPARTMENT OF BIOINTERACTIONS AND CROP PROTECTION, ROTHAMSTED RESEARCH, HARPENDEN, AL5 2JQ, UK, 2. BIOSCIENCES, UNIVERSITY OF EXETER, EXETER, EX4 4QD, UK

Abstract:

Fusarium Head Blight (FHB) is a devastating disease of cereal crops worldwide. It is primarily caused by the fungal pathogen *Fusarium graminearum,* infecting crops at anthesis. Infection causes shrivelled, damaged kernels laced with mycotoxins of the trichothecene class, rendering wheat grain unsuitable for both human and livestock consumption[1]. Current control methods are ineffective, and many questions remain unanswered regarding disease progression during host-plant tissue colonisation. Here, the well-studied trichothecene synthase gene Tri5, responsible for the biosynthesis of the potent mycotoxin deoxynivalenol (DON)[2], is re-evaluated. It is found that addition of DON to a DON-deficient *F. graminearum* strain does not restore the WT phenotype *in planta* and infection is still restricted to the infected spikelet. However, I present evidence that DON facilitates the crossing of cytoplasmic communication channels called plasmodesmata. This result poses new hypotheses surrounding the working disease model for *F. graminearum* and opens further avenues of exploration focusing on plasmodesmata.

References:

1. Eriksen and Pettersson (2004). Toxicological evaluation of trichothecenes in animal feed. *Anim. Feed Sci. Technol.* 114: 205-239. 2. Hohn et al. (1993). Evidence for a gene cluster involving trichothecene-pathway biosynthetic genes *in Fusarium sporotrichioides. Current Genetics*. 24: 291-295.

Erika Kroll, SAS-H

USING NETWORK ANALYSIS TO INVESTIGATE HOST-PATHOGEN INTERACTIONS BETWEEN WHEAT AND *FUSARIUM GRAMINEARUM*

ERIKA KROLL[1], MARTIN URBAN[1], NEIL BROWN[2], RYAN AMES[3] AND KIM HAMMOND-KOSACK[1]

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

Abstract:

Fusarium graminearum is the causative agent of the highly destructive fungal disease Fusarium Head Blight (FHB), which infects wheat and other cereals. It causes devastating crop losses by dramatically decreasing grain quality before harvest. Furthermore, the pathogen produces harmful toxins which deem grains unfit for human or animal consumption. Faced with a growing population, climate change, environmental pressures, and fungicide resistance; the ability to control fungal plant pathogens has become a global concern requiring urgent solutions. With *F. graminearum* being one of the most economically important plant pathogenic fungi, developing our understanding of its ability to infect and inflict disease is paramount.

Following the advances of fungal genomics and sequencing technologies (**1**), there have been a substantial number of studies investigating the genetic interaction between *F. graminearum* and its cereal hosts during infection (**2, 3**). These datasets can be synthesised and studied using weighted gene co-expression network analysis (WGCNA) (**4**) to predict and identify key disease-related genes and gene complexes involved in *F. graminearum* infection. Initially a network will be generated to solely study the expression of *F. graminearum* genes during *in planta* infections and compare this with expression during *in vitro* growth. However, this project also aims to eventually develop a dual pathogen-host combined expression network.

References:

1. King, Robert, Martin Urban, and Kim E. Hammond-Kosack. "Annotation of Fusarium graminearum (PH-1) version 5.0." *Genome announcements* 5.2 (2017): e01479-16
2. Kazan, Kemal, and Donald M Gardiner. Transcriptomics of cereal-Fusarium graminearum interactions: what we have learned so far. *Molecular plant pathology* vol. 19,3 (2018): 764-778. doi:10.1111/mpp.12561
3. Dilks, Tess, et al. "Non-canonical fungal G-protein coupled receptors promote Fusarium head blight on wheat." *PLoS pathogens* 15.4 (2019): e1007666.
4. Langfelder, Peter, and Steve Horvath. "WGCNA: an R package for weighted correlation network analysis." *BMC bioinformatics* 9.1 (2008): 1-13.

Mahassine Arhazzal, SAS-H

DOES WHEAT SELECT FOR BENEFICIAL SOIL MICROBIOME WHEN GROWN UNDER ABIOTIC STRESSES?

TIM MAUCHLINE[1], IAN CLARK[1], VANESSA NESSNER-KAVAMURA-NOGUCHI[1], JIM HARRIS[2], MARK PAWLETT[2], ADNANE BARGAZ[3]

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

Abstract:

The planet through climate change is facing many environmental changes that are negatively affecting its natural ecosystems, inducing water scarcity, longer periods of drought, arable land degradation and desertification. The plant microbiome, the full complement of microbes associated with a given plant host, holds promise in contributing to crop production in an environmentally friendly and sustainable way 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. In this work we investigate the ability of different wheat (*Triticum aestivum*) cultivars to select for a beneficial soil microbiome when grown under conditions of abiotic stress with and without fertiliser addition. 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 and salt tolerance. The microbial isolates will be identified by a 16S Sanger sequencing approach.

Tadesse Gashaw Asrat, SAS-H

COMPARISON OF PORTABLE AND BENCH-TOP SOIL SCANNING INSTRUMENTS AND CALIBRATIONS: FOR FERTILIZER DECISION MAKING PERSPECTIVE

[1]TADESSE GASHAW ASRAT, [1] RUBEN SAKRABANI, [1]RON CORSTANJE, [2]KIRSTY HASSALL, [1]TIMO BREURE, [2]STEPHAN M. HAEFELE, [3]FASSIL KEBEDE,

[1]CRANFIELD UNIVERSITY, CRANFIELD, UK; [2]ROTHAMSTED RESEARCH, HARPENDEN, UK; [3]MOHAMMED VI POLYTECHNIC UNIVERSITY, BEN GUERIR, MOROCCO.

Abstract:

Soil spectroscopy could be useful to improve fertilizer decision making in low-income countries where soil testing options are often limited and not accessible to many farmers. Hence, this study compared commercially available soil spectral sensing instrumentations viz., Neospectra, Fieldspec-4 with contact probe and mug light interfaces and Bruker Tensor-II, in their precision, uncertainty and ease of applicability to predict key soil properties for fertilizer decision making. The comparison was made by scanning 350 archived soil samples at Rothamsted Research which were collected from 0-20cm soil depth in agricultural farmlands of Ethiopia, Kenya and Tanzania. Six soil spectral pre-processing techniques and two sub-sampling methods for selecting train and test sets were evaluated for their effect on the prediction of soil properties using a PLSR model. Most of the soil properties (Exch-Al, Exch-Fe, pH, SOC, total N, Exch-Ca, Exch-K, Exch-Mg) were well predicted with a CCC value between 0.88-0.96 and RPIQ between 1.4-5.9 by all the soil scanning instrumentations compared. However, exchangeable iron, SOC and TN prediction precision using Neospectra were inferior to the other instrumentations. Ammonium-oxalate extract of P was predicted better than Olsen-p by all instrumentations, which signify that the conventional soil analysis method should be considered when predicting available soil P. Use of the predictions for the development of fertilizer recommendations gave promising results when compared to the use of the wet chemistry soil characters. In conclusion, the least cost and easily applicable Neospectra can be used to determine major soil properties with a reasonable precision for fertilizer decision making in East African agricultural soils.

Keywords: soil spectral tools and methods, PLSR model, Savitzky-Golay smoothing filter, GAP first derivative, Conditioned Latin Hypercubic, Kennard-Stone sampling.

Frank Gyan Okyere, PS

A NEURAL NETWORK BASED SEGMENTATION METHOD FOR HIGH THROUGHPUT PLANT PHENOTYPING

FRANK G. OKYERE[1], DANIEL K. CUDJOE[2], POURIA SADEGHI-TEHRAN[2], NICOLAS VIRLET[2], DANIEL SIMMS[3], MICHEL GHANEM[4], MANEL MHADA[4], FADY MOHAREB[3], MALCOLM J. HAWKESFORD[2*],

[1,2] ROTHAMSTED RESEARCH, HARPENDEN, UNITED KINGDOM, [3] CRANFIELD UNIVERISTY, CRANFIELD UNITED KINDOM
[4]UNIVERSITY OF MOHAMMED VI POLYTECHNIC, MOROCCO

Abstract:

Image segmentation is a fundamental but critical step to achieving automated plant phenotyping (Adams et al., 2020). For high throughput plant phenotyping, images are acquired from homogenous environments (glasshouse) or from dynamic and complex environments (field). Traditional segmentation methods perform satisfactorily well in environments with uniform background, however, the performance decreases when subjected to more complex environments (Sadeghi-Tehran et al., 2017). Conventional segmentation methods fail when there are disparities in illumination and colour, for example in nutrient deficient plants. This study aims to develop a neural network based robust segmentation tool to phenotype plants in both field and glasshouse environment in a high throughput manner to determine nutritional status.

Digital images from the glasshouse (cowpea and quinoa), subjected to different nutrient level and illumination, were collected over the full growth cycle of the plants. For environment variability, images were also acquired from the field on a phosphorus wheat experiment at flowering stage. Out of a total of 728 images, 30 were annotated using VGG annotator to get the foreground and background patches. Over 500,000 pixels from these patches were used to train 2- layer multi-layer perceptron (MLP), random Forest (SVM) and support vector machine (SVM) to segment the images. Again, traditional based methods combining colour indices, Excess Green (ExG) and Excess Green Red (ExGR), with Otsu segmentation were applied to segment the images. All methods are compared and evaluated using the following criteria: (1) comparison with ground truth images (2) variation with changes in environment (3) estimation of chlorophyll content of wheat based on the segmentation methods.

