MONOGRAM

CEREALS & GRASSES RESEARCH NETWORK

Programme Booklet Sponsored By:

BGI syngenta eurofins

2025

7 - 10 April

Hosted by

1872 PRIFYSGOL ABERYSTWYTH UNIVERSITY

ibers | CNYDAU GWYDN RESILIENT CROPS

About Monogram

The Monogram Network consists of UK based researchers with an active interest in small grain cereal and grass (including the C4 energy grasses) research. Commercial scientists and plant breeders are active members and provide the link between Monogram science and commercial exploitation. Monogram includes both basic and more applied research and its members span disciplines including plant genetics, physiology, pathology, breeding, and bioinformatics. We also have extensive expertise in outreach activities and links with industry.

Our aim is to promote:

Coordinated Research: Enhance coordination and information flow within the community, boosting visibility nationally and internationally to strengthen UK efforts.

Community Integration: Serve as the focal point for the UK grass and cereals community, representing it at the UK Plant Sciences Federation and integrating with the broader plant sciences community.

Lowering Entry Barriers: Facilitate entry for new researchers in the field.

Our Steering Group

Stéphanie Swarbreck
(NIAB), Chair

Elizabete Carmo-Silva
(Lancaster University)

Carmen Escudero-Martinez
(University of Dundee)

Rachel Goddard
(Limagrain)

Surbhi Grewal
(University of Nottingham)

Joshua Ham
(RAGT)

Carus John-Bejai
(KWS)

Christophe Lambing
(Rothamsted Research)

Paul Nicholson
(John Innes Centre)

Miriam Schreiber
(James Hutton Institute)

Aiswarya Girija
(Aberystwyth University)

Jake Bishop
(University of Reading)

Nikki Walter
(University of Nottingham)

Welcome

Welcome to Aberystwyth University and Monogram 2025

Aberystwyth University, Wales' first university college, has been a hub of teaching and research excellence for over 150 years, inspiring global change through knowledge and community building. It drives innovation, supports the Welsh language, and fosters a globally connected, prosperous Wales. Located on Wales' west coast, the university offers an inclusive, bilingual, and vibrant learning environment in a safe and welcoming community.

Institute of Biological, Environmental & Rural Sciences (IBERS).

IBERS' vision is to carry out research to ensure that humanity can sustainably produce the food, feed and plant based industrial resources it needs. It is a national capability in grassland and plant breeding science located at Gogerddan and is a leading research centre specialising in biological, environmental, and rural sciences. It focuses on innovation in agriculture, sustainability, and climate resilience, contributing to global food security and environmental conservation.

Work within IBERS is focused on crop science and plant breeding - forage crops, grains for health, and industrial crops. Our core capabilities include genomics, plant phenomics and Controlled Environment Agriculture at the National Plant Phenomics Centre, studying upland farmed ecosystems at the Pwllpeiran Upland Research Centre, downstream utilisation including biomass conversion and biorefining, and agricultural systems to deliver net-zero livestock systems.

On behalf of Monogram 2025 organizing committee

Aiswarya, Alison, Catherine, Gancho

Agenda

MONOGRAM: ECR Skill Building Pre-conference Workshop

13:30 - 14:00	**ECR registration**
14:00 - 14:15	Welcome by Nikki Walter, University of Birmingham
14:15 - 15:45	**Workshop1: Navigating Career Pathways after PhD;** Speakers: Laura Dixon (IPK), Carus John-Bejai (KWS), and Lorna McAusland (University of Nottingham)
15:45 - 16:15	Coffee Break with Snacks
16:15 - 17:30	**Workshop 2: Making the Most of Conferences;** Speaker: Elizabete Carmo-Silva (Lancaster University) and **Introduction to Mentoring;** Speaker: Stéphanie Swarbreck (NIAB)
17:30 - 18:30	Informal poster session with drinks
18:30 - 22:00	Dinner and Science Pub Quiz

MONOGRAM: Day 1, Tuesday 8 April 2025

8:30 - 9:30	Arrival and Registration with coffee
9:30 - 9:35	Welcome by Prof Iain Donnison, IBERS, Aberystwyth University
9:40 - 10:30	**SESSION 1: Rank Prize Session**
9:35 - 9:40	Session opening by Aiswarya Girija, IBERS
9:40 - 9:50	Introduction to Rank Prize by Michael Gooding
9:50 - 10:30	**Rank Prize Keynote Lecture by Janneke Balk, JIC, UK "Mineral biofortification of crops: from Arabidopsis to wheat field trials"**
10:30 - 11:00	Coffee Break
11:00 - 12:30	**SESSION 2: Crop Diversification for Food, Forage and Bioenergy:** Session chairs: Catherine Howarth (IBERS) and Carus John-Bejai (KWS)
11:00 - 11:30	**Keynote Speaker: Simon Griffiths, JIC "Breeding: Why we need to start all over again"**
11:30 - 11:45	Noam Chayut, JIC, UK "Genebank-Omics: A Vision for Diversifying Global Food Crops Exemplified by the A.E. Watkins Durum Landrace Project"
11:45 - 12:00	Maximillian Jones, JIC, UK "k-mer GWAS uncovers loci for trait improvement in the indigenous African cereal Tef"
12:00 - 12:15	Jake Hill, University of Nottingham, UK "Aegilops umbellulata: A wheat wild relative giving heat tolerance to wheat"
12:15 - 12:30	Jake Bishop, University of Reading, UK "Drivers of yield variability in major UK arable crops"
12:30 - 13:30	Lunch

13:30 - 15:00	**SESSION 3: Abiotic and Biotic Stress Management for Resilience:** Session chairs: Carmen Escudero-Martinez (University of Dundee) and Rachel Goddard (Limagrain)
13:30 - 14:00	**Keynote Speaker: Pallavi Singh, University of Essex, Let the "Hard Graft" begin: Understanding and enhancing water use efficiency in crops**
14:00 - 14:15	Emily Radford, Aberystwyth University, "Engineering myxobacterial super predators to fight crop disease"
14:15 - 14:30	Oliver Powell, King Abdullah University of Science and Technology "A wheat tandem kinase activates an NLR to trigger immunity"
14:30 - 14:45	Sibongile Zimba, University of Bristol "Uncovering mechanisms and pathways underlying root growth angle regulation in response to drought stress"
14:45 - 15:00	Jessica Shadbolt, The James Hutton Institute, Scotland, UK "Good copper, bad copper: Characterising the physiological implications of contrasting alleles of HvHMA5 in barley"
15:00 - 15:30	Coffee Break
15:30 - 18:00	**SESSION 4: Farm to Fork: Quality and Nutrition** Session chairs: Joshua (RAGT) and Petros Zafeiriou (JIC)
15:30 - 16:00	**Keynote Speaker: Catherine Howarth, IBERS, Aberystwyth University, "Improving the Oat Crop for Sustainability and Quality"**
16:00 - 16:20	Elena Baldoni, CNR-IBBA "Integrated GWAS and metabolomic analyses provide novel details about the genetic basis of free asparagine accumulation in durum wheat grains"
16:20 - 16:40	Ondrej Kosik, Rothamsted Research UK "Approaches to increase cereal dietary fibre content to help combat chronic diseases"
16:40 - 17:00	Aiswarya Girija, IBERS, Aberystwyth University "Sprouting for biofortification of cereal based foods"
17:00 - 17:30	Selected Poster Flash talks (2-minute presentations)
17:30 - 19:30	Poster Session in Medrus 1 with Welsh Whiskey and Cheese tasting session, followed by poster selection for awards by session chairs

MONOGRAM: Day 2, Wednesday 9 April 2025

8:00 - 9:00	**Stronger Together: Equality, Diversity & Inclusion Over Coffee:** Join us for an interactive and informal coffee session to engage in EDI conversions
9:00 - 11:00	**SESSION 5: Physiology and Resource Use** Session chairs: Philippa Borrill (JIC) and Guillermina Mendiondo (University of Nottingham)
9:00 - 9:30	**Keynote Speaker: Lorna McAusland, University of Nottingham "Turning up the heat; assessing photosynthetic acclimation to heat from wheat leaf to spike"**
9:30 - 9:50	Wanxin Chen, Rothamsted Research, UK "Mutation of Sucrose: Fructan 6-fructosyltransferase (6-sft) in Hexaploid wheat reduced susceptibility to biotrophic fungi"
9:50 - 10:10	Guy Golan, IPK "Variation in growth scaling shapes wheat adaptation"

10:10 - 10:30	Chen Ji, JIC, UK "Spatial Transcriptomics Reveals Key Mechanisms of Sucrose Transport in Wheat Grain Development"
10:30 - 11:00	Coffee Break
11:00 - 12:30	**SESSION 6: Crop Genomics and Bioinformatics** Session chairs: Christophe Lambing (Rothamsted Research) and Gancho Slavov (IBERS)
11:00 - 11:30	**Keynote Speaker: Martin Mascher, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) "Barley crop evolution through the lens of pangenomics"**
11:30 - 11:50	Surbhi Grewal, University of Nottingham "Chromosome-scale assembly of wheat wild relatives enables identification of new introgressions in wheat"
11:50 - 12:10	Delfi Dorussen, JIC, UK "Unravelling the role of DNA methylation in polyploid wheat using met1-1 mutants"
12:10 - 12:30	Chidimma Gift Omenoba-Nee Ubah, University of Bath "Location matters - Gene Expression and Fusarium Head Blight Response in diverse Wheat-Rye introgression lines"
12:30 - 13:30	Lunch
13:30 - 15:00	**SESSION 7: Below and Above Ground Development for Growth and Adaptation** Session chairs: Nikolai Adamski (JIC) and Laura Dixon (IPK)
13:30 - 14:00	**Keynote Speaker: Stéphanie Swarbreck, NIAB "Cereals for low input & regenerative agriculture"**
14:00 - 14:15	Stephen Pearce, Rothamsted Research "Beyond the Green Revolution: Novel dwarfing alleles for wheat and barley improvement"
14:15 - 14:30	Indi Lacey, University of Leeds "The fast and the floriferous: Accelerating winter wheat lifecycles using controlled conditions"
14:30 - 14:45	Deepak Kumar, Leibniz Institute of Plant Genetics and Crop Plant Research "Vision for hybrid wheat through key male trait integration: A path to optimized grain set"
14:45 - 15:00	Zhenru Guo, IPK "BRANCHED SHOOT 1, a key hub gene of whole plant architecture in bread wheat"
15:00 - 15:30	Coffee Break
15:30 - 15:45	**MONOGRAM GROUP Photo Session**
16:00 - 17:00	IBERS Gogerddan Optional Tour: National Plant Phenomics, Seed Biobank, Biorefining
19:30 - 21:30	**Gala Dinner in Medrus**

MONOGRAM: Day 3, Thursday 10 April 2025

8:30 - 9:00	Coffee
9:00 - 10:30	**SESSION 8: Phenomics and AI for precision crop improvement** Session chairs: Surbhi Grewal (University of Nottingham) and Jake Bishop (University of Reading)
9:00 - 9:30	**Keynote Speaker : Ji Zhou, NIAB, UK (Online via Teams) "The use of AI-powered analytics to study growth dynamics and their association to key yield components in wheat"**
9:30 - 9:45	Martin Vickers, JIC "Scaling up drone phenotyping at the John Innes Centre"
9:45 - 10:00	Andrew Riche, Rothamsted Research "Drone-based hyperspectral imaging for phenotyping small plot field experiments"
10:00 - 10:15	Lucy Mahony, Earlham Institute "Decoding the regulatory regions of wheat using bioinformatics and machine learning"
10:15 - 10:30	Nick Bird, KWS, UK "An efficient alternative system for hybrid wheat production"
10:30 - 11:00	Coffee Break
11:00 - 12:00	**SESSION 9: ECR New Lecture Rank Prize and Monogram Early Career Excellence Awards (MECEA) Winner Talks** Session chair: Malcolm Macaulay (James Hutton Institute)
11:00 - 11:20	ECR New Lecture Rank Prize, Jim Fouracre, University of Bristol "Harnessing SPL Transcription factors for real yield increases in false flax"
11:20 - 11:40	MECEA Winner PhD: Katie Long, JIC, UK "Mapping the Wheat Inflorescence with Spatial Transcriptomics"
11:40 - 12:00	MECEA Winner PhD: Isabel Faci-Gomez, JIC, UK "Temperature and photoperiod interaction: Releasing aerial branching in wheat"
12:00 - 12:30	Announcement of Best Poster Awards and MONOGRAM 2026
12:30 - 13:30	Lunch

RANK PRIZE

End of Conference

Speakers

Janneke Balk

John Innes Centre

Janneke Balk is a senior researcher in plant biochemistry, currently holding a joint position at the John Innes Centre and the University of East Anglia on the Norwich Research Park. She began her independent research group at the University of Cambridge in 2005, before relocating to Norwich in 2011 to further her internationally recognized work on iron metabolism in plants.

Her research focuses on how plants balance iron uptake with cellular and developmental demands. Using genetic and biochemical approaches, her lab studies the molecular mechanisms governing iron uptake from the soil, transport and distribution to different organs, and iron storage in seeds. Knowledge gained from the model organism Arabidopsis is transferred to crops such as wheat and pea, to test strategies for increasing the iron content and bioavailability in plant-based foods to address human nutritional deficiencies.

Simon Griffiths

John Innes Centre

Dr. Simon Griffiths is a prominent researcher in wheat genetics, serving as the leader of the Delivering Sustainable Wheat (DSW) Institute Strategic Programme (ISP). His work focuses on advancing sustainable agriculture by leveraging innovative genetic and genomic tools to improve wheat varieties. Dr. Griffiths and his team specialize in discovering and utilizing genetic diversity from the AE Watkins collection of bread wheat landraces, a unique resource of ancient wheat varieties. Their research translates these discoveries into practical breeding applications, targeting marker-assisted selection and gene editing. These priorities are defined in collaboration with the DSW Breeders Toolkit Committee, ensuring alignment with the needs of the wheat breeding community. Dr. Griffiths' team applies cutting-edge genetics and genomics techniques to dissect key traits that are critical for wheat improvement. Through close collaboration with breeders and stakeholders, Dr. Griffiths' work bridges the gap between fundamental science and applied breeding. His research is driving innovations that contribute to sustainable food systems and global food security.

Pallavi Singh

University of Essex

Dr. Pallavi Singh is a Lecturer in the School of Life Sciences, University of Essex, where she leads a research group dedicated to enhancing photosynthesis and plant productivity. Her work focuses on improving water use efficiency and overall plant water use strategies, employing both natural variation and advanced single-cell approaches to dissect these complex traits. Dr. Singh earned her Ph.D. from the National Institute of Plant Genome Research (NIPGR) in India, where she investigated the mechanisms underpinning flooding tolerance in rice. She then conducted postdoctoral research at Cornell University, USA, focusing on rice-pathogen interactions, and a Research Fellowship at Department of Plant Sciences, University of Cambridge working on transcriptional regulation of C4 photosynthesis and cereal grafting in 2024, Dr. Singh was awarded a prestigious UK Research and Innovation (UKRI) Future Leaders Fellowship, securing over £2 million in funding to develop climate change-resistant strains of rice. This project aims to adapt rice at a genetic level to cope with dwindling freshwater supplies, addressing the anticipated largest shortfall in the global rice market in two decades. As part of this initiative, she collaborates with farmers in Southeast Asia and the International Rice Research Institute (IRRI) to promote sustainable rice production. Dr. Singh's research employs advanced interdisciplinary technologies to drive significant advancements in agricultural productivity and sustainability.

Catherine Howarth

IBERS, Aberystwyth University

Dr. Catherine Howarth is a Reader at the Institute of Biological, Environmental, and Rural Sciences (IBERS) at Aberystwyth University. Her research focuses on utilizing DNA markers and trait analysis to understand the genetic and physiological foundations of key agronomic traits in cereals, particularly oats. She leads the oats breeding and improvement research in IBERS. Her work aims to enhance sustainable production, disease resistance, stress tolerance, and end-use quality through marker-assisted and phenotypic selection. Dr. Howarth's contributions significantly impact the field of plant genetics and breeding, promoting sustainable agriculture and food security.

Lorna McAusland

University of Nottingham

Dr. Lorna McAusland is a Research Fellow in the Faculty of Science at the University of Nottingham, specializing in plant physiology with a focus on photosynthesis and stomatal responses to environmental stimuli. She earned her Ph.D. in Plant Physiology from the University of Essex in 2014. Following her doctorate, Dr. McAusland contributed to the Realizing Increased Photosynthetic Efficiency (RIPE) project, investigating how multigene manipulation of photosynthetic carbon assimilation can enhance CO_2 fixation and biomass yield in tobacco. In 2015, she joined Professor Erik Murchie's group at the University of Nottingham as a postdoctoral fellow funded by Innovate UK, developing sensors and LED-based technologies to improve precision agriculture in glasshouse settings. From 2016 to 2019, she worked as a researcher with the International Wheat Yield Partnership (IWYP) at the University of Nottingham, developing systems for high-throughput phenotypic exploration of novel genetic variation to breed high biomass and yield in wheat. Currently, she is a research fellow on a BBSRC Newton-funded grant, focusing on identifying the role of nocturnal stomatal conductance in the temperature tolerance of Mexican wheat varieties in response to climate change. Her work continues to advance the understanding of plant responses to environmental changes, contributing to the development of crops with improved efficiency and resilience.

Martin Mascher

IPK, Gatersleben

Dr. Martin Mascher leads the Independent Research Group "Domestication Genomics" at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany. His research focuses on understanding the processes of domestication and adaptation, and their interactions with genetic diversity in cultivated plants and their wild relatives. He primarily concentrates on temperate cereals such as barley, wheat, rye, and oats. Dr. Mascher's work involves applying population genetics and genomics methods to sequence datasets, genetic marker data, and gene expression matrices to:

- Elucidate the relationships between cultivated plants and their wild progenitors.
- Trace the demographic development and adaptation of cereals from their domestication origins in the Fertile Crescent to their spread across Europe.
- Decode the molecular impacts of domestication, including effects on genetic diversity, gene expression, and regulation.

His research contributes significantly to the understanding of how domestication has shaped the genomes of important cereal crops, providing insights that can inform future breeding and conservation efforts.

Stéphanie Swarbeck

NIAB

Dr. Stéphanie Swarbreck is a group leader in Crop Molecular Physiology at the National Institute of Agricultural Botany (NIAB), based in the Plant Genetics Department at the Crop Science Centre in Cambridge, UK. Her research focuses on understanding how plants integrate and respond to various environmental conditions, such as nutrient availability, the presence of neighbouring plants (e.g., weeds), and different soil tillage levels. The goal is to develop crop varieties, particularly wheat, that are suitable for low-input regenerative agriculture practices while maintaining yield and quality. Her research involves understanding the regulation of nitrogen responsiveness in wheat and how it is modulated under varying nitrogen availability. The research investigates the role of strigolactone in wheat nitrogen responsiveness and its downregulation under increasing nitrogen availability. In collaboration with Dr. Nathan Morris (NIAB-Farming System), she also explores the impact of regenerative agronomic methods on soil health and the development of wheat varieties that perform well under these practices. Through her research, Dr. Swarbreck aims to provide valuable insights for developing sustainable agricultural practices and crop varieties that can thrive under diverse environmental conditions.

