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ASSOCIATION OF APPLIED BIOLOGISTS

# MONOGRAM

CEREALS & GRASSES RESEARCH NETWORK

# MONOGRAM'26

24 - 26th March 2026

Robinson College, University of Cambridge



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# MONOGRAM

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CEREALS & GRASSES RESEARCH NETWORK

The Monogram Network was established in 2005 and consists of mostly UK-based researchers with an active interest in small grain cereals and grass (including C4 energy grasses). A primary aim is to link academia with commercial science and crop breeding, Monogram 2026 will include both basic and more applied research and its members span disciplines including plant genetics, physiology, pathology, breeding, and bioinformatics.

Scientific Organisers of Monogram 2026: Stéphanie Swarbreck and Kostya Kanyuka

# Final Programme

# Tuesday 24th March 2026

0800 **Registration Opens**

0920 **Welcome**
**Stéphanie Swarbreck**

## 0930 Session 1: Staying Ahead of the Outbreak: Biotic Threats & Defences
**Chairs: Kostya Kanyuka and Nikki Walter**

0930- 1010 **RANK PRIZE SPEAKER**: **Cyrille Saintenac**
**Université Clermont Auvergne**
From resistance to susceptibility to *Septoria tritici* blotch: the Stb16q story

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1010-1025 **Jade van Wijk, Earlham Institute**
Using airborne DNA sequencing for cereal rust surveillance across multiple agricultural sites

1025-1040 **Katie Hawkins, University of Nottingham**
Exploiting wheat-wild relative introgression lines as a source of barley yellow dwarf virus (BYDV)

1040-1055 **Bernice Waweru, John Innes Centre**
From k-mers to candidates: Dissecting structural diversity and novel resistance haplotypes at the wheat Yr47/Lr52 locus backup







***Thanks to KWS for sponsoring Session 1***

1100-1130 **BREAK**

## 1130 Session 2: Cultivating Good Company: Probiotics for Plants
**Chairs: Fiona Leigh & Lu Lu**

1130-1210 **Tim Mauchline, Rothamsted Research**
Soil type, crop species and agrochemicals shape root microbiomes: new resources and insights

1210-1225 **Nikki Walter, University of Nottingham**
N it to win it: small package, big impact

1225-1240 **Cristina Barrero Sicilia, University of Hertfordshire**
Field performance evaluation of a carbon quantum dot–based crop enhancer on rice using yield and biomass traits

1230-1255 **Karol Kukula, University of Nottingham**
Optimizing nitrogen-use efficiency components: a comparison of landrace and elite malting barley

1300- 1400 **LUNCH**

## 1400 Session 3: Beyond Yield: Grain Quality & Human Nutrition
**Chairs: Carus John-Bejai and Becca Testa**

1400-1440 **Alison Lovegrove, Rothamsted Research**
Exploiting wheat diversity for improved human diet and health

1440-1455 **Anshu Prajapati, Ben-Gurion University of the Negev**
Enhancing barley nutritional quality for sustainable agriculture through genome editing of lysine metabolism

1455-1510 **Sibongile Zimba, University of Bristol**
Future-proof crops: uncovering effects of future climate stresses on root ideotypes and impact on wheat grain nutritional quality

1510-1525 **Nupur Tailor, Harper Adams University**
Genetic variation and genome-wide association analysis of β-glucan (mixed linkage) in a diverse spring naked barley panel

1530- 1600 **BREAK**

## 1600 Session 4: New Frontiers: Unlocking Opportunity Cereal
**Chairs: Stéphanie Swarbreck and Sibongile Zimba**

1600-1640 **Aiswarya Girija, Aberstywyth University**
Small Grain, Big Impact: Tef's role in the next generation of cereals

1640-1655 **Lizo Masters, Kew Gardens**
Genome assemblies of climate resilient millet crops Digitaira iburua and D. sanguinalis

1655-1710 **Crispus Mbaluto, University of Essex**
Hardy pearl millet rootstock makes rice tougher: a transcriptomic insight

1655-1710 **Miriam Schreiber, James Hutton Institute**
Breeding organic oat with high nutritional value

## 1710- 1730 Short Poster Talks (2-minute talks)
**Chair: Geraint Parry**

- **Natasha Brock, Rothamsted Research**
Re-engineering amino acid metabolism in wheat grain using CRISPR/Cas9

- **Agnes Aboagye, University of Nottingham**
An ontology-based semantic data integration framework for interoperability of crop phenotypic data

- **Chunhua Zhang, University of Nottingham**
Validation of root diameter as a key root trait for stress resilience

- **Kexin Liu, IPK-Gatersleben**
The Indeterminate Domain Protein BROAD LEAF 1 regulates the grain development in barley

- **Shanzay Qamar, James Hutton Institute**
Building better barley: Expanding the range of barley gene editing tool

- **Umali Herath, Harper Adams University**
Loss of Plastidal Phosphoglucoisomerase (PGIp) on physiology and carbohydrate metabolism in Wheat (*Triticum turgidum*)

- **Joshua Weblin, University of Nottingham**
Using next generational nitrogen sources for nitrogen use efficiency in spring barley genotypes

1730-1930 **Poster Session** *with Canapes and Drinks*

# Wednesday March 25th 2026

## 0900 Session 5: Climate-Proofing Monocots: Physiology that Delivers
**Chairs: Stella Edwards and Xavier Simón**

0900-0940 **Elizabete Carmo-Silva, Lancaster University**
Towards sustainable and temperature-resilient wheat photosynthetic productivity

0940-0955 **Miles Curl, John Innes Centre**
Exploring the role of NAM-2 in delaying drought-induced senescence in wheat

0955-1010 **Dominique Hirsz, IPK-Gatersleben**
Staggering towards new habits: exploring seasonality in wheat through alternative growth habits

1010-1025 **Catherine Famelton, Rothamsted Research**
Dissecting interactions between trehalose-6-phosphate, nitrogen and genotype in wheat physiology

1030-1100 **BREAK**




***Thanks to RAGT for sponsoring Session 5***

## 1100 Session 6: From Meristem to Harvest: Building the Plant
**Chairs: Nikolai Adamski and Amy Newell**

1100-1140 **Alex Webb, University of Cambridge**
Circadian Clocks in Wheat

1140-1220 **Sarah McKim, University of Dundee**
Does mother know best during grain development?

1220-1235 **Yunchuan Liu, John Innes Centre**
VRT2 increases rudimentary basal spikelet formation by delaying floret development in wheat

1235-1250 **Kenan Tan, IPK-Gatersleben**
Wind pollination and evolutionary innovation in grasses is driven by WAP1 enhancing pollen production and fertility

1250-1305 **Becca Testa, John Innes Centre**
Green be gone: transcription factor NAC3 regulates wheat senescence

1305-1400 **LUNCH**

## 1400 Session 7: Measure What Matters: Traits, Throughput, Translation

**Chairs: Joshua Ham and Denis-Florentin Sfrangeu**

1400-1440 **Malcolm Bennett, University of Nottingham**
Small processes, big effects: measuring the impact of anatomical traits on crop performance

1440-1455 **Lei Ju, Niab**
Trait-guided dual-view recognition of wheat varieties via knowledge distillation

1555-1510 **Maxwell Asiedu, University of Nottingham**
Root angle variation in the OzBarley population is driven by genetic variation in key EXPANSIN genes

1510-1525 **Annalene Hansen IBERS**
Thigmomorphogenesis: wheat phenotypic, transcriptomic and structural responses to mechanical stimulation

1530-1600 **BREAK**

## 1530 Session 8: Regenerative, Precision, Profitable: Practices that Work

**Chairs: Tally Wright and Bright Fiakeye**

1600-1640 **Christoph Dockter, Carlsberg**
The genetic basis of malt quality and pre-harvest sprouting

1640-1655 **Stephen Pearce, Rothamsted Research**
An expanded RHT1 allelic series enables tuneable control of wheat growth

1655-1710 **Anisa Blower, Niab**
Exploration of Niab's synthetic wheat as a new source of genetic resistance for effective control of *Septoria tritici* blotch disease

1710-1725 **Pooja Satpathy, IPK-Gatersleben**
Generation and validation of haploidy inducers in barley by Cas9-mediated knockout of PHOSPHOLIPASE A1

## 1830- 1915 Women in Crop Science and Allies Discussion Session

**Chair: Stéphanie Swarbreck**

**Dame Ottoline Leyser, Cambridge University**



## 1915- 2000 Drinks Reception

## 2000- late Conference dinner at Robinson College

*Must be booked as an optional extra*

# Thursday March 26th 2026

## 0930: Session 9: Decoding Monocots: Genetics for Impact

**Chairs: Miriam Schreiber and Beth Soanes**

0930-1010 **Eric Ober, Niab**
Navigating the GxExM landscape, and finding ways forward for crop improvement

1010-1025 **Emily Carr, University of Bristol**
A sticky situation: root exudate-substrate cohesion is modulated by an XTH gene

1025-1040 **David Ashworth, James Hutton Institute**
Can we develop novel algal biofertilisers from whisky co-products to produce barley sustainably?

1040-1055 **Denis-Florentin Sfrangeu, Niab**
Investigating the role of the 3D soil matrix in mediating root-to-root interactions between wheat and blackgrass

1100-1130 **BREAK**

1130-1215 New Lecturer Award Winner: **Jiorgos Kourelis, Imperial College**
From understanding to engineering: synthetic biology approaches to build made-to-order plant immune receptors

1215- 1230 **Monogram 2026 closing ceremony**
**Stéphanie Swarbreck, Kostya Kanyuka and Elizabete Carmo-Silva**

1215-1315 **LUNCH**

## 1315 Resources Workshop

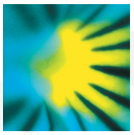
1315- 1445 **Sarah Dyer, Tally Wright and James Bedford, Niab**
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Ensembl plant population

1415-1500 **Burkhard Steuernagel, John Innes Centre**
Next-Gen Wheat Genomics Web Services, An initiative to update the wheat web services landscape

1500 **Meeting End**

# Poster Presentations

Poster Prize provided by The New Phytologist Foundation



New Phytologist

| Poster Presentations | | |
|---|---|---|
| P1-1 | **Fiona Leigh** | The Wheat Alliance: identification and characterisation of ancestral wheat microbiomes |
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| P2-1 | **Bright Fiakeye** | Exploiting wheat relatives to enhance brown rust resistance in bread wheat |
| P2-2 | **Lifeng Hou** | CRISPR/Cas9-guided knockout of TaZEP1 restricts multiple fungal pathogens growth in hexaploid wheat |
| P2-3 | **Tochukwu Chisom Iguh** | Tracking the molecular targets of stem rust in wheat |
| P2-4 | **Yao Fu** | Identification and Characterisation of Novel Barley Resistance to Aphids |
| P2-5 | **Saleem Mohammed** | **Hormetic UV-C Seed Treatment Enhances Barley Tolerance to Ramularia leaf spot** |
| | | |
| P3-1 | **Abdul Kader Al-abdullah** | Genome-Wide Analysis of Soluble Fibre Variation in Elite European Wheat |
| P3-2 | **Anoud Alsrwani** | Expanding Quinoa genetic diversity to improve nutritional quality and agricultural resilience in the UK |
| P3-3 | **Natasha Brock** | Re-engineering amino acid metabolism in wheat grain using CRISPR/Cas9 |
| P3-4 | **Muneta Grace Kangara** | Delivering a balanced diet for Southern Africa's farmers |
| P3-5 | **Emily Lyon** | Control of Grain Hydration and Germination Speed in Barley |
| P3-6 | **Nigel Muchiwanga** | Disentangling Genotypic, Environmental, and Agronomic Effects on Barley Starch Characteristics Relevant to Malting and Malt Quality |
| P3-7 | **Alejandro Perdomo Lopez** | Assessing Wheat Performance in Hydroponic and Vertical Farming Systems: Pathways to Reducing Urban Food Insecurity |
| P3-8 | **Workie Zegeye** | Harnessing Crop Wild Relatives Through Introgression Lines to Enhance Wheat Resilience and Grain Quality |
| | | |
| P4-1 | **James Bedford** | Building Foundations for 'Ensembl Plant Populations' |
| P4-2 | **Tansy Chia** | Chromosome-level genome assemblies for 48 Poaceae species |
| P4-3 | **Charlotte Grech** | Understanding the role of novel gene pathways in germination and their impact on the malting process. |
| P4-4 | **Camille HAQUET** | Impact of ph1 and ph2 mutation on homoeologous recombination in wheat |
| P4-5 | **Emilie Knight** | A protoplast-based method to identifying direct TARGETs of transcription factors in wheat |
| P4-6 | **Bach Nghiem** | Does the PRT6 N-degron pathway regulate the root growth response to heat stress in barley? |
| P4-7 | **Manel Othmeni** | Harnessing Genetic Variation from Wild Relatives for Durum Wheat Improvement |
| P4-8 | **Hardik Patel** | Towards identifying the key variables influencing lodging in tef (Eragrostis tef) |
| P4-9 | **Beth Soanes** | o-RYE-gins: using domestication genomics to support the development of perennial rye |
| P4-10 | **Mark Wilkinson** | Transformation of Crops and other Species at Rothamsted Research |

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| P4-11 | **Sadiye Hayta** | Recreating the Green Revolution in Wheat Through Gene Editing |
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| P5-1 | **Diana Amado-Sanchez** | Future Grains: Evaluating impacts of elevated CO2 and temperature on yield and grain quality in cereals |
| P5-2 | **Mouesanao Kandjoze** | Using embryonic monocot grafting as a tool for physiological trait transfer in Oryza sativa |
| P5-3 | **Zoë Kitching** | LAZY mediated control of root growth angle generates steep rooting phenotypes in wheat |
| P5-4 | **Lu Lu** | Exploring root exudate diversity and function to improve phosphorus efficiency in barley |
| P5-5 | **Hubert Matkowski** | The Nuclear Cap-Binding Complex Shapes ABA-Primed Drought Responses in Barley |
| P5-6 | **Kacper Milanowski** | Uncovering the role of negative modulator of ABA-driven stomatal closure in barley |
| P5-7 | **Md Khaled Mosharaf** | Hidden Hazards of Reused Wastewater: Physiological and Oxidative Effects of Sulfamethoxazole on Rice |
| P5-8 | **Keerthana Nagesh** | Elucidating the Gene Regulatory Network of ZmNAC111 in Maize under Drought Stress |
| P5-9 | **Amy Newell** | Developing an understanding of the molecular genetics of cold tolerance in winter wheat |
| P5-10 | **Xabier Simón** | Physiological assessment of rice-pearl millet inter-grafts under extreme drought |
| P5-11 | **Julia Stewart-Wood** | Temperature in wheat circadian oscillators:  from physiology to mechanisms |
| P5-12 | **Michael Voyt** | Are Winter Wheat Yields Warming Up? |
| P5-13 | **Joshua Weblin** | Using next generational nitrogen sources for nitrogen use efficiency in spring barley genotypes |
| P5-14 | **Ella Whiteley** | Investigating the Role of Aquaporins in Regulating Water-Use Efficiency in Rice |
| P5-15 | **Chunhua Zhang** | Validation of root diameter as a key root trait for stress resilience |
| P5-16 | Yarrow Beckman | Heat tolerance of Paragon Wheat over Space and Time |
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| P6-1 | **Kornelija Aleksejeva** | Unravelling polar chloroplast positioning in C4 photosynthesis |
| P6-2 | **Katie Jeal** | Investigating conserved awn and leaf developmental programs in barley |
| P6-3 | **Pauline Lemonnier** | Understanding how epidermal development in barley and wheat affect crop performance |
| P6-4 | **Kexin Liu** | The Indeterminate Domain Protein BROAD LEAF 1 regulates the grain development in barley |
| P6-5 | **Alanna McCutcheon** | Barley Surviving the Stress – Understanding Stress Induced Developmental Plasticity in Barley |
| P6-6 | **Vita Rakers** | Exploring genetic diversity for grain partitioning traits to enhance yield in spring barley |
| P6-7 | **Jennifer Shoesmith** | Evolution of Grain Shattering in the Triticeae |
| P6-8 | **liangyun wen** | Three-dimensional reconstruction reveals  stage-specific establishment of vascular architectureduring early barley spike development |
| P6-9 | **Yunqing Yu** | Dissecting the genetics of barley threshability |
| | | |
| P7-1 | **Agnes Aboagye** | An Ontology-Based Semantic Data Integration Framework for Interoperability of Crop Phenotypic Data |
| P7-2 | **Weronika Buchcik** | From gene to trait: effects of DWARF14 and DWARF53 mutations on barley morphology and transcriptome |

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| P7-3 | **Umali Herath** | Loss of Plastidal Phosphoglucoisomerase (PGIp) on Physiology and Carbohydrate Metabolism in Wheat (Triticum turgidum) |
| P7-4 | **Love Odunlami** | Genetic variation of expression of “elite” wheat genes |
| P7-5 | **Christy Smith** | Malting barley: A steep learning curve |
| P7-6 | **Christina Waesch** | Genetic basis and environmental plasticity of pollen and anther traits in rye (Secale cereale L.). |
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| P8-1 | **Eda Knights** | Evaluating wheat varieties for greenhouse gas emissions |
| P8-2 | **Shanzay Qamar-Macias** | Expanding the range of barley gene editing tools |
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| P9-1 | **Erwang Chen** | Unveiling centromeric retrotransposon dynamics through a near-complete rye genome assembly |
| P9-2 | **Fanny Combe** | Exploring how RNA splicing influences the transcriptional landscape of wheat |
| P9-3 | **Shane Fagan** | Linking Genome Diversity to Root Architecture and Growth Dynamics in Perennial Ryegrass |
| P9-4 | **Miguel Gonzalez Sanchez** | Next-Gen Wheat Genomics Web Services, An initiative to update the wheat web services landscape |
| P9-5 | **Maegan Green** | Capturing Genetic Diversity Without Compromising Genetic Diversity in Wheat Breeding |
| P9-6 | **Mustafa Emre Gul** | Transcriptome Profiling of Rht13 in Wheat to Understand Novel Height Variation |
| P9-7 | **Ruth Hamilton** | R-evolve: rapid evolution of wild barley |
| P9-8 | **Meng-Ting Hsieh** | I5: A Hidden Genetic Resource in Vietnamese Rice Landraces for Elite Breeding |
| P9-9 | **David Jones** | Unlocking Pooideae Diversity Through Comparative Pangenomics |
| P9-10 | **Anna Kocjan** | “Functional insights into aluminum response genes in barley” |
| P9-11 | **India Lacey** | A large gene family parTCPating in temperature adaptation in bread wheat |
| P9-12 | **Malcolm Macaulay** | Best Crop: Boosting photosynthesis in barley to deliver sustainable yield gains and circular bioeconomy value |
| P9-13 | **Zoe Marshall** | Utilising Bere barley landraces to genetically map manganese-efficiency and improve crop nutrient use |
| P9-14 | **Vanessa McMillan** | Exploring the use of genomic prediction approaches in barley DUS testing |
| P9-15 | **Nyien Nyein Myint** | Physiological responses of wheat to carbamazepine in reclaimed irrigation water |
| P9-16 | **Guy Naamati** | Utilizing Ensembl as a Resource for Comparative Pangenomics in Wheat |
| P9-17 | **Di Peng** | Going low to thrive high: towards unraveling the link between dwarfism and barley performance |
| P9-18 | **Amritha Raghavan** | Investigating homoeolog redundancy in polyploid wheat through machine learning and gene editing |
| P9-19 | **Ella Southin** | Characterising Male Sterile Two-Row Barley for a Hybrid System |
| P9-20 | **Ziyi Yang** | Complex structural genomic variations drive spikelet heterochrony to shape barley spike and domestication |

# Delegate List

## In-person Delegates

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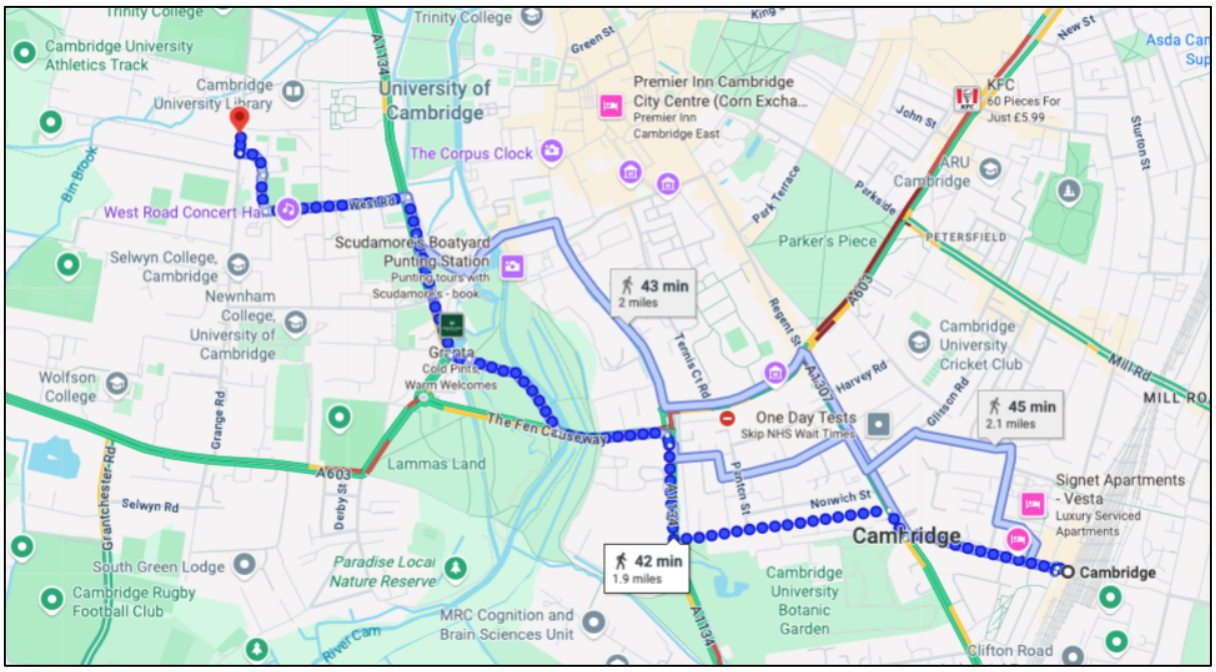
The meeting is at Robinson College at the University of Cambridge.

Address: Robinson College Grange Rd Cambridge, CB3 9AN
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The venue is 2-miles from Cambridge Train Station. Delegates can take a taxi from the train station or take a 20minute journey on the U1 Universal Bus to the Grange Road bus stop.

Bus timetable: https://www.whippetbus.co.uk/times/universal/u1/




If you require accessibility parking at Robinson College then please contact Geraint Parry (geraint@aab.org.uk).

The Monogram plenary sessions take place in Robinson College Auditorium.

On Tuesday March 24th registration opens at 8am on March 24th in the foyer outside the Auditorium.

All catering takes place in the Dining Hall, which is downstairs from the Auditorium.

Poster Boards will be located in the Dining Hall. Posters should be printed in portrait orientation, maximum size A0. Poster presenters will be able to hang their posters from 8am on Tuesday March 24th. Posters will be available for viewing throughout the meeting and the schedule poster session is from 1715-1900 on Tuesday March 24th. There will be canapes and wine provided at the poster session but no main meal. Delegates will be able to order other drinks from the bar but there is a limit on the bar-spend so please act responsibility when ordering.

On Wednesday March 25th the conference dinner is in the Dining Hall from 1930-2200. The Conference dinner must have been booked as an optional extra. Please contact Geraint Parry (geraint@aab.org.uk) if you have any queries about this booking. There is no seating plan so please sit wherever you would like.

The menu for dinner is: Balsamic glazed baby heritage beetroot tarte tatin, Lemon and Herb lamb/ Pithivier, Sticky toffee pudding

Wine and Water will be provided on the tables. Delegates will be able to order other drinks from the bar. There is a limit on the bar-spend so please act responsibility when ordering.

Eduroam and the college guest WiFi information is available during the meeting.

The Main meeting ends before lunch on Thursday March 26th. The closing ceremony will include the announcement of the location for Monogram 2027 and the award for the New Phytologist Foundation sponsored poster prize.

After lunch on Thursday March 26th there will be an interactive Resources Workshop. All delegates are welcome to attend this workshop.

Meeting oral presenters should either bring their talks on a USB drive or email them to geraint@aab.org.uk.

Online delegates can join the meeting at this zoom meeting
https://us02web.zoom.us/j/81337441266?pwd=2aGZJN2383GeC8BM8cPaRR63dRnaNm.1
Meeting ID: 813 3744 1266
Password: 887284

Following the meeting we will share recordings of all sessions. Oral presenters should let Geraint Parry know if they would NOT like their talks shared with other delegates. Recorded talks will not be shared online.

Please use #Monogram2026 to promote the meeting on social media but please do not post images on unpublished data without permission of the presenter.

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If you have any other questions about the meeting please contact Geraint Parry
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# *Oral Presentations*

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# *Session 1:*

# *Staying Ahead of the Outbreak: Biotic Threats & Defences*

# From resistance to susceptibility to Septoria tritici blotch: The *Stb16q* story

GAELLE MARLIAC[1], ANNE GENISSEL[2], BENJAMIN NOWAK[3], FREDERIC SUFFERT[2], ROMAIN VALADE[4], MARC-HENRI LEBRUN[5], THIERRY LANGIN[1] and CYRILLE SAINTENAC[1]

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## ABSTRACT

*Septoria tritici* blotch (STB), caused by *Zymoseptoria tritici*, is one of the most devastating wheat diseases. Over the past decade, major efforts have focused on identifying and deploying resistance genes and QTL to control this pathogen. Despite the identification of numerous QTL with variable phenotypic effects, the function of the genes located in these QTLs, their mechanisms of action, and their efficacy and durability remain poorly explored, limiting predictive resistance management. The *Stb16q* gene, identified 15 years ago in a synthetic wheat background, was initially described as a major broad-spectrum resistance QTL. It was subsequently cloned and shown to encode a cysteine-rich receptor-like kinase (CRK) interacting in a gene-for-gene manner with the fungal avirulence gene *AvrStb16q*, representing the first such mechanism described for a plant CRK. Following its introgression into French elite germplasm, *Stb16q* was rapidly deployed on more than 5% of the national French wheat acreage, by the mid-2010s, predominantly through a single variety. After this large-scale deployment, analysis of extensive national wheat field networks showed a complex spatiotemporal dynamic of *Stb16q* breakdown, exacerbated by the rainy 2016 season. It was particularly illustrated in most regions by higher disease levels on *Stb16q*-carrying varieties compared to a susceptible control, a striking pattern that may be explained by several non-exclusive hypotheses. The breakdown was accompanied by a marked increase in the frequency of *Z. tritici* isolates virulent against *Stb16q*. Analysis of these isolates revealed that virulence predominantly arose from the inactivation of *AvrStb16q* underscoring the strong evolutionary potential of *Z. tritici* to evade *Stb16q*-mediated recognition, with minimal impact on overall pathogenicity. Collectively, this case study illustrates the fast transition from effective major resistance to susceptibility following large-scale field deployment, and highlights the remarkable adaptive potential of this pathogen, raising questions about the achievement of durable resistance to STB.