The proposed method (MLP segmentation) outperformed the other traditional methods giving 87%, 87% and 12.5% segmented for reference consistency, image region consistency and error factor, respectively. It also outperformed the other methods in predicting plant chlorophyll accurately. The proposed method will be an essential tool for a data analysis pipeline development for glasshouse and field-based plant phenotyping.

References:

Adams, J., Qiu, Y., Xu, Y., & Schnable, J. C. (2020). Plant segmentation by supervised machine learning methods. Plant Phenome Journal, 3(1), 1–11. https://doi.org/10.1002/ppj2.20001
Sadeghi-Tehran, P., Virlet, N., Sabermanesh, K., & Hawkesford, M. J. (2017). Multi-feature machine learning model for automatic segmentation of green fractional vegetation cover for high-throughput field phenotyping. Plant Methods, 13(1), 1–17. https://doi.org/10.1186/s13007-017-0253-8

Bader Oulaid, SAS-H

GLOBAL SENSITIVITY ANALYSIS FOR THE CALIBRATION OF AQUACROP FOR WHEAT CROPS IN SEMI-ARID REGIONS

BADER OULAID[1, 2,3], DR ALICE MILNE[2], PROF. RON CORSTANJE[1], DR TOBY WAINE[1], DR RAFIQ EL ALAMI[3], PROF. MARYAM RAFIQI[3]
[1]CRANFIELD UNIVERSITY, CRANFIELD, UK
[2]ROTHAMSTED RESEARCH, HARPENDEN, UK
[3]MOHAMMED VI POLYTECHNIC UNIVERSITY, MOROCCO

Abstract:

Sensitivity analysis (SA) has grown in importance as a tool for analysing eco-system models and supporting model calibration. A global sensitivity analysis (GSA) assessment is carried out on the water driven model AquaCrop for the winter wheat crop in Morocco under different irrigation treatments. The main aim of SA is to identify model parameters that have a considerable impact on canopy cover, yield and above-ground biomass.

First, the Morris method was applied to identify a subset of relevant model parameters. Here, we identified 27 generally important parameters from a set of 29 analysed parameters. These parameters were then used as input for the Fourier Amplitude Sensitivity Test (FAST) in the second step. The overall sensitivity indices were calculated to offer a reliable sensitivity assessment for the AquaCrop model parameters. Finally, GSA-sensitive parameters were used as inputs for a particle swarm optimisation of the model.

The calculation of the main sensitivity indices provided a reliable sensitivity measure for the parameters of the AquaCrop model. The results demonstrated that output variable sensitivity varied in response to crop parameter variation and the sensitivities of the parameters were also shown to be stage-dependent from a day-by-day analysis of canopy cover and biomass simulations.

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Photo Call for Students

Outside Centenary Building

Poster Session

Fowden Hall

1. Izayana Sandoval-Carvajal (BCP)
3. Lisa Humbert (BCP)
5. Sandra Lucia Cortes Patiño (BCP)
7. Victoria Armer (BCP)
9. Erika Kroll (BCP)
11. Mahassine Arhazzal (SAS-H)
13. Tadesse Gashaw Asrat (SAS-H)
15. Frank Gyan Okyere (PS)
17. Bader Oulaid (SAS-H)

1

Izayana Sandoval-Carvajal, BCP

ASSESSING THE GENETIC DIVERSITY OF UK STRAINS OF BARLEY YELLOW DWARF VIRUS (BYDV)

IZAYANA SANDOVAL-CARVAJAL1,2, LAWRENCE BRAMHAM1, MARTIN WILLIAMSON1, GARY FOSTER2 & KIM HAMMOND-KOSACK1

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

Abstract:

Barley yellow dwarf virus (BYDV) is widespread in *Poaceae* family members and represents a notable threat to cereal cultivation, induction potential yield losses of up to 80% in some crops and regions. BYDV is vectored by more than 25 aphid species in a persistent non-propagative manner; however, transmission efficiency relies on aphid species and BYDV strain. There are different BYDV strains, GPV and SGV in the family *Solemoviridae* (genus *Sobemovirus*), and strains kerII, kerIII, MAV, PAS, and PAV in the family *Tombusviridae* (genus *Luteovirus*). BYDV has broad genetic diversity with a shifting taxonomy. One reason for this is the capacity for BYDV to undergo recombination. Currently, the diversity of BYDV across the UK has not been explored, with purely MAV and PAV strains reported. Understanding UK-wide BYDV diversity is crucial for generating novel strategies for mitigating BYDV-associated disease. These include the development of BYDV-resistant cultivars, as well as the development of refined assays for BYDV, enabling robust monitoring for disease. Work here aimed to explore UK BYDV diversity through the use of BYDV coat protein sequencing and phylogenetic analyses. An additional aim was to determine whether, besides MAV and PAV, other BYDV strains were apparent in the UK. Aphid samples of species *Sitobion avenae* and *Rhopalosiphum padi* were collected by the Rothamsted Insect Survey via suction traps located in Brooms barn, Edinburgh, Hereford, Starcross, and York. Total RNA from each sample was extracted after which an optimised RT-PCR reaction was carried out to partially amplify the BYDV coat protein gene. Besides BYDV-MAV and PAV previously reported in the UK, our preliminary results also suggest the presence of GAV and PAS strains in the UK; this has potentially significant ramifications and may be a key finding for improved future BYDV disease management.

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3

Lisa Humbert, BCP

FUNGAL SEX FACTORS AS NOVEL ANTIFUNGAL COMPOUNDS FOR CONTROL OF PLANT DISEASE

DR. DAVID WITHALL, PROF. PAUL DYER AND DR. MIKE BIRKETT

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, SCHOOL OF LIFE SCIENCE, UNIVERSITY OF NOTTINGHAM

Abstract:

Light Leaf Spot, caused by the phytopathogen *Pyrenopeziza brassicae*, is the main fungal disease of oilseed rape in the UK, causing up to £160M yield losses per year. It has also been identified across Northern Europe, Oceania and North America, infecting various brassicas vegetable crops.[1] Current disease management implying the use of common broad-spectrum fungicides, is largely compromised as the European populations are showing decreasing sensitivity to these conventional treatments, thus the development of novel more targeted disease control is required. [2,3] Described dispersal mechanisms outlined the role of both asexual and sexual reproduction during the spread of the pathogen with asexual sporulation being responsible for local spread within fields, whereas wind-borne ascospores (sexual spores) cause lesions to expand over greater distances.[4]

Previous studies demonstrated signalling molecules secreted from mated cultures of *P. brassicae* during their sexual cycle, referred to as Sex Factors (SF), have the ability to repress asexual sporulation and promote the development of fertile apothecia when supplemented on single isolates cultures.[5] This research project will focus on the isolation and characterisation of these phytopathogen's sexual hormones followed by investigating the molecular targets of the SF. Isolation of SF will be achieved through purification of the crude extract using reverse phase HPLC to narrow down the bioactive fraction, facilitating compounds identification by LCMS and NMR techniques. Structural information will allow synthetic access to the compounds in order to conduct investigation of the SF effects on larger scales (i.e. plant organs, individual plants, field trial) for its use as novel disease control agent.

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ROTHAMSTED
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5

Sandra Lucia Cortes Patiño, BCP

HERBIVORE-PLANT-SOIL MICROBE INTERACTIONS: WHO IS HELPING WHOM

SANDRA LUCIA CORTES PATIÑO[1,2], JOHN CAULFIELD[1], AMANDA RASMUSSEN[2], VANESSA NESSNER-KAVAMURA[3]

1. ROTHAMSTED RESEARCH, DEPARTMENT OF BIOINTERACTIONS AND CROP PROTECTION, 2. UNIVERSITY OF NOTTINGHAM, SCHOOL OF BIOSCIENCES, 3. ROTHAMSTED RESEARCH, DEPARTMENT OF SUSTAINABLE AGRICULTURE SCIENCES

Abstract:

Foliar, sap, and root-feeding herbivores are responsible for losses of more than 20% of food production worldwide (1). Finding ways to protect crops from pest damage requires understanding the interplay between biotic and abiotic factors that affect the plant responses to pest attacks. Growing evidence suggests that plant-microbe interactions in the rhizosphere can be involved in the plant defence response to herbivory. Root exudates are at the centre of this interaction acting as chemical signals and nutrients that help plants to influence the microbial communities in the rhizosphere (2,3). By shaping these communities, plants can alter the production of primary and secondary metabolites involved in direct and indirect defence (4). This project aims to understand how aboveground herbivory changes the chemistry belowground and how this, in turn, influences the rhizosphere microbiome affecting plant-microbe and plant-herbivore interactions. To achieve this, we will use wheat-aphid interactions as the plant-herbivore system and determine the composition of metabolites released above and belowground through volatile air entrainment collections and root exudates extraction. Furthermore, we will use a combination of genomics and community-level physiological profiling to understand the function of the altered microbial communities on the response to herbivory. We hope that the knowledge generated will contribute to the design of future agricultural systems that are sufficiently robust to protect crops from pests and provide balanced agroecosystems.