Ji Zhou

NIAB

Professor Ji Zhou is the Head of the Data Sciences Department at the National Institute of Agricultural Botany (NIAB), where he leads pioneering research in agricultural technologies, specifically in multi-scale plant phenotyping, computer vision, and artificial intelligence (AI). His work focuses on the development of advanced analytical solutions for improving agricultural productivity and sustainability. His research includes innovative projects such as SeedGerm for assessing seed quality and vigor, CropQuant-3D for screening nitrogen use efficiency in wheat varieties using LiDAR technology, and AirMeasurer for drone-based phenotyping of crop growth. He has also developed CropSight and YieldQuant-Mobile to monitor wheat growth and predict yields, among other technologies. With a strong background in crop phenotyping, Professor Zhou collaborates with renowned institutions, including the University of Cambridge, the John Innes Centre, and several leading universities in China and Japan, to advance the application of IoT sensing and AI in agriculture. A Fellow of the Royal Society of Biology (FRSB), Professor Zhou has published over 30 research articles in prestigious journals. He serves as an associate editor for Horticulture Research and Plant Phenomics and is a core member of PhenomUK, a network focused on crop phenotyping research. His innovative work in data-driven crop science continues to drive the integration of advanced technologies in agriculture, contributing to more efficient and sustainable farming practices worldwide.

Jim Fouracre

University of Bristol

Dr. Jim Fouracre is a Royal Society University Research Fellow and Proleptic Lecturer in the School of Biological Sciences at the University of Bristol. His research focuses on plant developmental biology, particularly the regulation of developmental timing in plants. He investigates how plants control when to transition between different stages of their life cycle, largely using vegetative phase change – the transition from the juvenile to the adult phase of vegetative growth – as a model system. Vegetative phase change, a highly conserved process regulated by the microRNA miR156, influences various traits including leaf morphology, shoot physiology, light use efficiency, and stress responses. In 2023, he was awarded the Rank Prize New Lecturer grant to work on enhancing the yield of Camelina sativa, an oilseed crop rich in omega-3 oils. By studying the genetics of developmental timing of this underutilized plant his research aims to improve its growth and robustness, offering potential for better human nutrition and sustainable production of essential omega-3 fatty acids.

Meeting Sponsors

MECEA Awards

MECEA PhD Winner 1

Katie long, JIC

Katie is a fourth-year PhD student in Cristobal Uauy's lab at the John Innes Centre. Her research focuses on optimizing spatial transcriptomic techniques for plant tissues. She is particularly interested in characterising gene expression in the wheat inflorescence to better understand the developmental processes that shape the wheat spike over time. Katie developed her passion for plant development during her BSc in Plant Sciences at the University of Edinburgh.

MECEA PhD Winner 2

Isabel Faci, JIC

Isabel Faci is a fourth-year PhD student at the John Innes Centre (JIC), researching the genetic mechanisms that regulate temperature and photoperiod integration in wheat. Her work involves detailed phenotyping and meristem transcriptomics of plants grown under various environmental conditions. She led the implementation of a Temperature-Free Air Controlled Enhancement (T-FACE) system, based on Kimball et al. (2005), to simulate future UK weather. She earned her Biotechnology degree from the Universidad Politécnica de Madrid, where she first gained experience in wheat research. During this time, she contributed to characterising a Spanish landrace collection for quality traits with the Mejora Genética Vegetal (Plant Breeding Research) team.

Further Information

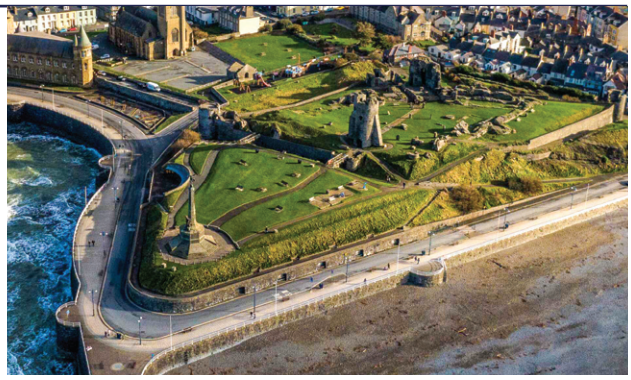
How to Get to Aberystwyth Town Centre

Bus: **301, T2, 512**

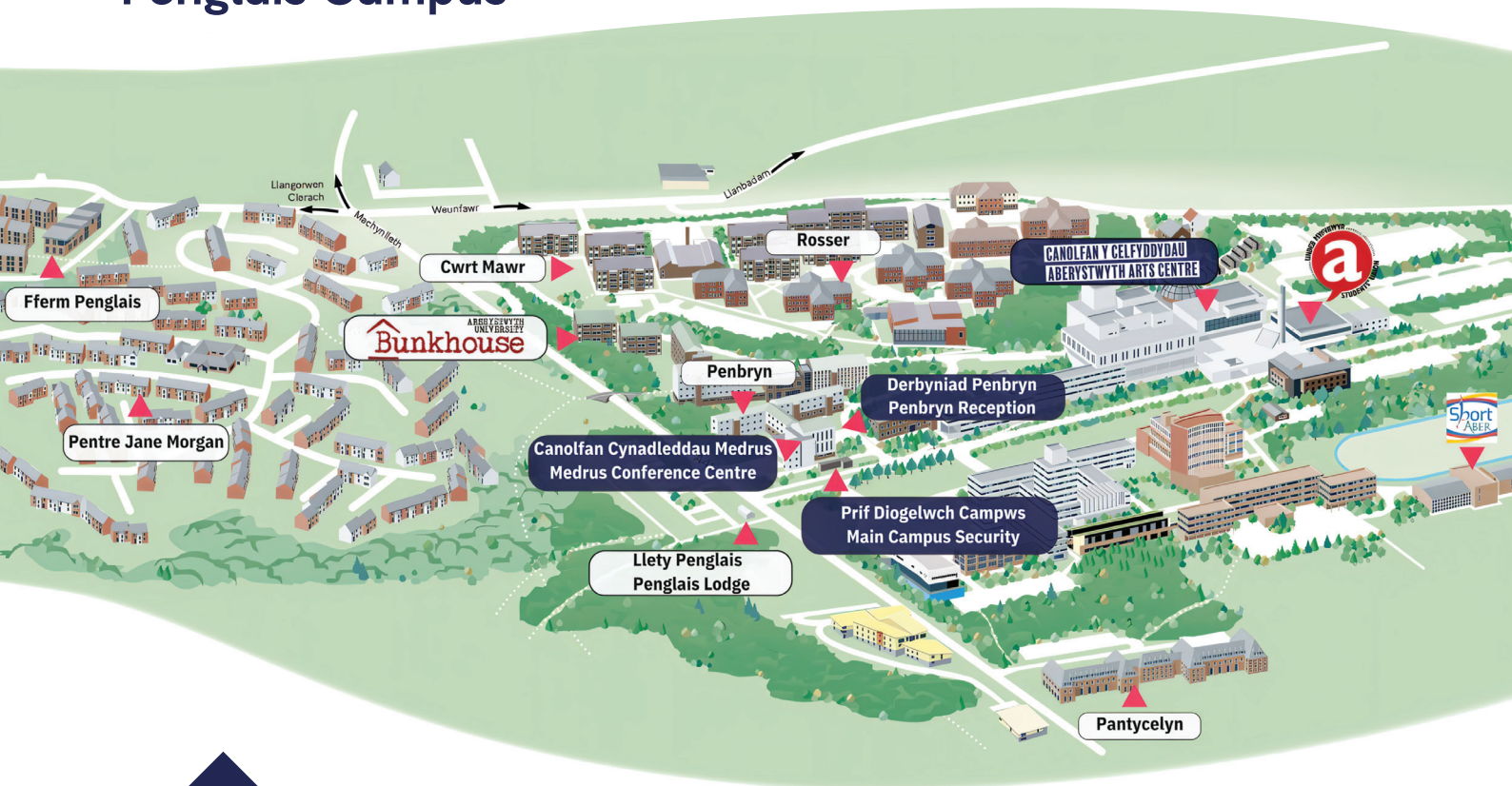
Taxi:	HopTon Taxis	Teifi Taxis	John's Taxis
	07487 523133	07999 567777	07792 906559

Nearby Tourist Attractions

1. Aberystwyth Cliff Railway
2. Aberystwyth Castle
3. Aberystwyth North Beach
4. Ceredigion Museum
5. Vale of Rheidol Railway



Penglais Campus



WE SEQUENCE, YOU DISCOVER

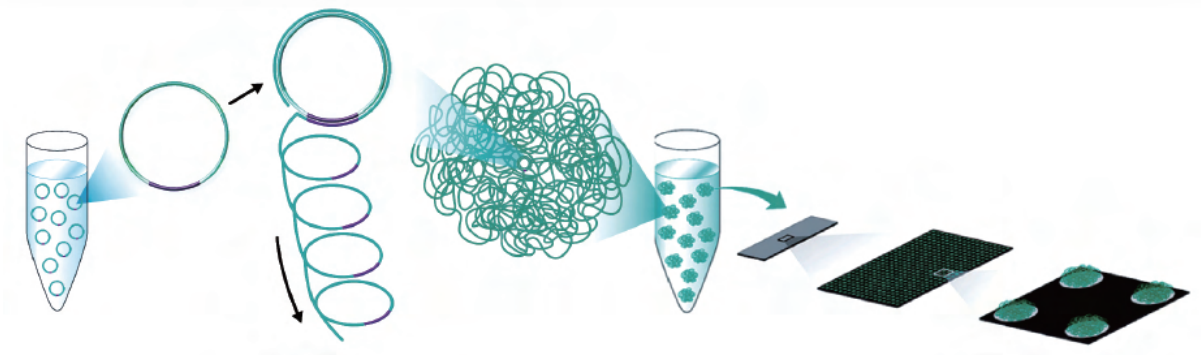
Genomics. Multi-Omics. And Beyond.

With over 20 years of sequencing experience, a global network of staff, a comprehensive service portfolio, and our own proprietary sequencing technology, we offer our customers a one-stop solution for reliable, cost-efficient and quality sequencing.

BGI's DNBSEQ™ Technology: Redefining Sequencing Quality

Proven DNBSEQ™ sequencing technology combines the power of DNA Nanoballs (DNB™), PCR-free Rolling Circle Replication, Patterned Nano Arrays and cPAS to deliver a new level of data clarity and affordability. The combination of linear amplification and DNB technology reduces the error rate while enhancing the signal, resulting in real advantages. BGI delivers thought leadership in the field of genomics with more than 4000+ peer-reviewed publications covering sequencing technology, methodologies, bioinformatics and applications.

- Highly accurate base calling.
- Much lower duplication rates for more usable data.
- Virtually no index mis-assignment for high throughput without loss of sample integrity.
- Higher sensitivity for identification of low-abundance/expressed species with high call confidence.



BGI offers multi-omics services to look across genomics, transcriptomics, epigenomics, proteomics and metabolomics, with the flexibility to customize solutions that meet your specific needs.

eurofins | Genomics

WHY PARTNER WITH EUROFINS GENOMICS FOR YOUR NEXT BREEDING OR RESEARCH PROJECT?

Benefit from our range of tailored, high throughput genotyping solutions to help you achieve your goals faster, for less.

Using new and established technologies, we can assist you to identify key marker-trait associations in your breeding populations using our range of discovery platforms, including **whole genome sequencing** using Illumina and MGI technologies, reduced representation library sequencing (GRAS-Di) or high density **microarrays**. Our Agrigenomics bioniformatics teams can help with marker selection for downstream applications. We offer **marker-assisted selection** via our flexible range of genotyping platforms, which can accommodate any level of complexity for marker-assisted selection strategies, with no compromise on accuracy, and with the speed required to make rapid breeding decisions. For eDNA and microbiome, we offer **NGS-based solutions** for metagenome analysis.

Our NGS-based and qPCR-based solutions are robust, flexible and deliver your data at very low costs, allowing you to accelerate your breeding programme, whilst keeping the costs down.

Contact us and find out how we can support you!

EUROFINS GENOMICS EUROPE AGRIGENOMICS PRODUCTS & SERVICES A/S Smedeskovvej 38 / 8464 Galten, Denmark
AG_agrigenomics_projects@genomics.eurofinseu.com / eurofinsgenomics.com / +45 7027 1170

Abstracts

ORAL TALKS

SESSION 1: Rank Prize Keynote Lecture

Keynote Speaker: Janneke Balk**,** Department of Biochemistry and Metabolism, John Innes Centre, Norwich, janneke.balk@jic.ac.uk

Mineral biofortification of crops: from Arabidopsis to wheat field trials

Enhancing the density of essential micronutrients, or biofortification, has been successfully implemented for e.g. vitamin A in maize and zinc in wheat (www.harvestplus.org). However, increasing iron in wheat and improve bioavailability is difficult to achieve by breeding. In the UK and many other countries, wheat flour is fortified with iron powder or iron salts to address widespread iron deficiency. We have recently completed a set of field trials that demonstrate a successful strategy to increase iron in wheat flour well above the UK requirement of 16.5 mg/kg. Fourteen years ago, we started with mapping iron homeostasis genes known from Arabidopsis and rice onto the wheat genome. We then cloned and tested iron transporter genes for overexpression in the wheat endosperm and combined this with a gene that improves mineral bioavailability. Interestingly, we later found examples of nature using a similar approach. In this talk I will also project forward to potential GE strategies following the discovery of the iron-sensing mechanism in plants

SESSION 2: Crop Diversification for food, forage and bioenergy

Keynote Speaker: Simon Griffiths, Delivering Sustainable Wheat (DSW) Programme Lead, John Innes Centre, Norwich, Simon.Griffiths@jic.ac.uk

Breeding: Why we need to start all over again

The humble wheat grain was central to the birth of civilisation and, together with rice and maize, continues as a global staple on which humanity depends. The statistics which support these statements are worth careful consideration. In the season 2023-24 global wheat production was almost 785 million tonnes. Production steadily increases, most years are a new record, perfectly tracking global population increase which is predicted to peak in 2050 with no new land available to expand production. Can wheat continue to deliver for us until then? This depends on the success of plant breeders who made possible the increases achieved so far. From the late nineteenth century a select and quite random group of unimproved landraces were sampled from limited geographical ranges and became the founders of

modern breeding programmes. We rely on the genetic gains delivered by reshuffling their genomes to this day! By reading the genetic code of global wheat landrace collection, assembled by AE Watkins in the early twentieth century an international team of researchers has shown that the foundations of modern wheat are simply too narrow and that most of the genetic diversity present in landraces has been unused in systematic breeding. Taking into account the existential challenges of climate change, biodiversity loss, declining soil health, and dietary crisis on top of our absolute need for food security I argue we need to revisit the origins of breeding and start again, enabled by the revolutionary technologies that underpin precision breeding.

T1: Genebank-Omics: A Vision for Diversifying Global Food Crops Exemplified by the A.E. Watkins Durum Landrace Project

Noam Chayut, John Innes Centre, UK, noam.chayut@jic.ac.uk
Keywords: Genebank, Genomics, Durum wheat, Landrace, Conservation

The UKRI-BBSRC Germplasm Resources National Bioscience Research Infrastructure (GR-NBRI) serves as the UK's public genebank for small grain cereals, with a focus on promoting Findable, Accessible, Interoperable, and Reproducible (FAIR) germplasm and data resources to drive modern crop science and breeding. This presentation reports on the development of a genebank-genomic resource for Durum wheat (Triticum durum), an underutilised crop with potential for diversifying UK arable rotations and contributing valuable allelic variation for bread wheat improvement. During the 1920s-1930s, A.E Watkins acquired thousands of landraces farmed globally prior to the green revolution. Of these, the 832 conserved bread-wheat accessions (Triticum aestivum) were profoundly studied, revealing a broad array of unique, beneficial and untapped genetic diversity and demonstrating a clear pathway of harnessing it to empower contemporary wheat breeding. In contrast, the 356 Watkins-Durum wheat landrace diversity, was thus far largely overlooked. This project dissects the Watkins-Durum wheat genomic diversity for high-resolution association genetics and downstream functional genomics. We used a K-Mer-based global genome diversity approximation to compare its breadths in the newly sequenced 356 AABB genomes with the recently published 1000+ bread-wheat AABB genomes. We show a significant proportion of novel untapped diversity. We conducted Genome-Wide Association Studies (GWAS) for >50 traits, evaluated in multisite replicated field trials over several years, spanning agronomy, grain quality, yield component, and pathology. The GWAS results are often confined to precise regions containing few dozen candidate genes. We ask if a systematic approach can validate the novel candidate gene function. Therefore, we evaluated targeted traits in >800 exome-sequenced mutagenised Durum lines (TILLING). We will present initial results to exemplify this gene-discovery pathway and showcase an early realised impact of the work by wheat breeders. Lastly, we will discuss how the GR-NBRI team envisages utilising genomics to improve global crop conservation.

T2: k-mer GWAS uncovers loci for trait improvement in the indigenous African cereal Tef

Maximillian Jones, John Innes Centre, UK, max.jones@jic.ac.uk
Keywords: Tef, Underutilised, GWAS, Resequencing, Metabolomics, Population genomics

Tef (*Eragrostis tef*) is an indigenous African cereal that is gaining global attention as a gluten-free "superfood" with high protein, mineral, and fibre contents. However, tef yields are limited by lodging and by losses during harvest owing to its small grain size (150x lighter than wheat). Breeders must also consider a strong cultural preference for white-grained over brown-grained varieties. Tef remains relatively understudied with limited "omics" resources. As part of an international collaboration, we resequenced 220 tef accessions from an Ethiopian diversity collection and conducted multi-locational phenotyping for 25 agronomic and grain traits. Additionally, grain metabolome profiling revealed differential accumulation of fatty acids and flavonoids between white and brown grains. We conducted k-mer-based genome wide association and uncovered novel marker-trait associations. A significant 70 kb peak for panicle morphology contained the tef orthologue of rice qSH1, a transcription factor regulating inflorescence morphology in cereals. We also observed a previously unknown relationship between grain size, colour, and fatty acids. These traits were highly associated with retrotransposon insertions in the two tef homoeologues orthologous to TRANSPARENT TESTA 2, a known regulator of grain colour. Our work provides valuable resources for tef research and breeding, facilitating the development of improved cultivars with desirable agronomic and nutritional properties. In particular, we provide insight into how breeders can combine desirable grain colour and grain size traits to reduce harvest losses while maintaining consumer appeal.

T3: *Aegilops umbellulata*: A wheat wild relative giving heat tolerance to wheat

Jake Hill, University of Nottingham, UK, Jake.hill@nottingham.ac.uk
Keywords: *Aegilops umbellulata*, Chlorophyll Fluorescence, Heat Tolerance, Wheat, Wheat Wild Relative

Global temperatures are rising, putting pressure on our wheat production systems. Predictions indicate that for every 1°C increase in temperature, wheat yields could decrease by 6%. This represents an approximate one million metric tonne loss in the UK yearly. Furthermore, the regions experiencing the largest temperature shifts align with some of the world's most food-insecure communities. The above highlights the importance of maintaining wheat yields under temperature stress in both the global north and south. Wild relatives of wheat may contain a solution for enhancing yields under elevated temperature stress. One such wild relative is Aegilops umbellulata, which can be found in Iran, Iraq, Turkey, and Syria areas that frequently experience temperatures exceeding 40°C. Consequently, these conditions have influenced the evolutionary development of Aegilops umbellulata to withstand high temperatures compared to bread wheat. We measured chlorophyll fluorescence to determine Tcrit (the temperature at which Fv/Fm shifts from a steady decline in efficiency to a rapid decline due to heat stress) in a collection of Aegilops umbellulata accessions and Aegilops umbellulata/Hexaploid Wheat

addition and substitution lines. Furthermore, we recorded plant yields and assessed seed morphology and elemental composition through image analysis, ICP-MS, and carbon-nitrogen analysis. Our findings suggest that chromosome 7U from Aegilops umbellulata may possess the ability to enhance the thermotolerance of bread wheat, therefore protecting yields under temperature stress.