# Using airborne DNA sequencing for cereal rust surveillance across multiple agricultural sites

JADE VAN WIJK[1], DARREN HEAVENS[1], CHARLOTTE HAYES[2], DIANE SAUNDERS[3], PAUL NICHOLSON[3], MATTHEW D CLARK[4] and RICHARD M LEGGETT[1]

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## ABSTRACT

Wheat provides roughly 20% of caloric intake worldwide, making it vitally important to protect. Some of the biggest threats to wheat include the cereal rusts *Puccinia striiformis* f. sp*. tritici (Pst)* and *P. triticina (Pt),* which cause yellow rust and brown rust respectively. Pst alone is known to cause yield losses of up to 5.5 million tonnes annually (Beddow *et al*., 2025). The obligate biotrophic nature of these pathogens also makes them impossible to culture and therefore difficult to study pre-infection. Here, we apply AirSeq, a novel sequencing-based approach for studying environmental bioaerosols, to monitor rust pathogens on wheat farms. This approach can be used to quantify fungal spores in the air before infection occurs, offering early warning of cereal rust infections and providing valuable insights to enable effective integrated pest management strategies (IPM). This environmentally conscious approach to IPM can aid farmers in reducing costs, while supporting sustainable farming practices. Here we present AirSeq surveillance data from commercial UK wheat breeding sites and from a research farm, monitored over several years. We demonstrate how quickly airborne spores translate into infections through benchmarking these datasets against field observations and leaf samples. Furthermore, we show the influence the weather has on disease spread through comparisons to meteorological data.

## References

**Beddow J M. *et al.* 2015**. *Nat Plants* **1**:15132.

# Exploiting wheat-wild relative introgression lines as a source of Barley Yellow Dwarf Virus (BYDV)

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## ABSTRACT

Barley Yellow Dwarf Virus (BYDV) is the single most important virus threatening wheat yield, a challenge exacerbated by climate change. To identify novel sources of resistance, this study exploits the genetic diversity found in wheat wild relatives. We characterised and screened introgression lines derived from *Aegilops speltoides*, *Aegilops mutica*, *Triticum timopheevii, Aegilops caudata, Thinopyrum bessarabicum,* and *Thinopyrum elongatum.*

Using a suite of genotyping tools, including KASP markers, genomic in situ hybridization (GISH), and skim-sequencing, introgressed wild segments were physically mapped within a bread wheat background. These lines were subsequently screened for BYDV resistance under controlled growth room conditions. By quantifying viral titre via ELISA, we have identified 7 lines exhibiting reduced viral accumulation compared to susceptible controls. Three of these lines are from *Ae. caudata,* 2 from *Th. elongatum,* and one from both *Th. bessarabicum* and *Ae. speltoides.* These putative resistant lines are currently undergoing validation in field trials, offering a promising genetic resource for breeding programs aiming to restore BYDV resilience in elite wheat cultivars.

# From *k*-mers to candidates: Dissecting structural diversity and novel resistance haplotypes at the wheat *Yr47/Lr52* locus

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## ABSTRACT

Wheat rust diseases remain among the most devastating threats to global food security, with emerging races (such as *Puccinia striiformis* virulent to *Yr15*) underscoring the urgent need for novel resistance sources. Traditional approaches based on read-mapping to a single reference genome often lack the resolution to capture structural diversity at resistance loci, motivating the development of scalable *k*-mer–based methods.

Here, we developed a *k*-mer haplotype pipeline to investigate the *Yr47/Lr52* locus on chromosome 5B using multiple reference assemblies. Using syntenic intervals as "baits", we derived 31-mers and used them to identify raw reads containing these 31-mers from two resistant Watkins landraces (WATDE0042, WATDE0776) with chromosome 5B-based resistance. We assembled the extracted reads into homoeolog specific contigs, from which haplotype-tagging *k*-mers were identified and evaluated in-silico across >1200 accessions using IBSpy.

Our analysis revealed striking structural variation at the *Yr47/Lr52* interval across pangenomes, with locus sizes ranging from 0.85 Mb in Lancer to 5.96 Mb in ArinaLrFor, harbouring between 0 and 17 annotated resistance genes (NLRs) depending on accession. Haplotype-specific *k*-mers from WATDE0042/WATDE0776 were present in only six accessions, indicating rare and potentially novel resistance alleles. Contigs bearing these *k*-mers contained an NLR, phylogenetically related to the susceptibility gene *Tsn1*, and with a potential neo-functionalisation towards rust resistance.

This work enabled the development and deployment of robust, haplotype-informed KASP markers to track a highly complex QTL, identify candidate resistance genes, and accelerate wheat improvement.



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# *Session 2:*

# *Cultivating Good Company: Probiotics for Plants*

# Soil type, crop species and agrochemicals shape root microbiomes: New resources and insights

TIM MAUCHLINE

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## ABSTRACT

This talk will introduce the UK Crop microbiome cryobank, the world's first publicly accessible resource designed to preserve and make accessible the microbial communities associated with the UK's major food crops. The resource focuses on wheat, barley, oats, oilseed rape, sugar beet, faba bean, and provides a bank of microbial cultures, cryopreserved samples, soil metadata and genomic resources from crop-associated microbiomes and detailed soil metadata to support research into crop–microbiome interactions. In addition, I will describe research into the impact of fertiliser and fungicide application on the wheat root microbiome. We demonstrate distinct, shifts in both fungal and bacterial community members within the rhizosphere and bulk soil, highlighting the broader ecological impacts of agrochemical use. Together, these efforts illustrate the value of curated microbiome resources and long-term experiments for understanding the impacts of agricultural practices on below-ground biodiversity.

# N It to Win It: Small package, big impact

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## ABSTRACT

Nitrogen (N) is essential for plants, playing a key role in growth, development and metabolism. Since the Green Revolution, N fertilisers have been provided extensively to crops to improve growth and yield, particularly in cereal crops. However, creating N fertilisers primarily involves converting atmospheric N ($N_2$) into ammonia ($NH_3$), using the energy-intensive and $CO_2$-producing HaberBosch process. This results in N fertilisers having a high carbon footprint alongside cost. N fertilisers additionally create environmental issues such as nitrification, and the release of nitrous oxide ($N_2O$) – a potent greenhouse gas.

Nitrogen-fixing bacteria are microorganisms that can convert atmospheric N (N2) gas into plant-available ammonia ($NH_3$) and represent a sustainable alternative or supplement to traditional N fertilisers. *Rhizobia* spp. are well documented N-fixing bacteria for Leguminous species. However, much less is known about N-fixing bacteria for broad-range crops. With cereals contributing significantly to global agricultural production, development of competitive bacterial strains to supplement N fertilisers represents a significant potential economic and environmental impact.

Here, bacterial strains with some evidence of N-fixation ability were screened for the nifH gene of nitrogenase, ammonia production and excretion. Promising strains were tested according to their ability to enhance yield in wheat, culminating in UK field and semi-controlled environment trials, where extended physiology measurements were taken. The most competitive strains are being taken forward to N-fixation validation assays, a bold approach often seen lack in many N-fixation efforts. Future work will involve evaluation across multiple crop species including maize and rice cultivars specific to Sub-Saharan Africa. Finally, the selected strain will be packaged in ultra-low volume packages at low cost to small-scale producers in Africa, delivering a sustainable and cheap source of N.

# Field performance evaluation of a carbon quantum dot–based crop enhancer on rice using yield and biomass traits

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## ABSTRACT

Translating novel crop enhancement technologies from laboratory development to field impact requires robust evaluation using agronomically relevant traits. In this study, a biomass-derived carbon quantum dot (CQD)–based crop enhancer was evaluated in a field trial in Sungai Burong, Malaysia, on rice during the second planting season, using yield- and biomass-based traits as primary performance indicators. Treatments were applied under normal fertilization practice and compared against an untreated control. Due to weed infestation in adjusted fertilization plots, analysis was restricted to normally fertilized plots.

The results show that CQD-treated plots achieved 23–36% higher grain yield compared to the control. In addition, total aboveground biomass increased by 80–90% in treated plots, demonstrating a substantial improvement in overall crop growth and productivity at the field scale. A reduction in harvest index was observed in treated plots, indicating that the increase in biomass was proportionally larger than the increase in grain yield, and highlighting assimilate partitioning as a potential target for further optimization.

Overall, this study demonstrates that the CQD-based crop enhancer delivers clear, measurable gains in key agronomic traits under field conditions without changes to standard fertilization practice. The results provide important phenotypic evidence supporting the translational potential of this technology from laboratory development to practical rice production.

Building on these outcomes, ongoing work is generating additional physiological, biochemical, and molecular data to elucidate the mechanisms underpinning CQD-mediated photosynthesis enhancement, including effects on photosystem performance and associated regulatory pathways, thereby supporting further optimisation and informed deployment of QD-based strategies across cereal crops.

# Optimizing Nitrogen-Use Efficiency components: A comparison of landrace and elite malting barley

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## ABSTRACT

Improving Nitrogen-Use Efficiency (NUE) in barley (*Hordeum vulgare* L.) is essential for more sustainable production with reduced artificial fertilizer inputs. This study examines the phenotypic variation in NUE components and responses to N availability within a diverse panel of spring malting barley, comparing elite UK and US varieties with landraces from Mexico, Iraq, Russia, and Scotland.

The panel was grown under high and low nitrogen (N) treatments over two years (2023, 2024), in glasshouse and field experiments at University of Nottingham, Leicestershire, UK. Measurements included grain yield and yield components, N-partitioning, and leaf/canopy measurements (NDVI and SPAD) used to calculate senescence kinetics. Significant associations were identified between senescence-related traits and NUE (grain dry matter/ N supply); specifically, delayed senescence was positively correlated with N-utilization efficiency (NUtE; grain DM/ aboveground N uptake) and N-remobilization efficiency.

Our field results showed yield was reduced by 17% under N limitation with a significant G x N interaction for grain yield each year, and under low N conditions genetic variation in NUE was primarily driven by N-uptake efficiency (aboveground N uptake/ N supply). Under high N conditions, elite UK varieties exhibited superior NUtE and N-partitioning efficiency, maintaining a high harvest index (grain DM/aboveground DM) and N-harvest index (grain N/aboveground N), while accumulating significantly lower grain N% compared to landraces. This produced a strong negative correlation between NUtE and grain N content. In contrast, some landraces, such as the Russian WB-269, exhibited a scavenging strategy, characterized by high post-anthesis N uptake.

These results highlight distinct strategies for enhancing NUE among genotypes for high and low N conditions, which could inform trait-based breeding for improved NUE. Analysis is ongoing to quantify these NUE traits in an AB InBev GWAS panel grown at Sutton Bonington in 2025 to identify molecular markers for deployment in plant breeding.

**Acknowledgments:** This work was supported by the Biotechnology and Biological Sciences Research Council (BBSRC) and AB InBev as part of the BARIToNE Collaborative Training Partnership (Barley Industrial Training Network) program.

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# *Short Poster Talks*

# Re-engineering amino acid metabolism in wheat grain using CRISP/Cas9

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## ABSTRACT

Unlike plants and microorganisms, humans and other animals cannot synthesise lysine, and so must acquire it in their diet. Wheat (*Triticum aestivum*) and other cereal grains are low in lysine and people who live a plant-based lifestyle or do not have access to meat can suffer from lysine deficiency and malnutrition. Soybeans and other legumes do contain higher concentrations of lysine, but if we are to reduce our dependency on meat, which is one of the recommendations for achieving net zero $CO_2$ emissions, a broader and more sustainable source of plant-based lysine will be required.

Lysine is synthesised by the DAP (diaminopimelate) pathway, of which the rate-limiting step is the conversion of L-aspartate semialdehyde and pyruvate into (4S)-4-hydroxy-2,3,4,5-tetrahydro-(2S)-dipicolinic acid, catalysed by the enzyme DHDPS (dihydrodipicolinate synthase). High levels of lysine are prevented from accumulating by feedback inhibition of DHDPS by lysine.

GM Mutant DHDPS wheat transformants have been generated through CRISPR and particle bombardment and subsequently analysed via HPLC. Ongoing work continues in an attempt to produce a gene edited, transgene free, high lysine line of wheat.

# An ontology-based semantic data integration framework for interoperability of crop phenotypic data

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## ABSTRACT

Underutilised crops are often nutritionally dense, climate-smart, and contribute to agrifood diversity. However, phenotypic data for associated genetic resources are highly heterogeneous across studies and collaborators, hindering access, reuse, and interoperability. Access to and comparison of commensurate trait datasets that characterise disparate crops is likely to accelerate the development and adoption of underutilised crops. To address these issues, we have developed an ontology-based semantic data access and integration framework, 'Framework for Ontology-based Comparison of Underutilised Species (FOCUS)', that harmonises phenotypic data of underutilised crops stored within the Germinate database platform into a unified semantic structure. Germinate is an established fully featured open-source plant genetic resources platform that incorporates a relational database for managing phenotypic, genetic, and trial data for a diverse range of crops. FOCUS incorporates a virtual knowledge graph representing the semantic layer, such as traits, crops, crop parts, and units, enhancing data access and integration. Existing annotations from the Open Biological and Biomedical Ontologies (OBO) Foundry Library were used to provide formal semantic definitions for phenotypic traits, anatomical structures, and measurements, thereby establishing a shared biological definition for the data and metadata. Ontology-based Data Integration (OBDI) involved systematic mapping between the formal OBO terms and the Germinate database fields and records. This now provides Germinate with a semantic capability that extends its capacity for knowledge discovery and crop data comparison across germplasm, experiments, and locations. We expect this ontology-based semantic integration and interoperability will provide a significant opportunity for data integration that will enable comparison and reuse of phenotype data already stored in Germinate. Mining such information can enable breeders and researchers to compare crops and identify traits and accessions needed to support the wider adoption of underutilised crops.

**Key words**: Ontology integration, phenotype data, semantic annotation, underutilised crops

# Validation of root diameter as a key root trait for stress resilience

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## ABSTRACT

Rice- the primary food crop in Asia/Africa is produced across six continents and is the staple food for ~3 billion people. With increasing population, Global Food Security is one of the major challenges facing world agriculture (Bailey-Serres *et al*., 2019). This is against the backdrop of global warming and increasing climate unpredictability. Crop production is especially vulnerable to extremes of environmental stress (drought/heat) leading to significant losses in yield and quality. To meet the future food demand, there is an urgent need to develop diverse, climate-ready and resilient agricultural systems (Bailey-Serres *et al*., 2019).

Root traits determine the plant's capacity to capture nutrients and water and therefore directly influence crop productivity. Previous studies have shown that nodal root diameter correlated positively with improved yield under drought stress (Liao *et al*., 2022; Siangliw *et al*., 2022). Interestingly, changes in root diameter have also been correlated with salt (Huang *et al*., 2022) and compaction (Huang *et al*., 2021) stresses.

As part of the GCRF strengthening grant, this project explores the heat tolerance/resilience of lines already selected for drought resilience in previous studies of the network partners using field-based studies and controlled environment studies. The poster will present some recent finding of these experiments including root architectural and anatomical studies using X-ray Computed Tomography and Laser Ablation Tomography.

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# The indeterminate domain protein BROAD LEAF 1 regulates the grain development in barley

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## ABSTRACT

Barley (*Hordeum vulgare* L.) represents an important crop that is cultivated world-wide for feed and forage for livestock, and for food and drinks for humans. Improving the barley grain yield and quality is a major priority of barley breeding. Barley grain quality is mainly determined by the content and composition of seed storage proteins (SSPs) especially the hordein levels. The grain yield is largely dependent on the starch content. However, the molecular mechanisms that regulate SSP and starch biosynthesis and their accumulation during grain development is poorly understood in barley.

The INDETERMINATE DOMAIN (IDD) protein BROAD LEAF 1(BLF1) is reported as a regulator of barley leaf width. In this study, we explored the function of the transcription factor BLF1 in grain development and its impact on SSP and starch synthesis. The knock-out mutants of *BLF1* in cv. Barke and cv. Golden promise exhibited a typical shrunken grain phenotype. The thousand grain weight, sucrose and starch content are significantly decreased, however the hordein levels are increased in the mutant grains.

We performed RNA-seq analysis at 5 and 8 days after flowering (DAF) and found most of *B-hordein* genes and starch metabolism genes differentially regulated in both stages. In addition, we performed a horomone measurement and found that auxin and ABA content are decreased, while the GA levels are increased in the mutants.

This study aims to clarify the molecular functions and gene regulative network (GRN) of BLF1 to better understand barley grain development.

# Building better barley: Expanding the range of barley gene editing tool

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## ABSTRACT

Gene editing (GE) provides precise and efficient methods for targeted genetic modifications, offering immense potential for crop improvement. However, its application in barley (Hordeum vulgare), an essential crop for food, beer, and whisky production, remains limited due to cultivar-dependent transformation efficiency. This project aims to expand the range of available GE tools and develop a comprehensive "BarEDIT" toolbox to enhance barley's genetic tractability across both transformable and recalcitrant cultivars.

Initial work focused on the model cultivar Golden Promise using multiple CRISPR-based systems, including intronized Cas9, mutated Cas9 (nickase), and Barley stripe mosaic virus (BSMV)-mediated delivery for transgene-free editing. Two primary gene targets were selected: HvPDS (a visual marker for assessing editing efficiency) and HvLDI (Limit Dextrinase Inhibitor), which influences malting quality. Over 20 LDI-edited lines were generated, with ten showing edits at three or more guide sites. Besides, constructs targeting HvMlo (mildew resistance) and HvSPY (seed germination regulation) were also developed to explore agronomic traits relevant to yield and quality.

Parallel optimization of tissue culture and transformation protocols was undertaken for recalcitrant whisky-related cultivars (Laureate, KWS Sassy, LG Diablo, SY Arrow, SY Tennyson, and Fairing) using a GUS reporter system. Results revealed cultivar-specific responses, with Laureate showing limited regeneration (2.8%) and others exhibiting localized GUS expression.

Ongoing work involves viral-vector–based editing using BSMV and evaluation of edited lines for malting performance through biochemical and micro-malting analyses. A vector has also been developed for introduction of the GRF4–GIF1 growth regulating factor complex for the recalcitrant varieties to improve regeneration efficiency. Collectively, these efforts will contribute to the development of a barley gene editing toolbox supporting genetic improvement of elite, industry-relevant cultivars for food and beverage production.

# Loss of plastidal phosphoglucoisomerase (PGIp) on physiology and carbohydrate metabolism in wheat (*Triticum turgidum*)

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## ABSTRACT

Transient storage of carbohydrates in leaves plays a vital role in maintaining daily energy balance and regulating plant metabolism. Carbohydrates accumulated in the leaves during the day are remobilised at night to support continued metabolic activity and growth when photosynthesis is absent. Phosphoglucose isomerase (PGI) in plants catalyses the reversible interconversion of glucose-6-phosphate (G6P) and fructose-6-phosphate (F6P). Through this enzymatic reaction, plastidial PGI (PGIp) regulates the flow of carbon between the Calvin cycle and starch biosynthesis within chloroplasts, making it a crucial regulatory point that influences starch metabolism. Two *Triticum turgidum* (wheat) mutant lines, with premature stop codons in each homoeologue of PGIp, (from the *T. turgidum* Targeting Induced Local Lesions in Genomes (TILLING) population), were crossed to obtain a double homozygous mutant progeny predicted to lack functional PGIp (*Ttpgip*). This mutant line and associated negative segregant (control) line were grown under controlled environmental conditions to assess carbohydrate accumulation and photosynthetic capacity – two phenotypes that were negatively impacted when PGIp mutants were previously studied in Arabidopsis. Transient starch accumulation was significantly impaired at the end of the day in the *Ttpgip* line, with near zero transient starch being accumulated, confirming the role of PGIp in transient starch metabolism in wheat. However, photosynthetic traits of the *Ttpgip* line, assessed via growth assimilation and photosynthetic capacity, remained unaffected. Preliminary analysis of starch granule size distributions within the seed also showed a significant increase of 15.1% in the diameter of B-type granules in the *Ttpgip* line, while A-type granule size remained unaffected. These findings suggest a potential species-specific role for PGIp and provide a unique opportunity to utilise wheat PGIp to assess the impact of modified transient carbohydrate pools with reduced secondary impacts, as well as investigate the role of PGIp in storage starch accumulation.

# Using next generational nitrogen sources for nitrogen use efficiency in spring barley genotypes

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## ABSTRACT

Spring barley (*Hordeum vulgare* L.) is a globally important crop for the malting industry, but its production relies heavily on nitrogen (N) fertilisers. This contributes to environmental impacts including nitrate leaching and greenhouse gas emissions, particularly nitrous oxide ($N_2O$). Improving nitrogen-use efficiency (NUE), the efficiency by which crops acquire and convert nitrogen into grain yield, is therefore essential for environmental sustainability and profitability. This study investigates the physiological and genetic basis of NUE in spring malting barley under contrasting N inputs and synergies with next-generation fertilisers. One experiment was conducted under glasshouse and field conditions in 2025 using a diverse panel of eleven genotypes, including elite UK cultivars, US breeding lines from Molson Coors, and landraces from the James Hutton Institute. Nitrogen treatments ranged from low (50 kg N $ha^{-1}$) to high (150 kg N $ha^{-1}$) application rates, with field trials incorporating three high N treatments (urea-based fertiliser, ammonium nitrate, and an ammonium nitrate + nitrification inhibitor) and a low N ammonium nitrate treatment. Our study aimed to identify traits and molecular markers associated with NUE. By integrating phenotypic assessments with molecular analyses, our work provides insights into breeding strategies for barley varieties that efficiently utilize nitrogen. Traits measured included leaf chlorophyll content and canopy size (NDVI) to determine senescence kinetics, grain yield, and the nitrogen analysis of plant components to determine NUE components. Results show there was a significant G × N interaction for canopy traits, but a less strong interaction for grain yield. Plant N measurements are ongoing for estimating G × N for NUE traits. The nitrification inhibitor treatment yielded similarly to the two other high N treatments. These experiments will be repeated in 2026 to identify further target traits for improving NUE in barley while maintaining high malting quality and synergies with next generational N fertilizers.

## Acknowledgements

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# *Session 3:*

# *Beyond Yield: Grain Quality & Human Nutrition*

# Exploiting wheat diversity for improved human diet and health

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## ABSTRACT

Wheat improvement is based on exploiting genetic diversity, including variation in grain composition and quality. Modern plant breeding has resulted in limited genetic diversity in modern wheat and therefore, it is necessary to identify wider sources of variation for improvement, including older “heritage” cultivars and landrace collections. A UK-China collaboration has recently reported genomic sequences of the Watkins collection over 800 wheat landraces, representing global diversity from about 100 years ago when the collection was assembled.

We have exploited the Watkins land race collection and other genetic resources, including elite genotypes and older types of wheat, to identify genetic sources for high grain mineral and dietary fibre content. Analyses of bi-parental populations and association mapping panels have identified genetic loci for the improved nutritional traits allowing the development of molecular markers, for use in conventional wheat breeding programmes, and identification of candidate genes. This will allow for the incorporation and stacking of these loci in new elite germplasm to deliver healthier staple foods. We relate these genetic improvements to measurable impacts on human health.

# Enhancing barley nutritional quality for sustainable agriculture through genome editing of lysine metabolism

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## ABSTRACT

This study aims to enhance the nutritional quality of barley by increasing its lysine content, an essential amino acid often limited in cereals but vital for human health and livestock nutrition. The approach combines CRISPR-based genome editing to disrupt lysine catabolic pathways and promote biosynthesis, with a breeding strategy to remove transgenes, ultimately producing non-GMO lines (Non-Genetically Modified Organism). In parallel, cytonuclear multi-parent population was used to investigate how interactions between nuclear and cytoplasmic genomes influence lysine accumulation. These lines, which share a common nuclear background but differ in cytoplasmic origin, enable the dissection of cytonuclear effects on lysine metabolism. Free lysine and total free amino acid levels were quantified across diverse cytonuclear backgrounds, revealing genotype-dependent variation likely driven by metabolic coordination between nuclear-encoded enzymes and chloroplast- or mitochondria-associated processes. The study further investigates both free and protein-bound lysine to evaluate overall improvement in seed nutritional value. Beyond barley, this work provides a proof of concept for applying lysine-targeted biofortification in other cereal crops. By addressing amino acid deficiencies in plant-based diets, the project supports global food security and sustainability through improved nutritional content, reduced reliance on external protein sources, and enhanced agricultural efficiency.

# Future-proof crops: Uncovering effects of future climate stresses on root ideotypes and impact on wheat grain nutritional quality

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## ABSTRACT

There is an urgent need to develop climate-resilient crops and agricultural systems to produce more food that is also more nutritious in a changing climate. The major driver of climate change is the rapid increase in atmospheric carbon dioxide ($CO_2$) concentration due to anthropogenic activities. These recent increases, along with the projected atmospheric $CO_2$ concentrations (estimated at above 550ppm by the end of the 21st century), represent a surge in an essential resource, surpassing anything plants have encountered. It has been understood for over two centuries that elevated $CO_2$ ($eCO_2$) concentrations enhance plant growth. This phenomenon, known as the 'carbon fertilization effect', profoundly influences plant physiology and metabolism, driving increased photosynthesis and yield. However, despite these potential benefits for crop productivity, $eCO_2$ is expected to alter plant elemental stoichiometry, with implications for grain nutritional quality such as iron, and zinc content in C3 staple crops like wheat. The extent and mechanisms of $CO_2$ driven changes in grain nutrient density remain poorly understood. At the same time, roots, critical for stress sensing and nutrient uptake are underexplored as targets for climate-resilience due to phenotyping bottlenecks. While individual stresses have been studied extensively in model plants, responses to combined stresses in wheat are largely unknown.

Using current and projected future climate scenarios, this work integrates root structural and anatomical characterisation with gene expression and grain mineral profiling to identify genetic drivers of nutritional and antinutritional responses to combined $eCO_2$, heat, and water stress, and to determine how these stresses interact to shape root–soil processes and wheat grain nutritional quality. The findings from this work will identify genetic targets to accelerate engineering of climate-resilient and nutrient-rich wheat. This cutting-edge research is timely and significant, aiming to ensure sustainable food and feed systems, and a nutrition-secure future for a healthier, population in a rapidly changing climate.