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Session 2

Chaired by Dr Sarah Raffan

Fowden Hall

Final Year Talks

Anastasia Sokolidi, BCP

SMART DETECTION OF AIRBORNE PATHOGENS FOR IMPROVED DISEASE MANAGEMENT IN THE UK TOMATO INDUSTRY

1. JON WEST, 2. JOHN CLARKSON, 3. PHIL MORLEY

1. ROTHAMSTED RESEARCH, HARPENDEN. 2. UNIVERSITY OF WARWICK, COVENTRY
3. APS GROUP, ISLE OF WIGHT

Abstract:

Technologies are constantly evolving that allow the early detection of plant pathogens in crops. The technology used in this project is spore trapping and it is the only technique that can detect the presence of pathogens before they infect the plant. It has been successfully used in the field to guide management strategies and reduce fungicide application or to reduce the use of expensive fungicide during low disease pressure (Mahaffee W.F., 2014). However, this technology isn't widely used in commercial greenhouses because of gaps in essential knowledge on the efficacy of spore trapping in such environments. In this project we have explored the capabilities of this technology to perform in a commercial tomato greenhouses to detect TPM (*Pseudoidium neolycopersici*) along with *Botrytis cinerea* and *Penicillium sp.*. We have used a combination of molecular tools (qPCR, LAMP), spore traps and spatial modelling to determine the efficacy of spore traps in commercial greenhouses and study the spread of *P. neolycopersici*. We have found that the height at which spore traps are placed in a commercial greenhouse don't affect measurements and that there is a strong variability between spore traps depending on the proximity to the source of infection. Even though this research highlights some findings and observations, further research is needed to back the aims that this project set to achieve.

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Henry Tidd, BCP

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

HENRY TIDD (1), KOSTYA KANYUKA (2), JASON RUDD (1), RUTH BRYANT (3), RUMIANA RAY (4)

1: ROTHAMSTED RESEARCH, HARPENDEN, HERTFORDSHIRE. 2: NIAB, CAMBRIDGE, CAMBRIDGESHIRE. 3: RAGT SEEDS, ICKLETON, CAMBRIDGESHIRE. 4: UNIVERSITY OF NOTTINGHAM, NOTTINGHAM, NOTTINGHAMSHIRE.

Abstract:

The fungus *Zymoseptoria tritici*, the causal agent of Septoria Tritici Blotch disease (STB), is one of the most destructive wheat (*Triticum aestivum*) pathogens in Europe and worldwide, causing crop losses of up to 50% under high risk conditions. Few traditional chemical controls remain fully effective against all strains of this fungus, and effective biological controls are not available. Therefore it is vital that existing *Stb* resistance genes are optimally used to protect elite wheat lines while maintaining their own durability against mutations and selection for virulence in *Z. tritici*.

In this project, I have screened 19 known *Stb* resistance genes in 17 wheat lines against an array of up to 90 UK *Z. tritici* field isolates (collected in 2015-2016 to broadly match the genetic diversity of current UK populations) to analyse the efficacy of each resistance. I have also developed KASP markers capable of tracking these *Stb* resistance genes in breeding populations. These data and tools will help to develop efficient breeding systems for the production of elite lines containing effective resistance genes for UK *Z. tritici* populations.

This data also suggests different models for the mechanisms of these different *Stb* genes, which I plan to further examine using fluorescent *Z. tritici* transformants and confocal microscopy. This could help to identify *Stb* resistance genes that would synergise best to improve resistance or durability in combination. I hope that these outcomes from existing and future work in this project will enable the development of wheat lines protected by pyramids of *Stb* resistance genes, providing broad and durable resistance to *Z. tritici* infection.

Manpartik. S. Gill, PS

REGULATION OF CANOPY ARCHITECTURE IN WHEAT BY MODULATING BRASSINOSTEROID PATHWAY GENES

MANPARTIK GILL1, ANDY PHILLIPS1, PETER HEDDEN1, JOHN FOULKES2, STEVE THOMAS1
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2 UNIVERSITY OF NOTTINGHAM, SUTTON BONINGTON CAMPUS, LEICESTERSHIRE LE12 5RD, UK

Abstract:

Due to increasing human population growth 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. A strategy for increasing grain number is to increase the spike density within the crop. This can potentially be achieved by altering canopy architecture to improve radiation use efficiency and allow a higher planting density. Brassinosteroids (BRs) are phytohormones that have an important role in controlling architecture and assimilate partitioning. It is well established that lesions in the BR biosynthesis and signalling pathway can produce more upright canopy architecture in cereals. For example, partial suppression of the *OsBRI1* gene in transgenic rice confers a beneficial erect-leaf phenotype that increases grain yield under higher planting density. In this study, we are investigating the effect of altering the BR pathway in wheat to increase leaf erectness, with a view to increasing spike density and grain yields. Based on studies in other cereals, we have selected the *TaBRI1*, *TaDWF1* and *TaDWF4* genes as candidates BR-related genes for controlling leaf angle. TILLING and EMS mutagenesis-based screens have identified homeologuous loss-of-function mutations. These have been stacked and their effect on canopy architecture has been assessed under glasshouse conditions. Interestingly, *Tabri1bd*, *Tabri1ad*, *Tadwf1abd* and *Tadwf4abd* mutants exhibit increased erectness of flag-leaf angle. To further test the agronomic and phenotypic performance under field conditions a field trial assessment of the BR mutants is currently in progress. Changes in leaf angle in BR mutants are associated with altered laminar joint development. As a strategy to understand the physiological and molecular mechanisms through which BRs control leaf angle, anatomical studies and transcript profiling of the BR mutants will be performed.

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Guest Speaker

Chaired by Claire Kanja

Science, partnerships and careers – my time in international development

Dr Julian Smith

Science Director - Protecting Crops and Environment
Rothamsted Research

Julian has a career in plant health and external affairs, focused on national biosecurity, crop protection and seed systems. In joining Rothamsted in 2021, he provides leadership on science strategy, alongside engagement with UK and overseas governments, academia, foundations and industry. In obtaining a degree (Agri Bot) and PhD (Rhizobia on faba beans) at Aberystwyth University, Julian joined CAB International (CABI) in 1992, addressing crop losses caused by pests and diseases of developing nations. Spanning the delivery and management of overseas field and laboratory projects, he also managed CABI's UK molecular biology laboratory and led on crop GM biosafety. His early research led to the first contained-use GM crop technology approvals for Kenya and South Africa. Julian's career has increasingly focused on plant pest risk assessment and biosecurity, and capacity strengthening of African nations. In moving to Fera Science Ltd in 2005, then Central Science Laboratory, he has furthered this cause under numerous initiatives of seed health and transborder trade. He has worked extensively on Banana Xanthomonas Wilt, Cassava Brown Streak Disease, Cassava Mosaic Disease and Maize Lethal Necrosis. In 2015 he authored a position paper on 'Africa's preparedness for plant pests and diseases under climate change' that informed the UNFCCC Paris Climate.

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Session 3

Chaired by Dr Maria Oszvald

Fowden Hall

Poster Introductions,
Final Year Talks & Poster Session

James Brett, PS

A MAJOR QTL FOR HIGH FIBRE IN WHEAT

JAMES A BRETT, SIMON GRIFFITHS, NOAM CHAYUT, PETER SHEWRY & ALISON LOVEGROVE

ROTHAMSTED RESEARCH, HARPENDEN. AND JOHN INNES CENTRE, NORWICH

Abstract:

Wheat is one of the most important crops in the UK. Wheat-based products are a vital source of dietary fibre, due to the quantity we consume. However, most people fall short of their recommended dietary fibre (DF) intake of 30g per day, per day, with people averaging ~20g. This can have knock-on effects on our health, including increased risk of diabetes, and contributing to poor gut health. Therefore, wheat is a primary target for DF improvement. We are working towards identifying quantitative trait loci (QTLs) associated with high arabinoxylan (AX), the main DF in wheat. To do this, we have 3 populations of Paragon x Watkins (ParW) crosses, which are phenotyped for viscosity and water-extractable (WE) pentosans, to quantify AX. We identified a major QTL on chromosome 1B, which undergo fine-mapping to add evidence for a candidate gene identified from RNA-Seq data on two cultivars Yumai-34 and Valoris, where populations detected the same 1B QTL. This will allow for the development of KASP markers for use in marker-assisted selective breeding programs.

A COMPARATIVE CROSS-OMICS ANALYSIS OF ANAEROBIC GERMINATION TOLERANCE IN RICE

GAVERS OPPONG1,2, HONGTAO ZHANG1, SHALABH DIXIT3, SMITA KURUP1, DARREN WELLS2, FREDERICA L. THEODOULOU1

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2 SCHOOL OF BIOSCIENCES, THE UNIVERSITY OF NOTTINGHAM, SUTTON BONINGTON, LE12 5RD UK
3 INTERNATIONAL RICE RESEARCH INSTITUTE, LOS BAÑOS, PHILIPPINES

Abstract:

Rice (*Oryza sativa*) serves as a staple for more than half of the global population, which makes it an important food security crop worldwide. 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). To elucidate the mechanisms underpinning AG, which are poorly understood, we compared gene and protein expression in a tolerant landrace, Ma Zhan Red, with that in an intolerant, elite cultivar, IR64. Previous studies reported significant transcriptome variation at different time points during AG in rice, indicating the importance of identifying an optimal time window for sampling. Therefore, we studied seedling phenotypes and the expression patterns of five known hypoxia responsive genes at different timepoints during aerobic and anaerobic germination. Subsequently, RNA-seq and quantitative proteomics analysis was performed with embryos and coleoptiles harvested two and four days after planting. Evaluation of RNA-seq and quantitative proteomics data reveals major differences in the transcriptomes and proteomes of the sensitive and tolerant genotypes under AG at both time points. Putative candidate genes related to tolerance in the tolerant variety have been identified for further functional characterization. Ultimately, it is hoped that understanding the mechanisms associated with AG will inform breeding of new varieties tolerant to anaerobic germination.