T4: Drivers of yield variability in major UK arable crops

Jake Bishop, School of Agriculture, Policy and Development, University of Reading, UK, j.bishop@reading.ac.uk
Keywords: Arable crops, Diversification, Yield

Agricultural diversification is seen as one route to resilience against a range of shocks or stressors. One factor that can limit diversification is the perceived gap in performance between major cereals and options for introducing diversity including minor cereals, oilseeds, potatoes and legumes. We sought to understand whether this performance gap exists, its size, and what can explain it. We linked yield and profitability information from c.2750 farms in England across 2014-2021 from the DEFRA Farm Business Survey to weather, land cover, and soil variables at the joint character area scale. Through several stages of selection using mixed models, we determined the most important variables that explain variation in the yield and profitability of the different crops. We show that major cereal crops are indeed generally more profitable and higher yielding than their alternatives, and they are also less variable in these aspects. Broadly, variation in the yield of legumes and other break crops was explained to a greater extent by weather compared to the cereals. Across all crops, soil and land cover information explained less variation, though the latter was generally more important for cereal crops.

SESSION 3: Abiotic and Biotic stress management for resilience

Keynote Speaker: Pallavi Singh, University of Essex, pallavi.singh@essex.ac.uk

Let the "Hard Graft" begin: Understanding and enhancing water use efficiency in crops

Water use efficiency is a multifactorial trait that represents the ability of crop to utilise water efficiently while maintaining optimal growth and productivity. The overarching aim of our research group is to enhance photosynthetic productivity by concentrating on the complementary requirement to balance plant water supply with carbon gain, maximising water use efficiency. In the talk, I will particularly highlight our approach, which employs grafting to improve yield resilience. Grafting, the joining of tissues from different plants, is widespread in horticulture and research, and has been used since antiquity for plant improvement. Our efforts have expanded this technique to include major cereal crops that could further inform our strategies for enhancing water use efficiency in crops.

T5: Engineering myxobacterial super predators to fight crop disease

Emily Radford, Aberystwyth University, emr33@aber.ac.uk
Keywords: Zymoseptoria, Myxobacteria, Predation, Biocontrol

Septoria leaf blotch (caused by the fungal phytopathogen Zymoseptoria tritici) is a widespread and devastating disease affecting wheat crops worldwide. Wheat (triticum asetivum) is a globally grown crop which is highly valued as a feedstock for both humans and livestock, but crops can suffer dramatically from poor quality and losses due to septoria leaf blotch. Myxobacteria (phylum Myxococcota) hold untapped potential as biocontrol agents to protect cereal crops from the damaging effects of fungal diseases. Often considered as a keystone taxon in the soil microbial community, myxobacteria have extremely wide prey ranges (including bacterial, oomycete and fungal prey) and as apex predators can profoundly influence the soil microbial community. We have used in vitro assays to demonstrate the predatory abilities of a range of myxobacterial strains against Z. tritici¸ including the ability of some to impact biofilm formation, evidencing the potential for myxobacterial strains to be utilised as biocontrol agents against Z. tritici. Optimisation of the infection protocol of wheat with Z. tritici is underway in preparation for assessing the predatory ability of myxobacteria in planta. In addition, we have taken a bioinformatics approach using myxobacterial pangenomics and a genome-wide association study (GWAS), to reveal individual myxobacterial genes with a significant correlation with predatory activity. These genes of interest are ideal candidates for gene editing with the aim of producing one or multiple engineered strains of myxobacteria with enhanced predatory activity. Such ‘super-predators’ will likely show improved predation against Z. tritici and contribute to the formulation of a biocontrol treatment for use in wheat plants, which may confer prophylactic and/or therapeutic effects against the widespread effects of septoria leaf blotch.

T6: A wheat tandem kinase activates an NLR to trigger immunity

Oliver Powell, King Abdullah University of Science and Technology, mail@oliverpowell.com
Keywords: Disease resistance, Stem rust, Kinase-fusion protein

The structure, function and mechanism of nucleotide-binding and leucine-rich repeat receptors (NLRs) in plant immunity is well studied. In comparison the mechanism of tandem kinases (TKs), an emerging class of immune receptors, that confer disease resistance in wheat and barley is poorly understood. In this study, we investigated the mechanism of Sr62TK, which imparts broad-spectrum resistance to stem rust. We cloned an NLR (Sr62NLR) required for the function of Sr62TK and demonstrate that the two genes form a digenic module at the SR62 locus. Additionally, we cloned the corresponding fungal effector (AvrSr62) and showed its interaction with Sr62TK. Recognition of AvrSr62 by the N-terminal kinase of Sr62TK triggers displacement of the C-terminal kinase of Sr62TK which activates Sr62NLR and leads to an immune response. AlphaFold modelling of the Sr62TK revealed that an unusual extended ß-finger motif in the N-terminal kinase of Sr62TK is crucial for effector recognition and homodimerization of Sr62TK. This extended ß-finger motif was also identified as a “hotspot” of natural amino acid variation in Sr62TK across Aegilops and Triticeae. We found that Sr62TK mutants with

mutations in the ß-finger motif disrupted the interaction of the effector with the N-terminal kinase in yeast 2-hybrid experiments and were auto-active in N. benthamiana leaves. These findings provide insights into the mechanism of TK-mediated immunity that will facilitate the engineering and breeding of plants with durable resistance.

T7: Uncovering mechanisms and pathways underlying root growth angle regulation in response to drought stress

Sibongile Zimba, University of Bristol, sibongile.zimba@bristol.ac.uk
Keywords: Root growth angle, Drought-stress, Developmental pathway, Molecular mechanisms

Optimising root phenotypes for improved resource capture under drought conditions, is an unexploited opportunity for sustainable agriculture in the context of climate change and global warming. Root system architecture (RSA) is potentially programmable component for crop improvement due to its plasticity. Root growth angle (RGA) is a significant agronomic trait and a major component of root system architecture. Knowledge of the molecular mechanisms underlying the effect of drought on root growth angle during drought remain limited. Sorghum is a naturally drought-adapted crop and a good model for investigating drought-mediated RSA changes. Here, we investigate mechanistic pathways underlying sorghum RGA regulation under drought conditions. We screened root traits using high-throughput phenotyping protocols in sorghum genotypes in varying drought water-stress and control conditions followed by high-throughput transcriptomic and gene expression analyses. Our results reveal that root architectural traits vary dramatically across genotypes that have differing drought adaptability. Further analyses shows that the nodal root growth angle is a significant component of this variation. This study demonstrated that the RGA of seedlings can support later field performance predictions, and therefore a potential target for breeding. It further shows that drought influences steeper, deeper rooting in water-stress-tolerant varieties. The study further identified drought-dependent regulation of auxin-responsive genes not yet characterised in sorghum, that may play a crucial role in regulating root architecture in response to drought stress. Our data provide a mechanistic and practical framework for the targeted selection of germplasm as valuable pre-breeding material of high-yielding varieties that are robust to climate change and have optimized growth in low-input conditions.

T8: Good copper, bad copper: Characterising the physiological implications of contrasting alleles of HvHMA5 in barley

Jessica Shadbolt, The James Hutton Institute, Scotland, UK, jessica.shadbolt@hutton.ac.uk
Keywords; Micronutrients, Element homeostasis, Stress tolerance, Sustainability

Copper (Cu) is an essential co-factor for metalloproteins and participates in key oxidation reactions in both plants and humans. However, in excess this micronutrient has severe physiological implications that result in Cu toxicity. Understanding the genetics of grain Cu accumulation in barley (H. vulgare) is important due to the underpinning nutritional role barley plays in the staple diets of the poorest populations, in addition to the increasing deposition of Cu into arable soils. In this presentation, I will

identify Heavy Metal ATPase-5 (HvHMA5) as the likely gene underlying a quantitative trait locus contributing to variation in barley grain micronutrient accumulation in a population of contemporary European 2-rowed barley cultivars. I will define the two distinct haplotypes of HvHMA5 present in cultivated barley, each associated with contrasting levels of Cu and other grain micronutrients. Through protein modelling I will demonstrate that the difference in nutrient accumulation of these alleles can likely be attributed to a single amino acid substitution. I will describe how an analysis of georeferenced genotypic data from diverse germplasm led to the tentative speculation that the HvHMA5 allele associated with increased grain Cu is under positive selection in cultivated germplasm. I will also discuss on-going experiments using a selection of chemical and CRISPR-Cas9-induced mutants that will answer remaining questions related to the role HvHMA5 in Cu stress tolerance. Through breeding approaches, the identified HvHMA5 alleles may facilitate the development of biofortified barley or varieties with increased heavy metal stress tolerance.

SESSION 4: Farm to fork

Keynote Speaker: Catherine Howarth, IBERS, Aberystwyth University, cnh@aber.ac.uk
Catherine Howarth, Jason Brook, Sandy Cowan, David Evershed, Aiswarya Girija, Irene Griffiths, Tim Langdon, Marc Loosely, Sara Tudor

Improving the Oat Crop for Sustainability and Quality

Oats in the U.K. are currently enjoying a strong resurgence with their production area doubling in the last 20 years. There are two important factors responsible. First, there is a strong consumer demand for oat products which combine validated health and satiety effects. Second, oats are resilient and can be grown with few inputs, leading to their use as a substitute for other crops which have failed in the face of extreme weather or the cost of pest and weed control. Maintaining grain quality of oats under a variable climate is critical for human nutrition, end-use functional properties and commodity value. Emphasis on grain yield can result in compromises in quality resulting in a 'quality gap' where the crop fails to reach threshold levels of quality required by the end-user. Breeding programmes thus face a huge challenge in addressing the complexity of factors affecting quantity and quality of yield, and in striking a balance between the two to maximise the value of the crop to the producer. This presentation will explore how environmental conditions and management practices that result in high grain yield, which is closely related to grain number m-2, do not necessarily result in high milling quality traits which are more closely associated with grain size features. In addition, there is an urgent need to increase the stability of oat yield and quality in the face of climate change and new cultivation practices.

T9: Integrated GWAS and metabolomic analyses provide novel details about the genetic basis of free asparagine accumulation in durum wheat grains

Elena Baldoni, CNR-IBBA, elena.baldoni@cnr.it
Keywords: Acrylamide, Free asparagine, Durum wheat, GWAS, Metabolomics

Free asparagine content is a key factor in acrylamide formation in wheat derivatives after high temperature processing. Therefore, the control of free asparagine levels is of interest in crop and food sciences. Our study aims to explore free asparagine natural variation in durum wheat grain to identify candidate genes controlling this trait. Two hundred and one durum wheat genotypes were selected from an international germplasm collection and sown in an experimental field for three years. Free asparagine content was measured on whole grain using an enzymatic assay. A genome-wide association study identified six associated quantitative trait nucleotides. Moreover, the whole grain metabolome of one-year samples was investigated to identify metabolic pathways associated to free asparagine accumulation. Specific enriched pathways involved in amino acids metabolism were detected and four candidate genes were identified. This study paved the way to characterize the genetic determinants of free asparagine accumulation in wheat grain.

T10: Approaches to increase cereal dietary fibre content to help combat chronic diseases

Ondrej Kosik, Rothamsted Research, ondrej.kosik@rothamsted.ac.uk
Ondrej Kosik[1], Anneke Prins[1], Heather Angus[1], Michelle-Leverington-Waite[2], Luzie Wingen[2], Abdul Kader Alabdullah[2], Simon Griffiths[2], James Brett[3], Rowan Mitchell[1], Lucia Segovia De La Revilla[4], Edward Joy[1,4,] Peter Shewry[1] and Alison Lovegrove[1]
[1] Rothamsted Research, Harpenden, UK
[2] John Innes Centre, Norwich, UK
[3] Earlham Institute, Norwich, UK
[4] London School of Hygiene and Tropical Medicine, UK
Keywords: Arabinoxylan, White flour, Chronic diseases, Dietary fibre

High intake of fibre and wholegrains has been linked to a risk reduction in non-communicable diseases, such as type-2 diabetes, cardiovascular disease, obesity and some types of cancer. Cell wall polysaccharides constitute a major source of dietary fibre (DF) in wheat endosperm. However, wheat is mostly (~80%) consumed after processing as white flour products such as white bread and pasta which markedly (over 60%) decreases the DF content. Fibre intake targets set by health authorities are rarely met. Yet, cereals provide around 40% of total fibre intake in the UK with bread delivering currently ~20% [1]. Our research focuses on improving the content of fibre in white flour so that the health benefits of increased fibre can be obtained without having to change eating preferences. Arabinoxylan (AX) is the major hemicellulose and DF in wheat endosperm. The major isoforms of glycosyl transferases (GTs) involved in AX biosynthesis and feruloylation (acyl-CoA dependent acyltransferases) have already been identified. We are identifying further sources of high fibre in white flour, using bi-parental populations

and association panels and have developed molecular markers for use in conventional wheat breeding programmes [2,3]. We are currently characterising genes responsible for the high-fibre trait to allow their identification or, if necessary, integration into elite germplasm by gene editing. We have also modelled the impact of the introduction of high-fibre white flour on fibre consumption in the UK [4]. Finally, we are establishing the effects of high-fibre bread on digestion using in-vitro models and working with commercial millers and bakers to determine the impact of higher-fibre flour on bread processing quality.

T11: Sprouting for biofortification of cereal based foods

Aiswarya Girija[1], Pilar Martinez Martin[2], Veda Krishnan[3], Amanda Lloyd[2]
[1]IBERS, [2]Aberystwyth University, [3]ICAR-IARI, India, aig15@aber.ac.uk
Keywords: Cereals, Functional foods, Metabolomics, Micronurtrients, Nutrition

The rise in lifestyle-related illnesses such as diabetes, irritable bowel syndrome (IBS), and gluten intolerance has led to growing requests for high quality, low glycemic potential (IGP) gluten free foods. Over the past decade, there has been a surge in the popularity of sprouted grains (germinated seeds) owing to their nutritional characteristics and enhanced sensory qualities, such as sweetness and flavor. This has sparked growing interest within the international food industry and among consumers in utilizing germinated grain flours for various food product developments aimed at improving nutritional content, sensory appeal, texture, and stability. Sprouting is a natural, flexible, cost-effective, and sustainable process of grain enrichment and this process can be adapted at home, and industrial settings to produce nutrient-dense products in a short time. This process will help to eliminate or reduce the major limitations in consuming whole grains such as anti-nutrients, allergens and indigestibility with better taste and flavor. During sprouting some biochemical changes occurs that positively influence nutritional profile and bioactive contents compared to ordinary grains. The current study aims to elucidate the nutritional profile using wheat, oats and gluten free cereals (pearl millet) sprouts and how sprouting impact the overall nutritional profile. Here we demonstrated the free phenolics, β-glucan, total sugars, free amino acids, micronutrients (Ca, Fe, Zn, Mg, Na, K, riboflavin, thiamine, niacin, vitamin B6, pantothenic acid, β-carotene) and anti-nutritional factor such as phytic acid.

SESSION 5: Physiology and Resource Use

Keynote Speaker: Lorna McAusland, University of Nottingham,
Lorna.McAusland@nottingham.ac.uk

Turning up the heat; assessing photosynthetic acclimation to heat from wheat leaf to spike

Historically, our knowledge of plant photosynthesis primarily derives from leaves, however, the photosynthetic potential of non-foliar structures is a major but less understood source of novel,

untapped variation. Inhabiting an unstable environment of high heat at the top of the canopy, the wheat spike is especially vulnerable to the rising global temperatures; with every 1ºC increase in maximum daytime temperatures resulting in up to 6% reduction in yield. With global temperatures predicted to rise between 1-6 ºC by 2050, and with heatwaves becoming more frequent and lasting longer, identifying and understanding spike Photosynthetic Heat Tolerance (PHT) is a means to understanding the non-foliar photosynthetic mechanisms vital for maintaining yields under greater climactic uncertainty. In this talk, I will discuss novel approaches to assessing spike PHT and present initial findings on the relationship between leaf and spike PHT under heat. Finally, I will draw on ecophysiological theory to understand how the wheat spike experiences heat compared to the leafy canopy below.

T12: Mutation of Sucrose: Fructan 6-fructosyltransferase (6-sft) in Hexaploid wheat reduced susceptibility to biotrophic fungi

Wanxin Chen, Rothamsted Research, UK, wanxin.chen@rothamsted.ac.uk
Wanxin Chen, Vinay Panwar, Wing-Sham Lee, Lucy Hyde, Martin Urban, Kostya Kanyuka and Kim Hammond-Kosack
Keywords: Wheat, Fructan, SUCROSE: FRUCTAN 6-FRUCTOSYLTRANSFERASE, Fungal disease resistance

Fructans are important storage compounds synthesised from sucrose in many grass species including wheat via the action of three enzymes: 6-SFT, 1-SST and 1-FFT. Fructans accumulate in stems and are remobilised to spikes and grain post- anthesis. Our previous studies indicated that fructans could act as host susceptibility factors contributing to Fusarium head blight (FHB) disease severity. 6-SFT and 1-SST knock-out mutants in the Cadenza background were generated using genome-editing (GE). Mutants with 61-70 bp deletions in the three 6-SFT homoeologues on 4AL, 7AS and 7DS, which lead to a frame shift and a gained stop codon, were identified. Phenotyping of T1 and T2 triple homozygous GE lines under controlled environment conditions has revealed most lines had no remarkable difference in plant growth comparing to controls, but some lines produced significantly larger grains. In T1 and T2 grains of triple GE lines, fructan content was significantly lower than in control non-GE lines and wildtype Cadenza, but starch content was similar in all T2 GE and non-GE lines. Yellow rust or powdery mildew leaf inoculations of homozygous T2 seedlings identified five and one moderate resistant lines out of two independent events, respectively. Preliminary result of T3 adult plants FHB phenotyping indicated one line was significantly less infected at 7 & 14 days after inoculation. Further phenotyping experiments are in progress. Simultaneously, the generation of triple 6-SFT TILLING mutants and Cadenza backcross lines are in progress. These GE and TILLING mutants will be explored as a new resource to be used in future breeding strategies to increase resilience against multiple fungal diseases.

T13: Variation in growth scaling shapes wheat adaptation

Guy Golan, Leibniz Institute,IPK, golan@ipk-gatersleben.de
Keywords: Growth, Scaling, Adaptation, Allocation, Genetics, Wheat

The rate of resource uptake and the expenditure of energy and resources are largely influenced by variations in organism size. Allometry describes the disproportionate change in an organism's morphology, physiology, and life-history traits relative to changes in its size. Growth rate, a fundamental biological trait determining plant resource use, is predicted to scale consistently with plant mass according to power laws, exhibiting remarkable constancy across taxa due to biophysical constraints and the optimization of natural selection. However, the applicability of this scaling to crop plants, shaped by artificial selection, and the potential consequences of deviations from these scaling predictions for crop performance remain unknown. We examined allometric relationships between plant mass and growth rate in 197 European winter wheat (Triticum aestivum L.) cultivars across seven developmental stages of spike growth, observing variation in scaling between developmental stages and cultivars. We found that genetic variation in scaling exponents, which describe how growth rate changes with plant size, was closely related to growth duration and biomass allocation. Specifically, plants that invest more in leaf production and develop quickly tend to increase their growth rate more efficiently as they grow larger. Phenotypic and genetic analysis revealed two main adaptive strategies among cultivars: large genotypes with low scaling exponents that grow slowly, enabling higher initiation of reproductive structures and enhancing yield potential, and small, fast-growing genotypes that favor reproductive effort and survival of floret primordia. Accordingly, we identified a shared genetic basis for growth allometry and Genotype-by-Environment interactions for grain yield, driven by a deletion in the promoter of Photoperiod response 1 (Ppd-1) that triggers an early boost of cell wall and metabolic genes promoting spike growth and confers adaptation to low precipitation. Our findings underscore the importance of growth allometry as a predictive framework for optimizing breeding strategies under diverse environmental conditions.