# Genetic variation and genome-wide association analysis of β-Glucan (mixed linkage) in a diverse spring naked barley panel

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## ABSTRACT

Barley grain is a rich source of the dietary fibre called β-glucan, which provides well-established health benefits including improved cholesterol regulation, enhanced glycaemic control and support for gastrointestinal function. However, despite its nutritional potential, widespread cultivation and long domestication history, barley is not well established as a food crop globally. In the United Kingdom (UK), it is the second most widely grown crop, yet none of this production is directly utilised for food. Furthermore, the genetic and agronomic factors that determine final β-glucan concentration in the grain remain poorly understood, partly because historical selection for malting quality has reduced natural variation for this trait. In this study, we investigated natural variation in grain β-glucan content within a genetically diverse panel of 300 naked spring barley accessions grown at Harper Adams University (Telford, UK) in a randomized complete block design. Near-Infrared Spectroscopy (NIRS) measured grain β-glucan concentration displayed a wide phenotypic range (1.57–7.30%), indicating substantial natural variation within the population.

Genome-wide association study (GWAS) analyses were conducted using multiple multi-locus statistical models MLMM, SUPER and BLINK and several marker-trait associations (MTAs) associated with grain β-glucan content were identified, with chromosome 5H consistently showing larger association signals, alongside additional loci on chromosomes 1H and 3H. Candidate gene analysis identified genes encoding a serine/threonine-protein kinase, a thioredoxin-like protein (HCF164), and a pentatricopeptide repeat-containing protein (DWY1), among others. These results highlight the polygenic architecture underlying grain β-glucan accumulation in barley and provide insights into genomic regions that may contribute to natural variation in the trait, indicating contributions from both biosynthetic and regulatory developmental pathways. These results provide a valuable foundation for the development of barley cultivars with enhanced β-glucan content and improved suitability for food applications.



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# *Session 4:*

# *New Frontiers: Unlocking Opportunity Cereal*

# Small grain, big impact: Tef's role is the next generation of cereals

AISWARYA GIRIJA[1], BAHAR HADDADI[2], HARDIK PATEL[2] and LUIS MUR[2]

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## ABSTRACT

Tef (*Eragrostis tef*) is an ancient cereal crop with increasing relevance for addressing contemporary challenges in global agriculture and food systems. Originating in Ethiopia, tef is valued for its adaptability to diverse agroecological conditions, nutritional quality, and gluten-free grain, yet it remains under-researched compared with major cereals (Girija, *et al*., 2022). As climate change, population growth, and nutritional demands place pressure on existing cropping systems, opportunity cereals such as tef offer promising pathways toward more resilient and diversified food systems. My research focuses on developing climate-smart and nutritious crops, especially niche cereals such as tef, millets and oats. In the talk, I will highlight our ongoing research in Tef, which employs integrated multi-omics approaches to dissect the molecular bases of drought, lodging and nutritional traits. By combining, metabolomics, transcriptomics and phenomics our work aims to identify gene and regulatory pathways that can accelerate tef breeding for improved resilience and performance. Our research contributes to unlocking tef's potential as a next-generation opportunity cereal and demonstrates how advanced molecular tools can be applied to underutilized crops to address climate resilience, productivity, and nutrition simultaneously.

## References

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# Genome assemblies of climate resilient millet crops *Digitaira iburua* and *D. sanguinalis*

LIZO MASTERS and RAFAL GUTAKER

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## ABSTRACT

Re-establishing underutilised crops across small-scale and commercial farming in lower- and middle-income countries increases food security. Many underutilised crops typically display high resistances to abiotic stressors e.g., drought and high temperatures making them promising candidates for rapidly changing climates. However, domestication traits such as non-shattering and plant architecture vary considerably in underutilised crop populations, and the genomic resources required to identify target genes underlying domestication traits are not always readily available. Numerous species in the grass genus *Digitaria* fall into the category of underutilised millet crops e.g., *D. exilis* (white fonio) and *D. iburua* (black fonio) from West Africa, *D. sanguinalis* (Polish millet) from Eurasia, and *D. compacta* (raishan) from Asia. Here we present genome assemblies for *D. iburua* and *D. sanguinalis*, millet species with underappreciated agricultural potential. Flow cytometry analysis and chromosome counts reveal that both species are tetraploids (2n = 4x = 36), which was confirmed by duplicated BUSCO gene recovery and k-mer copy number spectra for the respective primary assemblies. Subsequently, we have generated highly continuous chromosome scale tetraploid assemblies for *D. iburua* and *D. sanguinalis* and compared gene content across *Digitaria* crops. Conservancy of genome size and tetraploidy of these two millets is shared with *Digitaria exilis*. Further, preliminary results for reduced shattering in *D. exilis* show that Shattering1 (*sh1)* gene is an ideal candidate for gene editing in *Digitaria* millets. We chart the pathway to modernise millet species in the *Digitaria* genus to help meet global agricultural needs.

# Hardy pearl millet rootstock makes rice tougher: A transcriptomic insight

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## ABSTRACT

Rice (*Oryza sativa*) is a staple cereal crop feeding more than half of the world's population, yet its production is increasingly threatened by the recurring incidents of water shortages, intensified by climate change. Innovation to develop rice varieties that maintain high yields while using less water is therefore an urgent research priority. Embryonic cereal grafting of rice scions - onto drought tolerant cereal root stock such as pearl millet (*Pennisetum glaucum*) offers promising strategy to rapidly enhance rice stress resilience without genetic modification. Whereas the grafting of rice-pearl millet has shown enhanced physiological benefits, the underlying molecular mechanisms remain unknown.

We performed transcriptome profiling of grafted rice-pearl millet plants and non-grafted controls under controlled watering (CW) and soil field capacity (FC) either 100 % or 40 %. Overall, comparative RNA*seq* analyses reveal extensive transcriptional reprograming in the grafted rice scion at 40 % FC conditions. Under well-water conditions (CW), we observed fewer differentially expressed genes compared to genes induced under water limited conditions (40 % FC). In the talk, I will discuss our results that uncover the functional pathways and regulatory networks associated with the modulated genes.

Our finding provides first transcriptomic evidence that drought tolerant pearl millet rootstock can reprogram gene expression in rice to confer water-stress resilience. These results advance mechanistic understanding of interspecies grafting and highlight a rapid and non-transgenic approach to develop stress resilient and water efficient rice varieties.

**Key words**: Monocot grafting, transcriptomics, RNA*seq*, *Oryza sativa*, rice, *Pennisetum glaucum*, pearl millet, water-use-efficiency, drought, climate change

# Breeding organic oat with high nutritional value

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## ABSTRACT

Oat is a key crop for sustainable, high-yield agriculture, known for requiring minimal inputs. It is also considered one of the healthiest grains, packed with protein, minerals, antioxidants, and β-glucan fibre. This project aims to address the demand for oat varieties with enhanced nutritional value, specifically suited to sustainable organic farming. The primary goal is to create predictive models that combine nutritional quality, diversity, environmental conditions, and cultivation management. To do this, we examine 200 oat varieties and landraces from the Nordic region. These accessions will be genotyped for critical genes involved in β-glucan synthesis and phenotyped for various grain quality traits in multiple field trials across different environmental and management conditions. The resulting dataset will be used to identify oat varieties that are both nutritionally superior and yield-stable, providing valuable genetic material for breeders. Here, we will present an outline of the project and preliminary data.



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# *Session 5:*

# *Climate-Proofing Monocots: Physiology that Delivers*

# Towards sustainable and temperature-resilient wheat photosynthetic productivity

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## ABSTRACT

Wheat is a temperate crop that is increasingly experiencing unpredictable weather extremes during the growing season. For example, heatwaves alternated with cold snaps affect plant development and productivity. Photosynthesis is sensitive to changes in temperature and the leaf and cellular requirements for optimal photosynthetic efficiency are not the same in cool *versus* warm conditions. Rubisco catalyses the first step in the conversion of carbon from $CO_2$ into plant biomass: the carboxylation of ribulose-1,5-bisphosphate (RuBP). However, Rubisco is not very efficient and therefore wheat leaves allocate more than 50% of their protein content to Rubisco to maintain adequate photosynthetic capacity for plant growth and development. Despite this high abundance, Rubisco activity frequently limits carbon assimilation at the top of crop canopies, including in wheat. Under high temperatures, Rubisco activity is impaired by inhibition such that heatwaves experienced during the booting stage resulted in decreased grain yields. This talk will discuss approaches to make Rubisco activity more efficient and thermotolerant towards enhancing the sustainability and temperature resilience of wheat photosynthetic productivity.

# Exploring the role of *NAM-2* in delaying drought-induced senescence in wheat

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## ABSTRACT

Occurrences of drought within the UK continue to threaten wheat production due to decreased yields. Terminal drought can result in accelerated senescence and whole plant maturity, leading to decreased photosynthetic activity, and thus, wheat productivity. By targeting the transcriptional regulation of drought-induced senescence, we aimed to delay the onset of leaf senescence by utilising a stay-green phenotype to improve drought tolerance.

We used transcriptomics and Gene Regulatory Network (GRN) modelling from a controlled time-series drought experiment in wild-type *Triticum aestivum* cv. Cadenza to identify transcriptional regulators that control the process of drought-induced senescence. Using machine learning, we inferred a GRN from the time course data and ranked transcription factors based on their degree centrality, which describes the number of target genes. The homoeologs of NAC transcription factor, *NAM-2*, were identified as key transcription factors regulating a large number of downstream genes, indicating its potential significance in regulating drought-induced senescence.

To test the role of *NAM-2* in regulating drought-induced senescence, we conducted field drought experiments with TILLING mutants. We found a significant delay in whole plant, ear and peduncle senescence in homozygous triple mutant plants compared to the segregating wild-type and a significant increase in yield in rain-fed UK drought trials. No yield difference occurred in drought conditions in Spain, highlighting a GxE interaction. Exploration of *NAM-2* genetic variation in Watkins landrace and elite accessions highlighted multiple single nucleotide polymorphisms (SNPs) resulting in missense, intron and promoter variant mutations. We found that haplotypes were strongly associated with the geographic location of accessions and that clear haplotype variation was present between elite and Watkins accessions.

*NAM-2* was found to be an important regulator of drought-induced senescence, validated with field trials in terminal drought conditions. Furthermore, through SNP-based haplotype analysis, we identified distinct geographical variation both in landrace and modern elite germplasm.

# Staggering towards new habits: Exploring seasonality in wheat through alternative growth habits

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## ABSTRACT

Crops have been regionally adapted to respond favorably to a set of regular, combined environmental cues. In bread wheat (*Triticum aestivum*), the timing of the transition from vegetative to floral growth is largely regulated by the combination of photoperiod and temperature signals. Identifying and understanding the key genes which regulate the physiological responses to these environmental signals has been important to enable the efficient development of cultivars with different growth habits. Winter grown crops require an extended period of cold exposure called vernalisation, so are critically sensitive to the duration and level of winter temperatures. Therefore, there is a lot of variation in vernalisation response between cultivars defined as winter, yet not much is understood about the molecular makeup underpinning this variation. Through studying the effect of temperature and photoperiod in both controlled and field conditions, we aim to better understand the molecular response to the winter environment. We measured gene expression on both a long-term weekly basis and over varying short-term 24-hour conditions during the early developmental growth of the plants, which provides new insight into the vernalisation network. We have also worked to identify and understand the effect of different allelic variants of key vernalisation genes, through analysis of the Watkins collection and then testing the protein interactions of these different variants. Using these findings, we hope to support more specific adaptation of cultivars to regions experiencing different winter conditions, which will become increasingly important to ensure high yields with a changing climate.

# Dissecting interactions between trehalose-6-phosphate, nitrogen and genotype in wheat physiology

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## ABSTRACT

Staple cereal crops such as wheat face competing demands for higher yields to feed a growing population, lower nitrogen fertiliser inputs and climate resilience. Improving wheat yield sustainably requires increases in photosynthesis or “source” traits and grain capacity or “sink” traits. However, physiological gains often fail to translate across diverse genotypes, environments, and management due to strong G×E×M interactions. Identifying regulators that stabilise yield under variable nitrogen availability is therefore a priority for sustainable yield improvement.

Sucrose is the main carbon currency in plants, transported from leaf source to growing grain sinks. Plants sense the level of sucrose by converting some of it to trehalose-6-phosphate (T6P). T6P inhibits the regulatory kinase SnRK1, prompting cells to utilise sucrose and grow. Inspired by this endogenous signalling pathway, a synthetic light-activated T6P precursor enhances cellular T6P concentrations. Spraying this T6P precursor on wheat ears shows potential to boost yield, but with genotype and environment-dependent variation.

We are dissecting the basis of this variability by quantifying the interactions among T6P precursor treatment, nitrogen input, and genetic diversity in a controlled environment. Ranging from molecular to whole-plant scale, we assess impacts on source activity, sink strength and carbon allocation. This research aims to uncover new insights into how T6P regulates wheat physiology. Understanding T6P-nitrogen interactions could also contribute to climate resilient, nitrogen-efficient wheat which furthers sustainable intensification goals.

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# *Session 6:*

# *From Meristem to Harvest: Building the Plant*

# Circadian clocks in wheat

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## ABSTRACT

We have been investigating the structure and function of circadian oscillators in wheat, and their potential to be used as targets for yield-related traits. We have found structural and functional differences compared to the model plant Arabidopsis, specifically regarding the roles of *GIGANTEA* (*GI*) and *EARLY FLOWERING 3 (ELF3*). We discovered that wheat *ELF3* contributes to the regulation of heading date, with the loss of a single homoeologue sufficient to alter flowering time. ELF3 is a core component of the circadian oscillator, disrupting robust rhythms requires the loss of all its homoeologues, suggesting its effects on heading can be separated from its clock functions. Wheat *ELF3* transcript abundance peaks at dawn—anti-phased to the dusk-expressed *LUX ARRHYTHMO* (LUX)—whereas both peak at dusk in Arabidopsis. We have developed mathematical models of wheat circadian oscillators that suggest this dawn-phased expression is driven by TOC1-mediated repression of the *ELF3* promoter, highlighting a flexible circadian architecture that maintains robust rhythmic behaviour despite structural shifts. Similarly, GI is required for robust circadian rhythms in wheat, regulating the abundance of oscillator transcripts and chlorophyll fluorescence. The lack of functional GI results in later flowering under both long-day and short-day in controlled environments. Collectively, these studies demonstrate that the molecular pathways regulating photoperiodism and circadian timing in wheat are not fully conserved with those in Arabidopsis.

# Does mother know best during grain development?

SARAH McKIM

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## ABSTRACT

Cereal grain is a complex multigenerational unit. Originating from double fertilisation of the ovule's embryo sac, the endosperm and embryo lie embedded within the maternal ovule's nutritive and protective layers, which are surrounded further by the pericarp to form the 'caryopsis' or grain fruit. While the embryo grows and differentiates, the endosperm fills with starch, driving caryopsis expansion between the floret hulls. At the same time, maternal tissues form nutritive and/or protective structures which ultimately die, releasing nutrients and generating space crucial for normal grain fill. Our previous work suggested that the jasmonate phytohormone may contribute to the timing and extent of this programmed elimination. We tested this hypothesis using gene editing and found that blocking the synthesis of jasmonate led to extremely large grain uncoupled from floret hull dimensions, enlarged maternal tissues involved in nutrient transfer, and higher expression of genes linked to sucrose transport. These effects appear parentally derived and correlates with spatial transcriptomic profiles of JA metabolism within maternal tissues. Our work provides the first genetic dissection of JA in barley and suggests a key role in coordinating growth and death of maternal tissues with impacts on grain size and weight.

# VRT2 increases rudimentary basal spikelet formation by delaying floret development in wheat

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## ABSTRACT

Grain number per spike, a key determinant of wheat yield, depends on both the number of spikelets per spike and the grains within each spikelet. The two most basal spikelets often develop as rudimentary basal spikelets (RBS), which fail to produce grains, thereby limiting overall yield. However, the cellular and molecular basis of RBS formation remains poorly understood. In this study, we found that ectopic expression of VRT2 leads to elongated glume–leaf-like organ and significantly increases RBS. Scanning electron microscopy revealed that VRT2 ectopic expression delays floret development in basal sections of wheat spikes. We hypothesized that VRT2 promotes leaf meristem development, thereby limiting the development of spikelet meristem, and ultimately leading to delayed floret development and increased RBS. To investigate this mechanism, we established an in vitro culture system that enables tracking of spikelet and leaf primordium development at the late double ridge stage and used MorphoGraphX to quantify their developmental growth rates. Moreover, pull down assays and proteomic analyses revealed that VRT2 interacts in planta with key positive regulators of spikelet and floret development, including the MADS-box proteins VRN1, FUL2, FUL3, and AGL6. These results are consistent with yeast-two-hybrid data from Li et al and support ectopic VRT2-MADS-box interactions disrupting native protein complexes, delaying spikelet and floret development and thereby promoting RBS formation. We are currently evaluating VRT2-AGL6 interactions. Additionally, we will employ CUT&RUN and RNA-seq to identify downstream target genes of VRT2 at different developmental stages. Our work aims to construct a dynamic regulatory network centered on VRT2, providing valuable insights for enhancing basal spikelet development in wheat.

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# Wind Pollination and evolutionary innovation in grasses is driven by *WAP1* enhancing pollen production and fertility

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## ABSTRACT

Poaceae species predominantly rely on wind pollination, a reproductive strategy characterized by the production of large quantities of highly viable pollen. This strategy represents a classic evolutionary trade-off, favoring reproductive output over longevity and stress tolerance, and has contributed to the remarkable ecological success of grasses across diverse environments. However, the genetic mechanisms underlying enhanced pollen production in Poaceae remain poorly understood. Here, we integrated multi-tissue transcriptome datasets from multiple grass crops to identify reproductive pathways conserved across Poaceae. We discovered a previously uncharacterized, Poaceae-specific cysteine-rich peptide gene family, *WAP1* (*Wind-pollination Associated Peptide 1*), and reconstructed its plausible evolutionary origin and diversification. Phylogenetic and population genetic analyses revealed that *WAP1* emerged specifically within Poaceae and has been maintained under strong purifying selection, indicating an essential and conserved biological function. Functional analyses using transgenic and mutant lines in rice (*Oryza sativa* L.) and wheat (*Triticum aestivum* L.) demonstrated that *WAP1* positively regulates pollen number and viability, leading to significant effects on fertility without altering floral morphology. These results suggest that *WAP1* contributes directly to the high reproductive efficiency characteristic of wind-pollinated grasses. Together, our findings identify *WAP1* as a Poaceae-specific evolutionary innovation that enhances pollen production and viability, providing a molecular explanation for the reproductive strategy that underpins the ecological dominance and evolutionary success of grasses.

# Green be gone: Transcription factor *NAC3* regulates wheat senescence

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## ABSTRACT

Senescence is the last stage in wheat development when nutrients are remobilised from source tissues into the developing grain. Senescence regulation balances a trade-off between yield and protein content, which is a critical component of the grain for end uses like bread-making. Identifying transcription factors involved in regulating the timing of senescence is useful, as these could be manipulated to improve grain protein content without hindering yield.

We are investigating the role of *NAC3,* a NAC transcription factor, in regulating senescence using CRISPR/Cas9 gene-edited lines. Over two successive generations of phenotyping in the greenhouse, *nac3* CRISPR mutants show delays in reaching senescence of 3–4 days for the flag leaf and 1–6 days for the peduncle.

Furthermore, NAC transcription factors are known to act as heterodimers. To identify additional interactors of NAC3 at the protein level we are conducting an *in vitro* pull-down assay. Preliminary results identify several novel transcription factors as candidate interactors of NAC3, which will be verified using yeast two hybrid assays. This will reveal how NAC3 fits into the transcriptional regulation of wheat senescence and may identify new candidates involved in senescence regulation.

Overall, this project has confirmed *NAC3* as a senescence regulator. Ongoing work will expand our understanding of the genetic regulation of senescence, an agronomically important stage in wheat development.

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# *Session 7:*

# *Measure What Matters: Traits, Throughput, Translation*

# Small processes, big effects: Measuring the impact of anatomical traits on crop performance

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## ABSTRACT

Anatomical variation represents a promising source of traits for plant biology and crop breeding, but conventional screens for anatomical traits are very time consuming. I will describe an innovative high-throughput anatomical phenotyping approach termed Anatomics that combines laser ablation tomography and AI-based image analysis capable of rapidly screening thousands of field grown samples. I will illustrate the effectiveness of Anatomics by quantifying root anatomical variation in a pearl millet diversity panel exposed to drought stress in field trials in Senegal with French and Senegalese collaborators. Our Anatomics approach has revealed the critical importance of xylem size traits for drought resilience in pearl millet, highlighting that small processes can have big effects on crop performance.

# Trait-guided dual-view recognition of wheat varieties *via* knowledge distillation

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## ABSTRACT

Wheat (*Triticum aestivum* L.) variety identification is essential for cultivar purity, traceable supply chains, and genotype-specific agronomic decision-making. However, current identification practices remain constrained by subjective morphological scoring or large-scale genotyping, both of which are costly, slow, and labour-intensive. Here, we present an AI-driven pipeline that translates smartphone images into robust and explainable variety predictions under real field conditions.

Using a standardised imaging protocol at flowering to early grain-fill, we assembled a China–UK Wheat Traits dataset (CUWT) comprising 80 winter wheat varieties captured across two environments (Nanjing Agricultural University, Baima; and NIAB, Histon). To couple end-to-end variety prediction with biologically understandable spike morphology, we trained six trait-specific teacher models to learn robust image features for awn presence, width-to-height ratio, compactness, spikelet density, texture and colouration. We then transferred these learned trait features into a single Vision Transformer (ViT) based student classifier, so that when used, the system outputs both variety identity and trait scores in a single pass. This was performed using a model containing teacher networks and Vision Transformer (ViT) students

Across testing, the proposed model achieved a variety identification prediction accuracy of 89.3%, outperforming other state-of-the-art (SOTA) image-classification approaches, and trained more efficiently, which is impressive when you consider the visual similarity of varieties and the number of images in the training set. Trait ablation analysis showed the width-to-height ratio, texture and colouration contributed the largest single-trait improvements. Beyond accuracy, the resulting trait profiles provide a phenotypic “fingerprint” for each image and variety, enabling evidence to be audited when decisions are questioned and helping prioritise ambiguous samples for expert visual checks or genotyping. Taken together, this provides a practical route to high-throughput, trait-driven, in-field variety identification, with applications in commercial breeding, variety protection and seed certification, and research.

# Root angle variation in the OzBarley population is driven by genetic variation in key *EXPANSIN* genes

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## ABSTRACT

Roots are essential for water and nutrient uptake and carbon sequestration. Steep root angles enhance access to deep soil water and nitrogen, while shallow angles favour capture of topsoil resources. Root angle regulation involves several genes (Kirschner *et al*., 2024). In barley, *ENHANCED GRAVITROPISM1*(*EGT1*) and *ENHANCED GRAVITROPISM2* (*EGT2*) have been linked to root-angle control via cell wall mechanics (Fusi *et al*., 2022; Kirschner *et al*., 2021), though their downstream targets remain unknown. To explore this pathway, we used high-throughput phenotyping and genome-wide association studies (GWAS) on 214 diverse OzBarley lines. Haplotype analysis revealed no variants in *EGT2* and eight *EGT1* variants, forming four haplotypes, none of which were significantly associated with the root angle phenotype ($P$>0.1). However, GWAS identified a significant SNP ($-\log_{10} P$=6.16) on chromosome 1H within a gene encoding *EXPANSIN*, a key cell wall-loosening protein (Cosgrove, 2000). Two protein-coding variants for this *EXPANSIN* were found: a missense variant and a stop-gained variant. Both alleles were significantly associated with shallow root angles compared to genotypes with the reference allele ($P$<0.05), consistent with haplotype data ($P$<0.05). The stop-gained allele truncates the N-terminal domain of the Expansin protein, while AlphaFold modelling predicts the missense variant also disrupts protein function. These findings suggest that natural variation in *EXPANSIN* contributes to variation in root angle in the OzBarley panel and support the model in which *EGT1* (and *EGT2)* regulate wall extensibility by modulating enzymes such as Expansin. Functional validation through CRISPR knockouts and TILLING mutant screens in barley and other species could help validate the functional impact of *EXPANSIN*.

# Thigmomorphogenesis: Wheat phenotypic, transcriptomic and structural responses to mechanical stimulation

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## ABSTRACT

Mechanical stimulation, such as wind or rain, induces responses in plants collectively coined 'thigmomorphogenesis' (Jaffe, 1973) – including dwarfing, cell wall compositional alterations, transcriptomic changes and stem anatomical modifications. Japanese farmers have long utilised mechanical stimulation - treading on wheat seedlings to increase crop yield and resilience. While monocot grasses are vital for global food security, their thigmomorphogenic responses and underlying regulatory mechanisms remain underexplored compared to dicots. Recent work has begun to reveal monocot-specific transcriptional regulation associated with mechanical stress (Darwish, *et al*., 2023). To further characterise thigmomorphogenic responses in wheat, mechanical stimulation was imposed on two spring wheat and three winter wheat varieties for 2–4 weeks. Treatment dramatically altered transcriptomic profiles, increased chlorophyll content (up to 16%), decreased plant height (up to 35%) and increased stem stiffness (up to 80%). Potential drivers of increased stiffness were investigated, including cellulose crystallinity, lignin content and monomer composition, sclerenchyma thickness, stem cell density/area and pectin methyl esterase (PME) activity. Of these, only sclerenchyma thickness, syringyl:guaiacyl (S:G) lignin ratio and PME activity were significantly different between controls and mechanically treated wheat, with treatment increasing all these three parameters. These alterations suggest that anatomical and cell wall matrix modifications are likely major contributors to mechanically induced stiffening. Intervarietal variation strongly influenced thigmomorphogenic responses. Increased tillering was observed in both spring and winter wheat but was delayed in the latter. Cell wall lignin content responses were variable. While most varieties showed a decrease in main tiller grain volume and surface area, traits beneficial for milling, some did not show such decreases. Mechanical stimulation also doubled the phenolic content of whole grains, indicating nutritional benefits. However, the magnitude of this effect differed amongst varieties. Together, these findings highlight mechanical stimulation as a potentially underutilised strategy for crop resilience, yield and quality improvements, while underscoring the complexity and diversity of monocot thigmomorphogenic responses.