William Rickard, SAS-H

STRUCTURAL AND HYDRAULIC PROPERTIES OF THE EXTENDED SOIL PHENOTYPES ON HIGHFIELD

WILLIAM RICKARD, ANDY NEAL, RICHARD WHALLEY, SACHA MOONEY, JOHN CRAWFORD

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

Abstract:

If we are to fully realise the potential of soils in our environmental and climate regulation aims. We require a simple measurement system based upon fundamental soil processes. Soil can be described as the expression of biological activity that involves complex interactions between the microbiome and the abiotic parts of the soil. This interaction produces an environment where the structure and the gene abundance of the microbiome are unique. Presently, reading a soil's distinctive message requires techniques that cannot be scaled and relevant to farmers. We are trialling more accessible measurement methods that can be scaled up; these methods give information about soil structure and hydraulic properties. We are testing to see if these methods can be used as a proxy for measuring the soil phenotype and to develop a measurement system that farmers can use.

Munisath Khandoker, SAS-H

CAN SMARTPHONE APPLICATIONS REVOLUTIONISE HOW WE MEASURE AGGREGATE STABILITY?

STEPHAN HAEFELE, ANDY GREGORY, NICK OSTLE

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, LANCASTER UNIVERSITY

Abstract:

Aggregate stability describes the ability of soil aggregates to remain stable against external forces such as rapid wetting and raindrop impact. Stable aggregates can improve soil structure, water holding capacity, and protect organic matter. Aggregate stability is therefore an important physical indicator of soil health. Current methods to measure aggregate stability often involve disrupting soil aggregates in distilled water. These tests are time consuming, require specialised equipment and are usually done in laboratories.

The SLAKES: Soil Aggregate Stability smartphone application, developed by the University of Sydney, Australia, quantifies aggregate stability by measuring how quickly soil aggregates disintegrate once submerged in water. The SLAKES application requires three soil aggregates 1-2 cm in diameter to be placed in a petri dish. Water is added and the SLAKES app provides a measurement of aggregate stability within 10 minutes.

To determine the sensitivity of the SLAKES app, we compared its aggregate stability measurements with that of the established Le Bissonnais method. Soil samples of different texture were taken from under fallow, permanent grass, and continuous arable cropping management from four experimental sites. The SLAKES app was able to differentiate between different managements on clayey soil but, compared to Le Bissonnais, it was less sensitive when tested on sandy soil. Despite this, the SLAKES app is a legitimate method to measure aggregate stability. The app offers a simple, fast, and cheap alternative to standard laboratory methods, allowing land managers and non-scientists to actively test the quality of their soils.

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Mesfin K. Desta, SAS-H

LINKING ADSORPTION-DESORPTION CHARACTERISTICS WITH GRAIN ZN CONCENTRATIONS AND UPTAKE BY TEFF, WHEAT, AND MAIZE IN DIFFERENT LANDSCAPE POSITIONS IN ETHIOPIA

MESFIN K. DESTA1,2, MARTIN R. BROADLEY,1,2, STEVE P. MCGRATH1, JAVIER HERNANDEZ-ALLICA1, KIRSTY L. HASSALL 1, SAMUEL GAMEDA3, TILAHUN AMEDE4, STEPHAN M. HAEFELE1*

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2 FUTURE FOOD BEACON OF EXCELLENCE AND SCHOOL OF BIOSCIENCES, UNIVERSITY OF NOTTINGHAM, UK
3 INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTRE (CIMMYT), ADDIS ABABA, ETHIOPIA
4 AGRA, NAIROBI, KENYA
***STEPHAN.HAEFELE@ROTHAMSTED.AC.UK**

Abstract:

Introduction: The retention and release potential of Zn in soils affects its availability and subsequent uptake by crops and is associated with soil parameters that differ between landscape positions. This study aimed at understanding soil and management factors influencing Zn uptake and grain Zn concentrations of crops grown in a landscape position. **Materials and Methods:** Adsorption-desorption characteristics from a previous study were used to estimate the amount of net soil Zn potentially available for crop uptake. These estimates were compared with grain Zn concentrations and uptake of crops in three different Zn treatments (control/zero, Zn applied during planting (basal), during planting plus additional Zn at tillering (basal plus side dressing) in on-farm trials, and all are applied as solid. **Results and Discussion:** Soils from landscape positions with higher soil pH, SOC, and clay content tended to adsorb more Zn applied as fertilizer and resulted in lower Zn uptake and grain Zn concentrations than soils from landscape positions with lower soil pH, SOC and clay contents. Together, these three factors explained 37–49% of the observed variation in grain Zn concentration. We also found significant correlations of the grain Zn concentration with total Cu and Mg concentrations in soils and Cu and Ca concentrations in the grain, probably related to the Zn uptake from the soil and its translocation to the grain. **Conclusions:** In landscape positions where Zn adsorption is high, application of fertilizer Zn to the soil has little effect whereas in positions with low adsorption it is feasible to increase Zn uptake with applications to the soil. Wheat and teff seem to be more efficient in accumulating net Zn from the soil in the grain whereas maize is the least efficient. Knowledge of soil properties and crop characteristics can help to determine where basal Zn application can be effective and when foliar applications are the better approach.

Keywords: soil Zn, grain Zn, cereals, Zn application, East Africa,

Petros Sigalas, PS

WHEAT TILLERING CONTROL IN RESPONSE TO N SUPPLY: THE CASE OF STRIGOLACTONES

PETROS P. SIGALAS[1,2], PETER BUCHNER[1], STEPHEN G. THOMAS[1], FRANK JAMOIS[3], MUSTAPHA ARKOUN[4], JEAN-CLAUDE YVIN[4], MALCOLM J. BENNETT[2] AND MALCOLM J. HAWKESFORD[1]

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2 PLANT AND CROP SCIENCES, SCHOOL OF BIOSCIENCES, UNIVERSITY OF NOTTINGHAM, NOTTINGHAM, UK
3 PLATEFORMES ANALYTIQUES DE RECHERCHE, AGRO INNOVATION INTERNATIONAL-TIMAC AGRO, SAINT-MALO, FRANCE
4 LABORATOIRE DE NUTRITION VÉGÉTALE, AGRO INNOVATION INTERNATIONAL-TIMAC AGRO, SAINT-MALO, FRANCE

Abstract:

Major plant responses to nutrient-deficient conditions include changes in root and shoot architecture. Above ground plant architecture is shaped by modulating tillering patterns. To facilitate this response long-distance root to shoot signals coordinate plant growth at the whole-plant level. Tillering is known to be regulated by the interaction between 3 classes of phytohormones: auxin, cytokinins and strigolactones (SLs). SLs act as negative regulators of tillering and although they are induced under nutrient limitation, there is little information about their role in low nitrogen-mediated tiller suppression in wheat. To address this question, we studied the transcriptional response of SL metabolic and signalling genes in different tissues in nitrogen-deficient plants. In addition, we generated a DWARF17 (D17) triple knock-out mutant from the hexaploid wheat TILLING population. Transcriptomic analysis in high tillering *Tad17* triple homozygous mutant plants showed that lack of SL biosynthesis results in significant changes in nitrogen responsive genes, resource allocation, and other hormone pathways, highlighting the involvement of SLs in the fine-tuning of regulation of plant architecture in response to nitrogen limitation.

Mesfin K. Desta, SAS-H

EXPLOITING VARIATION IN GRAIN PROTEIN CONTENT AND QUALITY TO DETERMINE EFFECTS OF ENVIRONMENT ON PROCESSING QUALITY

ROHAN RICHARD[1], PETER SHEWRY[1], ALISON LOVEGROVE[1], PAOLA TOSI[2], SIMON GRIFFITHS[3], LUZIE WINGEN[3], AND MERVIN POOLE[4]

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, UNIVERSITY OF READING, READING. 3, JOHN INNES CENTRE, NORWICH. 4, HEYGATES LTD. NORTHAMPTON

Abstract:

A major limitation in breeding wheat combining high grain yield (GY) and grain protein content (GPC) is that these traits are negatively correlated. Monagham et al (2001) therefore suggested the use of the residuals from the linear regression line between GY and GPC, named Grain Protein Deviation (GPD), to identify cultivars with both high GPC and GY. The objective of this study is therefore to identify genomic regions associated with the GPD trait.

A double haploid population of 111 lines derived from a cross between the cultivars Hereward (with a high positive GPD value) and Malacca (which does not show GPD) was grown in two environments, at Rothamsted in 2019 and at Reading in 2020. Quantitative Trait Loci (QTL) analysis revealed a major QTL spanning 2cM chromosome 5B explaining 18% of the variation in GPD and overlapping with a region associated with protein content.