T14: Spatial Transcriptomics Reveals Key Mechanisms of Sucrose Transport in Wheat Grain Development

Chen Ji, JIC, UK, Chen.Ji@jic.ac.uk
Keywords: Wheat, Spatial Transcriptomics, Grain Development, Sucrose Transport

Wheat (*Triticum aestivum*) grain filling is coordinated with cell expansion that significantly enlarges the grain size. During this stage, the accumulation of starch and protein relies on the efficient transport of nutrients and signals between tissue compartments. Although different tissues (e.g. pericarp, endosperm) have been identified in the grain, we have limited knowledge about the diversity of cell types within these tissues and how they function. In this study, we use high-resolution metabolomics and transcriptomics to examine cell expansion, endosperm development, and nutrient accumulation in wheat grains at 12 and 18 days post-flowering. Using Stereo-seq spatial transcriptomics, we pioneered the profiling of gene expression patterns and identified distinct functional cell clusters distributed within

the grain, including the aleurone layer, modified aleurone, and embryo-adjacent endosperm (EAS) which are key transport interfaces during grain filling. Gene expression within spatially restricted compartments was validated using with RNA in situ hybridization. Using our spatial gene expression data and MALDI (Matrix-Assisted Laser Desorption/Ionization), we constructed a comprehensive model describing sucrose transport, as well as starch and protein storage dynamics. We provide an online resource that allows visualization of gene expression across the entire grain section using gene IDs. We present a case study demonstrating the utility of our spatial transcriptome approach in quickly identifying functionally relevant members from a gene family. We identified that sucrose transporter 1 (SUT1) exhibited specific expression in the aleurone, modified aleurone and scutellar epithelium and was the only sucrose transporter gene with this unique expression pattern. TILLING mutants in SUT1 exhibited disrupted sucrose transport and grain filling defects, leading to abnormal grain development and a significant reduction in kernel weight. These findings illustrate the power of resolving gene expression at the single-cell level in wheat grains and provide insights into improving wheat grain nutrient content.

SESSION 6: Crop Genomics and Bioinformatics

Keynote Speaker: Martin Mascher, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), mascher@ipk-gatersleben.de

Barley crop evolution through the lens of pangenomics

Pangenomes, which are collections of annotated genome sequences from multiple individuals of a species, provide valuable insights into structural variants that enhance genetic analysis in crop plants. This study presents a barley pangenome comprising long-read assemblies from 76 wild and domesticated genomes, supplemented by short-read data from 1,315 genotypes. The expanded variation catalog reveals structurally complex loci enriched in gene copy number variation. The utility of the pangenome is demonstrated through analysis of selected loci related to plant architecture, nutrient release, and trichome development. Novel allelic variations were identified, including a population-specific copy number gains in a vegetative branching regulator. Additionally, an expanded enzyme family in elite malting barley varieties was linked to altered enzymatic activity in micro-malting trials, and the deletion of an enhancer motif was associated with changes in the development of hairy appendages on barley grains. These findings suggest that allelic diversity at structurally complex loci has facilitated crop adaptation to selective pressures in agricultural environments.

T15: Chromosome-scale assembly of wheat wild relatives enables identification of new introgressions in wheat

Surbhi Grewal, University of Nottingham, surbhi.grewal@nottingham.ac.uk
Keywords: Genomics, Wheat, Introgressions, Bioinformatics

Bread wheat has become one of the most successful and widely cultivated crop species and is adapted to a wide range of climatic conditions. Continuous gene flow by natural and artificial introgressions from wild wheat relatives has increased the genetic diversity of bread wheat following a domestication bottleneck. Genome scans for regions under selection can reveal loci targeted by breeders as well as wider regions linked to selected loci with reduced haplotype diversity. Recently established high-quality reference genome sequences from various wheat wild relative species allow prediction of the size, frequency and identity of introgressed chromosome regions using read-mapping coverage analysis. We analysed the read mapping data from publicly available whole genome shotgun resequencing (WGS) data of 760 European winter wheat against a concantenated reference of Chinese Spring wheat RefSeq v.2.1 assembly and reference quality assemblies from 18 wild relative species from wheat's primary, secondary and tertiary gene pools. We identified 2,756 putative large introgression blocks (>5 Mb) from eight of these wild relative species spanning across all the wheat chromosomes. Some of these introgressions are well known, such as the 1B/1R from Secale cereale 2NS/2AS from Aegilops ventricosa. Others have been previously reported but with missing or misidentified wild relative sources. Here, we link the majority of the introgressions with the wild relative source species (where the genome assemblies are available) and provide an atlas of wild relative introgressions in the wheat genome. We also show that introgressions from different wild relative species sometimes overlap or occur consecutively along wheat chromosomes in these wheat accessions. We trace introgressions to early wheat cultivars and show that natural introgressions were utilised in early breeding history and still influence elite lines today.

T16: Unravelling the role of DNA methylation in polyploid wheat using met1-1 mutants

Delfi Dorussen, JIC, UK, delfi.dorussen@jic.ac.uk
Keywords: Epigenetics, DNA methylation, Transcriptomics, Homoeolog expression

DNA methylation is a central epigenetic mark in plants – changes in DNA methylation affect gene expression, transposable element activity, and genome stability, which can result in the generation of novel phenotypic variation. These (epi)genetic changes can be induced in plants with mutations in the epigenetic machinery, although such mutants are often lethal in crop species. Here, we present the first in-depth characterisation of an epigenetic mutant in wheat. We have exploited the partial redundancy between homoeologs in hexaploid wheat to generate viable mutants in the DNA Methyltransferase 1-1 (MET1-1) gene. Loss of four or more functional copies of MET1-1 is associated with a reduction in CG methylation, an increased number of differentially expressed genes, and abnormal developmental phenotypes, while full loss-of-function of MET1-1 is lethal. The partial met1-1 mutants have allowed

us to further investigate the relationship between DNA methylation and gene expression. Previously, CG methylation was found to be associated with homoeolog expression bias in wheat, as more highly expressed homoeologs have higher gene-body CG methylation than their less highly expressed counterparts. By perturbing DNA methylation in the met1-1 mutants, we have found that homoeolog expression bias is robust to moderate changes in gene-body CG methylation. Rather, homoeolog expression bias may be maintained by other epigenetic modifications, which often act redundantly. Large reductions in gene-body CG methylation, however, are associated with the suppression of homoeolog expression. Overall, our findings provide further insight into the interplay between DNA methylation and homoeolog expression bias, which could ultimately be used to generate novel homoeolog expression patterns.

T17: Location matters - Gene Expression and Fusarium Head Blight Response in diverse Wheat-Rye introgression lines

Chidimma Gift Omenoba-Nee Ubah[1], Ding Li2, Mark Winfield[2], Gary Baker[2], Keith Edwards[2], Hans-Wilhelm Nützmann[1,3]

[1]Life Sciences, University of Bath; [2]Biosciences, University of Bristol; [3]Biosciences, University of Exeter.

cgonu20@bath.ac.uk

Keywords: Wheat-rye introgression, Gene transcription, Genome interactions, Fusarium head blight, Deoxynivalenol mycotoxin

Bread wheat (Triticum aestivum), a vital global staple crop, provides about 20% of human caloric intake. Its evolution from the hybridization of *Aegilops tauschii* and Triticum turgidum ~10,000 years ago limits its genetic diversity, challenging breeders in creating resilient cultivars. Introgression, the transfer of genetic material from related species, enhances wheat's genetic diversity and introduces valuable traits. However, the genetic interaction between introgressed 'foreign' DNA elements and host genome as well as the biological effects of their integration sites remain poorly understood. Here, we studied a diverse set of introgression lines harbouring the short arm rye chromosome 1 (1RS) in different wheat genomes (1A, 1B, 1D) and at various locations within the 1D chromosome by RNA-sequencing, the updated TaNGv1.1 genotyping array, and plant pathogen assays. Transcriptional analysis revealed significant variation in gene expression depending on the size and genomic location of the introgression. The TaNGv1.1 array uncovered unexpected genotypic diversity among target lines, demonstrating its effectiveness in genome-wide variation detection. Fusarium head blight (FHB) assays with Fusarium graminearum revealed significant differences in disease progression, toxin accumulation, and fungal DNA levels among the analysed lines. These results highlight the enhanced resistance of wheat-rye introgression lines to fungal diseases. Overall, our study emphasizes the critical role of integration site in influencing gene expression, genome function, and disease resistance, underscoring its importance in developing future wheat varieties for changing climates.

SESSION 7: Below and Above Ground Development for growth and adaptation

Keynote Speaker: Stéphanie Swarbreck, NIAB, Stephanie.Swarbreck@niab.com

Cereals for low input & regenerative agriculture

Challenges experienced by crop plants grown in a field have been addressed traditionally by physical or chemical modification of their environment. However, regenerative agriculture practises such as no or low disturbance tillage as well as a reduction on nitrogen fertiliser application are likely to be less damaging to the environment and should be considered. While more and more farmers are adopting regenerative practises, it is unclear whether current commercially available cultivars are best suited. Niab has a long history of conducting research in agronomy, exploring ways to reduce tillage and build fertility; practises that are pillars of regenerative agriculture. We are currently involved in a multi-disciplinary research project encompassing agronomy, genetics and molecular plant physiology to assess established varieties as well as novel wheat genotypes under regenerative agriculture conditions.

T18: Beyond the Green Revolution: Novel dwarfing alleles for wheat and barley improvement

Stephen Pearce, Rothamsted Research, stephen.pearce@rothamsted.ac.uk
Keywords: Wheat, Gibberellin, Height, Breeding.

DELLA proteins are critical regulators of plant growth and development. They modulate transcription by interacting with hundreds of transcription factors and are targeted for degradation by the hormone gibberellin (GA). This dynamic system allows plants to respond precisely to developmental signals and environmental cues, making DELLA genes critical targets for crop improvement. During the 'Green Revolution,' breeders exploited semi-dwarf wheat varieties carrying GA-insensitive DELLA alleles to boost yields and lodging resistance. However, these alleles also confer drawbacks, such as reduced nitrogen use efficiency, highlighting the need for alternative strategies that separate desirable dwarfing traits from unwanted pleiotropic effects. We characterised IDD5, a C2H2 zinc-finger transcription factor in wheat, and its barley orthologue SDW3. Both IDD5 and SDW3 physically interact with DELLA proteins and positively regulate stem and leaf expansion. Loss-of-function mutations in these genes produce semi-dwarf plants of similar height to 'Green Revolution' wheat, but importantly, do not block GA-induced DELLA degradation. This suggests that IDD5 and SDW3 maintain a degree of GA responsiveness, potentially mitigating the negative traits associated with conventional 'Green Revolution' alleles. By dissecting the mechanisms by which these transcription factors control cell elongation, we aim to develop more targeted breeding strategies that preserve the lodging resistance of semi-dwarf cereals without compromising other key agronomic traits. Novel cereal dwarfing alleles provide breeders with new tools to enhance yield stability and sustainability.

T19: The fast and the floriferous: Accelerating winter wheat lifecycles using controlled conditions

Indi Lacey, University of Leeds, bs18isl@leeds.ac.uk
Keywords: Speed vernalisation, Winter cereals, Genetics, Flowering, Light, Temperature

Being able to grow crops throughout winter is essential to maintain global food security. While plant research has made major breakthroughs, facilitating improved growth and yield, much of it focuses on spring crops. This is partly because, for winter crops, including winter hexaploid bread wheat, vernalisation time is a major limit on the speed at which new traits can be researched. Therefore, reducing the duration to satisfy vernalisation will have a marked improvement on the potential rate of research. Speed vernalisation is a protocol which can reduce winter plant generation times through altering perceived vernalisation requirement in many winter cereals. We have shown it to reduce plant flowering time by up to 40 days without changing the vernalisation adaptation under field growth conditions. Using modern breeding cultivars, Watkins collection landraces and ancestral lines we have identified a broad range of responses to the speed vernalisation protocol as well as phenotypic indicators of positive and negative responses. With little to no expression of VRN1 or FT1 seen during speed vernalisation, we suspect an alternative pathway is used in the response to overcome the vernalisation block on flowering. Therefore, understanding the genetics of speed vernalisation will not only identify genetic loci to enable verification of whether a genotype can be speed vernalised but also identify potential novel genes with important roles in temperature and photoperiod response, which may be useful for future environmental adaptations. We have conducted qPCR and RNA-seq time courses and a GWAS using a large population of NILs to identify candidate genes. Here I will present our current understanding of the genetic pathway dictating speed vernalisation response and the genetic loci through which one would be able to select for speed vernalisation responsiveness in new breeding cultivars.

T20: Vision for hybrid wheat through key male trait integration: A path to optimized grain set

Deepak Kumar, Leibniz Institute of Plant Genetics and Crop Plant Research, dhathwal222@gmail.com
Keywords: Wheat, Hybrid breeding, Trait development, High-throughput phenotyping, Yield stability
By addressing the growing challenges to wheat (Triticum spp.) production and global food security posed by rapid environmental changes and population growth, hybrid breeding emerges as a viable solution. This study focuses on identifying and characterizing critical phenotypic male traits and integrating them into breeding programs to optimize parent selection for hybridization. We investigated the variability of key male traits—visual anther extrusion speed, pollen shedding capacity, and anther length—among 35 contrasting elite cultivars over two years under controlled greenhouse and field conditions at IPK in Gatersleben, Germany. A comprehensive phenotypic analysis revealed significant correlations between anther extrusion speed, pollen shedding capacity and anther length and their role

in cross-pollination ability and impact on final grain set in real-world hybrid production systems. Cultivars with longer anthers demonstrated faster extrusion speed and greater pollen-shedding capacities, which collectively enhanced cross-pollination efficiency and increased grain set in female tester lines. Interestingly, some genotypes deviated from this pattern by exhibiting compensatory mechanisms, such as lower pollen shedding capacity paired with higher anther extrusion speed or vice versa, underscoring a dynamic interplay among these traits. Moreover, a multiple regression analysis revealed that AES and PSC collectively explained 22–30% of the variation for grain set in the 35 elite lines. Despite the challenges associated with phenotyping these microscopic traits, their high heritability emphasizes their importance for developing proxy traits which are easy to phenotype and can reliably predict the final grain set. Furthermore, this also underscores their value in genetic studies for identifying markers that enable early selection and targeted improvement of superior male lines streamlining the hybrid breeding programs.

T21: BRANCHED SHOOT 1, a key hub gene of whole plant architecture in bread wheat

Zhenru Guo, IPK-Gatersleben, guoz@ipk-gatersleben.de

Keywords: Wheat, Plant architecture, Apical dominance, Aerial branching, Auxin response factor, dominant mutant

Higher plants establish their architecture post-embryonically through initiation and development at the shoot apex with diversity largely arising from the position and number of lateral organs. In grasses, like wheat (*Triticum aestivum L.*) and barley (*Hordeum vulgare L.*), shoot branches (tillers) typically form only at basal stem nodes. Here, we report a dominant wheat mutant allele, Branched shoot 1 (Bsh1), that produces ectopic shoots at aerial nodes, along with delayed flowering, reduced plant height, increased node numbers, a shorter plastochron, and abnormal inflorescence morphology. Using map-based cloning, we identified BSH-A1 as the causal gene encoding an auxin response factor (ARF) transcription factor. The dominant Bsh-A1 allele harbors a single amino acid substitution in the DNA-binding domain, that leads to auxin insensitivity and disruptions in auxin biosynthesis, metabolism and transport. Notably, analogous mutations in homoeologous BSH-B1 and BSH-D1 result in similar phenotypes. Furthermore, we show that the dominant Bsh-A1 allele represses the expression of TaSPL7 and TaSPL14, thereby modulating shoot and spike morphology. Our findings identify BSH1 as a critical regulator of plant architecture through the coordination of auxin homeostasis and global transcriptional repression, providing new insights into the role of ARF transcription factors in shaping wheat plant architecture.

SESSION 8: Phenomics and AI for precision crop improvement

Keynote Speaker: Ji Zhou, NIAB, UK, ji.zhou@niab.com (Online via Teams),

The use of AI-powered analytics to study growth dynamics and their association with key yield components in wheat

Artificial intelligence (AI) and deep learning (DL) are enabling novel biological discoveries in plant and crop research. Complex traits such as seed vigour, flowering and yield formation can now be quantified or modelled by AI-powered solutions, empowering breeders and plant researchers to identify desired traits under complex field conditions in a scalable and effective manner. In the talk, the speaker will start with multi-spectral seed imaging and seed germination analysis to quantify seed quality, seed vigour and their associated genetic mapping in wheat. Then, large-scale drone-based phenotyping will be introduced to verify seed vigour at early establishment in the field, followed by the examination of growth dynamics at key developmental phases (e.g. anthesis) using multi-modal modelling. In particular, the speak will introduce AI-powered analysis of key floral traits developed by his lab for cereal crops together with mapping genetics underlying desired floral characteristics that are key to yield and quality in crop production. At the end of the talk, the speaker will talk about how AI techniques have been developed by his lab to study Fusarium head blight (FHB) disease dynamics during yield formation.

T22: Scaling up drone phenotyping at the John Innes Centre

Martin Vickers, JIC, martin.vickers@jic.ac.uk

Keywords: Drone, Phenomics, Informatics, AI

This presentation outlines the John Innes Centre's (JIC) drone phenotyping initiative, launched in 2023 to comprehensively capture field trial data across its 100-hectare farm. The aim of this initiative is to provide all researchers at the JIC with access to high quality phenotype data from our farm trials. This reduces the barrier to entry for researchers, helps adopt community best practice, highlights opportunities to develop new methods, and introduces new people to the phenomics community. We capture image and point cloud data at both high spatial and temporal resolutions. Adopting the "data product" methodology of NASA/ESA missions, raw drone data undergoes calibration and processing, creating analysis-ready data products that are accessible to all JIC researchers and students. These include multispectral, high-resolution RGB (0.3m/px GSD), LIDAR and thermal. To democratise access, we provide training in open-source tools like QGIS and FieldImageR, empowering users to derive statistical data from their experimental plots. I will be presenting examples where scientists are leveraging drone-derived metrics—such as flowering time, yield prediction, plant height, emergence date, and thermal responses—without the traditional barriers of equipment costs, training time, or technical expertise required to set up individual drone programs. Furthermore, these datasets are being integrated into the JIC farm management database, which combines drone outputs with operational data (e.g., treatment schedules, weather records, harvester measurements) for a holistic overview. By also integrating these datasets with the JIC informatics platform, researchers harness machine learning

expertise, genomic resources, high-performance CPU/GPU computing, and our cloud-based analytics platform DEDAL (Distributed Ecosystem for Drone Analytics in Life-sciences), to build scalable pipelines. This collaborative framework not only accelerates discovery but also fosters open innovation to advance the plant phenomics community.

T23: Drone-based hyperspectral imaging for phenotyping small plot field experiments

Andrew Riche, Rothamsted Research, andrew.riche@rothamsted.ac.uk
Keywords: Hyperspectral imaging, UAV, Field experiment

Hyperspectral imaging offers advantages over simple multispectral approaches: many indices can be calculated simultaneously, new ones developed, whole spectral data can be used rather than specific wavebands, and where data is image based, intra as well as inter plot variation can be accounted for in field experiments. However, the sensor systems are inherently more complex to operate, and workflows more complicated than for multispectral sensors. In this paper we describe the workflow from flight to trait data for a hyperspectral UAV system collecting reflectance at 540 wavebands and 4cm ground resolution. The data have been used to calculate indices, yield prediction models using partial least squares regression, and yield prediction using several different machine learning and deep learning techniques, such as support vector machines and convolutional neural networks. The different methods are then compared to show whether more complicated systems result in better predictions. The dataset was collected from a winter wheat trial at Rothamsted Research, with 20 elite cultivars grown at three levels of nitrogen fertilization. Grain yield was measured at final harvest and was the main trait of interest against which the growth indices were compared, and against which the AI models were trained. Flights were carried out on 16 dates in 2023 between 21st February and 7th July with a total of 360 plots scanned on each date. The data workflow had to take into account small areas of missing data, changing light conditions and occasional anomalies due to sensor errors.