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# *Session 8:*

# *Regenerative, Precision, Profitable: Practices that Work*

# The genetic basis of malt quality and pre-harvest sprouting

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## ABSTRACT

*MKK3* (*Mitogen-activated Protein Kinase Kinase 3*) is a genetic determinant associated with increased post-harvest grain dormancy in East Asian elite malting barley varieties. Grain dormancy modulation is crucial for industrial application and in agricultural production to avoid preharvest sprouting (PHS). PHS is a global problem and is at risk of being further aggravated by climate change. To effectively breed barley varieties with reduced PHS risk, while maintaining malt quality, it is imperative to understand the molecular nature of the loci responsible for high PHS susceptibility. Here, we unravel the complexity of the barley *MKK3* locus through multi-year field trials of *MKK3* near-isogenic lines exposed to PHS-inducing conditions, combined with *in vitro* kinase activity assays and ddPCR-genotyping of contemporary and historical barley accessions. In-depth *MKK3* haplotype and expression analyses in the barley pan-genome and -transcriptome datasets reveal extensive structural variation at the *MKK3* locus including copy-number variation and respective changes in transcript abundance. The presence of variable *MKK3* copy-number and specific hyperactive protein haplotypes coincide with traditional and modern farming practices that are important for yield gain and grain quality. Our results suggest that the *MKK3* gene is the major determinant of grain dormancy selected across the globe to adapt to local climate and agricultural practices and that breeders must carefully choose *MKK3* haplotypes to balance malt quality and the risk of PHS.

# An expanded *RHT1* allelic series enables tuneable control of wheat growth

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## ABSTRACT

Green Revolution semi-dwarfing *Rht1* alleles remain central to modern wheat breeding because they improve lodging resistance and assimilate partitioning. However, negative pleiotropic effects, including weak early vigour, lower nitrogen use efficiency and limited flexibility in height control, restrict their utility in some environments, motivating the search for alternative dwarfing alleles.

By screening diverse collections of natural and chemically induced *RHT1* variation, we identified previously unexploited amino acid substitutions and premature stop codons across all three *RHT1* homoeologues, together conferring a wide range of height reductions. Ten *RHT-D1* alleles were introgressed into four elite UK winter wheat backgrounds and evaluated alongside the Green Revolution *Rht-D1b* allele in replicated field trials. Although the alternative alleles produced consistent and predictable height effects across genetic backgrounds, they differed markedly in yield potential.

In parallel, we used base editing to introduce precise *RHT1* variants directly into elite wheat cultivars, providing a rapid and efficient approach to generate tailored height alleles. Together, these complementary approaches establish an expanded *RHT1* allelic series that enables finer dissection of *RHT1*-mediated growth regulation across developmental pathways and provides new dwarfing alleles for direct deployment in wheat breeding programmes.

# Exploration of Niab's synthetic wheat as a new source of genetic resistance for effective control of *Septoria tritici* blotch disease

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## ABSTRACT

*Septoria tritici* blotch (STB) is an important fungal disease, caused by *Zymoseptoria tritici*, which results in significant wheat yield losses. Chemical treatment for STB control accounts for 70% of Northern European fungicide use. However, high levels of genetic diversity within the wild pathogen population rapidly results in the loss of fungicide effectiveness. Therefore, developing wheat varieties with a high level of STB resistance is a breeding priority. Niab have developed a series of synthetic hexaploid wheat (SHW) lines from crosses between different durum wheat and wild goat grass (*Aegilops tauschii*) genotypes, as a core resource in diversifying available wheat germplasm.

These SHWs, together with selected SHW-derived Nested Association Mapping populations, were screened for resistance to *Z. tritici* under controlled growth room conditions using recent UK field isolates, as well as under field conditions with natural infection. Phenotypic screening revealed that many primary SHW lines exhibit high levels of resistance to STB. Genome-wide association analysis of SHW-derived populations identified multiple genomic regions associated with STB resistance, highlighting the value of synthetic wheat as a source of novel resistance alleles. Overall, this work demonstrates the potential of Niab's synthetic wheat germplasm to contribute a valuable genetic resource for the breeding of multi-isolate resistant wheat and sustainable STB management.

# Generation and validation of haploidy inducers in barley by Cas9-mediated knockout of *PHOSPHOLIPASE A1*

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## ABSTRACT

The use of doubled haploid (DH) lines has become one of the most effective biotechnological tools in modern plant breeding. Individual DH lines are genetically unique products of meiotic recombination while also having the key advantage of being completely homozygous. Once a desirable DH line has been identified, it can be reliably and indefinitely propagated through self-pollination. In barley, DH lines can be efficiently produced by regenerating plants from cultivated microspores; however, the success of this approach can vary greatly depending on the genotype. An alternative concept for DH production involves the use of haploidy-inducing lines as paternal parents (Satpathy *et al.*, 2021). Among the progeny derived from such crosses, maternal haploids occur due to the elimination of the paternal genome during early embryogenesis. This phenomenon of uniparental genome elimination has been reported in mutants affecting genes such as *CENTROMERIC HISTONE 3* (*CenH3*), *PHOSPHOLIPASE* (*PLA1*, *PLD3*), and *DUF679 MEMBRANE PROTEINS* (*DMP*) across multiple plant species (Liu *et al.*, 2017). In this study, we generated *PLA1*-specific mutants of barley using genome editing. Pollination of wild-type plants with primary *pla1* knockout mutants resulted in about 6% haploid offspring. The haploidy-inducing capability of homozygous *pla1* $M_2$ mutants was then validated by pollinating diverse barley accessions, which resulted in haploid induction rates ranging from 6% to 16%. In a further approach, *Cas9*/gRNA-transgenic *pla1* mutant barley lines are being employed to deliver genome-editing components from sperm cells to zygotes via fertilization. This strategy enables targeted genome editing of genotypes of choice, while it is expected that in some cases the transgene-carrying paternal genome will be eliminated during early embryo development, leading to immediately transgene-free genome-edited plants (Budhagatapalli *et al.*, 2020). Overall, this approach holds great promise for barley genome editing with considerably reduced genotype dependency.

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# *Session 9:*

# *Decoding Monocots: Genetics for Impact*

# Navigating the GxExM landscape, and finding ways forward for crop improvement

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## ABSTRACT

Advances in genomics, phenomics and enviromics have had led to crop improvements, but the interactions between these factors that influence crop performance, the GxExM landscape, is less well navigated and under-exploited. This may explain in part the plateau in on-farm yields in recent years in the UK and across NW Europe. Genetic gains may not be fully realised on farm because of agronomic restraints, and improvements in management practices may not be matched with the variety most responsive to those practices. And the variety x agronomy combinations may not be optimally matched to exploit the spatial and temporal variation in environmental conditions across the farm and the rotation. Can the complex GxExM landscape be optimised to help close the gap between yield potential and actual yields? Recent work shows that process-based crop modelling, combined with statistical approaches using deep learning tools can make predictions about yield outcomes with specific combinations of plant traits and agronomic practices under a range of environmental conditions, while including measures of uncertainty around those predictions. Computational power was once a major constraint; now it is the availability of relevant, high quality datasets to train those models. There is also a growing trend to co-develop these digital tools with farmers, ensuring that the work is meaningful and applicable. To consider how these ideas might work in practice, new areas of work on genotype x soil microbiome interactions, variable rate N applications, precision planting, and variety blends for yield stability will be discussed in the GxExM context.

# A sticky situation: Root exudate-substrate cohesion is modulated by an XTH gene

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## ABSTRACT

The demand for staple crops like wheat is forecasted to increase, driven by increasing global population size. Land use changes towards cropland to meet this demand have been deemed responsible for 80% of annual soil erosion (Borrelli *et al.*, 2017). Extreme rain patterns caused by climate change and traditional farming methods such as tillage continue to contribute to the loss of arable land through soil erosion, exacerbating the issues facing food production. Root exudates pose a novel solution to reducing the loss of arable land, as they possess components with adhesive properties which can aggregate the soil together, preventing erosion. These components are also rich in carbon, meaning there is potential for engineered carbon storage in agricultural land. There is much to learn about root exudates and the pathways for their release, but two candidate genes, one an *XTH* and the other an *ABC* transporter, have been linked to changing exudate composition and stickiness. Uprooting experiments were conducted on *Arabidopsis* and Wheat CRISPR mutants which were made in house. To ensure root architecture had no effect on uprooting, X-ray CT scanning and a root hair analysis was conducted on the mutants. Root exudates were also extracted from the mutants using hydroponics, and used in a soil binding assay to compare their cohesive properties. For both experiments in both species, the *xth* mutants showed a fluctuation in their cohesion phenotype across repeats compared to Wild Type, but the *abc* mutant showed no differences. To understand the fluctuation observed in the *xth* mutant, the polysaccharide components of the exudates were analysed using biochemical assays. Overall, the *XTH* gene has been proposed as important for modulating the stickiness of root exudates, but further work is required to fully understand the mechanism.

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# Can we develop novel algal biofertilisers from whisky co-products to produce barley sustainably?

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## ABSTRACT

Inorganic fertilisers are essential for global food production, but their use is unsustainable due to depleting reserves of P and K and the energy intensity of the N-fixing Haber-Bosch process. To maintain crop yield and product quality while increasing sustainability, there is a search for alternative, sustainable fertilisers. Microalgae are one proposed source of sustainable fertilisers, with their efficacy proven in other crops including wheat, although their effect on yield, grain quality and malt quality of barley had not yet been investigated prior to this project.

We demonstrate that the microalga *Chlorella vulgaris* can effectively substitute for mineral fertiliser. In all experiments, algae and mineral fertiliser (positive control) were added to soil to meet 118 kg N $ha^{-1}$, the recommended rate for malting barley. In glasshouse and field trials, cv. Laureate grown with algae maintains biomass, tiller number, grain number, TGW and yield compared to mineral fertiliser, and shows statistically significant improvements over plants grown without any additional fertiliser as a negative control. After malting the grain from our field trials, there were no significant differences in hot water extract or predicted spirit yield between the algae or mineral fertiliser treatment, and both treatments gave significantly higher values for these traits than the plants grown with no additional fertiliser.

We are also exploring the relative transcriptomic changes in plants grown with algae or mineral fertiliser. We identified that plants grown with algae upregulate a tryptamine 5-hydroxylase that is posited to have a role in the immune response. Repeating our original experiment with mutants of this gene allows us to examine the perception of algal fertiliser by the crop. These experiments serve as a proof-of-concept that will be expanded to using algae grown on nutrient rich pot ale and spent lees, working towards a circular economy within the whisky value chain.

# Investigating the 3D soil matrix mediating root-to-root interactions between wheat and blackgrass

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## ABSTRACT

The 3D soil matrix is a complex and dynamic environment that plays a crucial role in the optimum growth and development of wheat (*Triticum aestivum* L.). In high-nutrient artificial media, wheat roots were negatively affected by neighbouring blackgrass (*Alopecurus myosuroides* Huds.). However, the impact of the 3D soil matrix in mediating the roots interaction between wheat and blackgrass remains largely unexplored. We hypothesised that (Moss *et al*., 2017) under high-nutrient soil-like conditions, as opposed to low-nutrient, wheat root architecture (e.g., spatial arrangement), topology (e.g., branching pattern), and morphology (e.g., root surface area) are more likely to be affected by the presence of a neighbouring plant; and that (Finch *et al*., 2017) blackgrass suppression by wheat is genetically dependent on wheat cultivar. To test our hypotheses, we (Moss *et al*., 2017) co-cultivated wheat and blackgrass seedlings for 10–14-days under two treatments (high-nutrient and low-nutrient) and three setups (wheat alone, intraspecific wheat-wheat, interspecific wheat-blackgrass); and (ii) conducted a randomised field trial with distinct Nitrogen treatments (high and low), tillage types (direct drilling and deep non-inversion), and 14 different cultivars. Our results indicate that in high-nutrient vermiculite: sand (1:1 ratio) substrates, wheat root surface area and volume in the intraspecific setup were significantly lower compared to the wheat alone setup but not lower compared to the interspecific setup. Moreover, in low-nutrient sieved soil substrates, wheat root dry biomass in the interspecific setup was significantly bigger compared to the intraspecific setup. Furthermore, field trials indicate that deep non-inversion tillage significantly reduced blackgrass aboveground dry biomass, particularly under high Nitrogen conditions. Moreover, blackgrass aboveground dry biomass was highest when surrounded by specific wheat cultivars compared to others. Our findings extend previous artificial-media experiments, highlighting the importance of substrate, nutrient availability, and wheat cultivars when investigating the underground competition of wheat and blackgrass.

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# From understanding to engineering: Synthetic biology approaches to build made-to-order plant immune receptors

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## ABSTRACT

Recurrent epidemics caused by plant pathogens pose a persistent and growing threat to global food security, with annual losses estimated at 22% in wheat and 30% in rice. Identifying natural resistance genes from wild relatives and introgressing them into elite varieties has been effective, but these gains can be rapidly eroded by the emergence of new pathogen strains. An attractive complementary strategy is to engineer immune receptors with defined recognition specificities, matched to pathogen genotypes present in the field.

My research programme addresses this challenge by first developing a mechanistic understanding of how intracellular nucleotide-binding leucine-rich repeat (NLR) immune receptors recognise pathogen effectors and activate immune signalling. A central insight from this work is that NLRs are modular receptors, with recognition and signalling functions encoded in distinct, interchangeable domains. Inspired by the natural integration of effector-target domains into NLR scaffolds over evolutionary time, we characterised the structural and functional constraints governing domain integration in the rice Pik NLR pair. These principles enabled the engineering of NLR-nanobody fusions, termed Pikobodies, which redirect NLR specificity towards user-defined targets. Pikobodies demonstrate that plant immune receptors can serve as effective scaffolds for custom binding domains, conferring resistance against pathogens and viruses delivering recognised molecules inside host cells.

Building on these foundations, my lab is now establishing tools designed to accelerate the discovery and engineering of immune receptors at scale. These include high-throughput cell-based screening platforms capable of evaluating thousands of receptor variants simultaneously, computational pipelines integrating AlphaFold3-based interaction prediction with large-scale genomic analyses, and a growing toolkit of bioengineered NLR scaffolds applicable across multiple crop systems. Drawing on nature's own solutions as a design guide, we are expanding this approach beyond model systems towards direct relevance for cereal crop improvement.

I will discuss how this integrated approach, from mechanistic understanding of NLR activation to the development of Pikobodies and next-generation screening platforms, provides a generalisable framework for engineering durable disease resistance in wheat, barley, and other cereal crops.



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# *Poster Abstracts*
# *P1. Cultivating Good Company: Probiotics for Plants*

# The Wheat Alliance: Identification and characterisation of ancestral wheat microbiomes

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## ABSTRACT

The Wheat Alliance Project is an international strategic partnership between the Collaborative Crop Resilience Program (CCRP), Niab and the Crop Science Centre (CSC) at University of Cambridge that aims to identify combinations of wheat genotypes and microbial strains that synergistically improve nutrient supply and increase wheat-resilience in low-input farming systems.

As climate change intensifies and natural resources become increasingly limited, there is an urgent need for sustainable solutions to increase resilience in agricultural systems. Plant-microbe interactions play a key role in supporting plant growth, enhancing productivity and increasing tolerance to environmental stress. Understanding how plant genetics influence the selection and assembly of beneficial microbiomes will help guide future breeding strategies and microbial applications toward more sustainable agricultural practices

Through the genetic bottlenecks imposed by crop domestication and modern breeding, the wheat varieties we rely on today may lack the range of genetic diversity needed to optimise microbial relationships which support plant resilience compared to their ancestral counterparts. Niab has created a large suite of wheat populations containing diverse introgressions from a range of wheat accessions including tetraploid wheat species (wild emmer, emmer and durum) and novel Synthetic Hexaploid Wheats (SHW).

We are performing a large-scale screening of a panel of the donors of these populations, consisting of wild, landrace, cultivated and SHW wheat lines, in both nutrient depleted and nutrient supplemented soils. This will identify optimal combinations of wheat accessions and beneficial microorganisms that can enhance nutrient acquisition from soil, improving crop resilience and productivity while reducing dependence on synthetic fertilizers.

The Wheat Alliance aims to create extensive plant and microbiome phenotypic data sets to develop predictive models of microbial functions and plant phenotypes associated with nitrogen and phosphorus benefit. A proof-of-concept framework for large scale microbiome-based breeding of resilient crops will be created to support sustainable agriculture.

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# *Poster Abstracts*
# *P2. Staying Ahead of the Outbreak: Biotic Threats & Defences*

# Exploiting wheat relatives to enhance brown rust resistance in bread wheat

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## ABSTRACT

Brown rust (*Puccinia triticina*) is an important fungal disease of wheat in the UK. The UK Cereal Pathogen Virulence Survey (UKCPVS) continues to show widespread virulence towards many resistance *Lr* genes, increasing the vulnerability of current varietal resistance. RGT Goldfinch is the only current variety on the AHDB Recommended List resistant to all tested UKCPVS isolates at the seedling stage (Davis *et al.*, 2025). These observations highlight the urgent need to broaden the genetic basis of brown rust resistance in UK wheat. Here, we evaluated tetraploid wheat accessions as novel sources of resistance for pre-breeding. Seedling screening against five broad-profile UK *P. triticina* isolates identified eight tetraploid accessions that consistently exhibited resistant infection types, demonstrating that the cultivated tetraploid gene pool is an under-exploited reservoir of effective all-stage resistance genes effective against contemporary UK pathogen populations. To assess the transferability of tetraploid-derived resistance, previously developed synthetic hexaploid wheat (SHW) lines incorporating resistant tetraploid donors were evaluated. In each case, resistance expressed in the tetraploid donors was maintained following introgression into hexaploid backgrounds, indicating successful transfer and expression of tetraploid-derived resistance. Together, these results support the deployment of tetraploid-derived alleles as a strategic resource for enhancing seedlings stage resistance in UK wheat. They also validate the Niab Tetraploid x Hexaploid (TetHex) and SHW-derived nested association mapping populations as platforms for forward genetic dissection and breeding-relevant delivery of improved brown rust resistance.

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# CRISPR/Cas9-guided knockout of *TaZEP1* restricts multiple fungal pathogens growth in hexaploid wheat

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## ABSTRACT

Wheat (*Triticum aestivum* L.), a cornerstone of global food security, faces persistent and severe threats from fungal diseases, particularly leaf rust, stripe rust and powdery mildew. Previous studies in tetraploid wheat have revealed that the *TaZEP1* gene functions as a negative regulator of plant immunity, its inhibition induces the accumulation of reactive oxygen species (ROS), thereby effectively restricting pathogen growth. However, it remains unclear whether knocking out *TaZEP1* in hexaploid bread wheat confers similar resistance. Therefore, we employed the CRISPR/Cas9 gene-editing system to precisely edit the *TaZEP1* gene in the transformation-amenable wheat cultivar 'Fielder'. Through self-pollination and marker-assisted selection, we successfully generated a series of homozygous mutants targeting the three *TaZEP1* homoeoalleles, including single- (aaBBDD, AAbbDD, AABBdd), double- (aabbDD, aaBBdd, AAbbdd), and triple-mutant (aabbdd) lines. We performed inoculation assays on eight homozygous lines (comprising the edited mutants and wild-type 'Fielder') using the highly virulent stripe rust race CYR32, the leaf rust race PHQS, and fresh spores of field-collected powdery mildew. The mutant lines exhibited a significant reduction in both the number and size of sporulation pustules, effectively impeding fungal proliferation. Notably, the triple mutant (aabbdd) displayed superior resistance compared to the single and double mutants, with pathogen growth rates significantly lower than those observed in the wild type. Collectively, these results confirm the conserved role of *TaZEP1* as a horizontal resistance gene in hexaploid wheat. The consistent ability of *TaZEP1* editing to suppress pathogen proliferation across different mutant genotypes and against multiple fungal species highlights it as a promising breeding target, suggesting that targeted manipulation of this gene holds significant potential for enhancing broad-spectrum disease resistance in elite wheat varieties.

# Tracking the molecular targets of stem rust in wheat

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## ABSTRACT

Stem rust is a devastating fungal disease of wheat and continues to pose a serious threat to global food security. The fungus infects wheat by delivering “effector” proteins into plant cells, where they suppress immune responses and reprogram host processes to support infection. Although several stem rust effectors have been identified, relatively little is known about how they function inside susceptible wheat plants. This project investigates wheat host proteins targeted by four stem rust effectors (AvrSr22, AvrSr26, AvrSr31, and AvrSr33) to improve understanding of host processes manipulated during infection. An initial yeast-based protein–protein interaction screen identified 18 candidate wheat proteins as potential effector interactors. However, when prioritised candidates were tested *in planta* using a split-GAL4 RUBY assay, no clear interaction signals were detected. To refine the candidate list, structural predictions generated using AlphaFold-Multimer were integrated with wheat RNA-seq expression data, enabling prioritisation of the most biologically plausible host targets. These high-confidence candidates are now being taken forward for independent validation using co-immunoprecipitation and functional assays. Defining how these host proteins contribute to susceptibility will advance understanding of stem rust pathogenesis and may help inform strategies for developing more durable disease resistance.

**Key words**: Stem rust**,** Effector–host interactions**,** Durable disease resistance

# Identification and characterisation of novel barley resistance to aphids

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## ABSTRACT

Aphids are major pests of barley, causing severe yield losses worldwide. However, the mechanisms underlying barley resistance and the quantitative variation among cultivars remain largely unknown. Thionins are small cysteine-rich peptides that have been suggested to play a role in barley defense against aphids. This study integrates gene family characterisation and quantitative resistance evaluation to investigate the evolutionary features of the thionin gene family and establish a framework for resistance assessment in barley.

A total of 56 thionin genes were identified from the barley Morex V3 reference genome. Phylogenetic analysis revealed pronounced chromosomal clustering, and structural characteristics and high sequence similarity indicate extensive tandem duplication within the family. Notably, thionin genes located on chromosomes 6H and 7H show extensive expansion and diversification, whereas those on chromosome 1H remain relatively conserved. Pan-genome analysis across 20 barley genotypes revealed substantial copy-number variation, particularly frequent expansion and contraction of thionin genes on chromosomes 6H and 7H. Moreover, pan-transcriptome analysis demonstrated clear tissue-specific expression patterns associated with chromosomal origin. The expression of thionin genes on chromosome 6H was further validated using RT-qPCR, highlighting the evolutionary diversification and complex regulation of this gene family. In parallel, a standardized aphid infestation system was established, and resistance was quantitatively evaluated using six aphid performance indicators reflecting aphid growth and reproduction. By integrating distance-based models, weighted composite indices, and multivariate clustering approaches, a quantitative resistance index was developed and applied to 20 barley cultivars.

Overall, this study provides new insights into the evolution and expression diversification of the barley thionin gene family. In addition, this study establishes a robust quantitative framework for aphid resistance evaluation in barley, supporting future studies of barley defense mechanisms and resistance breeding.

# Hormetic UV-C seed treatment enhances barley tolerance to *Ramularia leaf spot*

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**Abstract**

*Ramularia collo-cygni (Rcc),* the causal agent of Ramularia leaf spot (RLS), poses a major challenge to global barley production due to its latent infection, widespread fungicide resistance, and the absence of fully resistant genotypes. This study examined whether hormetic UV-C seed treatments can enhance barley resilience by modulating host immunity and maintaining holobiont functionality. Two field-infected barley genotypes with contrasting susceptibility to RLS were treated with mild and high-intensity pulsed UV-C at the seed stage. Disease severity, pathogen load, developmental traits, mineral composition, and root-associated microbial communities were assessed. Global transcriptome profiling and variant calling analyses were conducted to evaluate regulatory responses and genomic safety. UV-C treatment substantially reduced symptom severity without altering Rcc pathogen load in seed or shoot tissues, indicating enhanced host tolerance rather than resistance. Mild UV-C doses induced defence priming, while higher doses triggered immune-like transcriptional reprogramming, including upregulation of TIFY-domain (JAZ) repressors and modulation of jasmonate signalling, preventing the necrotrophy-associated oxidative transition of the pathogen. Although high UV-C doses caused shifts in microbial composition in the sensitive genotype, microbial functional capacity and nutrient assimilation remained stable, supporting holobiont integrity. SNP/INDEL Variant calling confirmed genomic safety across all UV-C treatments. These findings demonstrate that hormetic UV-C enhances barley resilience through immune recalibration and disease tolerance, decoupling pathogen load from symptom severity, while preserving functional stability of the associated microbiome. This work highlights the potential of abiotic elicitors to strengthen holobiont-level tolerance against necrotrophic pathogens, offering a sustainable strategy for crop protection.

MONOGRAM

CEREALS & GRASSES RESEARCH NETWORK

# *Poster Abstracts*
# *P3. Beyond Yield: Grain Quality & Human Nutrition*

# Genome-wide analysis of soluble fibre variation in elite European wheat

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## ABSTRACT

Dietary fibre is essential for health intake remains below recommended levels in many populations including the UK. Wheat is an important source of fibre, with most products being made from white flour which has a lower fibre content than wholemeal. Increasing the fibre content in white wheat flour therefore offers a scalable strategy to improve public health. Arabinoxylan (AX) is the principal fibre component in white flour, with the water-extractable (WE) fraction having benefits in the small intestine (reducing glycaemic response) and colon (being rapidly fermented). We assembled an Elite Fibre Panel (EFP) of 384 elite modern wheat genotypes and quantified the WE-AX content of wholemeal (as a proxy for WE-AX in white flour) across two UK field environments. This showed substantial quantitative variation, moderate genotype-by-environment interaction, and a broad-sense heritability of 0.68.

Genome-wide association analysis using 6,791 SNPs identified seven loci associated with WE-AX content. The largest and most stable effects were located on chromosomes 1B and 6B, previously implicated in AX regulation, with additional smaller and sometimes environment-dependent loci on chromosomes 3A, 5B, and 7A. Favourable alleles increased WE-AX content by approximately 5–15% and acted additively. Candidate genes within LD-defined intervals were associated with cell wall biosynthesis and modification. These findings demonstrate that soluble AX content can be increased by pyramiding existing alleles within elite germplasm, providing a practical breeding route to enhance fibre content in white flour.

# Expanding Quinoa genetic diversity to improve nutritional quality and agricultural resilience in the UK

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## ABSTRACT

Global agriculture depends on a few staple crops (rice, maize, wheat, and soybean), supplying about 75% of plant-based calories worldwide. Although vital for food security, this reliance increases vulnerability to climate variability and soil degradation. Diversifying cropping systems with resilient, nutritious species is therefore critical. Quinoa (*Chenopodium quinoa* Willd.) has gained prominence due to its high-quality, gluten-free protein, balanced amino acids, and rich micronutrient content, including iron, zinc, and magnesium. Quinoa tolerates abiotic stresses and contributes to agroecosystem services through biodiversity enhancement and rotational benefits. However, the genetic basis of quinoa nutritional traits remains underexplored, particularly for UK adaptation. Wild relatives, especially *Chenopodium berlandieri,* offer valuable genetic diversity to improve nutrition and resilience. At the University of Nottingham Farm, UK, field experiments were conducted to evaluate set of quinoa genotypes, including pre-breeding lines and commercial cultivars, under contrasting nitrogen regimes low-input and conventional systems. Agronomic performance and key nutritional traits in grain and leaves were assessed to explore genotype responses to environmental and management conditions. Preliminary results indicate that both genetic variation and environment influence nutrient accumulation in quinoa grain. Genotype significantly affected protein concentration. Under high nitrogen conditions, the pre-breeding lines, Q2 (material selected in Dubai at the International Center for Biosaline Agriculture (ICBA), Holtville 30_1, and 16_3, exhibited high protein content. For mineral contents, pre-breeding lines, Holtville 16_3 and 10_1 showed higher concentrations of potassium, magnesium, and zinc, under low nitrogen conditions. In contrast, the commercial variety Titicaca exhibited high calcium and iron concentrations under high nitrogen conditions. This work demonstrates the potential of leveraging wild *Chenopodium* genetic diversity to improve key nutritional traits while addressing genomic barriers in breeding. Integrating nutritional trait analysis with modern genomic tools provides a pathway to develop quinoa varieties adapted to UK environments that support climate resilience and human nutrition.