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ROTHAMSTED
RESEARCH

Poster Session

Fowden Hall

1. Izayana Sandoval-Carvajal (BCP)
3. Lisa Humbert (BCP)
5. Sandra Lucia Cortes Patiño (BCP)
19. James Brett (PS)
21. Gavers Oppong (PS)
23. William Rickard (SAS-H)
25. Munisath Khandoker (SAS-H)

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Training Session For Students

Fowden Hall

Close of day one

Click here to join the PhD Symposium - Meeting ID: 444 064 6523 - More ways to join your meeting
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Day Two

Wednesday, 2nd March 2022

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Session 5

Chaired by Victoria Armer

Fowden Hall

Poster Introductions, Final Year Talks & Poster Session

A SYSTEMS PERSPECTIVE ON FOOD WASTE: IDENTIFYING DETERMINANTS, IMPACTS AND TRADE-OFFS IN LOW- AND MIDDLE-INCOME COUNTRIES

HEIKE B ROLKER[1,2], MARK EISLER[1], LAURA CARDENAS[2], TARO TAKAHASHI[1,2]

[1] BRISTOL VETERINARY SCHOOL, UNIVERSITY OF BRISTOL, LANGFORD, UK, [2] ROTHAMSTED RESEARCH, NORTH WYKE, UK

Abstract:

The amount of food waste generated across global food value chains is increasing to date, and more rapidly amongst low-and-middle-income countries (LMICs). Reduction of food waste in LMICs provide multi-layered benefits for their sustainable development, through improved food security, enhanced rural income as well as the creation of environmentally friendly secondary markets (2–4). Food waste occurs in all food systems across the entire food value chain. Food systems, however, are often characterised by long and branching value chains, where narrow interventions to reduce food waste at a local scale do not always achieve a globally optimal outcome. Moreover, progress in waste reduction is hindered by a lack of understanding of indirect determinants and food system dynamics contributing to wastage (5). A system-wide analysis of determinants, intervention strategies and impacts across the full spectrum of value chains is therefore crucial to inform effective policymaking.

In my PhD project I am taking a system's perspective on food waste with the objectives to 1) define relevant sources of food waste in (LMICs) in consideration of expected impacts, unintended consequences, and trade-offs 2) identify and evaluate drivers, determinants and causes of food waste and predict the impact and trade-offs of food waste reduction for sustainable development, 3) determine the cost-effectiveness of food waste reduction strategies in consideration of expected impacts and trade-offs and 4) identify barriers to implementation of waste reduction strategies as described by policymakers, decision-makers and food value chain actors.

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Ed Pyne, BCP

LEVERAGING ANTAGONISTIC INTERACTIONS OF WOOD DECAY FUNGI AS BIOCONTROL OF THE DESTRUCTIVE FOREST PATHOGEN *ARMILLARIA*

ED PYNE(1,2), JOZSEF VUTS(2), SANDRA DENMAN(3), LYNNE BODDY(4), JAMES MCDONALD(1)

1, BANGOR UNIVERSITY 2, ROTHAMSTED RESEARCH, HARPENDEN. 3, FOREST RESEARCH, ALICE HOLT. 4, CARDIFF UNIVERSITY

Abstract:

Armillaria (Honey fungus) is a highly destructive necrotrophic fungal pathogen responsible for significant mortality of woody plants, particularly in heavily managed agronomic settings such as plantations, orchards and vineyards where its presence detrimentally impacts crop yields. Additionally, *Armillaria spp.* are well known secondary pathogens playing critical contributing roles in the most devastating tree disease epidemics in Europe. However, effective methods to manage *Armillaria* are lacking or are unsympathetic to woodland ecosystem function and biodiversity. After initial infection, Armillaria aggressively colonizes the roots and vascular tissues of trees, initiating rapid tissue necrosis and irreversible declines culminating in tree death. After tree death residual colonised wood fragments are able to colonise newly established trees decades after the initial incidence of disease, making *Armillaria* amongst the most challenging fungal pathogens of trees to manage. Dead wood fungi compete fiercely for space within wood to access nutrients. This makes some dead wood fungi highly combative, a trait that makes them ideal candidate biocontrol agents able to displace harmful pathogenic fungi in woodlands.

Our project aims to characterise the combative interactions between *Armillaria* and biocontrol candidates in their natural substrata, wood. We aim to combine RNA-seq on a subset of critical interactions alongside a characterisation of volatile organic compounds using produced during fungal combat (known to be critical determinants of interaction outcomes) using dynamics headspace collection. This data will provide the foundational knowledge required to develop the use of *H. fasciculare* as a potential biocontrol of Armillaria root rot. In addition, we aim to characterise hyphal level interactions between Armillaria and biocontrol candidates using light microscopy. Preliminary results from trials suggest that *Armillaria gallica* hyphae undergo morphological changes when interacting with *Hypholoma fasciculare* hyphae including enlargement, increased septation and apparent vacuolation.

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Sophia Bahddou, SAS-H

RUNOFF AND SOIL EROSION UNDER DIFFERENT SOIL SURFACE ROUGHNESS

SOPHIA BAHDDOU[1], PROF JANE RICKSON[1], PROF WILFRED OTTEN[1], DR RICHARD WHALLEY[2], DR HO-CHUL SHIN[2], DR MOHAMED EL GHAROUS[3]

[1]CRANFIELD UNIVERSITY, CRANFIELD, UK. [2]ROTHAMSTED RESEARCH, HARPENDEN, UK; [3]MOHAMMED VI POLYTECHNIC UNIVERSITY, BEN GUERIR, MOROCCO

Abstract:

Soil erosion is a result of detachment of particles or small aggregates from the soil surface followed by transport of the detached material. One factor that affects surface runoff and soil erosion is the soil surface roughness (SSR). Previous research shows that an increased roughness causes a decrease in runoff and soil loss, whilst other studies point towards the opposite.

To date there have been no studies into the effect of both magnitude and orientation of SSR on runoff, infiltration and soil erosion (i.e. by raindrop splash, and overland flow), occurring simultaneously. In this study, we compared the effects of up-down-slope oriented roughness, across-slope oriented roughness and random roughness, along with a smooth surface. We used a moderate slope gradient of 10%, a simulated rainfall intensity of 90 mm hr^{-1} and storm durations of 15 and 30 minutes. SSR was measured using the chain method before and after the rainfall event. Images of the soil surface were taken using a hand-held laser scanner to monitor the effect of rainfall and overland flow on the morphology.

The outcome of this study shows that rainfall erosivity increases roughness of the initially smooth surface and decreases SSR of the initially rough surfaces. In the random roughness treatment, this decrease was 64% of the pre-rainfall condition. This treatment generated significantly more runoff and soil loss and less infiltration than the other treatments ($p < 0.001$). Contrary to expectations, the across-slope oriented roughness did not always reduce runoff and soil erosion compared to the up-down-slope orientation and the smooth surface.

Keywords: Soil Surface Roughness, Runoff, Infiltration, Soil loss

Beth Roberts, SAS-H

QUANTIFYING THE TRUE COSTS OF FARMING SYSTEMS

BETH ROBERTS, DR. JONATHAN STORKEY, DR. TARO TAKAHASHI, DR. AISLINN PEARSON

1. ROTHAMSTED RESEARCH, HARPENDEN, UK. 2. UNIVERSITY OF BRISTOL, BRISTOL, UK

Abstract:

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).

This project aims 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 key trade-offs will be identified and practical methods to monitor natural capital on farms developed 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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Daniel Kingsley Cudjoe, PS

USING PROXIMAL SENSING PARAMETERS LINKED TO THE PHOTOSYNTHETIC CAPACITY TO ASSESS THE NUTRITIONAL STATUS AND YIELD POTENTIAL IN QUINOA

DANIEL K. CUDJOE[1,2,] FRANK G. OKYERE[1,2,] NICOLAS VIRLET[1], MARCH CASTLE[1], POURIA SADEGHI-TEHRAN[1], PETER BUCHNER[1], ANDREW RICHE[1], MANAL MAHDA[3], MICHEL GHANEM[3], TOBY WAINE[2] FADY MOHAREB[2], AND MALCOLM J. HAWKESFORD[1]

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

Abstract:

Proximal sensing (PS) offers a quick, non-destructive, and accurate assessment of crop N and status which is crucial for optimized fertilizer application and precision crop management. However, its exploitation in connection with the photosynthetic capacity and grain yield in quinoa has been limited. Therefore, any progress in utilizing PS parameters will offer a new paradigm to improve decision-making related to N fertilization in quinoa. The objectives of this study were to (i) evaluate SPAD chlorophyll readings (SPAD) and NDVI as an indicator of N status in quinoa, (ii) monitor N status across the season: how SPAD and NDVI are related over time, and (iii) how the N predictors (SPAD and NDVI) reflect the crop performance in terms of CO2 net assimilation and final grain yield. A nutritional experiment utilizing quinoa (Chenopodium quinoa Willd.) was conducted in the glasshouse at Cranfield University, UK. Quinoa plants were grown under varying N and P input designated as (HN-HP, HN-LP, LN-HP, and LN-LP, with H and L for high and low respectively) in pots in a randomized complete block design with 5 replications. Net assimilation was measured using a gas-exchange system LI-6400XT at 46 days after sowing (DAS) and the corresponding leaves were sampled for mineral analysis by leco combustion and ICP-OES. SPAD-502 and a Polypen were used to measure the chlorophyll index (SPAD) and spectral reflectance (NDVI) on a weekly basis. Furthermore, RGB (Red-Green-Blue) and hyperspectral images were captured using the Cranfield scanalyzer. Final harvest data were collected to assess grain yield. Our results show that NDVI and SPAD displayed similar efficiency as an indicator of N status and correlated strongly with the CO2 net assimilation during the vegetative growth stage. However, the use of the SPAD seems to be better correlated to grain yield in our conditions than NDVI. These present findings provide insights towards the understanding of the nutritional status of quinoa and the potential for proximal sensing tools to monitor crop performance across the growing season. Further analysis will be performed to compare the spectrally generated data with RGB-derived vegetation indices and hyperspectral data for high-throughput phenotyping analysis.