T24: Decoding the regulatory regions of wheat using bioinformatics and machine learning

Lucy Mahony, Earlham Institute, mahony@nbi.ac.uk
Keywords: Genomics, Machine Learning, Regulatory Regions.

Decoding the regulatory regions of wheat using bioinformatics and machine learning." Regulatory regions of genomes control the expression patterns of genes through multiple pre- and post-transcriptional processes. As such, regulatory regions provide a source of genetic variation that can be utilised to alter agronomically important traits in breeding. This is highlighted by the fact that an estimated 50% of causative mutations underlying crop domestication reside in the non-coding genome. However, regulatory regions are relatively uncharacterised, with the current understanding of their function constrained to specific genes. To address this, we have taken two approaches. The first is describing core promoters in wheat. Understanding core promoters is a pragmatic place to start

studying regulatory regions as the smallest region required for transcription and the integration of pretranscription regulatory signals. Using Cap Analysis of Gene Expression (CAGE) data, we mapped transcription start sites (TSSs) across three wheat varieties, refining annotations of core promoters and 5' UTRs. By analysing the distribution of short sequences within these regions, putative regulatory elements have been identified and linked to expression patterns. Due to the polyploidy nature of the wheat genome, alternative TSS usage and promoter elements in homologous genes have also been explored. Secondly, we have leveraged advances in large language models (LLMs) for genomic sequence analysis to predict gene expression from promoter and gene body sequences. AI is well suited to tackling research questions in genomics, as genomes are noisy complex datasets of which we have an ever-growing number of which to train on. In addition to making successful predictions, the models can be examined with the aim of elucidating the underlying biology. We applied pre-trained LLMs to Arabidopsis, soybean, and wheat datasets, successfully predicting gene expression patterns. Additionally, we employed model explanation techniques to identify putative functional regulatory regions, offering insights into the underlying gene regulation.

T25: An efficient alternative system for hybrid wheat production

Nick Bird, KWS, UK, nicholas.bird@kws.com
Keywords: Hybrid, Wheat, Nuclear male sterilty

Wheat is one of the most important global crops accounting for 20% of global calories and protein intake. Production of wheat globally is becoming increasingly challenging in a changing agricultural climate with increased yield and stability a requirement. Hybrid wheat has proven to have higher yields and be more stable under abiotic stressed conditions compared to in-bred wheat. However, the economic viability of hybrid wheat is a challenge due to the self-pollinating nature of the crop. For more than 10 years, KWS, in partnership with the University of Sydney, have been working on the Blue Aleurone (BLA) hybrid wheat system, a nuclear encoded male sterility system based on the Probus MS1 deletion. The system incorporates a monosomic addition chromosome carrying a blue aleurone phenotypic marker on the long arm and a fertility restorer on the short arm. When blue seed from the addition line are planted, the male-fertile plant will self-pollinate and generate normal and blue coloured seed in the ratio ranging from 1:1 to 3:1, thus maintaining the system as well as producing normal coloured, male-sterile seed for commercial hybrid seed production. During meiosis, the monosomic addition chromosome occasionally breaks resulting in sterile blue seeds or fertile normal colour seed which impacts hybrid seed production and system maintenance. To eliminate this issue, we worked with multiple techniques to rearrange the addition chromosome to reduce the rate and impact of breakage. Recently, a new version was identified, reducing the problems associated with breakage, making this improved version of the BLA hybrid system commercially viable. An update on our progress will be presented, demonstrating that the improved BLA system will provide a route to a productive, profitable and sustainable global wheat crop.

SESSION 9: ECR New Lecture Rank Prize

Rank Prize ECR New Lecture: Jim Fouracre, University of Bristol, jim.fouracre@bristol.ac.uk

Harnessing SPL Trascription factors for real yield increases in false flax

Work in my lab uses the highly conserved genetic network consisting of the microRNA miR156 and its targets in the *SPL* family of transcription factors to investigate the regulation of developmental timing in plants. High levels of miR156 maintains plants in a juvenile phase whereas increased *SPL* activity promotes a transition to adult development. Depending on the species, the transition between juvenile and adult phases of vegetative development is associated with dramatic changes to multiple traits, including agriculturally important ones such as branching, flowering time, leaf morphology, photosynthetic capacity and disease resistance. The miR156-*SPL* network is therefore an outstanding candidate for genetic engineering and is already a major focus for crop improvement in species as diverse as rice, wheat and alfalfa. Here, I will describe our preliminary work investigating whether modified *SPL* activity can lead to improved yields in the emerging brassica oilseed crop *Camelina sativa.*

MECEA Awardees

MECEA Winner 1-PhD, Katie Long, JIC, UK longk@nbi.ac.uk

T27: Mapping the Wheat Inflorescence with Spatial Transcriptomics

Keywords: Spatial transcriptomics, Developmental biology

In wheat (Triticum aestivum), the lanceolate-shaped inflorescence (spike) is defined by rudimentary spikelets at the base which initiate first but subsequently lag in development compared with central spikelets. While previous studies identified gene expression differences between central and basal inflorescence sections, the spatio-temporal dynamics and gradients along the apical-basal axis remain poorly resolved due to bulk tissue-level techniques. Using spatial transcriptomics, we profiled 200 genes across four stages of wheat inflorescence development to cellular resolution. Cell segmentation and unsupervised clustering identified 18 expression domains and their enriched genes, revealing dynamic spatio-temporal organisation along the apical-basal axis of the inflorescence. Along this axis, we uncovered distinct and spatially coordinated gene expression gradients patterning meristems prior to the visible delay in basal spikelet development. This study demonstrates the potential for spatial transcriptomics time-series to advance plant developmental biology.

MECEA Winner 2-PhD, Isabel Faci-Gomez, JIC, UK, Isabel.Faci-Gomez@jic.ac.uk

T28: Temperature and photoperiod interaction: Releasing aerial branching in wheat

Keywords: Branching, temperature, photoperiod, meristems

Across the world, wheat varieties are sown which are intimately adapted to their environment and growing season. Climate change poses a threat to wheat productivity by modifying the duration of the growing season, determined by the coordination of temperature and photoperiod. While climate change will affect temperatures, photoperiod cycles will remain constant. My aim is to understand the mechanisms governing temperature and photoperiod integration in wheat and elucidate how they impact the genetic pathways that coordinate shoot architecture. Shoot architecture is the result of synchronised adjustments in the development and determinacy of shoot meristems and branching patterns. While branching is a conserved process in plants, the outcomes of these branches differ, even in closely related species. For example, Brachypodium and maize have aerial branching, whereas wheat and barley do not. This means that in wheat, each tiller yields a single inflorescence/spike (compared to maize which has ears/cobs on its branches). We recently observed, unexpectedly, that a wheat landrace showed aerial branching under UK natural daylength but high temperature conditions. This suggests that the axillary meristems that would typically be dormant were derepressed under these conditions. To discover the mechanism underlying this phenomenon, we are using genetic approaches to identify the causal gene(s) and have performed RNA-sequencing analyses on derepressed and dormant meristems of this landrace. We are combining these approaches with spatial analyses, using massively multiplexed in-situ hybridisation methods in the aerial branching meristems. We aim to identify candidate genes which will be functionally validated through genome editing. With this research, we hope to contribute to our mechanistic understanding of the genetic and phenotypic responses of wheat under future climate conditions. Ultimately, we aim to deploy this knowledge to future proof wheat cultivars to a changing environment.

POSTER ABSTRACTS

P1: Crop Diversification – Exciting new cereals for the UK.

L. Salazar-Licea[1]; A. Aboagye[1]; C. Kirk[2], L. Williams[2]; R. Bhosale[1]; J. Brameld[2]; S. Mayes[13]; G. Mendiondo[1,*]

[1]Division of Plant and Crop Sciences, University of Nottingham

[2]Division of Food, Nutrition & Dietetics, University of Nottingham

[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India

*guillermina.mendiondo@nottingham.ac.uk

Keywords: Foxtail millet, Seed quality, Agronomic traits, Crop diversity

The UK food production system faces significant challenges, including climate change, a narrow crop diversity, and a reliance on a few major crops. Diversifying crop production is crucial for enhancing food security, reducing emissions, and adapting to changing environmental conditions. This study investigates the potential of foxtail millet (Setaria italica), a C4 grass with high drought and heat tolerance, as a novel and climate-resilient crop for the UK. Over the past three years, we have evaluated lines from an association genetics panel under UK field conditions. Our research has revealed significant phenotypic variation within the panel for key agronomic traits, including flowering time, plant height, and seed quality (protein, fat, and aroma). These findings demonstrate the potential for selecting genotypes well-suited to the UK environment. Furthermore, genome-wide association studies (GWAS) are being conducted to identify the genetic regions associated with these traits. Integrating phenotypic and genomic data will enable us to accelerate the development of high-yielding foxtail millet varieties adapted to UK conditions. The combination of the data presented here will allow for the best candidate selection for breeding varieties that will have the best yield under UK field conditions.

P2: GR-NBRI Operating FAIRly with Diverse Germplasm Resources

Simon Orford[1,*], Liz Sayers[1], Workie Zegeye[1,2], Ajay Silveru[1], Eleni Vikeli[1], Smitha Chundakkad[1], Alex Howard[1], Hang Gao[1,3], Pauline Stephenson[1], Richard Horler[1] and Noam Chayut[1]

[1].Germplasm Resources Unit, John Innes Centre, Norwich, UK;

[2].Department of Agricultural Biotechnology, University of Gondar, Ethiopia.

[3].University of East Anglia, Norwich UK

* simon.orford@jic.ac.uk

Keywords: Germplasm, Diversity, Genebank, Conservation, Genetic Resources

The UKRI-BBSRC Germplasm Resources National Bioscience Research Infrastructure (GR-NBRI) serves as the UK's public genebank for small grain cereals and legumes, with a focus on promoting Findable, Accessible, Interoperable, and Reproducible (FAIR) germplasm and data resources to drive modern crop science and breeding. The >50,000 accessions are highly used. During the previously reported 5 years (2018-2023), the GR-NBRI distributed >27,000 seed packets in support of >1700

project in 49 countries. Here we report on how the conserved diversity spans from natural crop wild relatives (CWR) to traditional landraces collected globally, and further to mapping and mutant populations and ultimately to modern cultivars. Links to in-house generated background data adds value to the material including phenotyping, genotyping and genomic data. To exemplify how our FAIR principles cause impact for current crop science and pre-breeding projects, we will follow a piece of T.urartu wheat gene-pool chromatin, sampled before the 1930s by the Reading University Society Expeditions and conserved by the GR-NBRI ancestral teams. The near 100 years of conservation activity allowed its utilisation by the Nottingham University CWR team of experts, working as part of the UKRI-BBSRC cross institute Designing Future Wheat (DFW) programme (2017-2022). The chromatin segment was introgressed into Paragon (Grewal et al., 2021) and deposited back to the GR-NBRI custodianship under the centralised Academic Tool-Kit (ATK) collection. The material is now forming part of the Pre-Breeding work conducted by the Horizon-Europe Protect and Promote CWR project, ProWild. ProWild field trials in INRAE, France and JIC, UK will evaluate (2025-2028) the beneficial potential of the T.urartu sampled chromatin, for enhancing wheat disease resistance, improving yields and grain nutritional quality. All the germplasm is available globally under the terms of the International Treaty for Plant Genetic Resources for Food and Agriculture, ensuring fair benefit sharing between germplasm donors, conservationists and users.

Ref: Grewal, S., Guwela, V., Newell, C., Yang, C. Y., Ashling, S., Scholefield, D., Hubbart-Edwards, S., Burridge, A., Stride, A., King, I. P., & King, J. (2021). Generation of doubled Haploid wheat-Triticum urartu introgression lines and their characterisation using chromosome-specific KASP markers. Frontiers in Plant Science, 12, 643636. www.seedstor.ac.uk JIC.geneticresources@jic.ac.uk Key words: Germplasm, Genebank, Diversity, Conservation, Genetic Resources.

P3: Detection of introgression from wild relative species to common wheat genome

Ding Li, Alexandra M. Przewieslik-Allen, University of Bristol, ux19101@bristol.ac.uk
Keywords: Genomics, Wheat, Introgression

Bread wheat is one of the world's most important crops which has complicated evolutionary history of hybridization and polyploidization. The wheat genome is considered to have widely gene flow with its relative species in the Aegilops-Triticum complex. However, few studies have shown the common wheat genome's interaction with its relatives in genomic scale. By skimmed-sequencing genome of 40 species of wheat relatives and using IBSpy pipeline for k-mer based identification, we detected segments of wheat genome which showed high identity of 50kb length bins. Theses bins illustrated either introgression between bread wheat and its relatives or the shared ancestors' phylogeny of the Aegilops-Triticum complex. By comparing the wild relatives datasets with the 11 available wheat reference genome, we reported the large scale of introgression and high identity of wheat genome and its relatives.

P4: Wheat Wild Relative Introgression Lines as a Source of BYDV Resistance

Katie Hawkins, University of Nottingham, katie.hawkins@nottingham.ac.uk
Keywords: Genetics, Genetic Variation, Plant Pathology, Wheat

Genetic Variation Bread wheat (*Triticum aestivum*) has undergone genetic bottlenecks that have reduced its genetic diversity, first when it was domesticated some 10,000 years ago and more recently through selective breeding for higher yield at the expense of other traits. Genetic diversity can be introduced from wild relatives of wheat such as Thinopyrum intermedium and *Th. elongatum*. Through crossing, introgression lines with segments of the wild relative in a wheat background can be produced. The location of these introgressions can be determined using SNP markers, GISH, and skim sequencing. Then, the material can be screened for desirable characteristics such as resistance to barley yellow dwarf virus (BYDV), thus indicating that the new desirable characteristic has been introduced as a result of the wild relative segment. I have carried out GISH on wheat x Th. intermedium lines, and both GISH and skim-sequencing on wheat x *Th. elongatum* lines to locate introgressions and have begun screening these species for BYDV resistance.

P5: Characterising rare and absent sequences in plant genomes

Jack Book, Amanda Clare, Wayne Aubrey.
Department of Computer Science, Aberystwyth University, jmb28@aber.ac.uk
Keywords: Nullomers, CpG islands, Plant genomics.

Absent or rare sequences in plant genomes are of interest in plant breeding because their absence may indicate otherwise harmful sequence. The extraction and characterisation of rare sequences enables us to better understand their properties and potential. Recent studies of nullomer sequences conducted using human genomes indicate that nullomers are particularly enriched for CpG dinucleotides and that methylated cytosines drive nullomer emergence. However, the mosaic methylation patterns of plants are known to be different to that of vertebrates and require further study. We began by examining 69 Arabdopsis thaliana genome assemblies to investigate the nullomers and rare sequences that are present and absent. We find that, while CpG sites are a strong factor influencing core, absent and rare sequences, the distribution of accessory nullomers is very variable across the genomes. Where rare sequences are present in a genome, we find that nearly 70% of these sequences are located between genes, and some sequences are located within the same gene when appearing only once per genome. The polyploidy nature of cereal crops and grasses provide additional bioinformatic complexity for nullomer analysis, as a nullomer may be absent from a single set of chomosomes but present in others. We compare the absent and rare sequences from the A. thaliana pan-genome to those in the hexaploid oat genome and discuss the contribution of CpG islands and methylation to rare and absent sequence in this crop species.

P6. Exploration of NIAB's synthetic wheat as a new source of genetic resistance for effective control of Septoria tritici blotch disease

Anisa Blower, NIAB/ University of Nottingham, anisa.blower@niab.com
Keywords: Septoria tritici blotch, Synthetic hexaploid wheat, Wheat disease resistance, Fine mapping

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 and derived select Nested Association Mapping and Chromosome Segment Substitution Line populations have been screened for resistance to Z. tritici both under controlled growth room conditions using recent UK field isolates of the fungus and in the field with natural infection. To date our results have revealed that primary SHWs are highly resistant to infection, both under artificial conditions and in the field. Further investigation of three SHW-derived mapping populations has identified several resistance loci, some of which appear to confer broad-spectrum resistance. Ongoing bulk segregant analysis is being used to refine these findings by narrowing down genomic regions associated with resistance, supporting fine-mapping efforts. This will provide a novel genetic armoury in the breeding of multi-isolate resistant wheat for sustainable STB management.

P7. Improving Annotation, Access and Comparison of Nutritional Composition Data for Underutilised Crops.

Aboagye A.[1], Raubach S[2], Salazar-Licea L.[1], Mayes S.[1,3,5,] Shaw P.[2] , Mendiondo G.[1] and King GJ,[3,4]
[1]School of Biosciences, University of Nottingham, Sutton Bonington, Leicestershire, LE12 5RD,
[2]Department of Information and Computational Sciences, The James Hutton Institute, Invergowrie, Dundee, Scotland DD2 5DA
[3]Crops For the Future UK, Chelmsford, Essex CM2 7PJ, England, UK 1
[4]Recombics, Alstonville, NSW 2477, Australia
[5]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, Telangana, 502324, India
Agnes.Aboagye@nottingham.ac.uk
Keywords: ontology, data integration, semantic web, database, controlled vocabulary, data comparison, FAIR data

Currently, there are limited dataset management systems available that provide ready query, visualisation, and comparison of nutritional data for underutilised crops. This is because the available data sources are syntactically and semantically heterogenous, posing significant interoperability and integration challenges. Therefore, in this work, diverse publicly available nutritional datasets were

assembled and managed within a consistent framework to increase their accessibility. The differences and similarities within the datasets were identified and then ontologies and semantic web technologies used for effective integration of these datasets. Overall, we are aiming to enhance trait comparison of underutilised crops (UCs) alongside major crops. Our main approach is to increase the Findability, Accessibility, Interoperability, and Reusability (FAIRness) of plant trait datasets by annotating them with appropriate ontology terms and classes from the plant science and nutrition domains. An ontology-based data access (ODBA) interface was developed to access the pooled relational dataset over a virtual knowledge graph. The latter represents the datasets enriched with the semantics of a global ontology constructed as a unified view of the nutritional datasets. The global ontology is a task-specific ontology to facilitate the data integration task. This semantic data integration allows the construction of joint queries, making the data accessible through a SPARQL endpoint. Overall, we expect the benefits of semantic data technology will facilitate collaborative research and contribute to the adoption and utilisation of underutilised crops.

P8: Discovering transcriptional regulators of drought-induced senescence in wheat

Miles Curl, John Innes Centre, miles.curl@jic.ac.uk
Keywords: Drought, Wheat, Senescence, Abiotic-stress, Yield, Sustainability

With the last 10 years officially the warmest decade on record, the world is facing a greater threat to crop production from abiotic stresses. Elevated temperatures are highly linked to decreases in soil water availability, often leading to agricultural drought conditions. Drought threatens wheat production and development by accelerating precocious senescence, ultimately impacting yield. Therefore, the aim of this research is to identify novel genetic regulators of senescence in drought conditions to ultimately breed more drought resilient wheat varieties. We have utilised transcriptomics and Gene Regulatory Network (GRN) modelling from controlled time-series drought simulation in wild-type Cadenza to identify transcriptional regulators that regulate the process of drought-induced senescence. OutPredict, a machine-learning, random forest-based computational approach, provided a quantitative value to the importance of transcription factors potentially acting on a given target gene. Transcription factors with greatest importance values were then ranked based on their degree-centrality, identifying the number of edges, or direct connections, to target genes. A subset of these ranked transcription factors, that were shown to be significantly upregulated in senescence and in known drought tolerant wheat lines, were explored through genotyping of elite wheat breeding germplasm. This identified a range of haplotypes associated with lines grown in drought-prone geographical regions. Through TILLING mutant characterisation, we hope to confirm the role of these transcription factors under drought stress and to validate the use GRNs in identification of key genes for abiotic stress resilience.