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# Re-engineering amino acid metabolism in wheat grain using CRISP/Cas9

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## ABSTRACT

Unlike plants and microorganisms, humans and other animals cannot synthesise lysine, and so must acquire it in their diet. Wheat (*Triticum aestivum*) and other cereal grains are low in lysine and people who live a plant-based lifestyle or do not have access to meat can suffer from lysine deficiency and malnutrition. Soybeans and other legumes do contain higher concentrations of lysine, but if we are to reduce our dependency on meat, which is one of the recommendations for achieving net zero $CO_2$ emissions, a broader and more sustainable source of plant-based lysine will be required.

Lysine is synthesised by the DAP (diaminopimelate) pathway, of which the rate-limiting step is the conversion of L-aspartate semialdehyde and pyruvate into (4S)-4-hydroxy-2,3,4,5-tetrahydro-(2S)-dipicolinic acid, catalysed by the enzyme DHDPS (dihydrodipicolinate synthase). High levels of lysine are prevented from accumulating by feedback inhibition of DHDPS by lysine.

GM Mutant DHDPS wheat transformants have been generated through CRISPR and particle bombardment and subsequently analysed via HPLC. Ongoing work continues in an attempt to produce a gene edited, transgene free, high lysine line of wheat.

# Delivering a balanced diet for Southern Africa's farmers

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## ABSTRACT

In Southern Africa biofortification has been used to increase the level of provitamin A and zinc (Zn) concentration throughmaize breeding. Farmers in this region commonly grow maize hybrids but native (landraces) varieties are still popular. The genetic diversity in the nutritional content of native varieties is largely unknown. A survey was conducted to explore nutritional traits of native maize varieties grown under contrasting management and agroecological regions in Zimbabwe. Additionally, researcher-managed on-station trials were also implemented to test the performance of five native maize varieties including a popular maize hybrid (as the control) under farmer managed conditions. Soil and grain samples were collected from 220 smallholder farmers and analysed for multi-elements including Zn and iron (Fe) using dry spectroscopy and wet chemistry.

A wider range in grain Zn and Fe concentration was observed in native maize varieties compared to hybrids, although averages were not significantly different. Specifically, grain Zn and Fe concentration in native maize varieties ranged from 13.5–40.0 (mean 24.1) and 10.7–43.7 (mean 21.6) mg $kg^{-1}$ respectively, while hybrids had Zn and Fe concentrations ranging from 19.9–35.8 (mean 25.1) and 13.3–29.1 (mean 21.3) mg $kg^{-1}$, respectively. Higher yields, resistance to pest and disease, better taste, medicinal and herbal benefits and seed knowledge conservation were highlighted by farmers as reasons for continued production of native maize varieties. The wider range in nutrient concentrations of native maize varieties reaching up to the optimal biofortification breeding threshold for Zn (38 mg $kg^{-1}$) and Fe (42 mg $kg^{-1}$) in cereals, indicates that these varieties could potentially compliment biofortified hybrids and offer a faster and more effective route into reducing dietary micronutrient deficiencies in Southern Africa.

# Control of grain hydration and germination speed in barley

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## ABSTRACT

Barley is an economically important crop in Scotland, with 52.5% of the 1.33 million tonnes of spring barley produced in 2021 used for malting. Malting involves controlled soaking, germination, and drying of barley grain, and improving water and process efficiency is a major industry goal. Traits such as grain hydration and germination speed are therefore of significant interest. Water uptake during steeping initiates germination and is influenced by environmental conditions and genetic background through effects on grain composition and structure.

A study of six barley varieties grown across 13 trial sites examined the roles of genetics, environment and their interaction (G×E) in regulating grain water uptake. Environment accounted for most of the variation, indicating that growing conditions strongly influence this trait. A genome-wide association study (GWAS) using over 220 malting varieties did not find any significantly associated genomic regions, suggesting that grain hydration is a complex, polygenic trait potentially controlled by many small-effect alleles.

To investigate germination speed, the 220 malting varieties mentioned above, and a bi-parental mapping population developed by Syngenta have been phenotyped for quantitative trait loci (QTL) identification. QTL identification and analysis is currently ongoing. Future work will focus on transcriptome analysis of the mapping population parents at multiple timepoints during germination to explain differences in germination speed. Identifying loci linked to faster germination could improve malting efficiency and sustainability.

# Disentangling genotypic, environmental, and agronomic effects on barley starch characteristics relevant to malting and malt quality

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## ABSTRACT

Climate change and new agronomic practices in major barley-growing regions may alter malt-processing quality. These changes could compromise profitability, product uniformity, and quality consistency in the brewing industry. Observed varietal and seasonal variation in key malt quality traits indicates that both genotype and growing environment influence malting quality; however, their relative contributions remain poorly understood. This study examines how genotype and growing environment affect barley starch structure and composition, aiming to identify key traits that predict malting and brewing performance.

In 2024, field trials were established at four sites across the USA, Argentina, and the UK, representing diverse climatic and agronomic conditions. Six commercial malting barley varieties (ABI Cardinal, ABI Eagle, ABI Fina, ABI Raptor, ABI Voyager, and Merit 57) were used. Weather variables and agronomic data were recorded at each site. Harvested grain samples were analysed for malting quality and starch composition. Samples were micromalted and mashed at laboratory scale to produce wort for standard brewing quality analysis. Thermal and pasting properties were characterised using Differential Scanning Calorimetry and Rapid Visco Analysis, respectively. Analysis of variance was used to quantify genotypic (G), environmental (E), and G × E effects, while correlation and regression analyses examined relationships among starch properties, weather conditions, management factors, and malting quality.

Results from the 2024/25 season indicate a stronger environmental influence on malting quality than genotypic effects. Warmer temperatures during grain-filling at Fort Collins, USA, resulted in significantly higher protein content and higher starch gelatinisation temperatures. In contrast, UK samples, produced under cooler and wetter conditions, showed higher fine grind extract values and greater peak and breakdown viscosities. Significant correlations between gelatinisation temperature, hot water extract, and protein content suggest that starch thermal properties have potential as predictors of malting quality in barley. Analysis of starch granule distribution and amylose content is in progress.

# Assessing wheat performance in hydroponic and vertical farming systems: Pathways to reducing urban food insecurity

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## ABSTRACT

Meeting the projected 50-70% increase in global food demand by 2050 requires innovative agricultural strategies capable of overcoming the intensifying effects of climate change. Rising temperatures of 1.5–5.5 °C and more frequent severe droughts are already reshaping where and how crops can be grown. Since most food production relies on soil-based systems, food security is tightly linked to land availability. However, agricultural expansion has historically driven ecosystem loss and pollution. Urban food insecurity further compounds these challenges, as rapid urbanisation and dependence on external food supplies leave billions, particularly those in informal settlements, vulnerable to limited access, high prices, and poor nutritional quality food.

To address these pressures, alternative production systems that are climate-resilient and land efficient are urgently needed. Hydroponics and vertical farming offer substantial potential, providing highly controlled, resource-efficient, and space saving environments that minimise pest pressures and operate independently of climate constraints.

This study evaluated seven double dwarf wheat genotypes from CIMMYT, valorising breeding program byproducts for commercial use, alongside a commercial cultivar grown under hydroponic, vertical farming, and compost-based glasshouse conditions. Results show that hydroponic cultivation produced the greatest biomass and grain yield. Similarly, both hydroponics and vertical farming enhanced grain micronutrient concentrations, with zinc accumulation in vertically farmed wheat reaching up to 5.5-fold higher than in compost-grown plants.

These findings demonstrate that hydroponic and vertical farming systems can successfully produce high value crops such as wheat with superior nutritional quality. Implementing such systems in urban settings could strengthen local food production, improve access to nutrient dense foods, and contribute to more resilient urban food security.

# Harnessing crop wild relatives through introgression lines to enhance wheat resilience and grain quality

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## ABSTRACT

The systematic exploitation of crop wild relatives to broaden wheat's genetic diversity is the primary objective of the Horizon Europe PRO-WILD project, which aims to deliver pre-breeding ready genetic resources for wheat improvement. In alignment with PRO-WILD deliverables focused on trait discovery, characterisation, and prioritisation of introgressed materials, we conducted a phenotypic evaluation of 360 wheat introgression lines (ILs) developed by crossing diverse wild relative donors into elite wheat backgrounds.

Plants were evaluated under controlled glasshouse conditions for key grain size traits, including thousand grain weight (TGW), grain length, and grain width, as well as grain quality traits relevant to nutrition and end-use quality, namely iron, zinc, grain protein, gluten, starch content, and grain hardness. Substantial phenotypic variation was observed across all traits, with distributions extending beyond the recurrent parent's range, indicating successful capture of novel alleles from wild relatives. Several ILs exhibited transgressive phenotypes, indicating favourable combinations of wild and elite alleles that are immediately relevant to pre-breeding pipelines.

Trait distributions varied across donor-derived IL subsets, highlighting donor-specific effects on grain architecture and nutritional composition and supporting wild relative donor prioritization strategies within PRO-WILD. Correlation analyses revealed strong positive associations among grain size components, protein and gluten, and starch and grain hardness. In contrast, negative relationships between protein and starch, and between starch and gluten, underscored key trade-offs relevant to quality-oriented breeding decisions. In parallel, seedling-stage screening in the growth chamber via artificial inoculation for Septoria tritici identified a subset of ILs with enhanced resistance.

Collectively, this deliverable provides a phenotypic foundation for the PRO-WILD objective of advancing CWR-derived diversity in wheat improvement. By integrating trait performance with donor origin and future marker-based validation, this study enables prioritisation of introgressed segments and supports their targeted deployment in elite breeding programs.

**Key Words**: Crop wild relatives, introgression lines, grain quality, pre-breeding, PRO-WILD, *Septoria tritici*

MONOGRAM

CEREALS & GRASSES RESEARCH NETWORK

# *Poster Abstracts*
# *P4. New Frontiers: Unlocking Opportunity Cereals*

# Building foundations for 'Ensembl Plant Populations'

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## ABSTRACT

The United Kingdom has strong capabilities in plant research, with extensive expertise in germplasm resource development, trait discovery platforms, and genomics. However, integrating these areas has historically been challenging, requiring significant technical expertise. The 'Ensembl Plant Populations' initiative is a collaborative effort between Ensembl and Niab, that has been funded by the BBSRC to address these challenges head-on. This open-source online platform will provide researchers with the necessary tools for robust genome-wide association analyses and candidate gene assessment for 12 already genotypically defined and publicly available plant populations.

Focusing on seven key plant species - *Arabidopsis*, barley, oat, oilseed rape, rice, tomato, and wheat - the project combines carefully curated genotype data with genetic analysis pipelines to ensure statistical integrity. Researchers will be able to access seed from the relevant Germplasm Resource Unit, make their measurements and observations, before uploading their phenotypic data to 'Ensembl Plant Populations'. This platform will then perform association studies and candidate gene assessment and the user will receive expert guidance through an interactive visualisation tool to identify key genetic components, and directly link to the existing Ensembl Plants infrastructure, enabling further bioinformatic exploration of resulting genetic regions of interest. This project will enable a significant step forward in the community's ability to explore the genetic basis of important plant traits, in a number of key species, streamlining the research process and fostering collaborative discovery.

# Chromosome-level genome assemblies for 48 Poaceae species

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## ABSTRACT

The project 'AEGIS: Ancient Environmental Genomics Initiative for Sustainability', led by the University of Copenhagen and funded by Novo Nordisk Foundation and the Wellcome Trust, aims to develop methods to use ancient environmental DNA (eDNA) to identify important organismal associations and genetic adaptations in natural and agro-ecosystems that will improve future food security under climate change. This will be achieved by (1) Studying how climate change and human activities have shaped species composition and genetic diversity in natural ecosystems over time; (2) Investigating how crops and farming systems have changed as climate and farming methods have evolved; (3) Identifying beneficial genetic traits and ecosystem processes from the past that could enhance crop resilience; (4) Applying these climate-adaptive traits to improve the productivity, sustainability and resilience of modern farming systems.

A central 'Data Engine' will analyse and priorities genes and variants identified from ancient eDNA. To support this, new chromosome-level genome assemblies will be generated for species which currently lack such resources, to help interpret ancient eDNA datasets. As part of this effort, Niab has sourced, grown and harvested tissue for 94 plant species of agricultural relevance for genome sequencing at the Wellcome Sanger Institute. These span 10 plant families, and include vegetables (celeriac, gourd, scorzonera), fodder crops (e.g. clovers, medics, sulla, lupins), herbs (e.g. carroway, dill, fenugreek, parsley, tarragon), oil crops (field gromwell), and fruits (quince, medlar, blackberry).

Within the **Poaceae, 48 species from 40 genera** were selected, including all the species on the European Common Catalogue of Plants and Vegetable Species that currently lack reference genomes (e.g. brome and canary grasses, black oat, fescues), as well as grass weeds and species adapted to a wide range of ecogeographic environments. The resulting genomic resources will be shared with the Poaceae Pangenome Consortium, and made publicly available to support Poaceae R&D.

# Understanding the role of novel gene pathways in germination and their impact on the malting process

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## ABSTRACT

Seed dormancy and germination represent one of the most consequential developmental decisions in the plant life cycle, yet how environmental information is integrated to control this transition remains poorly understood. While hormonal and genetic regulators of dormancy have been extensively studied, light as an instructive environmental signal during cereal germination has been largely excluded from mainstream models. This omission represents a major conceptual gap in seed biology.

The MAP kinase MKK3 has emerged as a central regulator of seed dormancy and abscisic acid (ABA) signalling in wheat and barley. However, its potential role as an integrator of environmental cues, particularly light perception, has never been explored. In parallel, the N-degron pathway component PRT6 regulates dormancy by targeting proteins involved in hormonal and environmental responses; disruption of PRT6 enhances ABA sensitivity and reinforces dormancy, particularly under stress conditions such as hypoxia. Together, these pathways suggest the existence of an integrated signalling network linking environmental perception, intracellular signalling cascades, and hormonal control. We propose that domestication and selective breeding for low-dormancy phenotypes, beneficial for malting quality, have rewired ancient regulatory modules, weakened environmental responsiveness and increasing susceptibility to pre-harvest sprouting. By exploiting wild barley accessions as reservoirs of ancestral signalling architectures, we aim to uncover genetic variants and regulatory interactions involving MKK3, PRT6, and ABA/GA signalling that are absent or diminished in elite cultivars. Using a combination of physiological assays, molecular analyses, and CRISPR/Cas9-based gene editing, we will dissect how light, hypoxia, temperature and hormonal signals converge on these pathways to determine dormancy depth and germination timing. This work seeks not merely to refine existing models but to redefine them by positioning environmental signal integration at the core of dormancy regulation. Insights from this research have direct relevance for barley improvement, offering routes to mitigate pre-harvest sprouting while enabling precise, synchronous germination essential for high-quality malting.

# Impact of ph1 and ph2 mutation on homoeologous recombination in wheat

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## ABSTRACT

Diversification of the hexaploid wheat genetic pool using wild genetic resources relies on effective meiotic recombination (crossover) between wheat chromosomes and their counterparts from related species (homoeologues), (Mercier *et al*., 2015). However, crossover between homoeologues is normally suppressed by two major genes, ZIP4-5B (Ph1) and MSH7-3D (Ph2), (Mello-Sampayo & Lorente. 1968; Sears & Okamoto, 1958). We investigated the effect of introducing zip4-5B and/or msh7-3D mutations into interspecific hybrids derived from crosses between wheat and Aegilops variabilis. Single and double mutants were exploited in Chinese Spring (CS) and Cadenza (Cad) genetic backgrounds, as well as in a CS/Cad recombinant background. The number of univalents, bivalents and multivalents was scored from meiotic cells at metaphase I, from which numbers of chiasmata were deduced. We demonstrated a non-cumulative effect of simultaneous zip4-5B and msh7-3D mutations on homoeologous recombination, as homoeologous crossovers reached a maximum when ZIP4-5B alone was mutated. We also showed that hybrids carrying both the zip4-5B and msh7-3D mutations in the same genetic background exhibited more effective recombination compared to a double mutant in the CS/Cad recombinant background. Thus, our study significantly contributes to the optimization of the introgression of beneficial alleles from wild relatives into elite wheat germplasm; first by demonstrating the efficiency of ZIP4-5B and MSH7-3D mutations independently and in combination and second by elucidating the influence of the genetic background in which these mutations are present in an interspecific hybrid context.

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# A protoplast-based method to identify direct TARGETs of transcription factors in wheat

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## ABSTRACT

Transcription factors (TFs) are key regulators of numerous genes. In wheat, many gene networks still need to be deciphered, notably the identification of target genes of TFs. Methods developed for this purpose are not yet adequate. For example, ChIP-seq requires transgenic plants which is still a lengthy process in wheat, or *in vitro* techniques such as DAP-seq are not effective on all families of TFs. To overcome these limitations, we have adapted a protoplast-based system for the rapid identification of targets of TFs.

Wheat protoplasts are isolated from young leaves and transformed with a construct carrying a TF of interest, coupled with a Glucocorticoid Receptor (GR). Transformed cells express GFP and are therefore selected by Fluorescence Activated Cell Sorting (FACS). Treatment of the sorted cells with dexamethasone breaks down the TF-GR complex and allows the TF to move to the nucleus where it can interact with its targets. A pre-treatment with cycloheximide prevents protein translation and thus ensures no secondary targets of the TF are triggered . Transcriptome analysis of the treated versus non treated cells leads to the identification of the direct targets of the TF of interest.

We have tested the method independently with two types of TFs: a NAC and a bHLH. In both cases we identified direct targets of each TF, including expected targets. Promoter sequences of target genes were enriched for conserved binding motifs for each TF. Finally, expected GO terms were identified for targets of each TF. These combined results confirm the efficacy of this method.

Further studies are now being carried out to establish whether the FACS step could be omitted from the method allowing for more samples to be run per experiment and speed up the technique.

In summary, this protoplast-based system is a promising route to decipher gene networks in wheat.

# Does the PRT6 N-degron pathway regulate the root growth response to heat stress in barley?

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## ABSTRACT

Climate change, driven by the accumulation of greenhouse gas emissions due to human activities, is disrupting weather patterns, intensifying extreme weather events, and raising global average temperatures. This phenomenon poses significant challenges to global food security, exacerbated by growing population and shrinking in arable land. Understanding how crop plants respond to temperature is essential for developing crop varieties that can adapt to high-temperature stress.

The N-degron pathway is a proteolytic system that targets proteins with N-terminal residues for degradation through proteasome. Ubiquitin-mediated proteolysis via the Plant Cysteine Oxidase (PCO) branch of the PRT6 N-degron pathway control plant response to environmental cues by facilitating changes to the proteome involved in sensing and may improve plant performance under several abiotic stresses (Vicente *et al*., 2017). Recent work has revealed salicylic acid as an upstream regulator that represses PRT6 activity in rice (Xu *et al*., 2025).

In barley, reduction in PRT6 was reported to benefit plant growth and development in several abiotic stresses, including waterlogging and salinity stress (Mendiondo *et al*., 2016; Vicente *et al*., 2017). The role of the N-degron pathway (especially PRT6) in heat stress remains unclear, with improved survival under extreme heat reported in Arabidopsis but not under moderately high temperatures (Vicente *et al*., 2017). Furthermore, UBR7, another N-recognin within the pathway, regulates autophagy through selective degradation of ATG8a during heat stress recovery, highlighting the pathway's diverse roles in thermotolerance (Kim *et al*., 2025). In this project, we aim to dissect how barley responds to high temperature stress, with the PRT6 N-degron pathway as the central sensor and regulator. Preliminary findings from our research indicate that barley roots exhibit sensitivity to extreme heat, with *Hvprt6* mutant lines displaying altered root growth dynamics and anatomy under high temperatures. This suggests that PRT6 may play a crucial role in root-specific heat stress responses in cereals.

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# Harnessing genetic variation from wild relatives for durum wheat improvement

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## ABSTRACT

Climate change combined with the reduction in arable land and the rapid growth of the global population is significantly impacting wheat production worldwide. Durum wheat, like other crops, is not immune to these challenges. One promising solution lies in harnessing the genetic variation found in wild relatives of wheat. Accessing this untapped diversity can lead to the identification of novel alleles that enhance adaptability and boost yield. At the Wheat Research Centre (WRC) in Nottingham, over 1000 wild relative's introgression lines were developed in the hexaploid wheat background. Efforts are now underway to transfer these valuable introgressions into durum wheat. A crossing program was established to transfer wild relatives introgressions from 96 introgression lines selected from seven wild relatives; *Aegilops caudata*, *Ae. speltoides*, *Ae. mutica*, *Thinopyrum bessarabicum*, *Th. elongatum*, *Triticum timopheevii*, and *T. urartu* into the background of two durum wheat cultivars. Approximately 97% of these lines were successfully crossed, producing F1 seed with at least one of the durum genotypes. Originally developed for bread wheat, around 1000 KASP markers were tested for their ability to track the wild segments in the durum wheat background. The number of usable markers ranged from 215 to 474, depending on the species. High level of segment retention was identified, especially in *T. timopheevii* population. Genotyping of the BC1 and BC2 generations confirmed the presence of new, smaller introgressions due to recombination with the durum genome. The program has now progressed to the BC2F1 stage, with tetraploid introgression lines identified across several populations. Once homozygous, these lines will be phenotyped for multiple agronomic traits of interest.

# Towards identifying the key variables influencing lodging in tef (*Eragrostis tef*)

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## ABSTRACT

Lodging in tef (*Eragrostis tef*) is a major agronomic challenge that limits yield potential and complicates harvesting. Tef is particularly prone to root lodging, where the entire plant tilts from the base rather than snapping at the stem. Lodging resistance has previously been associated with dwarfing genes (e.g., *Rht1* and *BRI1*) and cell wall biosynthesis genes (e.g., *COMT1, CAD8C, CESA1*, and *CESA4*). In this study, we conducted a multifaceted assessment of lodging in 61 tef genotypes sourced from the GRIN seedbank (https://www.ars-grin.gov/). Based on field assessments, genotypes had been classified as resistant (R, n = 23), susceptible (S, n = 24), or moderately resistant (MR, n = 14). Plants were grown for five weeks as single individuals in 15 cm pots filled with F2 compost (Levingtons Ltd) to prevent nutritional limitation. Lodging characteristics were confirmed both observationally and through measurements of Young's modulus (stem stiffness), which indicated that lodging was primarily due to root failure rather than stem breakage. Phenomic analysis included traits such as plant height, plant area, stem count, angle, hull area, canopy spread, convexity, and pixel-based colour metrics (% red, orange, yellow, green, and cyan). These analyses revealed that MR genotypes were distinctive, showing lower canopy spread, plant area, and canopy spread. Stem cross-sectional analysis, combined with quantitative phloroglucinol staining for lignin, revealed a counterintuitive result: R genotypes had significantly lower lignin content. Hyperspectral imaging of the lower stem did not support lignin (typically detected in the 1100–1600 nm range) as a major variable in R genotypes. Instead, absorption features around 983–992 nm suggested the presence of primary metabolites such as sugars (possibly indicating hemicellulose or cellulose content), amino acids, and lipids. Hyperspectral data indicated that MR genotypes were the most metabolically distinctive. Stem metabolite profiling using high-resolution mass spectrometry supported this, showing that lodging resistance was linked to phenylpropanoid metabolism, particularly the production of cross-linking metabolites such as ferulate, rather than lignification. These findings will be further validated through transcriptomic analyses, but they suggest that enhancing cell wall cross-linking may be a promising breeding target to improve lodging resistance in tef.

# o-RYE-gins: Using domestication genomics to support the development of perennial rye

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## ABSTRACT

Perenniality, the ability of plants to regrow after seed set, represents a promising alternative growth habit for agriculture, with potential applications in dual-purpose, cover, and other sustainable cropping systems. In Australia, an introgression between *Secale strictum* and *S. cereale* has produced mountain rye, a perennial rye currently undergoing domestication. A deeper understanding of the genetic and regulatory basis of flowering in this material holds promise for integrating perenniality into practical cropping systems. To enhance the agronomic potential of perennial mountain rye, we are developing a haplotype phased chromosome-scale genome assembly of this novel accession, together with assemblies for four additional *Secale* accessions from the IPK genebank spanning key species within the genus. In parallel, genotype-by-sequencing (GBS) was performed on over 130 mountain rye individuals and analysed alongside 1,397 publicly available rye GBS datasets, representing 356 accessions across five species. After filtering, 112,946 SNPs were retained with genotype calls in at least 90% of individuals, capturing extensive genome-wide variation across the panel. Subsequent population structure analyses reflect the recent and complex domestication history of rye, highlighting considerable gene flow among *Secale* species. The integration of haplotype-resolved assemblies with population-scale variation data offers a powerful framework to disentangle the contribution of *S. strictum*, the perennial wild relative of cultivated rye, to both historical and current domestication processes. The ongoing development of diverse rye genomic and transcriptomic resources in this study aim to establish a foundation for exploiting the substantial genetic diversity present in rye, enabling the targeted introgression of valuable traits - including perenniality - into cultivated cereals.

# Transformation of crops and other species at Rothamsted Research

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## ABSTRACT

The Crop Transformation Unit was established at Rothamsted in mid- late 1990s. Its main focus initially was the transformation of elite bread wheat cultivars using particle bombardment and over 40 elite cultivars have now been transformed using this method. The transformation of tetraploid Durum (pasta wheat) was also successfully achieved. To maintain its relevance and importance in the transformation field of research it began to expand its portfolio of species transformation to include *Brassica napus* and rice, where successful transformation systems have now been established using *Agrobacterium* mediated methodologies. Triticale has also been transformed using particle bombardment. Transformation systems for soybean, broad bean, potato, tomato and black grass using *Agrobacterium* are being developed. It has also successfully generated gene edited wheat and *Brassica napus* lines now awaiting further analysis and field trial testing. This poster will highlight the breadth of our transformation services.