Keywords: Proximal sensing, N status, photosynthetic capacity, quinoa, high-throughput phenotyping

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Beth Roberts, SAS-H

BIO-PROSPECTING FOR PLANT-GROWTH-PROMOTING MICROBES: RICH SEAMS IN LONG-TERM AGRICULTURAL FIELD EXPERIMENTS?

OWEN THORNTON[1,2], GLYN BARRETT[2], IAN CLARK[1], ROBERT JACKSON[2,3], TIM MAUCHLINE[1]

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

Abstract:

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 each of the different combinations of these treatments have acted continuously on resident soil microbes over the last 175+ years. Moreover, crop plants repeatedly cultivated under these specific conditions may promote or supress specific members of their associated microbial communities accordingly, further increasing the diversity of relevant plant-microbe associations fostered by the experiment. High-throughput characterisation of a library of ~5000 root-associated microbes recently isolated from a selection of Broadbalk treatment plots has begun to reveal the distribution of key traits and will enhance our interpretation of a comprehensive field-wide amplicon sequencing survey aimed at dissecting the determinants of effective microbial plant-growth-promotion in the field.

Claire Kanja, BCP

AN ‘EFFECTIVE’ WAY TO INFECT YOUR HOST

CLAIRE KANJA[1,2], JASON RUDD[1], MATT DICKENSON[2], KIM HAMMOND-KOSACK[1]

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

Abstract:

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 (FHB), one of the most destructive diseases threatening wheat production worldwide.

Effectors are small secreted proteins produced by a pathogen that manipulate the host to aid colonisation. 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 2012, finding candidates suitable for functional studies from a pool of almost 300 secreted proteins with unknown functions remains problematic.

I have adopted *in silico* bioinformatic pipelines that consider a multifaceted approach to effector discovery such as transcriptional analysis (RNA-seq and microarray), proteomics, taxonomic distribution analysis and the genomic location of candidates. This has proven to be successful in finding clusters of candidate effectors in multiple filamentous phytopathogens. By taking a two-pronged approach for the functional characterisation of candidates, I have identified a paralogous pair of effectors that are expressed during the early symptomless stage of *F. graminearum* infection. These effectors, FgSSP34 and FgSSP53 are adjacent to each other on the *F. graminearum* chromosome and divergently orientated. Both effectors, in this orientation are highly conserved within the wider *F. graminearum* species complex (FGSC). Of the pair, FgSSP53 induces cell death in the non-host *Nicotiana benthamiana,* however, the second isoform of FgSSP53 found within FGSC does not. Within the host system, viral overexpression of FgSSP53 using BSMV-VOX in wheat, reduces disease severity of FHB. FgSSP53 deletion mutants have reduced pathogenicity in both wheat coleoptiles and mature wheat ears.

Jesus Castillo, SAS-H

INTENSIFICATION OF DIFERENT TEMPERATE RICE ROTATIONS AND IT IMPLICANCES IN TERMS OF NITROGEN

JESUS CASTILLO [1,2,3], GUY KIRK [2], JORDANA RIVERO [1], JOSE TERRA [3], WALTER AYALA [3], STEPHAN HAEFELE [1]

1, ROTHAMSTED RESEARCH, HARPENDEN. 2, CRANFIELD UNIVERSITY. 3, INIA URUGUAY

Abstract:

Based on a nitrogen (N) circular economy strategy, the Uruguayan rice-livestock system has been capable to combine high productivity with high N efficiency parameters values sustainably. Nevertheless, the system has been recently intensifying, adding more fertiliser N, or including other crops to the rotation but without considering the externalities of these changes. Here, we assessed three rice rotations: continuous rice (Ri-Ri), rice-soybean (Ri-Soy) and the business-as-usual rice-pasture-livestock rotation (Ri-Liv), in terms of N balance (N-BAL = N inputs minus all the N outputs), N surplus (N-SUR = N inputs minus N in food products) and the full chain N use efficiency (FCh-NUE= ratio among N in food and all the N inputs). Nitrogen inputs considered were fertiliser, biological fixation and atmospheric depositions, whereas N outputs considered were N in food products, gaseous losses and leaching. We assessed field and modeled data from 9 years of a rice-long term experiment. N inputs were different (108, 79 and 39 kg N ha^{-1} yr^{-1} for Ri-Ri, Ri-Soy and Ri-Liv respectively), while N outputs of Ri-Soy and Ri-Ri (90 and 82 kg N ha^{-1} yr^{-1} respectively) were higher than Ri-Liv (42 kg N ha^{-1} yr^{-1}). The N-BAL was positive for Ri-Ri (26 kg N ha^{-1} yr^{-1}) and negative for Ri-Soy and Ri-Liv (-12 and -3 kg N ha^{-1} yr^{-1} respectively) while the annual N-SUR was different (102, 73 and 29 kg N ha^{-1} for Ri-Ri, Ri-Soy and Ri-Liv respectively). The FCh-NUE was higher in the Ri-Soy (98%) compared with Ri-Ri and Ri-Liv (64 and 57% respectively). Environmentally, the high FCh-NUE of the Ri-Soy could indicate a soil N mining risk while high losses to the environment are likely for the Ri-Ri system. Further improvement of N management must be done to successfully intensify the rice rotations without generate negative environmental issues.

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Pei-Tzu Kao (Mandy), SAS-NW

IS THE FORM (ORGANIC/INORGANIC) OF MINERAL SUPPLEMENT TO SHEEP A SIGNIFICANT FACTOR TO THE AVAILABILITY OF MICRONUTRIENTS TO GRASS FROM SOIL APPLIED WITH THE SHEEP EXCRETA?

P.-T. KAO[1,4], H. WARREN[2], T. DARCH[1], S. MCGRATH[3], H.L. BUSS[4], M.R.F. LEE[1,4]

1, ROTHAMSTED RESEARCH, NORTH WYKE. 2, ALLTECH BIOSCIENCE CENTRE. 3, ROTHAMSTED RESEARCH, HARPENDEN. 4, UNIVERSITY OF BRISTOL.

Abstract:

In a grazing livestock system, mineral supplements are often given to the animals prophylactically and routinely as part of the standard practice to prevent potential micronutrient deficiency. Substantial studies have been conducted to investigate the absorbability of mineral supplements of different chemical forms in animals. However, there is no study, to the author's knowledge, investigating whether the administration of mineral supplements would alter the ultimate availability of micronutrients to grass in soil applied with the excreta of the animal given the supplementation. To investigate the impact of the mineral supplement on the flux micronutrient in a pasture system, a sheep experiment and a lysimeter-pot experiment were carried out. Twenty-four sheep were given organic/inorganic minerals (Cu, Mn, Zn and Se) at European industrial levels for 2 weeks. The concentrations and total output of nutrients in urine and faeces were analysed. The results showed that the supplemental mineral form did not significantly influence the partitioning and total excretion of the micronutrients in urine and faeces. Afterwards, soils of different OM contents were applied with the urine, faeces or the combination collected from the sheep experiment. Perennial ryegrass (*Lolium perenne*) was grown in the soils for 6 weeks (3 harvests). The total uptake by grass and the concentrations of micronutrients in grass, soil and leachate were analysed. The results indicate that the supplemental mineral form had no consistent influence on the grass uptake and leaching of Zn, Cu, Mn and Se. Compared to the supplemental mineral form, soil OM content and excreta type had a more significant and consistent impact on micronutrients uptake by perennial ryegrass. Among the excreta types, urine played a more important role than faeces due to the synergistic effect between macronutrients and micronutrients. The Se uptake by grass was dominated by soil OM content. The treatment of excreta might have driven microbial reduction which transformed the Se into a less-mobile form that was fixed by soil OM or Fe oxides and, therefore, became less available to the grass.

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ROTHAMSTED
RESEARCH

Poster Session

Fowden Hall

2. Hannah Romanowski (BCP)
4. Aishwarya Shankhapal (PS)
6. Leena Sarah Farhat (Bangor University)
8. Heike Rolker (SAS-NW)
10. Ed Pyne (BCP)
12. Sophia Bahddou (SAS-H)
14. Beth Roberts (SAS-H)
16. Daniel Kingsley Cudjoe (PS)
18. Owen Thornton (SAS-H)

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Hannah Romanowski, BCP

IS BEING SMOOTH THE NEW TREND?