P9: Effects of heat stress on reproductive traits and gene interactions in barley

Aziza zerrouk, Experimental Station Aula Dei - The Spanish Research Council (CSIC), azerrouk@eead.csic.es

Keywords: Barley, Heat, Near-isogenic lines, HvVRN1, HvCEN

Heat stress is a critical abiotic factor that negatively affects barley yield and productivity, especially when it occurs during key reproductive stages. Understanding this threat and identifying genetic sources of resilience is essential. Here, we investigated the interactive effects of key flowering time genes (HvCEN and VrnH1) on barley reproductive traits under heat stress, as well as their influence on inflorescence development under controlled conditions. To evaluate how heat stress affects reproductive traits at flowering and maturity stages, a field experiment was conducted using four contrasting near-isogenic lines with different allele combinations of HvCEN and VrnH1. Heat stress was induced using portable tents with transparent polyethylene films, increasing the ambient temperature by ~6°C at either pre-flowering or seven days post-flowering. Control plots remained under the same environmental conditions without tents. Key agronomic traits, including grain number, grain size, spikelet number, spike number per plant, spike fertility, and thousand-kernel weight, were recorded. Exposure to heat stress at pre- and post-anthesis resulted in significant yield penalties, mainly due to reduced grain number and grain weight, two critical components of cereal crop yield. Results confirmed an interaction between HvCEN and VrnH1, particularly affecting thousand-kernel weight, with heat stress at pre- and post-anthesis also slightly impacting seed set. A differential effect of heat stress on VrnH1 was also observed, indicating that this gene responds differently depending on the genetic background and the environmental conditions of the plants. These findings will provide additional insights into how VrnH1 and HvCEN influence barley development under varying environmental conditions.

P10: Use of Thinopyrum species to improve salt tolerance in bread wheat

Jack Walker[1,2,4,*,] Stella Edwards[2], Caiyun Yang[2], Duncan Schofield[2], Stephen Ashling[2], Jonathon Atkinson[1,3], Malcolm Hawkesford[4], Darren Wells[1,3], Ian King[2], Julie King[2], Surbhi Grewal[2].

[1]Future Food Beacon, University of Nottingham, Sutton Bonington Campus, Loughborough, United Kingdom

[2]Nottingham BBSRC Wheat Research Centre, School of Biosciences, University of Nottingham, Sutton Bonington Campus, Loughborough, United Kingdom

[3]School of Biosciences, University of Nottingham, Sutton Bonington Campus, Loughborough, United Kingdom 4Rothamsted Research, West Common, Harpenden, United Kingdom

Jack.Walker2@nottingham.ac.uk, Surbhi.Grewal@nottingham.ac.uk

Keywords: Salt-tolerant, Wild-relative, Introgression, Wheat

Soil salinization negatively effects plant growth. Twenty percent of cultivated land and thirty-three percent of irrigated land are salt affected and degraded. To increase food security, an increase in food production on saline soils is particularly important. Bread wheat is slightly salt tolerant, however several of its wild relatives are highly salt tolerant, particularly Thinopyrum species. In this study, a high

throughput hydroponic screening system was developed to evaluate salt tolerance of wheat and its wild relatives during the vegetative growth stage. Plants were subjected to varying levels of salt stress for three weeks, after which shoot dry weight, tiller number and leaf ion content were measured. Under severe salt stress, Thinopyrum elongatum and its linkage group 1 introgression lines outperformed wheat in shoot dry weight while maintaining low sodium content in leaves. Additionally, a separate experiment assessed salt effect on root growth during germination, revealing superior performance of linkage group 1 introgression lines compared to their wheat parent. These screening systems will be applied to evaluate salt tolerance in Thinopyrum ponticum and elongatum introgression lines developed at the Wheat Research Centre (WRC), with a focus on linkage group 1, which have shown enhanced salt stress tolerance.

P11: Investigating Rht GA3-sensitive genes to enhance drought tolerance in durum wheat

Giuseppina Angione, Concetta Lotti, Salvatore Esposito, Pasquale De Vita, Philippa Borrill
University of Foggia, giuseppina.angione@unifg.it
Keywords: Wheat Green Revolution, Coleoptile length, Gibberellic acid-insensitive genes, QTL mapping, Transcriptome analysis

The discovery of gibberellic acid-insensitive dwarfing genes (e.g., Rht-B1b and Rht-D1b) during the Wheat Green Revolution reform the wheat ideotype. The reduction in plant height and the pleiotropic effect of the Rht genes on spike fertility significantly increased grain yield. However, GA3-insensitive genes negatively affect coleoptile length and early seedling vigor, traits that are favorable for improving grain yield in water-limited environments. In contrast, GA3-sensitive dwarfing genes reduce plant height without compromising coleoptile length, allowing deeper sowing and better crop establishment, especially in arid and semi-arid conditions. In this study, a F2 population of durum wheat (Triticum durum Desf.), obtained by crossing Castelporziano (GA3-sensitive dwarfing genes) and Atoudur (GA3-insensitive dwarfing genes), was grown under controlled conditions to map QTL and identify candidate genes for coleoptile and shoot length. Based on phenotypic distributions, two contrasting bulks (CS: short and CL: long) were created and sequenced using an exome capture platform. Using the QTL-seq approach, genome regions associated with coleoptile and shoot length were identified and revealed approximately 15,000 genes within these regions. To strengthen candidate gene identification, transcriptome analysis allowed to identify genes differentially expressed between the parents. Of the 15,000 genes associated with QTLs, 192 were differentially expressed genes (DEGs). Moreover, Gene Ontology analysis revealed that many of the upregulated genes in Castelporziano were associated with key processes such as cell growth, cell cycle regulation, and transcriptional control, which are essential for cellular expansion and division, suggesting a control of the coleoptile length in Castelporziano compared to Atoudur. To clarify the role of the selected candidate genes a screening of mutants in the Kronos TILLING population will be performed. Obtained results could be useful to undertake plan breeding plan to improve wheat yield under various conditions.

P12: Manipulating targeted proteolysis to improve barley resilience: characterising novel environmental stress regulators.

Alasimi S., Nghiem B., Moroyoqui Parra M., Derecka K., Foulkes J. and Mendiondo G
Division of Plant and Crop Science, University of Nottingham, Sutton Bonington, Nottinghamshire, UK.
guillermina.mendiondo@nottingham.ac.uk
Keywords: PRT6 N-Degron pathway , barley, roots , root cortical senescence

Impact of changing climatic conditions on global crop production. We need to increase the population to feed the world while reducing the reliance on fertiliser application. One solution is to develop varieties that have improved soil resource capture and thus improved yield under suboptimal conditions. Crop yields are globally affected by abiotic stresses such as drought, salinity and waterlogging. Ubiquitin-mediated proteolysis via the Plant Cysteine Oxidase (PCO) branch of the PRT6 N-Degron pathway controls the plant response by regulating the turnover of proteins involved in sensing and/or conferring tolerance to abiotic stresses. The importance of the root cortical senescence (RCS) trait towards this especially improving yield while reducing the metabolic burden of maintaining cortical tissues under abiotic stresses. RCS is a very important breeding target for edaphic stress tolerance. The fundamental understanding of genes and mechanisms controlling this process is missing. Interestingly, we recently observed that barley mutants in the PRT6 N-degron pathway have increased RCS. In addition, we are evaluating the impact of the heat stress responses in barley roots. This project focuses on newly discovered and uncharacterized N-Degron pathway substrates to shed light on their specific downstream stress regulation functions, offering new opportunities for stress resilience research. We identified two such substrates, BERF1 and RAF; in this project, we are studying their specific roles as key regulators of environmental stress. A recent paper showed RAF and BERF1 were upregulated in a transcriptional analysis, which indicated the important role of these genes in the development of root cortical senescence. This project, therefore, combines fundamental research into understanding the drivers for abiotic stress resilience, with application to generate resilient barley for deployment. The barley N-Degron pathway mutants are under field characterization and resilience evaluation.

P13: Investigating the effects of disrupting wheat yellow rust disease susceptibility factors

Sarah L. Bailey, John Innes Centre, baileys@nbi.ac.uk
Keywords: Wheat, Yellow rust, Pathology, Breeding, Phenotyping

Wheat yellow rust, caused by the fungus Puccinia striiformis f. sp. tritici (Pst), poses a constant threat to global wheat production. One way to tackle this disease is to disrupt the function of wheat susceptibility factors that are essential for supporting Pst disease progression. However, these susceptibility factors are often components of important plant pathways, and their disruption could have pleiotropic and detrimental effects. The aim of this study is to evaluate the effect on plant development of disrupting three previously identified Pst susceptibility factors (TaBCAT1 [1], TaCSP41a [2] and TaICL [3]). In each case, the disruption of a single homoeolog was sufficient to reduce Pst infection, reducing

the chance of a detrimental effect as the gene function of the remaining homoeologs is preserved whilst still reducing Pst susceptibility. To evaluate impact on growth and development, CRISPR-Cas9 gene edited lines of TaBCAT1, TaCSP41a and TaICL were developed in multiple wheat varieties. Preliminary growth and development analysis of TaBCAT1 mutants in glasshouse conditions suggests performance comparable to wild type plants, evidencing the potential of this gene disruption for disease resistance breeding. In parallel, we have also begun combining these three single homoeolog disruptions into a single wheat line, which will be instrumental for evaluating the potential of this approach in resistance breeding. Double homozygous combined disruption mutants have now been generated and will be assessed for susceptibility to Pst. Overall, these findings could contribute to the search for durable disease resistance against yellow rust, addressing challenges in global wheat cultivation.

[1] Corredor-Moreno et al., 2021, Plant Cell
[2] Corredor-Moreno et al., 2022, Commun. Biol.
[3] Ibe et al., 2024, TPJ.

P14: Thigmomorphogenic responses: crops phenotypic and structural responses to mechanical stimulation

Annalene Hansen, Maurice Bosch
Aberystwyth University IBERS, anh98@aber.ac.uk
Keywords: Cereals, Wheat, Mechanical stimulation, Thigmomorphogenesis, Biomechanics, Cell wall

Mechanical stimulation, such as rain or wind, induces responses in plants collectively known as thigmomorphogenesis, including dwarfing, changes in cell wall composition and stem anatomical features. Japanese farmers have utilised mechanical stimulation for centuries, a process called mugifúmi[1] – treading on wheat and barley seedlings to increase crop yield and resilie nce, but improper application can lead to adverse effects. While most thigmomorphogenic studies focus on dicots, monocot grasses like cereals are vital for global food security. Grasses exhibit some unique responses, such as increased tiller number in wheat, in an age- and dose- responsive way[2], and monocot-unique transcriptional regulation is beginning to be illuminated[3]. Similarities to dicots include increased stem structural rigidity, which may be in part due to increases in cell wall thickness and lignin content[2,4,5] . In winter wheat, higher chlorophyll content has been observed following mechanical treatment, similar to dicots[6,7], while in spring wheat, grain colour changes were noted in one of the two varieties tested. Grain number and weight decreased in Brachypodium and winter wheat varieties, but not in spring varieties. These findings suggest species and varietal differences in thigmomorphogenic responses, though further research is needed to establish general patterns. Mechanical stimulation may offer an underexplored strategy to increase crop resilience to environmental stresses by activating broad, non-specific defense pathways, as reported in dicots[8–10]. However, the underlying mechanisms in monocot grasses remain poorly understood. Can mechanical stimulation be harnessed to improve agricultural practices for sustainable crop production?

P15: Metabolite signatures of drought stress at seedling stage in two spring wheat (*Triticum aestivum*) cultivars over a diurnal cycle.

Rachel Dye, Aberystwyth University IBERS, rad35@aber.ac.uk
Keywords: Circadian, Drought, Diurnal, Metabolites, Wheat

It is well established that drought will be a limiting factor upon grain production in the changing climate. However, little is known about the effects that water scarcity will have on wheat over a diurnal period. Therefore, determining the cultivar specific impact of drought is important for selecting the superior genotypes. An ideal environment in early growth stages is important in ensuring a successful crop is achieved. We hypothesised that cultivar-specific differences, therefore, would be reflected in metabolic differences that reflect the underlying biochemical pathways involved the response to drought over a 48 hour period. As a test case we investigated the impact of severe drought in three spring wheats (Paragon (drought sensitive), Gladius (drought tolerant), and 810 (an Afghan variety)) during seedling stage under controlled growth conditions.

Key differences were found between metabolite profiles between treatments and genotypes. Gladius appeared to maintain rhythmicity under drought over its control. Paragon and 810, on the other hand, decreased in the number of rhythmic compounds under drought, both losing rhythmicity in nearly half of their compounds. Heatmap results of the most significantly active metabolites also revealed that Gladius matched the activity of its controls for key metabolites whereas Paragon and 810 both showed larger variance. 810 showing the largest difference across the timeframe between control and droughted samples. This suggests that metabolic profiling could be an easily scalable method for selecting robust germplasms based on the response at different times of day.

P16. Impact of two different water deficits on physiological traits of the flag leaf and the ear and grain yield of three wheat varieties grown under a climate change scenario.

Ismael Gutiérrez-Fernández, Institute of Natural Resources and Agrobiology of Salamanca (IRNASA-CSIC), ismael.gutierrez@irnasa.csic.es
Keywords: Climate change, Ear, Flag leaf, Water deficit, Wheat, Grain yield

The improvement of wheat adaptation to future environments and dryer soils will be crucial for ensuring global food security. The objective of this study was to evaluate the physiological and biochemical responses of the wheat flag leaf and ear at the grain filling stage when wheat production is more affected by water scarcity. Two wheat bread (Gazul and 41-CIMMYT) and one durum (Regallo) varieties were grown at 900 ppm CO2 and temperatures 4 oC higher than the current ones in Salamanca region (Spain). Water treatments included: i) 100% field capacity (control); ii) (long) water deficit (65% FC) applied after the development of the fourth leaf (LWD), and iii) (terminal) water deficit (50% FC) imposed at the booting stage (TWD). Physiological and biochemical traits were measured in the wheat flag leaf and ear seven days after anthesis, while plant growth and grain yield were evaluated at maturity. The

results showed that Regallo, the least productive variety, decreased the overall biomass of the plant under LWD, whereas TWD reduced the leaf photosynthesis and the ear weight, resulting in lower grain weight. By contrast, 41-CIMMYT, the variety with the highest yield, showed higher photosynthesis, flavonoids and proline content in the leaves, and fructans and starch in the ears, but lower NBI regardless of the water deficit applied. In Gazul, the foliar traits were not significantly affected by water deficits, whereas glucose and fructose content in the ear increased under both water deficits. TWD also increased sucrose and starch content in the ear. Despite the overall reduction in grain yield and grain number induced by the water deficits, this study highlights that these effects of water stress clearly depend on the variety, identifying relevant traits associated with variation in wheat production.

P17. Elucidating the signalling network linking biotic stress and free-asparagine accumulation in wheat

Navneet Kaur, Rothamsted Research, Harpenden, AL5 2JQ, UK, navneet.kaur@rothamsted.ac.uk
Keywords: Asparagine, Fusarium, Wheat

Asparagine (Asn), in its free form, plays a vital role in nitrogen storage and transport in plants. However, it also serves as a precursor to acrylamide, a processing contaminant classified as a Group 2A carcinogen. Asn levels increase significantly during seed germination and in response to various abiotic and biotic stresses. In wheat, fusarium head blight (FHB), caused by Fusarium graminearum (Fg), not only reduces crop yield but also contaminates grains with harmful mycotoxins like deoxynivalenol (DON). DON exposure in wheat has been shown to elevate levels of free Asn, glutamine (Gln), and aspartate (Asp). In plants, sucrose non-fermenting 1-related protein kinase 1 (SnRK1) integrates metabolic and stress signalling, aiding stress responses and improving crop performance. During FHB infection, Fusarium secretes the effector protein OSP24, which binds to SnRK1 and accelerates its degradation. On the other hand, a wheat orphan protein TaFROG, competes with OSP24 for SnRK1 binding, thereby protecting SnRK1 from degradation. These are important findings, but the downstream signalling pathways, including proteins and transcription factors that contribute to Asn accumulation during Fg infection, remain poorly understood. This study aims to elucidate the molecular network underlying Asn accumulation in wheat during Fg infection. To achieve this, a combination of F. graminearum mutants, RNA sequencing (RNA-seq), and proximity labelling has been employed. Key components of the identified signalling hub will be validated by virus-induced gene silencing (VIGS). The findings from this study will provide insights into the regulatory mechanisms of Asn accumulation and support the development of crop improvement strategies to enhance wheat resistance to Fg and DON.

P18: Allele Mining in the Watkins Landrace Collection of Durum Wheat for Improved Grain Nutritional Quality

Ajay Siluveru, John Innes Centre, Ajay.Siluveru@jic.ac.uk
Keywords: Wheat landraces, GWAS, Biofortification, A.E Watkins.

The UKRI-BBSRC Germplasm Resources National Bioscience Research Infrastructure (GR-NBRI) serves as the UK's public genebank for small grain cereals, with a focus on promoting Findable, Accessible, Interoperable, and Reproducible (FAIR) germplasm and data resources to drive modern crop science and breeding. Durum wheat (*Triticum turgidum* L. ssp. durum) is an important global staple crop with the potential to diversify UK arable crop rotation and as an alternative source of allelic variation for bread wheat improvement. Enhancing grain nutritional quality (biofortification) without sacrificing yield requires identifying new allelic variations. We, therefore, evaluated macro/ micronutrients (e.g., protein, starch, fibre, Fe, Zn) and their trade-offs with yield components in an untapped 356-accessible wheat landrace resource collected by A.E Watkins from 23 countries. The landraces presented a broad phenotypic diversity range: Thousand Grain Weight (TGW) 33 – 70g, Grain Zinc Content (GZC) 22 - 50ppm, Grain Protein Content (GPC) 11 – 22%, and Grain Carotenoids Content (GCC) 0.4 – 2.7ug/g. Whole genome re-sequencing (short reads, Illumina x>20) of the resource allowed us to conduct a high-resolution genome-wide association study (GWAS) to uncover genomic regions regulating the phenotypic variation. We will present the most promising GWAS peak associations for the measured traits. Multi-environment field trials have been conducted to strengthen these findings further, and grain phenotyping efforts for GWAS are ongoing. Future work will focus on candidate gene validation using a pre-screened library (n=828) of durum wheat mutants from the Kronos TILLING collection evaluated for macro/ micronutrients and yield components by assessing the accumulative effect of each mutated gene found under a GWAS peak in comparison to the Kronos (WT) control and the TILLING population performance average. This study highlights the breadth of diversity in the A.E Watkins durum wheat landrace pre-dating the green revolution global genetic bottleneck. It paves a path for its utilisation in breeding.

P19: Flour Power! Enhancing Iron and Zinc Bioaccessibility in Biofortified Wheat

Kristel June D. Sartagoda, John Innes Centre, kristel-june.sartagoda@jic.ac.uk
Keywords: Wheat, Iron, Iron-Deficiency Anemia, Biofortification

Wheat has long been fundamental to global food and nutritional security, providing approximately 20% of human dietary calories worldwide. Despite its importance, wheat products generally lack sufficient bioavailable minerals like iron and zinc, leading to deficiencies in populations relying heavily on wheat as a staple, like North India and Pakistan. To combat this, fortifying foods with iron during industrial milling is a common practice around the world and is mandatory in 81 countries, including the UK. However, this approach faces challenges because of the poor bioavailability of fortificants, potential dysbiosis, and sustainability concerns. Biofortification of wheat has emerged as a promising solution.