# Recreating the green revolution in wheat through gene editing

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## ABSTRACT

We harnessed gene editing technologies to fully exploit the rich genetic diversity of the Watkins wheat collection. This unique resource enables the development of novel pedigrees that integrate diversity accumulated over 10,000 years across a wide range of environments, ensuring the preservation and utilization of valuable adaptive traits for future crop improvement.

The primary goal of the Watkins Precision-Bred pedigree is to produce lines with improvements suitable for inbred breeding programs. Our precision breeding program focuses on the fixation of four key alleles:

- RHT-1 (height regulation)
- PPD-1 (day-length sensitivity)
- R (sprouting resistance)

In this presentation, we will demonstrate how advanced gene-editing platforms, including Base Editing, Prime Editing, and CRISPR-Cas9, are being deployed to precisely introduce and recreate these alleles directly.



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# *Poster Abstracts*
# *P5. Climate-Proofing Monocots: Physiology that Delivers*

# Future grains: Evaluating impacts of elevated $CO_2$ and temperature on yield and grain quality in cereals

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## ABSTRACT

Future climate conditions in North West Europe (Intergovernmental Panel on Climate Change. 2013), characterised by elevated $CO_2$ and increased temperatures, are expected to impact plant development. Previous studies have shown reduced nutritional content under either elevated $CO_2$ or high temperature (wheat and rice) (Schmid *et al*., 2015). However, the combined effect on grain quality has not been studied in detail (Hampton *et al*., 2013). This represents a critical knowledge gap with implications for the brewing and malting industry. It has been reported that higher $CO_2$ concentrations could act as a fertiliser for plants, counteracting temperature effects and increasing biomass and yield. However, this could severely reduce the nutritional content of the final crops, lowering protein and mineral contents. As each crop has specific requirements for different uses, ensuring that future crops meet minimum requirements is a challenge that needs to be addressed now. In this study, we evaluated barley, rye, and wheat in two controlled environments: ambient conditions (425 mg $l^{-1}$ and 18°C) and future conditions based on the worst-case scenario reported by the IPCC (1000 ppm and 22°C). Several measurements were taken, including phenotypic measurements and the determination of grain quality using ionomics and HSI techniques. Results showed that total yield (g) was highly affected under future conditions: barley (–27.8%), wheat (–36.9%), and rye (+16.2%). Grain volume ($mm^3$ spike) was also decreased: barley (–19.2%), wheat (–23.5%), and rye (–8.7%). Ionomics showed reductions in nutrients ranging between 20% and 40%. The objective of this experiment is to explore how a future scenario could affect plant development and the nutritional content of the grain.

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# Using embryonic monocot grafting as a tool for physiological trait transfer in *Oryza sativa*

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## ABSTRACT

Grafting is an ancient horticultural practice of physically joining two plants so that they can grow as one. This technique has long been used to transfer desirable traits between different rootstock and scion, both within and across species. Recently, Reeves *et al*. (2022) overturned the longstanding consensus that monocotyledonous plants cannot be grafted. They demonstrated that several monocot species, including cereals and grasses, can be successfully grafted at the embryonic root-shoot interface, thereby opening new possibilities for studying root–shoot communication and transferring desirable traits in these crops. Here, we aimed to test whether the transfer of physiological traits from a photosynthetically efficient rootstock to a less efficient scion can improve whole-plant photosynthesis and water-use efficiency traits. We used a non-invasive, digital high-throughput phenotyping technique (Phenospex-Planteye), alongside infra-red gas exchange measurements (LICOR-6800), to screen a sub-panel of eight Asian rice cultivars (*Oryza sativa* L.) for photosynthetic performance and biomass accumulation. Among these, Azucena, (tropical japonica subspecies), and Sarali, (indica two subspecies), exhibited high photosynthetic performance and biomass accumulation, whereas IR64 (indica one subspecies) showed reduced performance in both traits. We then successfully grafted the Sarali rootstock onto IR64 scions, which were also measured for photosynthetic performance and biomass accumulation. Notably, net photosynthetic assimilation response curves revealed that grafted plants exhibited consistently higher rates of carbon fixation compared with non-grafted IR64 controls, indicating that the rootstock confers a measurable enhancement in photosynthetic capacity.

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# *LAZY* mediated control of root growth angle generates steep rooting phenotypes in wheat

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## ABSTRACT

Root system architecture (RSA) is a key determinant of plant performance, governing access to water and nutrients, while also contributing to soil function through pore formation, particle stabilisation, and carbon inputs. As such, RSA has been proposed as a target for crop improvement to enhance both resource acquisition and soil health. In particular, steeper, deeper root architectures are predicted to improve nitrogen and water uptake and increase carbon sequestration in subsoils.

Root growth angle is strongly regulated by gravity, with LAZY proteins acting as central modulators of gravitropism and branch angle control. Here, we describe a novel point mutation in a root-specific *LAZY* gene that confers steep rooting phenotypes in hexaploid spring wheat (*Triticum aestivum*) via a key role in gravity sensing and response. Phenotyping across 2D and 3D colander soil-based systems revealed significantly steeper seminal and crown root angles in mutant lines compared with the wild type. Importantly, this altered root architecture occurred without detectable changes to above-ground traits, as assessed in both 2D soil systems and colander-grown plants.

Together, these results identify a genetic route to selectively modify wheat root architecture without pleiotropic shoot effects, highlighting the potential of LAZY-mediated gravitropic regulation as a breeding target for improved resource capture, drought tolerance and soil function.

# Exploring root exudate diversity and function to improve phosphorus efficiency in barley

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## ABSTRACT

Several organic compounds released by roots can directly or indirectly improve the ability of plants to acquire phosphorus (P) from sparingly available pools present in the soil. The chemical composition and quantity of root exudates vary considerably depending on the growth conditions, plant species, and even different genotypes of the same plant species. However, still little is known about the extent of variability of the chemical composition of root exudates of cereal crops, such as barley, and how potential genetic variations impact the functional role of these exudates in facilitating P acquisition. Therefore, we explored the concentration of up to 20 amino acids and 8 organic acids in the root exudates of 38 spring-type, six-rowed barley accessions representing three major global-wide subpopulations. Substantial variation was detected for the concentration of many organic acids and amino acids in root exudates and root extracts. We were also able to identify accessions that preferentially secreted citrate or malate, two organic acids with high P mobilization capacity. An RNA-seq analysis of roots and shoots of cv. Morex, a genotype that preferentially secretes malate, identified the GO term “organic acid transport” among the genes up-regulated in response to low P in roots. Only one member of the aluminum-activated malate transporter (ALMT) family was significantly up-regulated specifically in roots of P-deficient plants. We are currently investigating whether the candidate ALMT mediates malate export and to what extent it contributes to the identified genotypic variation in malate secretion in barley.

# The nuclear cap-binding complex shapes ABA-primed drought responses in barley

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## ABSTRACT

In the face of ongoing climate change and the growing risk of drought, which significantly reduce crop yields, it is essential to explore mechanisms that increase plant tolerance to water deficit. One promising approach is priming, which prepares plants for stress through prior exposure to a stimulus that induces a defensive response. A key regulator of drought response is abscisic acid (ABA), which initiates signaling cascades leading to reduced transpiration and reprogramming of cellular processes. Mutants in the Cap-Binding Complex (CBC) genes including the *Cap-Binding Protein 20 (CBP20)* and *Cap-Binding Protein 80 (CBP80)* demonstrate increased sensitivity to ABA and improved drought tolerance. Therefore, we investigated how barley mutants in the CBC genes respond to ABA pretreatment followed by drought, and whether CBC affects priming efficiency in barley. In our study, we used the *hvcbp20.ab* and *hvcbp80.b* mutants obtained using TILLING approach in the genetic background of the 'Sebastian' cultivar (WT), as well as a double mutant obtained by crossing. We pretreated plants with ABA at the tillering stage and applied drought at the booting stage. We integrated physiological measurements including stomatal conductance ($g_s$) and chlorophyll *a* fluorescence, performed after drought and rewatering with transcriptome analysis, focusing on changes in gene expression and alternative splicing. ABA priming did not further reduce $g_s$ relative to drought-only, whereas differences between genotypes were more pronounced in chlorophyll fluorescence parameters, where ABA priming induced genotype-dependent changes in PSII efficiency. Transcriptome analysis revealed that ABA priming triggers stress response reprogramming with changes in ABA, stress, redox, and chloroplast pathways. Collectively, the results indicate that CBC shapes how ABA signals translate into plant function under drought by regulating responses at the transcriptome level.

This work was supported by the National Science Center, Poland project SONATA BIS10 '(QUEST) Quest for climate-smart barley–the multilayered genomic study of CBC function in ABA signaling' (2020/38/E/NZ9/00346).

# Uncovering the role of negative modulator of ABA-driven stomatal closure in barley

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## ABSTRACT

Drought presents one of the most severe dangers related to crop productivity, which paired with the incidence of drought events increasing worldwide makes a search for solutions that can improve the response of plants to drought stress a key priority for sustainable agriculture. One of the first and fastest plant responses to stress is the rapid closure of stomata, driven by plant hormone called abscisic acid (ABA). This process helps plants conserve water by lowering transpiration rate in leaves and thus improving plant water status. ABA and its role regulating plant abiotic stress response, as well as its core signaling pathway have been extensively characterized. However, the mechanisms that modulate the strength and timing of this response still remain incompletely understood.

In this study, we investigated the contribution of the cap-binding complex (CBC), a key regulator of mRNA metabolism, also linked to ABA-dependent stomatal regulation in barley. We compared wild-type plants with mutant lines identified with use of TILLING approach in genes encoding both subunits of CBC (hvcbp20.ab, hvcbp80.b, hvcbp20.ab/hvcbp80), which were exposed to exogenous ABA and to conditions of high vapor-pressure deficit (VPD), which mimicks atmosphere drought-like conditions through increased transpiration, lowering leaf water potential and activating ABA-dependent pathways. Mutations in genes encoding CBC in barley resulted in pronounced changes in stomatal conductance and was accompanied by distinct transcriptional responses, revealing altered expression of ABA-responsive genes. Together, these findings identify the CBC as an important negative regulator of ABA signaling, suggesting that it plays a role in fine-tuning stomatal behavior and optimizing plant responses to drought stress.

This work was supported by the National Science Center, Poland project SONATA BIS10 ‘(QUEST) Quest for climate-smart barley–the multilayered genomic study of CBC function in ABA signaling’ (2020/38/E/NZ9/00346).

# Hidden hazards of reused wastewater: Physiological and oxidative effects of Sulfamethoxazole on rice

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## ABSTRACT

Rapid industrialization and wastewater reuse in agriculture to tackle water shortage for irrigation has led to the introduction of pharmaceutical pollutants in the environment. In this study, we have evaluated the impact of Sulfamethoxazole (SMX), a common pharmaceutical pollutant reported in wastewater, on rice (*Oryza sativa* L.) growth and physiology. Two different concentrations of SMX were chosen: one from reported environmental concentration and the other was the first concentration at which we found SMX affected seed germination. Rice plants treated with SMX showed significantly lower photosynthetic rate at higher concentrations compared to control plants. The oxidative responses of plants to SMX and their underlying mechanisms were also investigated. Higher concentration of pollutant significantly increased peroxide level, malondialdehyde, proline content and ion leakage indicating membrane lipid peroxidation and cell membrane damage. In line with changes to reactive oxygen species, we also observed increases in antioxidant enzyme activities such as catalase, ascorbate peroxidase, superoxide dismutase, in plants treated with SMX. Transcriptome analysis of SMX treated plants further supported the finding that oxidative pathways are enhanced. These findings emphasize that, in the absence of adequate treatment and regulatory oversight, wastewater irrigation may pose a substantial risk to agricultural sustainability and crop production.

# Elucidating the gene regulatory network of *ZmNAC111* in maize under drought stress

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## ABSTRACT

Drought stress significantly limits maize production, making the identification of genetic tolerance mechanisms a priority for crop improvement. Through a genome-wide association study (GWAS) of natural variation in maize, researchers previously identified an 82-bp miniature inverted-repeat transposable element (MITE) insertion in the promoter of *ZmNAC111* (Zm00001eb405590) associated with drought susceptibility in temperate germplasm (Mao *et al*., 2015). This MITE insertion represses ZmNAC111 expression via RNA-directed DNA methylation and H3K9 dimethylation (Mao *et al*., 2015). Conversely, increasing ZmNAC111 expression in transgenic maize enhances seedling drought tolerance and water-use efficiency by upregulating various stress-responsive genes (Mao *et al*., 2015).

This project aims to identify and validate drought-responsive genes regulated by ZmNAC111. Our goal is to establish the *ZmNAC111* gene regulatory network. To achieve this, we conducted DNA affinity purification sequencing (DAP-seq) of ZmNAC111 using maize libraries from both control and water-deprived conditions. Through our comparative analysis, we identified both known and novel drought-responsive genes. Currently, validation of selected target genes is being done using luciferase reporter assays in maize protoplasts and electrophoretic mobility shift assays (EMSA). Furthermore, we aim to quantitatively validate the expression of these targets via reverse transcription quantitative polymerase chain reaction (RT-qPCR) in *ZmNAC111* mutants under drought stress.

Our innovative approach will elucidate the intrinsic regulatory network of ZmNAC111-mediated drought resistance. This knowledge can be leveraged further to breed drought-resilient maize lines for temperate regions in the face of climate change.

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# Developing an understanding of the molecular genetics of cold tolerance in winter wheat

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## ABSTRACT

Unpredictable weather events are becoming increasingly common due to climate change. This is leading to increased fluctuations in cold weather. Whilst winter wheat requires cold weather for vernalisation, severe cold snaps at certain stages in development can greatly reduce yields. Further, some varieties are more cold tolerant than others. Despite some important loci for cold tolerance being known, there is still much to discover about the specific pathways that lead to cold tolerance and the appropriate experimental conditions that will allow us to uncover these in the laboratory.

Here we share our efforts towards the optimisation of controlled environment cold treatment conditions that will enable the harvesting of tissues in cold susceptible and cold tolerant wheat varieties. We will also present our initial characterisation of gene expression changes during cold treatment. Future work will focus on single cell level responses to uncover key differences between these varieties at the genetic level to build a framework to investigate stress responses and identify new targets for the improvement of crops.

# Physiological assessment of rice-pearl millet inter-grafts under extreme drought

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## ABSTRACT

Global food security is increasingly threatened by the impact of extreme drought events on crop productivity. Despite feeding more than half of the global population, rice remains one of the most water-intensive crops, making its yield highly vulnerable to water scarcity (Caine *et al*., 2023). Therefore, developing rice varieties capable of withstanding extreme drought is essential. While grafting, the physical joining of different rootstocks and shoots to combine traits, has historically been exploited to improve horticultural crops, its application in monocotyledonous cereals has remained a significant challenge. Recently discovered embryonic monocot grafting approach offers unprecedented potential for developing climate-resilient cereal varieties by combining beneficial traits from different shoot and rootstock (Reeves *et al*., 2021).

We have optimised cereal grafting in rice and pearl millet, specifically evaluating the physiological impact of self- and intra-grafting on the photosynthetic performance and growth. Our results demonstrate that the grafting process induce minimal influence on photosynthetic activity, stomatal behaviour and water-use efficiency at the leaf level in rice and pearl millet. Furthermore, we successfully generated inter-species grafts by grafting pearl millet rootstocks with rice scions. We found that the grafted plants showed improved drought resilience and photosynthetic performance under extreme drought conditions, compared to non-grafted controls. These findings underscore the potential of embryonic monocot grafting as a viable tool for the development of stress-tolerant cereal varieties.

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# Temperature in wheat circadian oscillators: From physiology to mechanisms

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## ABSTRACT

Understanding the drivers of wheat yields is critical to global efforts to sustainably increase production. Circadian clocks are internal biochemical oscillators that allow plants to anticipate environmental cycles, conferring advantages to growth and survival (Dodd *et al.*, 2005). Circadian oscillators regulate numerous pathways underlying yield-related traits, including temperature responses (Steed *et al*., 2021). Temperature is both a crucial environmental input to wheat circadian oscillators and a physiological variable regulated by circadian clocks through stomatal aperture control (Webb 2003; Wittern *et al.,* 2023). Therefore, an improved understanding of the impact of temperature on wheat circadian oscillators and the development of tools to measure circadian rhythms in crop plants could facilitate agricultural improvements.

By combining thermal imaging with physiological and molecular analyses, we are investigating how wheat circadian oscillators sense, integrate, and respond to temperature. We present our optimisation of low-cost, adaptable systems for using measurements of leaf temperature to non-invasively characterise circadian rhythms in *Triticum turgidum*. These systems have the potential to be used in both controlled environmental systems and agriculture to quantify circadian rhythms in non-model crop species, providing the capacity to better incorporate chronobiology into agricultural practices. We have also found that wheat circadian oscillators robustly function under warmer temperatures and heat stress, but that large daily fluctuations in temperature inhibit normal circadian oscillator function. Lastly, we have demonstrated that the circadian oscillator component EARLY FLOWERING 3 (ELF3) is necessary for temperature integration into wheat circadian oscillators despite ELF3 lacking a predicted temperature sensitive domain present in its *Arabidopsis thaliana* ortholog (Zhu *et al.*, 2024). Overall, this work bridges scales to build our understanding of how temperature is perceived and processed by wheat circadian oscillators, offering insights for optimizing temperature resilience in breeding programs and understanding the impact that a changing climate may have on this key crop.

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# Are winter wheat yields warming up?

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## ABSTRACT

As in other winter crops, springtime flowering in wheat is promoted by the colder temperatures experienced during previous months through the process of vernalization. Overwinter, critical decisions occur in the developing wheat meristem which will determine the plant's capacity for yield at harvest.

Globally, warmer winter temperatures are predicted to have a significant and negative impact on crop yields. Yet, there is some indication that winter warming could increase yields in UK wheat. This is, however, largely untested. Furthermore, it remains unclear how warming impacts physiology at the meristem and plant level, and what molecular mechanisms underpin these traits.

To address these questions, we have prepared a field-scale warming trial using a combination of gentle soil warming cables and mesh tenting to increase ambient air temperature by 2.5–3°C and soil temperature by 6–8°C. We chose two 45 day periods covering the period across the end of vernalization and the beginning of the floral transition, with environmental monitoring and weekly sampling for phenology and transcriptomics.

While warming has had a significant effect on size and development of both the meristem and whole plant, the full impact this will have on yield cannot be determined until harvest. At the end of this trial, we aim to demonstrate the effects of warming on development and yield and identify temperature responsive targets which will enable breeders to enhance yield under a wider variety of conditions.

# Using next generational nitrogen sources for nitrogen use efficiency in spring barley genotypes

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## ABSTRACT

Spring barley (*Hordeum vulgare* L.) is a globally important crop for the malting industry, but its production relies heavily on nitrogen (N) fertilisers. This contributes to environmental impacts including nitrate leaching and greenhouse gas emissions, particularly nitrous oxide ($N_2O$). Improving nitrogen-use efficiency (NUE), the efficiency by which crops acquire and convert nitrogen into grain yield, is therefore essential for environmental sustainability and profitability. This study investigates the physiological and genetic basis of NUE in spring malting barley under contrasting N inputs and synergies with next-generation fertilisers. One experiment was conducted under glasshouse and field conditions in 2025 using a diverse panel of eleven genotypes, including elite UK cultivars, US breeding lines from Molson Coors, and landraces from the James Hutton Institute. Nitrogen treatments ranged from low (50 kg N $ha^{-1}$) to high (150 kg N $ha^{-1}$) application rates, with field trials incorporating three high N treatments (urea-based fertiliser, ammonium nitrate, and an ammonium nitrate + nitrification inhibitor) and a low N ammonium nitrate treatment. Our study aimed to identify traits and molecular markers associated with NUE. By integrating phenotypic assessments with molecular analyses, our work provides insights into breeding strategies for barley varieties that efficiently utilize nitrogen. Traits measured included leaf chlorophyll content and canopy size (NDVI) to determine senescence kinetics, grain yield, and the nitrogen analysis of plant components to determine NUE components. Results show there was a significant G × N interaction for canopy traits, but a less strong interaction for grain yield. Plant N measurements are ongoing for estimating G × N for NUE traits. The nitrification inhibitor treatment yielded similarly to the two other high N treatments. These experiments will be repeated in 2026 to identify further target traits for improving NUE in barley while maintaining high malting quality and synergies with next generational N fertilizers.

## Acknowledgements

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# Investigating the role of aquaporins in regulating water-use efficiency in rice

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## ABSTRACT

Plant aquaporins, or plasma membrane intrinsic proteins (PIPs), are channel proteins which are involved in the transport of water and solutes, such as $CO_2$, across plant membranes (Hanba *et al*., 2004; Sakurai *et al.,* 2005). Aquaporin isoform *PIP2;1* has previously been shown to play a role in water transport for many species, including Arabidopsis, rice, and barely (Da Ines *et al.,* 2010; Ding *et al*., 2019; Hanba *et al*., 2004). The role of *PIP2;1* in $CO_2$ diffusion and mesophyll conductance is unclear, and it has been suggested that there is potential to improve plant productivity by manipulating aquaporin expression if its role in photosynthesis is better understood (Heckwolf *et al.*, 2011; Kromdijk *et al.*, 2020; Uehlein *et al*., 2012). For example, overexpression of *PIP2;1* may enhance mesophyll conductance and photosynthetic carbon assimilation, whereas reduced *PIP2;1* expression may constrain photosynthesis but improve intrinsic water-use efficiency (WUE), a trade off that could be advantageous for developing climate resilient crops under water-limited conditions.

My work explores the hypothesis that modulating the expression of *OsPIP2;1* alters hydraulic conductivity in rice, rebalancing water transport and carbon assimilation to sustain photosynthetic performance under limited water conditions. *OsPIP2;1* RNAi knockdown lines, null segregants and wild-type plants were assessed phenotypically using multi-spectral 3-D measurements (Phenospex Planteye), and physiologically using infra-red gas exchange analyses (LI-6800). Here, I will discuss data that gives mechanistic insights into the role of *OsPIP2;1*, and its influence on photosynthetic, stomatal and water-use efficiency traits in rice.

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# Validation of root diameter as a key root trait for stress resilience

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## ABSTRACT

Rice- the primary food crop in Asia/Africa is produced across six continents and is the staple food for ~3 billion people. With increasing population, Global Food Security is one of the major challenges facing world agriculture (Bailey-Serres *et al*., 2019). This is against the backdrop of global warming and increasing climate unpredictability. Crop production is especially vulnerable to extremes of environmental stress (drought/heat) leading to significant losses in yield and quality. To meet the future food demand, there is an urgent need to develop diverse, climate-ready and resilient agricultural systems (Bailey-Serres *et al*., 2019).

Root traits determine the plant's capacity to capture nutrients and water and therefore directly influence crop productivity. Previous studies have shown that nodal root diameter correlated positively with improved yield under drought stress (Liao *et al*., 2022; Siangliw *et al*., 2022). Interestingly, changes in root diameter have also been correlated with salt (Huang *et al*., 2022) and compaction (Huang *et al*., 2021) stresses.

As part of the GCRF strengthening grant, this project explores the heat tolerance/resilience of lines already selected for drought resilience in previous studies of the network partners using field-based studies and controlled environment studies. The poster will present some recent finding of these experiments including root architectural and anatomical studies using X-ray Computed Tomography and Laser Ablation Tomography.

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# Heat tolerance of paragon wheat over space and time

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## ABSTRACT

Climate change, particularly increased temperature, threatens global wheat production (Porter *et al*., 2014; Asseng *et al*., 2015). As such, researching genetic and physiological variations which can result in improved wheat heat tolerance is essential.

A widely accepted technique for evaluating heat tolerance in crop plants is the calculation of the variable "$T_{Crit}$", defined as the critical temperature at which incipient damage to photosystem II (PSII) occurs. Rather than heat-stressing an entire plant, this technique involves taking a leaf cutting, and repeatedly measuring its photosynthetic output (Fv/Fm) as the leaf cutting is heated (Ferguson *et al*., 2020).

Said leaf cutting is generally taken from the centre of a wheat plant's flag leaf, and the procedure carried out at whichever developmental stage is most relevant to a particular experiment. This allows wheat plants of different genetic backgrounds, and/or which have undergone different treatments, to be compared (Coast *et al*., 2022; Posch *et al*., 2022; Coast *et al*., 2024).

However, variety within a wheat plant has yet to be explored. This study investigates how $T_{Crit}$ changes depending on the location of the leaf sample (leaf height, cutting area) and the plant's developmental stage. The aim is to provide a holistic overview of variation in PSII heat tolerance over space and time. This information should aid the global effort to developing more robust, climate-resilient wheat, both by providing context for current data, and allowing sampling strategies to be refined in future if necessary.

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# *Poster Abstracts*
# *P6. From Meristem to Harvest: Building the Plant*

# Unravelling polar chloroplast positioning in C4 photosynthesis

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## ABSTRACT

To reach global food requirements and sustain our ever-growing population, we must focus our efforts on developing more efficient crops. Plant productivity is underpinned by photosynthetic reactions taking place in chloroplasts within leaf tissues. Several species have naturally evolved a more efficient photosynthetic mechanism, known as $C_4$ photosynthesis, which splits photosynthetic reactions between the leaf mesophyll and bundle sheath cells. Kranz anatomy is a characteristic feature of $C_4$ species, encompassing a range of anatomical modifications that complement biochemical changes. When combined, these changes boost photosynthetic efficiency, water use efficiency, and biomass accumulation. One understudied feature of Kranz anatomy, is the polar organisation of chloroplasts in bundle sheath cells to either a centrifugal (adjacent to the mesophyll cells) or centripetal (adjacent to the vasculature) orientation. My research utilises genetics, molecular and cellular biology, and advanced imaging techniques to track how light induction paves the way towards cytoskeleton-mediated chloroplast movement in both centrifugal (*Zea mays*, *Sorghum bicolor*) and centripetal (*Gynandropsis gynandra*) $C_4$ species. Harnessing knowledge from photorelocation movement studies in *Arabidopsis*, this work explores how conserved the roles of *CHLOROPLAST UNUSUAL POSITIONING1* (*CHUP1*) and *KINESIN-LIKE PROTEIN FOR ACTIN-BASED CHLOROPLAST MOVEMENT1* (*KAC1*) are in $C_4$ species and whether loss-of-function mutations in these genes influences chloroplast position on the micro scale, and photosynthetic efficiency on the macro scale. Furthermore, I investigate how potential CHUP1-KAC1 protein complexes at membrane contact sites play a role in proper organelle position and communication. By developing new tools to cell-specifically disrupt chloroplast actin dynamics, and new methodologies to quantify the extent of organelle polarisation, this work aims to have a significant impact on understanding the cellular biology of $C_4$ Kranz anatomy. In the long term, this project will inform attempts to engineer more efficient crops needed for global food security.