H ROMANOWSKI[1,2], G. JONES[1], J. BELL[2], K. HASSELL[2]. K. BOUGHEY[3], S. NEWSON[4],

1, BRISTOL UNIVERSITY. 2, ROTHAMSTED RESEARCH. 3, BAT CONSERVATION. 4, BRITISH TRUST FOR ORNITHOLOGY TRUST

Abstract:

The methods behind estimating population trends from survey data is an evolving process that aims to accurately capture the changes in population abundance, usually over long periods of time with large datasets. Recently, studies have used non-linear, as supposed to traditional linear relationships, to produce a more informative output that captures the fluctuations and subtleties of population change over increasingly longer periods of time. This study uses world-class survey data collected by the British Trust for Ornithology (BTO) and Bat Conservation Trust (BCT) to estimate population trends for two bird and three bat species over 25 years, using generalised additive models (GAMs). Data for both is collected annually by citizen science approaches, in which volunteers use standardised methods to count species at multiple sites. The UK trends produced here successfully reproduce those published by the BTO and BCT. Swallows (*Hirundo rustica*) and swifts (*Apus apus*) were found to be in decline, while pipistrelle bat species (*Pipistrellus pipistrellus* and *Pipistrellus pygmaeus*) were found to be significantly increasing. Greater horseshoe bats (*Rhinolophus ferrumequinum*) were found to have increased significantly since the start of data collection, however numbers in the UK are known to be low and these trends must not result in complacency of conservation efforts. The contrast between trends in insectivorous birds and bats is another far-reaching but interesting observation. Dissecting the reasons for success in bat species, as supposed to birds with a similar diet, may enlighten us on the drivers of declines in aerial birds.

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Aishwarya R Shankhapal, PS

MESOCOTYL ELONGATION FOR DIRECT SEEDING OF RICE VARIETIES

AISHWARYA R SHANKHAPAL[1,2], GUILLAUME MENARD[1], LEAH BAND[2], MALCOLM BENNETTE[2], SMITA KURUP[1], PETER EASTMOND[1]
[1]ROTHAMSTED RESEARCH (HARPENDEN), [2]UNIVERSITY OF NOTTINGHAM

Abstract:

More than half of the world's population relies on rice cultivation as it is a staple food for them. Puddled transplanting is the most traditional and widely used method for cultivation of rice (Farooq et al., 2010). Though this transplanting system leads to high losses of water and reduces soil permeability. Huge water inputs, labour costs, labour requirements lead to reduced profit margins (Pandey and Velasco, 1999). Due to all these reasons, farmers are switching from puddled transplanting of rice to dry direct seeding of rice (DSR). Apart from high economic returns, DSR has several advantages such as DSR crops are faster and easier (Farooq et al., 2008) to plant, less labour intensive and consume less water (Bhushan et al., 2007, Jehangir et al., 2005). Mesocotyl elongation is important for seedling vigour in direct seeding as it helps the shoot emerge from the soil after germination. Elongation of this organ varies between genotypes (Wu et al., 2015) and gets affected by various parameters such light exposure, temperature, and water (Feng et al., 2017), so the aim of the project is to investigate the genetic regulation behind mesocotyl elongation. Genome wide association studies (GWAS) (Menard et al.,2021) and comparative transcriptomics by RNA seq has been performed in our group for finding the promising candidate genes which might have a role in mesocotyl elongation. Transgenic cv. IR64 rice lines have been made that overexpress the shortlisted candidate genes or knock them out (CRISPR-Cas9). The PhD involves characterizing these lines and validating the function of the gene(s). It also compromises of investigating how environment contributes to the control of mesocotyl length.

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Leena Sarah Farhat, Bangor University

BRINGING BIG-DATA TO SOCIALSCIENCE

L. S. FARHAT, J. ROBERTS, W. TEAHAN

BANGOR UNIVERSITY

Abstract:

This project seeks to combine these data to holistically value nature's contributions to people, drawing on existing data from a range of several national surveys. Using Supercomputing Wales, Natural Language Processing (NLP) will be applied to analyse the quantitative data within these surveys. Then advanced visualization techniques will be developed to enable the comparison of the qualitative free text responses and quantitative survey data, which includes distance travelled and length and regularity of visits. All of this will allow for quick and simple data analysis geared towards social science. The ability to visualize both quantitative and qualitative data at national-scales may transform sustainable decision-making.

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Guest Speaker

Chaired by Mollie Langdon

What’s Next?

Dr Joanna Scales

Project Lead,
AgriFood Africa Connect

Joanna works in the AgriFood team at Innovate UK KTN on the GCRF AgriFood Africa programme which builds connections and supports innovation between the UK and Africa. Joanna completed her PhD on the heat tolerance of wheat at Rothamsted Research and the University of Essex. After her PhD Joanna worked in science policy in the UK before moving to East Africa to work on delivering agricultural services for smallholder farmers across a range of different supply chains.

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Session 6

Chaired by Dr Guillaume Menard

Fowden Hall

Poster Introductions,
Final Year Talks & Poster Session

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Marieme Drame, SAS-NW

INCLUSION OF UREASE INHIBITORS WITH UREA TO EFFECTIVELY REDUCE AMMONIA EMISSIONS FROM SOIL AT HIGH TEMPERATURES

AUTHORS: MARIEME DRAME[1,2], ALISON CARSWELL[1], SIGRID HEUER[4], MARTIN JEMO[3], GUY KIRK[2], MARK PAWLETT[2], WILLIAM ROBERTS[1], MARIA OSZVALD[5], TOM MISSELBROOK[1]

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Abstract:

Inclusion of urease inhibitors (UI) with urea can effectively reduce ammonia (NH_3) emissions from surface-applied urea. However, research into the efficacy of UI has predominantly focussed on temperate regions, whereas little is known about UI efficacy at high temperatures (> 25°C) favourable to rapid nitrogen (N) turnover.

This study explores the efficacy of UI at high temperatures, in terms of reducing NH_3 emissions and their impact on nitrous oxide (N_2O) emissions. The UI were evaluated over a 35-day incubation at 15, 25 and 35°C within controlled environments, laid out in a randomized complete block design, with three replications of four fertiliser treatments: urea; urea with a single UI (N-(n-butyl) thiophosphoric triamide (NBPT)); urea with two UI (NBPT and N-(n-propyl) thiophosphoric triamide (NPPT)) and a zero-N control.

Inclusion of UI with urea, relative to urea alone, delayed and reduced the NH_3 emission peak by three days and 91% at 15°C, by one day and 80% at 25°C, and by one day and 67% at 35°C. Under all fertiliser treatments soil-NH_3 emission was negligible 14 days after fertilisation at 15 and 25°C. However, at 35°C, NH_3 emission was marginal at 20-25 days after fertiliser addition. The inclusion of UI with urea reduced cumulative NH_3 losses by 87, 75 and 48% relative to urea alone, at 15, 25 and 35°C, respectively. For N_2O emissions, temperature had a significant impact on cumulative N_2O emission, with greater emissions at 35°C relative to 25°C. Cumulative N_2O emissions generally increased (non-significantly) when UI were included with urea, representing 1.9% of applied N compared to 1.7% for urea. Our results suggest that inclusion of UI with urea effectively reduces NH_3 losses from urea at temperatures reaching 35°C, but may slightly increase N_2O emissions, making UI a viable strategy for mitigating NH3 emissions from urea within warmer climates.

Keywords: Nitrogen fertiliser; Urease enzyme; Greenhouse gas; Mitigation strategy; Sub-Saharan Africa

Acknowledgements: This work was conducted as part of the Rothamsted Research, Cranfield University and Mohammed VI Polytechnic University collaboration under the SAFA programme, funded by OCP group. We gratefully acknowledge Origin Fertilisers (UK) and Diamond Fertilisers (UK) for providing the fertiliser products.

Joseph Oddy, PS

GENETIC AND ENVIRONMENTAL REGULATION OF FREE ASPARAGINE IN WHEAT GRAIN

JOSEPH ODDY[1], MARK WILKINSON[1], J. STEPHEN ELMORE[2], STEPHEN PEARCE[1], NIGEL G. HALFORD[1],

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2. DEPARTMENT OF FOOD & NUTRITIONAL SCIENCES, UNIVERSITY OF READING, WHITEKNIGHTS, READING, RG6 6DZ, UNITED KINGDOM

Abstract:

Understanding the genetic and environmental regulation of grain asparagine content in wheat is important in order to reduce dietary intake of acrylamide, a processing contaminant that forms from asparagine during baking. Quantitative trait loci (QTL) controlling grain asparagine content have been sought since the discovery of acrylamide in food in the early 2000s, but stable QTL across environments have been lacking. We recently identified a QTL controlling grain asparagine content in sulphur sufficient environments that is caused by a deletion of the asparagine synthetase 2 homeologue *TaASN-B2*. To identify and characterise further QTL, we are also analysing a soft wheat mapping population for amino acids and other quality traits. Finally, we are investigating the optimal agronomic strategies for controlling grain asparagine content through a series of field trials. Combining genetic and agronomic strategies for the control of grain asparagine content represents a promising strategy for controlling dietary acrylamide intake.

References:

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Imane El Fartassi, SAS-H

AGENT-BASED MODELLING OF CROP MANAGEMENT

[A,B,C] IMANE EL FARTASSI, [A]ALICE MILNE, [B]RONALD CORSTANJE, [C]RAFIQ EL ALAMI, [C]MARYAM RAFIQI, [B]TOBY WAINE

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Abstract:

Climate change poses substantial challenges to Africa and threatens the viability of many sectors, mainly agriculture. Therefore, understanding how farmers respond to climate change and factors that influence the choice of crop management would contribute to determining farmers adaptive capacity and willingness to engage in cooperative strategies as a mitigation solution to alleviate the negative impacts of climate change. Surveys were distributed to farming stakeholders and professionals who worked across the contrasting environments of Morocco. There were 277 responses recorded in total. This study employed both descriptive statistics and the Poisson model to estimate the factors influencing farmers' decision-making. The results show that Moroccan agriculture is characterized by the dominance of cereals and olive trees, conventional tillage, drip irrigation and chemical fertilizer use. We found that that agricultural management practices are mainly impacted by environmental factors and crop profile characteristics. Moreover, achieving a high-income yield and getting access to a range of fertilisers at competitive prices are the crucial factors impacting fertilizers consumption. We also note that the dominance of low-input cropping systems mainly cereal monoculture is the key driver of biodiversity loss, and no contingency strategy is anticipated to face severe drought when farmers are not yet affected by water shortages.