Over the past decade, the Balk and Uauy groups have developed transgenic wheat overexpressing the wheat TaVIT2-D gene and the rice OsNAS2 gene, which significantly increases zinc levels and redistributes iron to white flour fractions. These new lines are currently in field trials. My research aims to determine if the products of the NAS enzyme can outcompete anti-nutrient phytic acid for mineral binding, potentially enhancing iron bioavailability and absorption in the human gut. The results of this research will help develop strategies for using biofortified wheat in food systems in the UK and globally.

P20: Exploring Genetic Diversity for Enhancing Wheat Nutritional Quality: Insights from the A. E. Watkins Landrace Collection

Petros Sigalas, Rothamsted Research, petros.sigalas@rothamsted.ac.uk
Keywords: Wheat grain, Mineral micronutrients, Nutritional quality, Genetic mapping

Wheat is an important source of mineral micronutrients for human and livestock nutrition. It is well-established that commercial wheat cultivars exhibit low genetic diversity compared to older varieties, including landraces. By exploiting the A. E. Watkins landrace cultivar collection, a historical germplasm collection dating back a century, we aim to identify novel alleles for enhancing the accumulation of essential minerals in wheat grains and provide valuable germplasm for breeding programs. Our approach involves a multilayered exploitation of the genetic diversity in mineral content, through screening the recently sequenced 821 Watkins landraces, along with the development of bi-parental populations for Quantitative Trait Loci (QTL) analysis and Nested Association Mapping (NAM) panels for Genome-Wide Association Studies (GWAS). These populations were grown in successive years in replicated trials at Rothamsted. Traits such as grain and straw yield were recorded along with mineral analysis by ICP-OES. Genetic analysis in three biparental populations, developed from crosses between the spring cultivar Paragon and three selected Watkins landraces, led to the construction of a QTL atlas including 23 strong QTLs for essential minerals in the grain. Additionally, a ZnNAM panel was developed using 25 Watkins founders showing variation in grain Zn concentration and genotyped by a 35K breeders array. GWAS analysis in this panel identified significant markers not only for Zn but also for other essential minerals. In parallel, data from screening the entire population is being subjected to GWAS analysis, which may reveal novel loci involved in these traits. The identification of beneficial alleles and SNP markers establishes a foundation for advancing the nutritional quality of wheat grains. Our findings contribute valuable insights for improving wheat varieties with enhanced nutritional profiles, offering significant implications for sustainable global food systems.

P21: Investigating the oligomerization of PTST1 and GBSS during starch synthesis

Carol Huang, John Innes Centre, carol.huang@jic.ac.uk
Keywords: Starch, Biosynthesis, Amylose, Protein oligomerization, Wheat

Starch is an important carbohydrate polymer for both plant metabolism and human consumption, and it accumulates in large amounts in cereal crops, such as maize, wheat, and rice. Starch naturally forms

semi-crystalline granules consisting of the polymers, amylose and amylopectin. However, the amylose to amylopectin ratio varies hugely across different species of cereals, as well as within species, where some varieties have been specifically bred for their low amylose content. For example, varieties that produce amylose-free (waxy) starch are of great industrial interest for its stickiness and high freeze-thaw stability. GBSS and PTST1 are the two main proteins involved in amylose synthesis, and they interact with each other. However, we recently discovered that wheat BGC1, a paralog of PTST1 that is involved in starch granule initiation, can form dimers. Here, we used a range of experiments including co-IP, protein crosslinking, and mass photometry to investigate whether PTST1 or GBSS can form oligomers and determine their degree of oligomerization. We discovered that PTST1 forms stable dimers, suggesting dimerization is conserved among members of the PTST family. As previously reported, GBSS formed oligomers, but did not have a specific degree of oligomerization in our case, indicating that it could exist as multiple oligomerisation states. Overall, our findings reveal oligomerisation of biosynthetic proteins as a new layer of protein regulation in amylose biosynthesis. We are currently identifying the sites of protein dimerization or oligomerization, as well as investigating the function of oligomerisation in vivo, to gain a better mechanistic understanding the regulation of GBSS and PTST1 during amylose synthesis. This builds a foundation for engineering different amylose to amylopectin ratios in crops.

P22: Re-engineering amino acid metabolism in wheat grain to reduce the risk of acrylamide formation during processing and improve nutritional value

Nigel Halford, Rothamsted Research, nigel.halford@rothamsted.ac.uk
Keywords: CRISPR/Cas9, Asparagine, Food safety, Pathogen infection, Lysine, Nutritional improvement

Acrylamide is a carcinogenic processing contaminant that forms from free (non-protein) asparagine and reducing sugars during high-temperature cooking and processing of cereal grains and other plant products. Food businesses face the prospect of the European Union setting Maximum Levels for acrylamide in food later this year. Compliance would be greatly facilitated by the development of crop varieties with reduced acrylamide-forming potential. We have used CRISPR/Cas9 to knock out the asparagine synthetase-1 and -2 (TaASN1 and TaASN2) genes of bread wheat. Wheat lines with mutations in the A, B and D genome TaASN2 genes have also been identified in a TILLING population produced by chemical mutagenesis, and the mutations have been stacked to produce a total TaASN2 knockout. We have also assessed the effect of a natural deletion of B genome TaASN2 in some varieties. Data from field trials show the CRISPR lines to have significant reductions in free asparagine concentration and a concomitant decrease in acrylamide formation in heated flour, biscuits and bread, especially after toasting. These approaches to reduce free asparagine accumulation are being undertaken alongside experiments on fertilisation rates, especially of sulphur, and disease control, with the signalling hub through which pathogen infection induces free asparagine accumulation being elucidated in detail. We are also extending our re-engineering of amino acid metabolism by targeting genes that encode DHDPS, the enzyme that catalyses the first committed step in lysine biosynthesis

and is feedback-inhibited by lysine. Wheat and other cereal grains are deficient in lysine, which is an essential dietary amino acid for humans and other monogastric animals, such as pigs and chickens. The acrylamide issue in cereal products is the subject of the ACRYRED COST Action (https://acryred.eu/) and the aims, objectives and activities of ACRYRED will be introduced.

P23: Engineering Starch Granule Morphology in Wheat for Industrial Use and Nutrition

Petros Zafeiriou, John Innes Centre, petros.zafeiriou@jic.ac.uk
Keywords: Wheat, Starch, Starch Granule Morphology, Food processing, Digestibility, Quality

Wheat starch granules come in two sizes—large A granules and small B granules—creating challenges for standardising and optimising industrial processes. This size variation affects key aspects like starch digestibility, food texture, nutritional properties, and processing efficiency. Through our research, we have developed novel approaches to engineer starch granule morphology in wheat using genetics. By targeting key proteins that control the initiation of starch granules, which are distinct from the proteins that synthesise the starch polymers, we can specifically modify starch granule size and shape, opening up new possibilities for food processing and nutrition. In this project, we are evaluating the functional properties of durum wheat lines with modified granule morphology, producing pasta from the lines and assessing their quality, and using in vitro digestion models to evaluate nutritional benefits. We are also expanding the technology for use in bread wheat and maize crops. This approach has the potential to improve the health benefits of staple foods by increasing resistant starch and reducing glycaemic index. Additionally, it can improve quality for pasta- and bread-making, and lead to more efficient industrial starch processing. We aim to attract industry interest and move this innovative technology from early-stage research to commercial application.

P24: Investigating master regulators of Fe homeostasis in wheat

Adam Gicgier, John Innes Centre, adam.gicgier@jic.ac.uk
Keywords: Fe, bHLH, Biofortification, Molecular biology, Wheat

Iron (Fe) is an essential element for life – it enables the oxidative phosphorylation to take place in mitochondria, as well as chlorophyll biosynthesis. However, Fe can also be toxic in higher concentrations due to the release of damaging reactive oxygen species through the Fenton reaction. Therefore, its amount in the plant is tightly controlled via a cascade of transcription factors. The primary iron sensor is thought to be a highly conserved ubiquitin ligase HRZ (BTS in Arabidopsis), which labels bHLH subgroup IVc TF – PRI (Positive Regulator of Iron homeostasis) for degradation when Fe is abundant. When Fe is scarce, the PRI activate Fe deficiency response in plant. Previously, it has been shown that mutating the PRI-HRZ interaction site (-PxA motif) leads to constitutively active Fe uptake pathways, causing increased Fe content in leaves and seeds of Arabidopsis and tobacco. The aim of this project is to utilise this approach for wheat biofortification, as deficiencies in micronutrients such as iron have serious consequences on human health. Firstly, we have investigated the conservation of

interaction between the PRI transcription factors and HRZ ubiquitin ligase in hexaploid wheat. Yeast 2 hybrid assay was used to test the interaction of four PRI and two HRZ proteins. We identified novel differences in the interaction pattern, namely TaHRZ2 interacts only with TaPRI2, in contrast to previously published results in rice where OsHRZ1 and OsHRZ2 partners were the same. These results could help elucidate the different roles of paralogous genes. We selected Cadenza TILLING lines with a premature stop codon in the HRZ-interacting region of TaPRIs. The Fe content of seeds in those TILLING lines will be measured using ICP-OES. A phylogenetic analysis revealed high conservation of the -PxA motif among land plants, as well as Chlorophyta and even red algae, suggesting this mechanism of Fe homeostasis in evolutionarily ancient. This project offers new insights into potential avenues to improve the iron content of bread wheat.

P25: Genetic and Environmental Control of Malting Quality in a Changing Climate

Emily Lyon, James Hutton Institute - University of Dundee, emily.lyon@hutton.ac.uk
Keywords: Barley, Malting, Germination, GxE

Barley is the fourth most widely produced cereal globally. In the UK, 1.5 million tonnes of malt is produced annually from malting barley, primarily for the brewing and distilling industries. Malt is made by steeping, germinating and drying grain to convert starch into fermentable sugars. During the steep stage, even water uptake across the batch is required to hydrate the endosperm sufficiently and ensure high malt quality. Water uptake into grain is influenced by grain composition and structure, which can be heavily affected by both genotype and environment, meaning climate change threatens the production of high-quality malt. To breed malting varieties resilient to climate change, we need a better understanding of the genetic and environmental factors which regulate water uptake and malt quality. This 4-year project seeks to understand how genetic background and environment can affect water uptake during steeping. In a panel of 17 varieties from the same field trial, significant differences were observed in the weight of water taken up at 24 hours, indicating water uptake is at least partially genetically controlled. To investigate this, Quantitate Trait Loci (QTL) mapping for water uptake will be performed on a 270-line biparental mapping population supplied by the project's industry partner, Syngenta, from two UK field trial locations. Additionally, a Genome Wide Association Study (GWAS) will be performed on 245 spring barley varieties from a 2024 field trial and two 2025 European field trials. Physiological data gathered from these trials hopes to reveal how environment, timing of flowering, senescence and grain maturity influences grain development, and thus water uptake and malt quality. In 2023, 6 spring malting varieties were grown in 13 locations across 5 European countries by Syngenta and this germplasm collection hopes to further elucidate the G x E interactions for water uptake, grain composition/structure and malt quality.

P26: Grain Nutritional Quality Diversity in Mutagenized Tetraploid Wheat Population (cv Kronos TILLING Collection)

Hang Gao, John Innes Centre, hang.gao@jic.ac.uk
Keywords: Wheat TILLING Mutant, Forward Genetics, Biofortification, Iron, Zinc

Germplasm Resources National Bioscience Research Infrastructure (GR-NBRI) serves as the UK's public genebank for small grain cereals, with a focus on promoting Findable, Accessible, Interoperable, and Reproducible (FAIR) germplasm and data resources to drive modern crop science and breeding. The GR-NBRI wheat TILLING exome-sequenced EMS-mutagenised populations are highly utilised resources. Users browse for mutations in their genes of interest on Ensembl-Plants; www.plants.ensembl.org and order the corresponding seed on www.SeedStor.ac.uk, most commonly for functional gene validation, known as reverse genetics. To add value to the resources and support a joint effort for wheat grain nutritional improvement, we asked whether screening the TILLING populations using forward genetics could link unknown genes' mutations to (loss of) function expressed phenotypically as altered grain nutrient content. We therefore screened a tetraploid wheat TILLING population for macro/micronutrients by non-destructive Near Infrared and X-ray fluorescence spectrometry. The Kronos TILLING population exhibited significant variation in grain iron (Fe) and zinc (Zn), ranging from 28.7–60.5ppm and 19.6–74.3ppm respectively (n=828). Fe and Zn levels positively correlated (R = 0.4332 Pv<0.001). Grain Protein Content (GPC) and Thousand-Grain Weight (TGW) also revealed broad phenotypic diversity ranging from 14–27% and 21–65g, respectively (n=350). We investigated the trade-off between GPC and existing yield data (kindly provided by James Simonds, Uauy lab, JIC) and confirmed a significant negative correlation (R=0.571 Pv<0.001) between the two components. We then assigned a Grain Protein Deviation (GPD) for each line as a quantitative indicator for nitrogen use efficiency ranging from -7 to 5 (% protein). The results demonstrate an extensive variation in the mutants' nutrient content. Future efforts will concentrate on adapting the necessary bioinformatic methodologies for linking the discovered phenotypic changes with the mutated genes. Additionally, lines high in Fe and Zn with a positive GPD will be identified for Pre-breeding.

P27: Barley Starch Structure and Quality for Brewing: Impacts of genotype, environment and crop management.

Nigel Muchiwanga, University of Nottingham, nigel.Muchiwanga@nottingham.ac.uk
Keywords: Barley, Brewing, GxE, Starch, Quality

Inconsistent quality of raw materials hinders efforts to maintain product uniformity and quality in the brewing industry. Varietal and seasonal variations have been noted in key malt processing parameters such as gelatinisation temperature of malting barley. We aim to elucidate the relative importance of genotype, environment and crop management conditions in determining starch structure, composition and quality for brewing in barley, particularly starch gelatinization temperature. We also aim to determine if thermal and pasting parameters can be used to predict malting/brewing quality in malting barley.

We characterized thirteen barley samples with abnormally high gelatinisation temperatures to provide an initial snapshot on the significance of genotype. The samples were sourced from 3 distinct sites in the USA and Mexico during the 2021/22 season.Thermal properties measured by Differential Scanning Calorimetry (DSC) showed that genotypes significantly differed in peak (Gp) and endset (Ge) gelatinisation temperatures with differences across growing locations being more significant compared to differences across different genotypes grown the same location. Rapid Visco Analysis (RVA) results showed significant differences in pasting properties of the samples including pasting temperature (PT), peak (PV), break down (BD) and final (FV) viscosities. The samples were micromalted and evaluated for parameters related to starch breakdown during mashing. Fine extract, specific gravity and colour were found to have significant negative correlations with Gp and Ge. The parameters were also negatively correlated with PT, time to peak viscosity (TTPV), PV and FV. We noted that some DSC & RVA parameters have the potential of predicting brewing quality in barley. We are currently determining starch composition and structure of the samples. Additionally, grain samples from a replicated field trial with 6 malting genotypes evaluated at Fort Collins (USA) , Sutton Bonington Campus (UK) and two other sites in Argentina will be analysed to determine the effect of growing conditions on starch structure, composition and functional properties in brewing.

P28: Better Bread. Novel Milling processes for improved nutrition

Pilar Martinez-Martin, Aberystwyth University, mam167@aber.ac.uk
Keywords: Flour, Fortification, Nutritional profiling

Wheat grain is a major source of carbohydrates as well as containing significant protein, fibre, and minor components such as lipids, minerals, vitamins, and phytochemicals. Modern white flour milling processes, however, remove the nutrient-rich aleurone, bran, and germ, which contain 40 to 60% of the total minerals, vitamins (for example 80% of the total niacin and folate), as well as most of the fibre (Brouns et al., 2012). Current mandatory fortification aims to reintroduce much of this nutritional content to all non-whole wheat flour. In the Innovate UK funded Better Bread project, Shipton Mill and Aberystwyth University are nutritionally profiling Shipton's milling streams and final flours to identify sources of nutrient loss throughout the milling process. We aim to determine which stream combinations will deliver a final product that retains as high a natural nutritional value in the white flour as possible, thus minimising the need for artificial fortification, whilst meeting consumer demands for 'white' bread. Our analyses are concentrated on protein (incl. amino acid profile), vitamins, minerals (incl. copper, iron, manganese, sodium, zinc), soluble (e.g., beta-glucan) and insoluble fibre, oil, and starch content. The project is also harnessing the nutritional properties of other crops such as spelt, rye, barley, peas, beans, oats, and pearl millet to consider in formulating white flour blends with improved nutritional quality and enhanced health benefits. Brouns, F., Hemery, Y., Price, R., & Anson, N. M. 2012. Wheat Aleurone: Separation, Composition, Health Aspects, and Potential Food Use. Critical Reviews in Food Science and Nutrition, 52(6), 553–568. https://doi.org/10.1080/10408398.2011.589540

P30. Enhancing milling quality through variety development

P29. Enhancing milling quality through variety development

Irene Griffiths*, Sandy Cowan, Marc Loosley, Sara Tudor, Catherine Howarth
Aberystwyth University, SY23 3EE, Wales, UK, *igg@aber.ac.uk
Keywords: Oats, Milling, Quality, Variety development

There has been an oat breeding program based in Aberystwyth since 1919 producing varieties primarily for the U.K. Since 2001, over 30 winter and spring oat varieties have been included on the UK National Variety and Recommended Lists. This includes a number of innovative oat varieties including the winter oat, Gerald which won the NIAB Cereals Cup voted as the variety most profitable by farmers and Mascani which is at present grown on the vast majority of the winter oat area. In 2024, varieties of winter oats bred at Aberystwyth University made up over 96% of the market in the United Kingdom. The general targets are to produce economically competitive varieties which are high yielding, disease resistant, easy to crop and meet end user requirements. In the UK, approximately 70% of oats grown are used for human consumption and the market for cereal products is expanding. For the milling industry, the goals are high yielding varieties with high specific weight, high kernel content, that are easy to dehull combined with appropriate grain composition. The programme has strong links with the UK milling industry, which provides validation of breeding targets and undertakes analysis of the milling quality of selected varieties.Producing new varieties is a long process. The first stage is to identify genetic variation for the traits of interest and to incorporate that into U.K. adapted material. Following the initial cross a rigorous selection process is undertaken integrating a range of high throughput phenotypic and genetic tools. In early generations plants are selected for traits such as height, disease resistance, flowering time and maturity. As selections progress through the breeding program, multi-locational field trials are used and grain quality traits (e.g thousand grain weight, specific weight, kernel content, hullability and β-glucan content) are assessed as well as grain yield. Together with the agronomy results these criteria form the basis for variety creation. Quicker and more efficient methods of DNA analysis are allowing the integration of marker technology into the breeding program. This enables a more directed selection approach in which only plants with the desired markers for traits of interest are taken forward into the next generation. The application of these techniques with regards to the development of high quality milling oats will be discussed.