# Investigating conserved awn and leaf developmental programs in barley

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## ABSTRACT

In the grass family (Poaceae), awned lemmas have been repeatedly gained and lost, with both awn morphology and function varying widely between species. For example, straight awns in barley photosynthesise, contributing to yield, whereas hygroscopic awns in oat twist to aid in seed burial. Awns are likely homologous to the leaf blade, suggesting that the genetic pathways regulating awn development may result from the reuse of conserved leaf developmental programs. This raises the hypothesis that developmental constraint, through redeployment of leaf blade gene expression in the lemma, has facilitated the repeated emergence of awns across grasses.

To investigate this, barley awn mutants are used as an experimental system to identify genes regulating awn initiation and development. Despite the homology between leaves and lemmas, awn mutants exhibit contrasting leaf and lemma phenotypes, indicating that conserved developmental programs can be differentially regulated between homologous organs. Analysis of developmental series from wild-type and awn mutant barley inflorescences reveals that their developmental trajectories diverge early, identifying key stages at which awn initiation and growth are disrupted and highlighting target stages for future comparative transcriptomic analyses. If leaf and awn developmental programs are conserved, genes involved in leaf blade development are expected to be downregulated in awnless barley mutant lemmas compared with wild type.

To test whether these regulatory mechanisms are conserved beyond barley, loss-of-function mutants of orthologues of known leaf developmental genes have been generated in the model grass *Brachypodium distachyon*. This comparative approach enables direct testing of whether similar genetic disruption produces corresponding leaf and lemma phenotypes across grasses, providing insight into how conserved developmental programs are modified to generate awn diversity.

# Understanding how epidermal development in barley and wheat affect crop performance

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## ABSTRACT

Epidermal features play major roles in adapting plants to their environment. During differentiation, epidermal cells commit to different fates producing either pavement cells, stomata or trichome (hairs) and others depending on the species. For instance, in grasses, epidermal cell files can form stomata, which develop as a four-cell complex composed of a central guard cell pair, flanked by subsidiary cells, as well as prickle hairs and silica cells. Stomata are well known to regulate water and carbon dioxide exchange between the plant and the atmosphere, impacting the efficiency of photosynthesis and water use. While establishing diverse cell fates, epidermal cells also secrete their cuticle which, amongst other roles, helps prevent non-stomatal water loss and increases irradiance, potentially protecting plants against drought and heat stress. Interestingly, several glossy mutants in barley which lack certain types of epicuticular waxes also have modified stomatal patterning suggesting a link between the two developmental pathways. However, the coordinating mechanisms are still poorly understood. Here, we focus on several *eceriferum* mutants (*cer*, “not bearing wax”) in barley as well as their orthologues in durum wheat identified from mutagenised TILLING populations to better understand the roles of this group of genes in coordinating epidermal development and cuticle deposition. Specifically, we assess how the impacted stomatal and cuticular traits may affect physiological processes such as photosynthesis, stomatal and cuticular conductance and heat regulation, and ultimately cereal crop performance under different environments through techniques including infrared gas exchange measurements and thermal imaging.

# The indeterminate domain protein BROAD LEAF 1 regulates the grain development in barley

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## ABSTRACT

Barley (*Hordeum vulgare* L.) represents an important crop that is cultivated world-wide for feed and forage for livestock, and for food and drinks for humans. Improving the barley grain yield and quality is a major priority of barley breeding. Barley grain quality is mainly determined by the content and composition of seed storage proteins (SSPs) especially the hordein levels. The grain yield is largely dependent on the starch content. However, the molecular mechanisms that regulate SSP and starch biosynthesis and their accumulation during grain development is poorly understood in barley.

The INDETERMINATE DOMAIN (IDD) protein BROAD LEAF 1(BLF1) is reported as a regulator of barley leaf width. In this study, we explored the function of the transcription factor BLF1 in grain development and its impact on SSP and starch synthesis. The knock-out mutants of *BLF1* in cv. Barke and cv. Golden promise exhibited a typical shrunken grain phenotype. The thousand grain weight, sucrose and starch content are significantly decreased, however the hordein levels are increased in the mutant grains.

We performed RNA-seq analysis at 5 and 8 days after flowering (DAF) and found most of *B-hordein* genes and starch metabolism genes differentially regulated in both stages. In addition, we performed a horomone measurement and found that auxin and ABA content are decreased, while the GA levels are increased in the mutants.

This study aims to clarify the molecular functions and gene regulative network (GRN) of BLF1 to better understand barley grain development.

# Barley surviving the stress – Understanding stress induced developmental plasticity in barley

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## ABSTRACT

Plants are sessile organisms growing in a continuously changing environment. Their ability to alter development to dynamic stresses is crucial to survival. With the changing climate we expect increasingly plastic responses from vital crops such as barley. However, our understanding of developmental plasticity and how it could safeguard yield is limited.

We discovered that expression levels of a key transcription factor (TF) modulate development and growth in barley, with higher levels causing later flowering and stem elongation. Using a combination of stress experiments, genetic analysis and RNA-sequencing we show that this TF developmental control is environmentally sensitive. Under an episode of heat and drought, barley lines with increased levels of the TF show a complete developmental arrest. Strikingly, lines showing this stress-induced growth arrest showed a higher grain yield after plants recovered post-stress, compared to other lines. This indicates a possible role for stress-induced growth arrest in resilience. We also show through RNA-sequencing that increased levels result in a larger number of unique differentially expressed genes between environmental conditions than lines with lower levels. Further functional analysis has revealed enriched pathways that may been altered under stress by this TF to evoke the arrest response. Finally, network analysis isolated candidate interactor genes of this TF that may be critical for this response. We propose levels of the TF function modulate developmental progression, especially under stress, by these key developmental pathways and genes. We aim to further elucidate the mechanisms of this plasticity in barley, to predict and adapt future barley responses to increasing environmental stresses.

# Exploring genetic diversity for grain partitioning traits to enhance yield in spring barley

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## ABSTRACT

Yield progress in recent decades in cereals was mainly due to a higher harvest index (HI; grain dry matter / above-ground dry matter) (Xiao *et al*., 2012, Beche *et al*., 2014). Under optimal conditions the genetic variation in grains $m^{-2}$ is the product of biomass at anthesis, spike partitioning index (spike DM / above-ground DM) and fruiting efficiency (grains per g spike DM at anthesis). Additionally, grain filling may be limited by the joint source and sink capacity in modern cultivars, indicating a need to research the co-limitation of yield by both photosynthesis and grain sink strength. The source refers to photosynthetic capacity to fill the grains, while sink refers to the capacity of the grains to store assimilate. The objectives were to identify traits for enhanced grain partitioning for deployment in barley breeding. A glasshouse and field experiment were carried out with spring barley genotypes provided by KWS Ltd at University of Nottingham Farm, Leicestershire, UK. Samples were collected at anthesis and maturity to determine biomass at anthesis, spike partitioning index and fruiting efficiency as well as grain yield, HI and yield components. The extent to which post-anthesis source may be limiting final grain size was estimated by partial degraining of spikes , while a defoliation treatment was used to estimate if excess photosynthetic capacity existed. A positive relation was found between grain number and biomass at anthesis in both experiments. Moreover, degraining increased the weight for the remaining grains. The positive response to degraining could indicate a source limitation to grain growth. Next year a repetition of these experiments will be done to further determine which traits underpin grain number and HI and quantify the extent of sink or source limitation in the genotypes.

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# Evolution of grain shattering in the *Triticeae*

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## ABSTRACT

The grass tribe *Triticeae* includes three of the world's major cereal crops: wheat, barley, and rye. In wild species of *Triticeae* inflorescences shatter at maturity to aid grain dispersal. During domestication of cereal crops, a non-shattering trait was selected to facilitate harvest. Disarticulation (the separation of grains) in *Triticeae* can occur at the rachis or rachilla with rachilla disarticulation being the ancestral type. Rachis disarticulation is further categorized as occurring above (wedge type) or below (barrel type) the node. Wild species are increasingly being used in pre-breeding, as orphan crops or as forage crops. Therefore, understanding the genetics and evolution of disarticulation in wild species is critical for crop improvement.

Wild barley has wedge-type disarticulation, which is controlled by the domestication genes *non-Brittle Rachis 1 (BTR1)* and *BTR2*. *BTRs* are unique to the Triticeae and appear to have evolved from a duplication of *BTR1-like and BTR2-like* genes found throughout the Poaceae. In contrast, *Aegilops tauschii*, a wild wheat progenitor, displays barrel-type disarticulation. Its genome reveals loss of *BTR1* and duplication of *BTR2*, though how these changes influence disarticulation type is unresolved. It is also unknown if *BTR* function in shattering is specific to the rachis or if they are also involved in rachilla disarticulation. We hypothesise that through evolutionary time the spatial expression of *BTRs* and other genes has shifted from rachilla to rachis.

RNA-sequencing will be performed on six different species of Triticeae with two species of each disarticulation type at two developmental stages in both rachis and rachilla DZs. We will determine if *BTRs* are expressed in rachilla DZ tissue and which other genes and co-expression networks are conserved between species and disarticulation types. This work will further our understanding of the evolution of shattering in the *Triticeae*.

# Three-dimensional reconstruction reveals stage-specific establishment of vascular architectureduring early barley spike development

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## ABSTRACT

Vascular anatomy of the cereal inflorescence is poorly understood despite its obvious relevance for crop yield. Here we investigate the early establishment of the barley spike vasculature from the transition apex (Waddington stage W1.5) until maximum yield potential (Waddington stage W5.0). Results were obtained by serial sectioning analysis of resin embedded probes combined with three-dimensional (3D) reconstruction.-

The vegetative shoot meristem (W0.0) lacks intrinsic vasculature which develops from the third plastochron onwards. After transforming into a inflorescence meristem, the early spike initially remains without any visible vasculature. The first traces of spike vasculature arise around stage W2.0 with the initiation of the lateral veins in the lower half of the developing rachis. By stage W3.0 as multiple central veins have arisen in between the lateral veins, the spikelets are still devoid of any visible vascular structures. Approaching stage W5.0 the lay-out of the rachis vasculature is completed while veins initiating within the spikelet organs start growing towards and connecting to the rachis vasculature.

Together, these results define a stage-specific and highly ordered program of vascular establishment during early barley spike development, providing a three-dimensional anatomical framework for understanding how transport capacity is progressively constructed prior to MYP.

# Dissecting the genetics of barley threshability

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## ABSTRACT

Barley (*Hordeum vulgare* ssp. *vulgare*) is a cereal crop important for the drinks industry, animal feed, and human food. At harvest, prior to use, the grain needs to be separated from the straw by a process known as threshing. Incomplete threshing reduces post-harvest grain yield, while over-threshing is associated with grain damage. Therefore, easy threshability has been selected during barley domestication and subsequent crop improvement.

Threshability is controlled differently in different cereals. In hulled barley, in which the outer husk (lemma and palea) is tightly attached to the grain, threshing requires separating the grain below the husk from the chaff and straw (rachis and other floral structures). Neither the structural basis that leads to easy threshability nor its genetic control is known in barley. Genetic studies using crosses between easy-thresh barley cultivars and hard-thresh wild barley (*H. vulgare* ssp. *spontaneum*, *Hvs*) have identified a single genetic locus, *thresh-1*, on the long arm of chromosome 1H (Schmalenbach *et al*., 2011).

This project aims to characterise threshability at the cellular and genetic levels in barley, using a Bowman near isogenic line (NIL) BW878 that exhibits a hard-thresh phenotype. BW878 is derived from a cross between Bowman and a wild barley accession, resulting in a NIL with a single *Hvs*-derived introgression on chromosome 1HL that overlaps with the *thresh-1* locus. Preliminary results revealed higher lignin content at the base of the grain in BW878 compared with Bowman. Fine mapping of the *thresh-1* locus identified a *MYB* gene present in BW878 and wild barley but absent in multiple barley cultivars. Real-time PCR and RNA-Seq analysis confirmed the expression of this *MYB* in the rachilla and lemma of BW878 but no expression was found in Bowman. Further experiments are required to validate whether the presence of the *MYB* gene is responsible for the hard-thresh phenotype.

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CEREALS & GRASSES RESEARCH NETWORK

# *Poster Abstracts*
# *P7. Measure What Matters: Traits, Throughput, Translation*

# An ontology-based semantic data integration framework for interoperability of crop phenotypic data

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## ABSTRACT

Underutilised crops are often nutritionally dense, climate-smart, and contribute to agrifood diversity. However, phenotypic data for associated genetic resources are highly heterogeneous across studies and collaborators, hindering access, reuse, and interoperability. Access to and comparison of commensurate trait datasets that characterise disparate crops is likely to accelerate the development and adoption of underutilised crops. To address these issues, we have developed an ontology-based semantic data access and integration framework, 'Framework for Ontology-based Comparison of Underutilised Species (FOCUS)', that harmonises phenotypic data of underutilised crops stored within the Germinate database platform into a unified semantic structure. Germinate is an established fully featured open-source plant genetic resources platform that incorporates a relational database for managing phenotypic, genetic, and trial data for a diverse range of crops. FOCUS incorporates a virtual knowledge graph representing the semantic layer, such as traits, crops, crop parts, and units, enhancing data access and integration. Existing annotations from the Open Biological and Biomedical Ontologies (OBO) Foundry Library were used to provide formal semantic definitions for phenotypic traits, anatomical structures, and measurements, thereby establishing a shared biological definition for the data and metadata. Ontology-based Data Integration (OBDI) involved systematic mapping between the formal OBO terms and the Germinate database fields and records. This now provides Germinate with a semantic capability that extends its capacity for knowledge discovery and crop data comparison across germplasm, experiments, and locations. We expect this ontology-based semantic integration and interoperability will provide a significant opportunity for data integration that will enable comparison and reuse of phenotype data already stored in Germinate. Mining such information can enable breeders and researchers to compare crops and identify traits and accessions needed to support the wider adoption of underutilised crops.

**Key words**: Ontology integration, phenotype data, semantic annotation, underutilised crops

# From gene to trait: Effects of *DWARF14* and *DWARF53* mutations on barley morphology and transcriptome

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## ABSTRACT

Strigolactones (SLs) are carotenoid-derived class of plant hormones that regulate various developmental processes and responses to environmental conditions in plants. SL molecules are recognized and bind by the SL receptor DWARF14 (D14), which changes the conformation of the D14 protein, and next activates the SCF complex (SKP1-CULLIN-F-BOX). This complex binds the SL repressor DWARF53 (D53) and carries out its proteasomal degradation. Following degradation of the D53 repressor, SL-dependent transcription factors (TFs) and their target genes become activated. The regulatory mechanisms underlying SL-dependent gene expression in *Hordeum vulgare* (barley) have yet to be elucidated.

Hence, the *Hor*TILLUS (*Hordeum*-TILLING-University of Silesia) population, developed for spring barley cultivar Sebastian after double-treatment with sodium azide ($NaN_3$) and N-methyl-N-nitrosourea (MNU), was used to identify SL mutants in genes encoding components from SL signalling pathways. Mutant *hvd14.d* is a semi-dwarf that produces almost twice as many tillers as the wild-type. Mutant *hvd53.f* displays the opposite phenotype including a reduction in tillering. The double mutant *hvd14.d hvd53.f* was generated to test whether the *hvd53.f* allele is epistatic to *hvd14.d*, which would indicate that HvD53 acts downstream of the HvD14 receptor in the SL signaling cascade.

In the presented work, we performed shoot and root phenotype analyses, as well as analyses of RNAseq data for the shoot, root and tillering node for the wild-type, both signalling mutants and double mutant *hvd53.f hvd14.d*. Obtained results allowed us to conclude that the phenotype of the double mutant is intermediate relative to those of the two single mutants. RNAseq data let us establish how many differentially expressed genes (DEGs) are upregulated and downregulated. Moreover, we identified TFs that potentially regulate DEGs in barley mutants impaired in SL signalling.

This work was supported by a research grant from the National Science Centre in Poland (Sonata Bis 2023/50/E/NZ3/00236).

# Loss of Plastidal Phosphoglucoisomerase (PGIp) on physiology and carbohydrate metabolism in wheat (*Triticum turgidum*)

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## ABSTRACT

Transient storage of carbohydrates in leaves plays a vital role in maintaining daily energy balance and regulating plant metabolism. Carbohydrates accumulated in the leaves during the day are remobilised at night to support continued metabolic activity and growth when photosynthesis is absent. Phosphoglucose isomerase (PGI) in plants catalyses the reversible interconversion of glucose-6-phosphate (G6P) and fructose-6-phosphate (F6P). Through this enzymatic reaction, plastidial PGI (PGIp) regulates the flow of carbon between the Calvin cycle and starch biosynthesis within chloroplasts, making it a crucial regulatory point that influences starch metabolism. Two *Triticum turgidum* (wheat) mutant lines, with premature stop codons in each homoeologue of PGIp, (from the *T. turgidum* Targeting Induced Local Lesions in Genomes (TILLING) population), were crossed to obtain a double homozygous mutant progeny predicted to lack functional PGIp (*Ttpgip*). This mutant line and associated negative segregant (control) line were grown under controlled environmental conditions to assess carbohydrate accumulation and photosynthetic capacity – two phenotypes that were negatively impacted when PGIp mutants were previously studied in Arabidopsis. Transient starch accumulation was significantly impaired at the end of the day in the *Ttpgip* line, with near zero transient starch being accumulated, confirming the role of PGIp in transient starch metabolism in wheat. However, photosynthetic traits of the *Ttpgip* line, assessed via growth assimilation and photosynthetic capacity, remained unaffected. Preliminary analysis of starch granule size distributions within the seed also showed a significant increase of 15.1% in the diameter of B-type granules in the *Ttpgip* line, while A-type granule size remained unaffected. These findings suggest a potential species-specific role for PGIp and provide a unique opportunity to utilise wheat PGIp to assess the impact of modified transient carbohydrate pools with reduced secondary impacts, as well as investigate the role of PGIp in storage starch accumulation.

# Genetic variation of expression of “elite” wheat genes

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## ABSTRACT

Most of our understanding of genetic variation in wheat comes from analysing mutations in well-annotated protein coding regions, where non-synonymous and truncating changes are detected easily. However, natural diversity in the control and regulation of gene expression is also likely to make a major contribution to agronomically important traits.

This project aims to understand the regulatory control of a defined set of elite genes; genes underlying key breeding targets such as flowering time, vernalisation response, biotic and abiotic stress tolerance, and plant architecture. Using pan-transcriptomic data from the 10+ wheat genomes, UK cultivars, and the Watkins core collection, I will quantify diversity in elite gene expression at the homeolog level and relate this to underlying genetic mechanisms, including cis regulatory variation, eQTLs, copy number changes, and DNA methylation. I will then test the effects of selected markers and alleles on elite gene expression using Paragon × Watkins near isogenic lines, providing experimental validation of regulatory variants.

Preliminary analysis of 159 biotic stress related genes already reveals extensive expression variation across wheat lines, supporting the hypothesis that genetic regulation of gene expression can be systematically identified and harnessed for breeding.

# Malting barley: A steep learning curve

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## ABSTRACT

Steeping, the initial stage of malting, hydrates barley grains to initiate germination so that the grains produce enzymes essential for converting starch into sugars during brewing. This process profoundly influences malt quality, process efficiency, and yield. Although seemingly straightforward, the rate of water uptake and uniformity of germination are controlled by a complex interplay of genetic, environmental, post-harvest, and technological factors. Barley genotype and growing conditions shape endosperm structure, storage protein composition, β-glucan content, water sensitivity, and dormancy, all of which determine how grains interact with water. Understanding these interactions is critical for optimising the malting process while reducing the water footprint.

This study evaluated 10 hydration- and germination-related traits across 27 barley varieties grown at two sites in Lincolnshire and one in Dundee. Analysis of variance showed that β-glucan content and thousand-grain weight were largely genetically determined, whereas endosperm hydration was mostly influenced by the environment the barley was grown in. Final moisture was equally affected by genetics and environment with moderate genotype-by-environment interaction (GxE). Oxygen consumption and germination energy showed substantial varietal variation depending on the site, highlighting both adaptability and genetic control.

Understanding which traits are mainly influenced by genetics and which are shaped by growing conditions helps improve both barley breeding and malting practices. By bringing together information from crop genetics, crop physiological, and processing perspectives, the work aims to investigate why certain genotypes exhibit enhanced water uptake efficiency or more reliable germination behaviour. This evaluation could also identify barley lines suitable for “one steep” steeping methods, which use considerably less water yet still allow rapid, uniform germination and therefore high-quality malt. The aim is to support breeding programs develop barley varieties and malting practices that use less water while still producing high-quality malt, helping to make the malting industry more sustainable.

# Genetic basis and environmental plasticity of pollen and anther traits in rye (*Secale cereale* L.)

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## ABSTRACT

Pollination mode is reflected in a species' reproductive traits, shaping pollination efficiency and influencing adaptation to changing environments. In wind-pollinated grasses such as rye (*Secale cereale* L.), anthers are typically large and produce abundant pollen with smooth pollen surfaces, yet the genetic and environmental drivers of intraspecific variation in these traits remain poorly understood. To address this gap, we investigated quantitative variation in pollen and anther morphology across diverse rye germplasm and examined how these traits respond to long-term nutrient deficiency resulting from more than 140 years of rye monoculture.

We analysed a rye diversity panel including domesticated, feral, and wild accessions to characterize the genetic basis of male reproductive traits. Pollen size was quantified in 286 individuals using multispectral imaging flow cytometry, and anther length was measured in 314 individuals via light microscopy, revealing substantial intraspecific diversity. Genome-wide association scans identified five genomic regions associated with pollen size and eight associated with anther length, several of which overlapped with domestication-related loci of previously unknown function. $P_{ST}$-$F_{ST}$ comparisons and population genomic analyses also indicated selection during domestication, consistent with larger pollen and longer anthers in domesticated rye.

To assess environmental influences on male reproductive traits, we evaluated two rye populations, one population variety and one diversity panel, grown under soil nutrient enrichment and deficiency conditions. Soil nutrient deficiency, compared to nutrient enrichment, significantly reduced anther length and pollen number per anther, but not pollen size and viability. We detected shifts in the resource allocation strategy, resulting in phenotypic trade-offs, in response to the soil nutrient treatment. Correspondingly, soil environment-specific QTLs were detected for anther and pollen size.

Together, these findings uncover the genetic basis of pollen and anther morphology in rye and demonstrate how domestication and soil nutrient availability have shaped these key reproductive traits.

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# *Poster Abstracts*
# *P8. Regenerative, Precision, Profitable: Practices that Work*

# Evaluating wheat varieties for greenhouse gas emissions

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## ABSTRACT

Agriculture, forestry and other land uses accounted for 22% of total net anthropogenic greenhouse gas (GHG) emissions in 2019. Within agricultural systems, nitrogen (N) fertiliser application and associated field operations together account for over 70% of total GHG intensity from UK arable farms. The Haber-Bosch process used to manufacture synthetic N fertiliser is responsible for an estimated 1.5% of global anthropogenic carbon dioxide ($CO_2$) emissions. N fertiliser application to the crop also leads to N losses: via leachate through the soil, leading to diffuse pollution and eutrophication of aquatic ecosystems, or through volatilisation (e.g. $NH_3$) and GHG emissions, particularly nitrous oxide ($N_2O$), a potent GHG with approximately 300 times the global warming potential of $CO_2$. These environmental and economic pressures have driven interest in regenerative agriculture, which aims to improve ecosystem function through practices such as reduced tillage, cover cropping, and optimised nutrient management. Additionally, expanding genetic diversity in wheat through synthetic hexaploid wheat (SHW) lines may offer opportunities to identify varieties with improved nitrogen use efficiency and reduced GHG emissions.

This research investigates whether GHG emissions from wheat production can be reduced through genotype selection and agronomic practices associated with regenerative agriculture. Field trials were conducted under different tillage regimes and nitrogen treatments to evaluate commercial and synthetic winter wheat lines. Preliminary data indicate that nitrogen application rate did not significantly affect $N_2O$ fluxes, likely due to unusually dry conditions during the trial period, though some differences were observed between tillage treatments and varieties. Further field trials under varying environmental conditions are planned to clarify these relationships.

# Expanding the range of barley gene editing tool

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## ABSTRACT

Gene editing (GE) provides precise and efficient methods for targeted genetic modifications, offering immense potential for crop improvement. However, its application in barley (Hordeum vulgare), an essential crop for food, beer, and whisky production, remains limited due to cultivar-dependent transformation efficiency. This project aims to expand the range of available GE tools and develop a comprehensive "BarEDIT" toolbox to enhance barley's genetic tractability across both transformable and recalcitrant cultivars.

Initial work focused on the model cultivar Golden Promise using multiple CRISPR-based systems, including intronized Cas9, mutated Cas9 (nickase), and Barley stripe mosaic virus (BSMV)-mediated delivery for transgene-free editing. Two primary gene targets were selected: HvPDS (a visual marker for assessing editing efficiency) and HvLDI (Limit Dextrinase Inhibitor), which influences malting quality. Over 20 LDI-edited lines were generated, with ten showing edits at three or more guide sites. Besides, constructs targeting HvMlo (mildew resistance) and HvSPY (seed germination regulation) were also developed to explore agronomic traits relevant to yield and quality.

Parallel optimization of tissue culture and transformation protocols was undertaken for recalcitrant whisky-related cultivars (Laureate, KWS Sassy, LG Diablo, SY Arrow, SY Tennyson, and Fairing) using a GUS reporter system. Results revealed cultivar-specific responses, with Laureate showing limited regeneration (2.8%) and others exhibiting localized GUS expression.

Ongoing work involves viral-vector–based editing using BSMV and evaluation of edited lines for malting performance through biochemical and micro-malting analyses. A vector has also been developed for introduction of the GRF4–GIF1 growth regulating factor complex for the recalcitrant varieties to improve regeneration efficiency. Collectively, these efforts will contribute to the development of a barley gene editing toolbox supporting genetic improvement of elite, industry-relevant cultivars for food and beverage production.



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# *Poster Abstracts*
# *P9. Decoding Monocots: Genetics for Impact*

# Unveiling centromeric retrotransposon dynamics through a near-complete rye genome assembly

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## ABSTRACT

Rye (*Secale cereale* L.) is an important cereal crop known for its high yield potential and tolerance to biotic and abiotic stresses. However, its large, repeat-rich, and heterozygous genome has posed challenges for assembly compared to related species such as wheat and barley. Here, we present a high-quality, chromosome-scale genome assembly of the inbred line Lo7, generated using PacBio HiFi, Oxford Nanopore, Hi-C, and BioNano technologies using the TRITEX pipeline. The resulting Lo7_V3 assembly spans 6.76 Gb with a contig N50 of 128 Mb, correcting previous misorientations and achieving complete centromere assemblies across all seven chromosomes. Repetitive clusters containing rye-specific satellite sequences (pSc200 and pSc250) were contiguously assembled. Their chromosomal positions were validated using FISH. Centromeric retrotransposon analysis highlighted *RLG_Abia* and *RLG_Abigail* as a prominent element in rye, showing signs of recent activity and high abundance, unlike in wheat. Collectively, the new Lo7_V3 genome assembly provides a highly improved resource that will support future genomic research and crop improvement efforts in rye and related cereal species.