Musa Kisiriko, CAS

AGRICULTURAL BIOPRODUCTS FROM MEDICINAL AND AROMATIC PLANTS

MUSA KISIRIKO[1, 2, 3], JANE L. WARD[1], MICHAEL H. BEALE[1], MARIA ANASTASIADI[2], LEON A. TERRY[2], MANSOUR SOBEH[3]

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Abstract:

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

Biostimulants and bioprotectants (bioproducts) are ecologically friendly and potentially sustainable options derived from natural sources [2]. Extracts from plants, in particular medicinal and aromatic plants (MAPS) present major sources of bioactives [3]. MAPs are abundant in arid areas of Morocco but many of them have not been assessed for their bioactive potential. This research seeks to identify active entities from MAP extracts and develop novel bioproduct formulations for use in African agriculture.

Extracts of selected MAPs from Morocco have been screened using NMR, LC-MS, and GC-MS to characterise compounds comprising their metabolomes. Crude extracts have been trialled in biostimulant and bioprotectant assays to provide indications of bioactivity. In biostimulant tests, germination assays using wheat and pot experiments using tomatoes have been completed. For bioprotectant assessment, initial antifungal assays on pathogens relevant to major African (Moroccan) crops have also been done.

Several compounds from both the polar and non-polar metabolomes including novel metabolites have been identified from *Acacia gummifera*, *Origanum compactum*, *Origanum majorana* and *Ammodaucus leucotrichus*. In wheat germination assays, *A. gummifera* and *A. leucotrichus* showed the highest biostimulant effects. *A. gummifera* increased root lengths, dry weights, and seedling vigour by up to 23%, 15% and 25% respectively. *A. leucotrichus* increased shoot lengths and fresh weights by up to 30% and 24% respectively. None of the extracts, both polar and non-polar has had any antifungal effect on the tested pathogens and further tests are to be undertaken.

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Mollie Langdon, PS

UNLOCKING THE POTENTIAL OF THE POD: INCREASING SEED YIELDS BY MODULATING SEED NUMBER AND SEED SIZE

MOLLIE LANGDON[1], DR GUILLAUME MENARD[1], DR LAURA SILES-SUAREZ[1], DR PETER EASTMOND[1], DR HANS-WILHELM NUETZMANN[2], DR JAMES DOUGHTY[2] AND DR SMITA KURUP[1]

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Abstract:

In a world facing climate change and increasing populations, 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 yields could be to improve parameters that control yield, such as 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 to 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 seeds 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 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.

On the other hand, seed yields can 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) on seed yields of crops such as *Brassica oleracea*.

Overall, this PhD project aims to investigate the impact of manipulating seed number and seed size on seed yields in *Arabidopsis* and *Brassica*.

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Rahul Nitnavare, PS

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

RAHUL NITNAVARE[1,2]*, MALCOLM HAWKESFORD[2]*, JOHN FOULKES[1]*, ANDREW RICHE[2], PETER BUCHNER[2], LUZIE WINGEN[3] AND SIMON GRIFFITHS[3]

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Abstract:

The excess use of nitrogen (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 Nitrogen-use efficiency (NUE). In wheat, there is relatively small genetic variation in adapted elite germplasm in N-uptake efficiency (NUpE) and N-utilization efficiency (NUtE), which are two key components of the NUE. This study therefore aims to identify novel variation for NUE and associated traits by screening diverse wheat germplasm. The BBSRC Designing Future Wheat (DFW) Breeder's Diversity Toolkit of hexaploid wheat, including near-isogenic lines (NILs) derived from Watkins's landraces backcrossed to Paragon, was screened at two different locations (Rothamsted Research and Sutton Bonington) in 2018-19. These NILs were phenotyped in addition at Rothamsted Research in 2019-20. The NILs with QTLs related to NUE traits like aboveground dry matter (AGDM), straw DM and grain filling thermal time (GFPTT) with alleles from Watkins's landraces had significantly higher Normalised Difference Vegetative Index (NDVI) than Paragon at anthesis. These NILs showed higher biomass and grain yield than positive check line paragon. The grain yield at Rothamsted site was higher (1-1.8 t/ha) as compared to Nottingham site in 2018-19. Based on the results in the field experiments in 2018-19 and 2019-20, a subset of 5 NILs with QTLs previously identified for aboveground DM (AGDM), Combine grain weight (COMGRWT) and Combine Straw weight (COMSTR) was selected for the RNAseq analysis. The RNAseq field experiment was carried out under high and low N on flag leaf samples at post anthesis in 2020-21. The RNAseq data are being analysed to identify the candidate genes having differential expression. Moreover, an *In-silico* QTLs data analysis is being carried out as a parallel approach to identify candidate genes. Subsequently, shortlisted genes will be used for targeted mutagenesis experiment in the future.

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Tom Oliver, SAS-H

THE IMPACT OF NOVEL INSECTICIDES ON BUMBLEBEE FLIGHT CAPABILITIES

TOM OLIVER, PAUL CROSS, ANDY REYNOLDS, JAMES MAKINSON AND LARS CHITTKA
1, ROTHAMSTED RESEARCH, HARPENDEN. 2, BANGOR UNIVERSITY, BANGOR

Abstract:

Since the ban of ‘bee-killing’ neonicotinoid pesticides across the EU, a number of novel pesticides with similar chemical structures have become commercially available. The impact these pesticides may have on key pollinator species such as bumblebees remains unknown. Through the use of tethered flight mills I aim to quantify the impacts of sublethal exposure of two novel pesticides on *Bombus terrestris* flight behaviour.

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Poster Session

Fowden Hall

2. Hannah Romanowski (BCP)
4. Aishwarya Shankhapal (PS)
6. Leena Sarah Farhat (Bangor University)
20. Marieme Drame (SAS-NW)
22. Joseph Oddy (PS)
24. Imane El Fartassi (SAS-H)
26. Musa Kisiriko (CAS)
40. Alexander Borg (BCP) – not in attendance

ROTHAMSTED
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Alexander Borg, BCP

ELUCIDATING THE MECHANISMS OF APHID RESISTANCE IN *TRITICUM MONOCOCCUM* L. (POACEAE)

ALEXANDER BORG[1,2], JOHN CAULFIELD[1], JOZSEF VUTS[1], JOHN FOULKES[2], MICHAEL BIRKETT[1]

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2: DIVISION OF PLANT AND CROP SCIENCE, SCHOOL OF BIOSCIENCES, UNIVERSITY OF NOTTINGHAM, SUTTON BONINGTON, LOUGHBOROUGH, LEICESTERSHIRE LE12 5RD, UK

Abstract:

Previous studies have identified greater aphid resistance in the wheat ancestor *Triticum monococcum,* compared to modern wheat varieties. The aim of this study is to characterise the antibiotic mechanisms underlying aphid resistance in *T. monococcum* MDR049, focusing on the role of its secondary metabolites (SMs). Two hypotheses were tested: (i) induction of aphid resistance in MDR049 is aphid density-dependent and (ii) aphid resistance mechanisms are systematically induced upon aphid feeding. The hypotheses were tested using artificial feeding assays to assess *Sitobion avenae* responses to leaf extracts, followed by bioassay-guided fractionation to identify and isolate the bioactive compounds. Extracts were collected from plants at 0, 1, 5, 10 and 25 *S. avenae* infestation densities and *T. aestivum* cv. Solstice was used as an aphid-susceptible control. HPLC and LCMS analyses were used to assess the leaf extract chemistry.

MDR049 leaf extracts were antibiotic against *S. avenae* after 24hrs and 48hrs, reducing adult survival and number of nymphs. MDR049 has a threshold of 5 aphids to induce a significant antibiotic activity at the aphid feeding site. This activity is reversed on the same leaf near the feeding site and not affected on a different leaf. PCA analysis of MDR049 leaf SMs, identified by LCMS, shows changes in trends with increasing aphid density compared to Solstice, with signs of a systemic reaction to aphid feeding on the same leaf as the feeding site. Bioassay-guided fractionation has identified peaks potentially responsible for the antibiotic activity observed in MDR049.

In conclusion, SM changes in MDR049 are aphid density-dependent and may be related to its aphid resistance mechanisms. MDR049 shows signs of a systematic response to aphid feeding. The SMs potentially responsible for this aphid antibiotic activity have been isolated. Ongoing work is identifying and confirming activity of these SMs.

Key words: *Triticum monococcum*, *Sitobion avenae*, secondary metabolites, antibiosis

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VOTING OPENS!

Students only, please vote for best in category here!

Feedback and Close of Event

Andrew Mead

Fowden Hall

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Thank you for attending!

We would like to say thank you to…..

The students for attending and taking part in the event. With a special thanks to the students and staff who have helped with the organisation of the event and the chairing of sessions.

The Rothamsted Conference Centre staff for all they have done in the preparation and hosting of the event.

VCU for printing posters and for taking the group photo.

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