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# Exploring how RNA splicing influences the transcriptional landscape of wheat

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## ABSTRACT

Alternative splicing is a widespread regulatory mechanism that generates multiple RNA isoforms from a single gene, leading to altered gene expression or increased protein diversity. In plants, there is evidence that alternative splicing is involved in the control of agronomically important traits, including developmental changes and responses to biotic and abiotic stress. Hexaploid bread wheat *Triticum aestivum* is the world's most widely cultivated crop and is essential for global food security. Alternative splicing in wheat is likely to contribute substantially to phenotypic diversity. However, the extent and functional relevance of splice variation remain poorly characterised with most previous studies relying on short-read RNA sequencing followed by the reconstruction of full-length isoforms. These approaches can lead to the identification of incorrect splice junctions and spurious isoforms, a challenge exacerbated in polyploid genomes where high sequence similarity exists between homoeologous genes.

My PhD project addresses these challenges by integrating PacBio Iso-Seq and Oxford Nanopore long-read transcriptomic datasets to build an annotation pipeline for characterising alternative splicing in wheat. Using full-length transcript data, I aim to describe and compare isoform landscapes across wheat subgenomes, tissues, and cultivars. In later stages, I will extend these analyses across plant species of the *Triticeae* to investigate the conservation and evolution of isoforms. Overall, this work aims to provide a clearer view of isoform diversity in wheat and its potential contribution to gene regulation and crop improvement.

# Linking genome diversity to root architecture and growth dynamics in perennial ryegrass

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## ABSTRACT

Future temperate climates are predicted to experience more frequent and severe summer droughts alongside increased winter rainfall and flooding, threatening future grassland productivity (Kew *et al*., 2024). This creates a unique challenge for grass breeding, where cultivars must tolerate both water excess and deficit. Consequently, targeted breeding programs may benefit from focusing on cultivars exhibiting combined tolerance to both waterlogging and drought. Therefore, traits associated with root systems are of particular interest, yet remain relatively understudied in perennial ryegrass (PRG)

This project focuses on the genes and mechanisms underlying variation in root architecture in PRG, with particular emphasis on traits such as root length and rooting depth. An initial screen a diverse set of 200 PRG genotypes revealed a large variation in root phenotypes and rooting depths. Using rhizoboxes combined with semi-automated photographic analysis, root traits such as rooting depth were quantified in a selected of genotypes. This approach enabled the identification of stably reproducing shallow and deep rooting PRG genotype. RNA-sequencing was subsequentially performed on a further reduced subset of PRG genotypes to identify gene expression profiles associated with each root phenotype. This analysis revealed key differentially expressed genes (DEGs), likely contributing to observed variations in root architectures. Gene variations such as deletions and SNPs have been identified through whole genome sequencing, with the aim of linking genetic variation and changes in gene expression to differences in rooting depth across genetically distinct PRG lines.

Integrating rhizobox derived phenotypic data with RNA sequencing data provides combined phenotypic and transcriptomic profiles for individual plants. This could support breeding programmes by enabling the identification of genetic markers associated with key root traits.

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# An initiative to update the wheat web services landscape

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## ABSTRACT

Wheat-related web services that present data or support analyses serve thousands of active users across the research and breeding community. However, rapid advances in genomic data, reference genomes, and analytical methods have left many tools outdated, with underlying technologies increasingly unsupported.

This is a community call for action.

We are presenting this initiative to attract partners and gather feedback on the next steps.

Our goal is to modernise, connect, and future-proof the wheat web services so they remain powerful, efficient, and easy to use. We want to link tools that are commonly used together, keep essential resources up to date, and identify new research outputs that should be delivered as web services. We are also exploring whether recent advances in AI could provide new interfaces and smarter ways to access data.

Tell us:

- How could the existing web services and tools be improved?
- Which tools are more/less useful?
- What new tool would help you?
- Could you contribute any new tools?

Get involved and help shape the next generation of wheat web services.

**wheat-tools.jic.ac.uk**

# Capturing genetic diversity without compromising adaptation in wheat breeding

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## ABSTRACT

Global food security is increasingly threatened by climate change and increasing population-driven demand, requiring the enhancement of genetic diversity in wheat breeding programs. Plant genetic resources (PGRs), including wild relatives, landraces, and isolated breeding gene pools, represent a largely underutilised host of diversity with potential to improve yield and resilience. However, the introgression of beneficial traits from PGRs into elite germplasm remains constrained by cost and complexity. This study develops and evaluates simulation-based strategies combined with general combining ability (GCA) estimation to identify elite parental lines that facilitate the effective introgression of PGR-derived diversity without compromising local adaptation. Emphasis is placed on key adaptive traits, plant height, flowering time, and growth habit, controlled by major loci *Rht*, *Ppd1*, and *Vrn1*.

A tester-based crossing design is employed to generate training populations that enhance GCA prediction accuracy and facilitate diversity capture in both inbred and hybrid breeding contexts. Simulation outputs will be validated against empirical data to assess predictive performance. Additionally, a decision-support R-based tool is under development to optimise diversity capture in backcross breeding schemes, enabling efficient incorporation of PGRs while preserving local adaptation. This integrative framework offers a resource for enriching genetic diversity in wheat breeding pipelines through the strategic use of simulation and predictive breeding tools.

# Transcriptome profiling of Rht13 in wheat to understand novel height variation

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## ABSTRACT

Wheat is a major staple crop and an important part of human nutrition. Demand is increasing for more nutritious, resilient and sustainable wheat varieties and there is a pressing need to improve yield and yield stability. Hybrid wheat holds strong potential to increase wheat yields and stability, but successful hybrid breeding requires additional genetic variation across key traits, including plant height. Recently, a gibberellic acid sensitive single-copy semi-dwarfing gene, *Rht13*, was cloned and proposed as a useful source of variation for breeding.

To understand the pathways through which *Rht13* acts, we characterised transcriptional differences between *Rht13* wild type and mutant plants using peduncle and coleoptile tissues. We found mutant peduncle showed 5,286 differentially expressed genes (DEGs) compared to wild type peduncle. Gene Ontology enrichment indicated that up-regulated genes were mainly related to stress responses, while down-regulated genes were mainly related to cell wall regulation and protein synthesis. To prioritise changes which are more likely to be related to *Rht13* effects on height, we restricted analyses to genes differentially expressed only in mutant peduncle vs. wild type peduncle, and not in any other contrast (i.e. not in coleoptile), resulting in 1,719 DEGs. In this focused set, down-regulated enrichment remained similar, while up-regulated enrichment was limited to responses to hypoxia and nitric oxide (NO) biosynthesis.

From the 1,719 peduncle-specific DEGs, we prioritised 160 candidate genes (66 up-regulated; 94 down-regulated) for further validation; a subset will be tested through mutants and/or gene editing. These candidate genes include transcription factors and cell wall-associated genes. Ultimately this work will contribute to our understanding of how height is controlled in wheat and provide opportunities for wheat improvement.

# R-evolve: Rapid evolution of wild barley

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## ABSTRACT

Traditional crop breeding methods have improved yield but have resulted in a significant loss of genetic variation. Novel genetic variation has the potential to improve yield stability and enhance resilience in crops. Wild barley (*Hordeum vulgare ssp. spontaneum)* is more genetically diverse than current elite lines and can survive harsh environments with no inputs. Capturing these resilient traits can help meet sustainable breeding goals. Introducing exotic variation into the barley breeding genepool is challenging, screening unadapted material for advantageous alleles is difficult due to traits like seed shattering at maturity. In barley, very few introgressions from wild barley have been utilised in modern varieties with most exotic alleles originating from landraces.

The R-evolve project seeks to overcome some of these issues of utilising the broader wild genepool. Traditional approaches use exotic material to identify and transfer beneficial traits into elite material. We have reversed this approach and selected for the modern elite version of key domestication genes to recreate the domestication process. This ensures the part-wild material is usable in the field while maximizing the wild diversity. Our part-wild population has been tested as inbred lines and as $F_1$ hybrid parents to screen for promising breeding material. The R-evolve project has rapidly replicated domestication in 4 years instead of 10,000 years, acting as proof of concept for efficiently capturing diversity from undomesticated material.

# I5: A hidden genetic resource in Vietnamese rice landraces for elite breeding

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## ABSTRACT

Preserving global crop genetic diversity is crucial for food security. Over the last few decades, the rapid development of modern technologies has brought significant improvements to agriculture and crop breeding. However, its effects on global crop genetic diversity remain unclear. A unique indica subpopulation, I5, was found in the previous Vietnamese rice study with an admix-like population structure. I5 mainly consists of traditional low-yielding lowland landraces. We suggested that I5 has specific environmental or culinary value and is thus preserved in the low-altitude area around the Red River Delta. By investigating variations in I5, this project aims to provide potential genetic resources for future crop improvement and to understand how artificial selection shapes population structure and its effects on genetic diversity over time. We constructed and annotated an I5 reference genome. While an annotation-based pan-genome didn't show any special megabase-scale structural variation, a SNP-based introgression mapping method revealed multiple short non-indica regions. To navigate the further details of these introgression regions, including their sources, when and how they introgressed, we are reconstructing the relationship between I5 and other rice subpopulations using population-genetics-based tools. Afterwards, we will include herbarium specimens to explore population history, understand the reasons for introgression, and identify unique genetic resources in I5 that have been lost from elite varieties and could be integrated into modern breeding programs.

# Unlocking Pooideae diversity through comparative pangenomics

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## ABSTRACT

Pangenomes, which attempt to capture the complete genetic content of multiple individuals or closely related species, represent a powerful genomic resource for understanding evolutionary relationships and trait variation. The Pooideae, a globally distributed grass subfamily encompassing major cereals including wheat, barley, and rye, exhibits significant ecological and phenotypic diversity across its constituent genera. We are developing a pangenome for Pooideae grasses, integrating chromosome-scale genome assemblies with genomic analyses across a broad selection of lineages. As initial components of this resource, we have completed reference-quality genome assemblies for the species *Stipa capillata* and *Elymus angulatus*, representing two distinct evolutionary lineages within Pooideae. In parallel, we are validating and integrating publicly available sequencing data from diverse Pooideae accessions. This pangenomic framework is directly relevant to adaptation and resilience in cool-season grasses, enabling the analysis of conserved and dynamic gene content, lineage-specific structural variation, and genomic innovations associated with ecological differentiation and climate-related stress responses.

# Functional insights into aluminum response genes in barley

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## ABSTRACT

Aluminum (Al) is the third most abundant element in the Earth's crust after oxygen (O) and silicon (Si). In neutral and alkaline soils, Al occurs mainly in stable, non-toxic mineral forms. Under acidic conditions, however, Al becomes soluble and forms highly reactive and phytotoxic $Al^{3+}$ ions. Currently, more than half of the world's soils are acidic, and increasing industrialization together with the intensive use of ammonium-based and other acidifying fertilizers continues to exacerbate soil acidification, representing a major challenge for agriculture.

Plants have evolved several mechanisms to mitigate Al toxicity, including the secretion of organic acid anions (OAs) into the rhizosphere to chelate $Al^{3+}$ and the sequestration of Al into vacuoles for detoxification. These responses are largely regulated by the transcription factor STOP1 (*Sensitive To Proton Rhizotoxicity 1*), which controls the expression of genes involved in Al tolerance. Among them, the ABC-family transporter ALS1 plays a key role by mediating the vacuolar transport of $Al^{3+}$–OA complexes.

Ours study examines the aluminum stress response in barley (*Hordeum vulgare*), which ranks fourth most important cereal crop worldwide, primarily cultivated for animal feed and considered one of the most Al-sensitive crop species. We present the functional analysis of barley Al-toxicity related genes. The analyses were conducted using mutant lines identified through a TILLING approach within the *HorTILLUs* population.

These findings provide new insights into the molecular mechanisms underlying Al tolerance in barley, a species in which the roles of these genes under Al stress have not previously been investigated.

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# A large gene family parTCPating in temperature adaptation in bread wheat

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## ABSTRACT

Adaptation to climate is an important factor in cultivar selection to maximise crop yield. Identification of genes involved in temperature or stress tolerance can improve cultivar performance predictions and assist in selective breeding. The TCP (*TB1, Cycloidia,* and *Proliferating Cell Factor)* gene family are a large family of transcription factors involved in temperature dependent plant development and cell fate determination. Previous work has demonstrated the role of *TB1* in cereal spike architecture however the roles of other TCPs has been investigated predominantly in model dicot plants.

We first wanted to determine how different TCP genes may be involved in temperature regulation of different developmental stages. To do this we have explored expression of the TCP family in spring and winter cultivars across different plant tissues in different temperatures. Based on these expression profiles we identified gene candidates that may be involved in temperature regulation of floral development. To verify if these genes may be active in existing temperature regulated flowering gene pathways, we conducted yeast hybrid interaction studies and co-segregation analysis using Watkins haplotype data. We observed that TCP activity and allele type may be influential in bread wheat growth habit and identified a selection of TCPs involved in photoperiod, temperature, and circadian networks.

Understanding how these genes are involved in temperature dependant regulation of flowering time and floral architecture will assist selection for better adapted cultivars to help maintain and improve crop yield.

# Best crop: Boosting photosynthesis in barley to deliver sustainable yield gains and circular bioeconomy value

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## ABSTRACT

Improving crop productivity while reducing environmental impact is a major challenge for agriculture. The EU Horizon Europe project BEST-CROP (Boosting photosynthESis To deliver novel CROPs for the circular bioeconomy) addresses this challenge by targeting photosynthetic efficiency and biomass quality in barley (*Hordeum vulgare*), a strategically important cereal for food, feed and industrial uses.

BEST-CROP brings together 18 Partners from seven EU countries and the UK including geneticists, physiologists, breeders and industrial partners. The project explores natural and induced genetic variation affecting key photosynthetic traits, including chlorophyll content, canopy architecture, stomatal regulation and dynamic photosynthetic responses to fluctuating light. These traits are assessed using a combination of controlled-environment phenotyping, field trials and high-throughput physiological measurements, enabling the identification of genotypes with superior performance under realistic agronomic conditions.

In parallel, BEST-CROP evaluates straw quantity and quality to support circular bioeconomy applications such as animal feed, bio-composites and bio-based materials, aiming to increase whole-crop value without compromising grain yield or quality. Early project outcomes demonstrate significant genetic diversity for photosynthesis-related traits and highlight opportunities to decouple yield improvement from increased inputs.

By translating advances in photosynthesis research into breeding-relevant trait targets, BEST-CROP seeks to provide breeders and agronomists with practical guidance on which physiological traits offer the greatest potential for sustainable yield improvement. The project aims to support the development of barley varieties better adapted to future production systems, contributing to resilient arable farming and circular bioeconomy goals.

# Utilising Bere barley landraces to genetically map manganese-efficiency and improve crop nutrient use

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## ABSTRACT

Artificial selection for high-input systems has driven a loss of key resilience traits in modern barley varieties, including nutrient use efficiency traits. Older, locally adapted barley landraces can represent a valuable source of alleles for restoring these lost traits. “Bere” barley is an ancient Scottish landrace that was widely replaced by modern cultivars over the last 200 years, but has persisted on Scottish islands such as Orkney and the Outer Hebrides, in part due to an ability to thrive on the alkaline, manganese (Mn)-deficient soils present. In Mn-deficient conditions, Bere retains more vigorous green growth, stronger photosynthesis and larger grain yields than modern elite lines (Cope *et al*., 2020). Manganese deficiency is a global issue that drives yield losses of up to 60%, but the mechanisms underlying Mn-use in barley are poorly understood, so Bere offers a key opportunity to genetically map Mn-efficiency.

Through mapping of a previously developed biparental population produced from a cross of Bere Unst and the Mn-inefficient elite line KWS Irina, this project aims to genetically characterise Bere’s Mn-efficiency trait. A large, tri-replicate field trial of 428 fixed $F_7$ lines has been performed on Orkney and measurements of chlorophyll fluorescence and leaf Mn levels have been taken to assess Mn-use efficiency. Spatial mapping revealed trends in Mn deficiency across the field, which were accounted for by “Spatial Analysis of Field Trials with Splines” spatial modelling with the “SpATS” package in RStudio. The final adjusted phenotype data is being combined with genotype data to map the genetic regions (QTLs) associated with Mn-efficiency in a traditional segregant analysis. Subsequent fine mapping will be performed help to identify useful breeding markers, which could help produce elite barley varieties that are more tolerant to marginal soils and require fewer inputs and thus contribute to sustainable farming goals across Britain.

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# Exploring the use of genomic prediction approaches in barley DUS testing

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## ABSTRACT

To be marketed and/or awarded Plant Breeders' Rights (PBR) in the UK, all agricultural plant varieties must pass DUS (Distinctness, Uniformity and Stability) tests. DUS testing ensures that new varieties are unique, with distinctness determined by visually comparing candidate varieties against other varieties in common knowledge (the 'variety collection'). In the UK, barley DUS testing is carried out by Niab, on behalf of the Animal and Plant Health Agency (APHA). The DUS test is normally conducted over two independent growing cycles and involves the assessment of 29 DUS 'characteristics' (phenotypes). Provisional descriptions of candidate varieties, generated in the first growing cycle, are used to select the most similar varieties from the variety collection for distinctness comparisons in the second growing cycle. A third growing cycle is often required to establish distinctness for spring barley varieties due to their close phenotypic similarities.

Genomic prediction-based approaches, focussed on prediction of individual barley DUS characteristics, were investigated to explore whether they could be used to facilitate distinctness comparisons earlier in the testing process. Genomic and DUS phenotypic data were assembled for 1,086 barley genotypes from the variety collection. Genomic prediction methodologies were tested, including Random Forest (RF) and Ridge Regression Best Linear Unbiased Predictor (rr-BLUP), with prediction accuracies varying depending on the approach used and characteristic heritability. Comparisons made using the RF model with historic DUS data showed a good overlap (>70%) between the most similar varieties identified using predicted phenotypes compared to observed, providing proof of concept for the use of genomic prediction approaches to streamline DUS testing procedures.

Further work as part of a third Defra funded project is underway to genotype the complete UK spring barley variety collection, optimise and validate the genomic prediction models in parallel to current DUS testing procedures, and explore technical barriers to implementation.

# Physiological responses of wheat to carbamazepine in reclaimed irrigation water

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## ABSTRACT

The reuse of reclaimed wastewater for irrigation is increasing in arid and semi-arid regions, raising concerns about the entry of persistent pharmaceutical residues such as carbamazepine (CBZ) into agricultural systems. CBZ is frequently detected in treated wastewater and soil aquifer treatment effluents; however, its direct physiological effects on crop growth and root system architecture remain poorly characterized. We hypothesized that CBZ exposure alters wheat growth by selectively disrupting root architectural traits critical for water and nutrient acquisition. To test this hypothesis, tetraploid wheat (Triticum turgidum ssp. durum cv. Kronos) seedlings were grown hydroponically under control conditions (0 mg $L^{-1}$ CBZ) or CBZ treatment (2 mg $L^{-1}$) from 7 to 22 days after germination (DAG). Phenological, above-ground, and below-ground traits were quantified every three days. CBZ exposure significantly reduced shoot growth, including plant height, leaf length, leaf width, and leaf area, with differences becoming pronounced after 13 DAG ($P$<0.000001). By 22 DAG, CBZ-treated plants exhibited approximately 40% reductions in plant height and leaf area compared to controls ($P$<0.000001). Root system development was strongly affected by CBZ. Total root length was significantly reduced from early developmental stages, exceeding a 44% reduction relative to controls by 22 DAG ($P$<0.000001). Lateral root formation was particularly sensitive, with CBZ treatment causing reductions of more than 70% by 22 DAG ($P$<0.000001). In contrast, seminal root number remained unchanged throughout the experiment ($P$>0.05), indicating that CBZ specifically impairs root branching rather than root initiation. Together, these results demonstrate that CBZ selectively disrupts wheat root architectural plasticity while constraining overall vegetative growth. The strong inhibition of lateral root development suggests potential limitations in resource acquisition under reclaimed wastewater irrigation, highlighting the importance of considering pharmaceutical contaminants when evaluating crop performance and sustainability in water-limited environments.

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# utilizing Ensembl as a resource for comparative pangenomics in wheat

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## ABSTRACT

Ensembl is an open platform for visualising and exploring publicly available genomic data, including over 130 plant species. Annotated genes and genomic features such as repeat regions and variants can be viewed through the genome browser.

Ensembl's comparative genomics analyses produce whole-genome alignments, gene trees, and inferred homologies across plant species, supporting pangenome exploration through integrated views.

I will present two case studies to illustrate this:

**1**. A structural inversion detected between Chinese Spring and the cultivar Jagger from whole genome alignments, which revealed a strand orientation switch. This inversion, potentially affecting stress granule biology, demonstrates how Ensembl's visualisation tools uncover functionally relevant rearrangements.

**2**. Inspection of the cultivar Mace showed no annotated orthologue for a thionin-related gene; pairwise alignment suggested a missed annotation. These examples highlight Ensembl's capacity to detect structural variation and reveal functionally significant annotation gaps.

# Going low to thrive high: Towards unraveling the link between dwarfism and barley performance

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## ABSTRACT

Plant phenotypic plasticity is central to adaptation under fluctuating environments, yet plastic responses can incur costs, and excessive morphological adjustments under stress may reduce structural stability and compromise yield potential. In an attempt to understand the genetic underpinnings of reproductive organ survival, we have discovered a negative genetic correlation between floral survival and internode morphogenesis.

We found that in the classic barley (*Hordeum vulgare* L.) semi-dwarf mutant *uzu*, reduced stem elongation is associated with enhanced tip growth and increased floret survival, consistent with an underlying trade-off in source–sink allocation during morphogenesis. Further analyses showed that, compared with the wild type (WT), the *uzu* mutant exhibited an increased number and greater thickness of sclerenchyma layers, potentially forming a constitutively reinforced peripheral mechanical ring. Such structural reinforcement may dampen morphological plasticity, consistent with our observation that the *uzu* mutant displayed reduced phenotypic plasticity under resource-limited conditions, including high planting density and low nitrogen (N) availability.

We propose that the inherent strengthening of vascular tissues, combined with a more determinate growth pattern (lower plasticity), may contribute to the mutant's enhanced tolerance under environmental constraints. These anatomical traits may also support improved lodging resistance, although this requires further validation. Overall, our results align with theoretical frameworks emphasizing both the adaptive role and limits of plasticity, and highlight the potential of optimizing plasticity to improve crop resilience and performance in barley.

# Investigating homoeolog redundancy in polyploid wheat through machine learning and gene editing

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## ABSTRACT

Functional redundancy occurs when a gene is able to phenotypically compensate for the loss of another gene. *Triticum aestivum* (bread wheat) is hexaploid, so contains three copies (homoeologs) of many genes which together are known as a triad. Functional redundancy between homoeologs spans a spectrum of full redundancy, partial redundancy, and non-redundancy. It is unclear, however, what causes this range, making it difficult to predict, and therefore compensate for, redundancy when generating loss-of-function mutants.

This project aims to train a machine-learning pipeline to predict gene redundancy in *T. aestivum* homoeolog triads. Using epigenomic, transcriptomic, and genomic datasets, we developed a training and testing pipeline, aiming to predict redundancy in homoeolog triads throughout the bread wheat genome. This model provides further insight into characteristics that could contribute to functional redundancy, allowing for more efficient generation of mutants, and better characterisation of homoeolog triads in the wheat genome. Alongside this, we aim to better understand differences in editing efficiency between homoeologs, in order to more effectively screen mutants. We aim to characterise CRISPR-Cas9 homoeolog editing efficiency in wheat protoplasts. As well as potentially confirming the reliability of our machine learning pipeline, this will provide understanding into factors that affect gene editing efficiency. Overall, this project will develop our knowledge of homoeolog redundancy and provide a pathway for increasing efficiency of gene editing in bread wheat.

# Characterising male sterile two-row barley for a hybrid system

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## ABSTRACT

A key strategy for crop improvement has been harnessing hybrid vigour, which has seen great success in maize and rice production. The production of hybrid seeds involves the crosspollination of two genetically dissimilar parents to combine desirable traits from both genotypes in the resulting offspring, with increasing genetic distance being positively correlated with hybrid vigour. Hybrid vigour, or heterosis, is a phenomena that means hybrid offspring consistently outperform the parental lines in yield, stress tolerance, size and speed of development (Baranwal *et al*., 2012).

Domesticated barley has been bred to self-pollinate, leading to small inaccessible flowers that cannot be reliably manually emasculated on an industrial scale; research has therefore turned to genic male sterility (Colombo & Galmarini, 2017). My project aims to discover novel environmentally sensitive genic male sterile lines using a forward genetic approach and map the loci in approximately three near isogenic mutant lines. These would act as a maternal line in a two line system that can be crosspollinated under nonpermissive conditions but can recover fertility and self pollinate under permissive conditions (Vasupalli *et al*., 2025). This will be paired with advanced phenotyping for maternal fitness traits to maximise crosspollination. Current hybrid efforts utilise cytoplasmic male sterility from mitochondrial mutations to create a three line system, whereas environmentally sensitive mutants in this project can create a two line system with lower cost, more diverse parental combinations and higher yield hybrid offspring.

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# Complex structural genomic variations drive spikelet heterochrony to shape barley spike and domestication

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## ABSTRACT

Plant inflorescence shape is often patterned by the modular arrangement of structural units that differ in size or shape along a proximal–distal axis. Such a morphological gradient is central to reproductive success and crop yield performance, yet mechanisms coordinating the size, number and position of these modules remain unclear.

*Triticeae* inflorescence, called spike, provides an attractive model to address this question because of its simplified branching form, where repeated leaf–spikelet modules are progressively generated along a single axis called rachis. One aspect of spike shape is its bidirectional gradient in spikelet size, which we show can arise from developmental conflicts between the leaf and the spikelet within each module, leading to heterochronic spikelet development.

We demonstrate that this spikelet heterochrony is driven by complex structural genomic variations at the *VRN-H2* locus acting independently of flowering time. *VRN-H2* accomplishes this by retaining developmental potential in the leaf, thereby constraining spikelet outgrowth. Such a developmental constraint, however, can be further tinkered by time and by additional mutations affecting leaf–spikelet interactions. Finally, we provide evidence that a more uniform shape is associated with yield-related traits. The *vrn2* knockout mutant exhibits an increase in spikelet number and a significant increase in grain weight. Our results delineate a design principle of inflorescence shape with direct implications for crop domestication and improvement.

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