P30. Strigolactone Perception in Wheat Nitrogen Responsiveness

Anusree Saha, National Institute of Agricultural Botany (NIAB), anusree.saha@niab.com
Keywords: Strigolactones, Nitrogen use efficiency, TILLING, wheat

Nitrogen (N) is an essential nutrient element for crop growth, mainly supplied by application of N fertilizer in agriculture. However, N fertilizer represents a significant cost of production for the growers and also have environmental impacts through nitrate leaching and gaseous emissions. Wheat (Triticum aestivum L.) is a major crop in the UK and worldwide, that provides 20% of calories globally. Sufficient N supply is required to produce high wheat yield as well as ensuring good grain quality. Hence, understanding how major crops respond to available nitrogen followed by selection and development of crop varieties

that can grow with lower nitrogen input is of great importance. Our main research interest is to gain fundamental understanding of role of Strigolactones (SLs) in driving nitrogen responsiveness in wheat. Strigolactones (SL) are a relatively recently characterized phytohormones that regulate branching/tillering and its synthesis and exudation are often linked with nutrient availability although their role in N responsiveness has not yet been demonstrated. The major genes involved in SL perception pathway have been identified in many species. In a nutshell, SL binds to D14 which is a α/β-hydrolase protein, which acts as the receptor protein, the complex then binds to a F-box leucin rich repeat protein (D3), which is responsible for ubiquitination and degradation of targeted proteins. D53 and members of the same family have been identified as degradation targets. Using TILLING mutant lines, we are testing whether perception of SL affects the capacity to respond to different external N availability in wheat. RNA-Seq based transcriptomics study on the mutant lines is underway to delve deeper into gene expression pattern of the downstream genes and analyze the molecular mechanism underlying SL mediated nitrogen responsiveness.

P31: It's about time: Conserved and divergent functions of EARLY FLOWERING 3 in wheat circadian oscillators

Julia Stewart-Wood, Department of Plant Sciences, University of Cambridge, United Kingdom
js2442@cam.ac.uk
Keywords: Circadian rhythms, Wheat, ELF3, Evening complex, Photosynthesis

Plant circadian oscillators regulate numerous pathways underlying yield-related traits, including photosynthesis, flowering time, and temperature responses. EARLY FLOWERING 3 (ELF3), a key circadian oscillator component, integrates environmental signals such as light and temperature into circadian oscillators and regulates these downstream pathways. Crop plants, such as wheat (Triticum species), have differences in ELF3 transcriptional dynamics and protein structure relative to well-studied model plants such as Arabidopsis thaliana. ELF3 is a critical component of wheat circadian oscillators [1]. However, the mechanisms underlying its different transcriptional timing relative to Arabidopsis and the impact its altered structure has on the protein's functions in temperature responses and photoperiod-dependent flowering time remain unclear [2]. Here, we present an analysis of ELF3 at the transcriptional, molecular, and physiological levels. We hypothesize that wheat ELF3 is regulated by the circadian oscillator transcription factor TOC1, contrasting with CCA1-mediated regulation in the model plant Arabidopsis thaliana [3]. We have explored the role of ELF3 in global transcription patterns and found that ELF3 is an important regulator of rhythmic transcription in wheat. Furthermore, we have explored the roles of ELF3 in regulating circadian oscillations in photosynthesis through chlorophyll fluorescence imaging and found that the role of ELF3 in integrating light and temperature signals into circadian oscillators is not impaired by heat stress. In vivo assays have indicated that the ability of the ELF3 protein to interact with A. thaliana circadian clock proteins and proteins involved in temperature responses is partially conserved in wheat ELF3. Overall, these findings enhance our understanding of the roles of ELF3 in wheat circadian biology, offering insights for optimizing photoperiod-dependent

flowering and temperature resilience in wheat breeding programs and understanding the impact that a changing climate may have on this key crop.

References: [1] L. Wittern, G. Steed, L. J. Taylor, D. Cano Ramirez, G. Pingarron-Cardenas, K. Gardner, A. Greenland, M. A. Hannah, A. A. R. Webb, Wheat EARLY FLOWERING 3 affects heading date without disrupting circadian oscillations. Plant Physiology 191, 1383–1403 (2023). [2] G. Steed, D. Cano Ramirez, M. A. Hannah, A. A. R. Webb, Chronoculture, harnessing the circadian clock to improve crop yield and sustainability. Science 372 (2021). [3] A. Upadhyay, J. Rowland-Chandler, J. Stewart-Wood, G. Pingarron-Cardenas, I. Tokuda, A. A. R. Webb, J. C. W. Locke (in preparation), Data-driven mathematical modelling explains altered timing of EARLY FLOWERING 3 in wheat circadian oscillators.

P32: Enhancing nutrient content of cereals using the endophytic insect-pathogenic fungus *Beauveria bassiana*: a proof of concept in the model plant Arabidopsis thaliana.

Alex Jennings, University of Nottingham, alex.jennings@nottingham.ac.uk

Keywords: Nutrient translocation, Fungal colonisation, Arabidopsis, Roots

Beauveria bassiana is a commercially available insect-pathogenic fungus capable of forming intimate associations with plants. It can benefit plants by inducing plant defences to insect pests, reducing damage, and contributing to protecting plant health by competing with soilborne pathogens. Additionally, emerging evidence suggests that entomopathogenic fungi can facilitate nutrient exchange with plants, but the extent of such interactions remains unclear. This research investigates nutrient translocation between Arabidopsis thaliana Col-0 and *B. bassiana* to determine whether fungal colonisation enhances plant nutrient content and whether there are associated nutritional and phenotypic trade-offs. We have quantified changes in macro and micronutrient composition in A. thaliana shoots inoculated with *B. bassiana* using Inductively Coupled Plasma Mass Spectrometry (ICP-MS). Additionally, we have examined the changes in root and shoot phenotypes in fungal-colonised A. thaliana plants across a gradient of nutritional conditions. Our findings will serve as a proof of concept for future experiments evaluating *B. bassiana*'s potential application in cereal production to improve nutrient content while simultaneously protecting against insect pests.

P33: Delivery of biologically fixed N for cereals in ultra-low volume packages for Small Scale Producers (SSPs)

Nikki Walter, University of Nottingham, nikki.walter@nottingham.ac.uk

Keywords: Nitrogen, Fixation, Roots, Below-ground, Bacteria, Biological

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. However, creating N fertilisers primarily involves converting atmospheric N (N2) into ammonia (NH3), using the energy-intensive and CO2-producing Haber Bosch 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 (N2O) – a potent greenhouse gas. Nitrogen-fixing bacteria are microorganisms that can convert atmospheric N (N2) gas into plant-available ammonia (NH3), 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 will be screened for the nifH gene of nitrogenase, ammonia production and excretion. Promising strains will be tested according to their ability to enhance yield in maize, rice and wheat, culminating in field trials in the UK and Sub-Saharan Africa. The most competitive strains will be selected for N fixation quantification for validation. 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.

P34. Malting barley: a steep learning curve.

Christabel Smith, University of Nottingham, stxcs19@nottingham.ac.uk
Keywords: Barley, Malting, Germination.

Water is essential in malting, particularly during steeping, where barley grains absorb water to trigger germination. Enzymatic activity during germination releases sugars and other essential nutrients for brewing. However, with climate change disrupting weather patterns and limiting freshwater availability, the malting industry must reduce water consumption while maintaining malt quality. Innovations such as water treatment and circulation of steep water show promise, but the response of malting barley varieties to these methods remains largely unknown. This project aims to identify barley lines that germinate uniformly and rapidly under water-efficient steeping conditions. Evaluation of 29 elite malting lines for germination energy, index, water sensitivity, protein content, thousand kernel weight, moisture uptake and grain hydration after steeping has revealed significant phenotypic differences. These findings highlight variation in elite malting lines that can be exploited in breeding programs to develop new varieties that produce high-quality malt with less water.

To further investigate, a larger panel of barley varieties will be tested using ‘Optisteep,’ a single-steep system that enhances water oxygenation, reduces germination inhibitors, and is expected to accelerate water uptake. The performance of these varieties in Optisteep will be assessed to determine their adaptability to water-efficient steeping. Subsequent genotyping will identify genetic regions linked to efficient water use and malt quality, enabling plant breeders to develop malting barley varieties optimized for sustainable steeping practices.

P35. Evaluation of Oat Varieties for Agronomic and Spectral Traits in Ireland: Preliminary Insights from Oat Frontiers Project

Atikur Rahman , TEAGASC, atikur.rahman@teagasc.ie
Keywords: Agronomy, Physiology, Grain Quality, Vegetation Index, Adaptability, NDVI

Oat (*Avena sativa L.*) is the third major cereal crop grown in Ireland and is well known for its resilience and cereal break-crop in tillage rotation. Despite the potential, the availability of high-yielding adaptive varieties remains a major constraint for Irish oat cultivation. To address this knowledge gap, the Oat Frontiers project (2023-2026) is evaluating >390 oats recurrent population, genotyped by SNP markers, in multi-location trials. The project aims to assess agronomic adaptability and identify genes associated with key traits. In addition, 28 oat varieties from European breeders are also being evaluated for their agronomical and grain quality traits. In the spring of 2024, the first year of the two-years trial, 28 varieties were sown in a replicated trial in Teagasc, Carlow, Ireland. Critical phenological and agronomic data were recorded. Spectral data was collected by a multispectral sensor attached to an Unmanned Aerial Vehicle and Vegetation Indices for critical growth stages were calculated. Preliminary first-year results show that yield varied among varieties, with Raven exhibiting the highest yield (approximately 8 t/ha), while Pol had the lowest (5.2 t/ha). WPB Isabel exhibited stable grain quality for multiple quality parameters. Varieties showed greater differences in panicle filling duration (PFD) (i.e. panicle emergence to maturity) than panicle emergence duration (PED). Regression analysis with the top and bottom five yielding varieties shows PFD had explained 37% of yield variation (r2=0.37), suggesting a moderate association compared to PED (r2=0.04). A regression analysis of NDVI/day at the grain filling stage showed a preliminary association with yield (r2=0.75). Notably, NDVI/day at GS80 distinguished between low- and high-yielding varieties. Preliminary data from a single-year trial suggest that a slower NDVI decline (canopy greenness retention) may lead to higher yields in Ireland's cool climate. However, this needs further validation through studies of pre- and post-anthesis RUE variation among varieties.

P36: Novel Tools for Cereal Genetic Resources Management derived from barley and wheat Genebank-Genomic projects

Workie Zegeye, John Innes Centre, workie.zegeye@jic.ac.uk
Keywords: DNA Barcoding, Genebank, KASP Marker, Minimal marker, Watkins Landraces

DNA Barcoding, Genebank, KASP Marker, Minimal marker, Watkins Landraces The UKRI-BBSRC Germplasm Resources National Bioscience Research Infrastructure (GR-NBRI), the UK's public genebank for small grain cereals, focuses on promoting FAIR (Findable, Accessible, Interoperable, and Reproducible) germplasm and data resources to advance crop science and breeding. Genomic barcoding has emerged as a promising tool for effectively managing plant genetic resources, however sequencing large collections is often cost-prohibitive. Furthermore, sequence or saturated marker data is unnecessarily complex to suit efficient routine quality control and quality assurance tools for germplasm regeneration and distribution, respectively. Therefore, we develop cost-effective minimal

KASP marker sets capable of separating all genetic backgrounds from each other in the GR-NBRI crop collections. Here we report on the approach of filtering, choosing, and validating 25 markers for Durum wheat (Triticum Durum) and barley (Hordeum vulgare) molecular barcoding. For Durum, we used 345 accessions of the Watkins Collection of Landrace wheat genotyped by the 35K-Axiom® array and achieved 98.8% discrimination. These 25 markers fully resolved all the available (n=160) GR-NBRI conserved cultivars and 92% of a global panel (n=556) acquired from ICARDA and the USDA. In barley, the 25 markers were filtered from 171,263 bi-allelic SNPs and provided 100% separation for the tested GR-NBRI modern cultivars (n=94), and 98.6% for landraces (n=352). These results highlight minimal marker sets' robustness, accuracy, and cost-effectiveness for genebank management in avoiding duplications, identifying mislabelled plants and seeds, and resolving field harvest mix-ups. A future application of molecular barcoded genebank collections is a quicker response to emerging diseases. Since lines could be identified by low-cost DNA sampling, no labelling and separating accessions during phenotyping are needed. Therefore, identification of resistance strains could theoretically be conducted on farmer fields in the infected area rather than in specialised breeding stations. The GR-NBRI team in collaboration with ICARDA and the Global Crop Trust, are experimentally testing this vision.

P37: Chromosomal location oat crown rust resistance gene Pc101 disease resistance, DArTseq, marker assisted selection, Puccinia coronata f. sp. avenae

Edyta Paczos-Grzeda, Sylwia Sowa, Joanna Lech, Tim Langdon, University of Life Sciences in Lublin
edyta.paczos@up.lublin.pl
Keywords: Disease resistance, DArTseq, Marker assisted selection, *Puccinia coronata* f. sp. avenae

Crown rust is one of the most destructive fungal diseases of oats worldwide, caused by Puccinia coronata f. sp. avenae. Breeding disease-resistant oat cultivars is the preferred method of preventing the spread of rust and potential epidemics. The subject of the study was Pc101, a race-specific seedling crown rust resistance gene, highly effective at all growth stages, derived from A. sterilis PI 334961 originating from Haifa, Israel. The surveys carried out for more than 10 years in Poland have shown that virulence against this gene is extremely rare and most often the symptoms of infection are accompanied by many signs of the immune response of the infected plant in the form of chlorosis or necrosis and small-sized uredinia. Crown rust response tests were performed and the proportions of phenotypes in segregating population derived from a cross Pc101 differential line with crown rust susceptible Polish oat cultivar, Kasztan × Pc101, confirmed the monogenic inheritance of the gene. Effective gene introgression depends on reliable gene identification at early stages of plant development, so the study aimed to develop molecular markers closely linked to Pc101. Segregating populations of Kasztan × Pc101 were genotyped using DArTseq™ technology based on Illumina next-generation short-read sequencing. Markers associated with Pc101 were located on chromosome 2D of the oat reference genomes, Avena sativa cv. Sang [1] in the region between 170 Gb and 174 GB bp. Based on the SNPs discovered in this region, allele-specific markers were subsequently developed using TaqMan technology. The newly developed co-dominant markers will be a valuable tool for marker-assisted selection in breeding programmes and may be useful for oat improvement.

P38: Multiplex Genome Editing in Wheat: Designing Efficient Experiments and High-Throughput Screening Strategies

Valentina Buffagni, John Innes Centre, valentina.buffagni@jia.ac.uk
Keywords: Multiplex Genome Editing in Wheat: Designing Efficient Experiments and High-Throughput Screening Strategies

Genome editing, Wheat breeding, Next-Generation Sequencing (NGS), CRISPR/Cas9 Recent dvancements in gene editing (GE) technology have revolutionized wheat breeding, significantly enhancing transformation efficiency and cultivar flexibility. Concurrently, the ongoing amendments to EU legislation on New Genomic Techniques (NGTs) mark a promising milestone for the future of genome editing, enabling a landmark for plant breeding and research. This study details the comprehensive strategy for crafting efficient GE experiments, targeting multiple loci, using CRISPR/Cas9 constructs, and employing delivery methods suited for wheat's polyploid genome. Additionally, we describe the screening strategy for transgenic progeny, showcasing the use of next-generation sequencing (NGS) as a high-throughput, cost-effective approach for detecting successful edits in multiplex GE experiments. Our methodology underscores the effectiveness of NGS in screening multiple targets, accelerating genetic advancements in wheat, and fostering the future of innovative crop improvement.

P39: The Dynamic Regulatory Network of VRT2 in Controlling Rudimentary Basal Spikelet Formation in Wheat

Yunchuan Liu, Sophie Carpenter, Katie Long, Nikolai Adamski, Max Jones, Cristobal Uauy, John Innes Centre, yunchuan.liu@jic.ac.uk
Keywords: Wheat, Rudimentary Basal Spikelet Formation, VRT2, spikelet development, Regulatory Network

Wheat, Rudimentary Basal Spikelet Formation, VRT2, spikelet development, Regulatory Network 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 (RBSs), which fail to produce grains, thereby limiting overall yield. Currently, the molecular mechanisms behind RBS formation remain poorly understood. In this study, we investigate the role of VRT2, a MADS-box transcription factor, in controlling RBS formation through its dynamic regulatory network. Our preliminary results reveal that in VRT2 ectopic expression lines, the VRT2 protein interacts with key positive regulators of spikelet development, including SQUAMOSA MADS-box proteins VRN1, FUL2, and FUL3, across different developmental stages. These VRT2-SQUAMOSA interactions are hypothesized to disrupt the native protein complexes, delaying spikelet meristem development and increasing RBS formation. Furthermore, VRT2 interacts with other transcription factors, including SPL14 and SOC1, linking the photoperiod and age pathways, highlighting its putative role in the precise regulation of spike development. To further investigate these mechanisms, we will functionally

characterize these proposed genetic interactions. Additionally, we will employ CUT&RUN 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.

P40: Supporting the Monogram community with Ensembl

Jorge Alvarez-Jarreta, EMBL-EBI, jalvarez@ebi.ac.uk
Keywords: Ensembl, Poaceae, Genomics, Variation, Pangenome, Watkins

Ensembl is an open platform which integrates publicly available genomic data to support exploration of gene annotations, genetic variation and comparative genomics. Increasing numbers of genomes are available for agriculturally relevant species, with multiple high quality genomes now being generated in the case of certain crops. Furthermore, a considerable volume of genetic variation data is now available to research and industry communities alike. Providing ways to explore this genomic data is key to supporting research and breeding efforts for agricultural species. Ensembl Plants (https://plants.ensembl.org) latest release (60) now holds 70 genomes from the Poaceae family, including pangenomes for wheat (17) and rice (15). In release 61, coming in March 2025, we will include the barley pangenome (https://www.nature.com/articles/s41586-024-08187-1) covering 2 existing and 75 new genomes, and in release 62, scheduled for September 2025, the oat pangenome (https://www.biorxiv.org/content/10.1101/2024.10.23.619697v1) will be released with 2 existing and 31 new oats. Moreover, we are also expanding our variation support for the community, with the incorporation of ~90 million variants from the Watkins Landrace Wheat Collection (https://www.nature.com/articles/s41586-024-07682-9) into our resources. We are also actively working on our new site, Ensembl Beta (https://beta.ensembl.org), which brings together all species across the tree of life, including over 100 plant genomes. This new site includes all the species and additional features previously available in Ensembl Rapid, aiming to ultimately become the single Ensembl site in the future. As such, an additional 2 Poaceae species, Phragmites australis (common reed) and Bromus sterilis (barren brome), are available in Ensembl Beta, on top of the species available in Ensembl Plants, making a total of 179 Poaceae genomes available across Ensembl sites before the end of 2025.

P41. Identifying direct TARGETs of transcription factors in wheat

Emilie Knight, John Innes Centre, emilie.knight@jic.ac.uk
Keywords: Transcription factor, TARGET, Protoplast

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 the Arabidopsis thaliana TARGET system (Transient

Assay Reporting Genome-wide Effects of Transcription factors) developed by Bargmann et al., to wheat. This system allows for the rapid identification of direct regulated genome-wide targets of TFs. Here we have used the well-characterised senescence regulator NAM-A1 as an example for this technique. 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 can therefore be 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. Using this technique, we have identified 11,311 direct targets of NAM-A1, including known targets of this TF, which confirms the efficacy of this method. The promoter sequences of target genes are currently being analysed for conserved motifs. In summary, the TARGET system is a promising route to decipher gene networks in wheat.

P42. iTAG Barley - Inheritance of Traits and Genes Teaching and Training resource using Oregon Wolfe Barley

Malcolm Macaulay[1], Kelly Houston[1], Chiara Campoli [1], & Robbie Waugh [1,2]
[1]James Hutton Institute
[2]University of Dundee, malcolm.macaulay@hutton.ac.uk
Keywords: Barley, Teaching Resource, Genes, Traits Inheritance

Understanding the relationship between genotype and phenotype is fundamental to biology but remains challenging for students and novice researchers. The Inheritance of Traits and Genes (iTAG) module leverages the Oregon Wolfe Barley (OWB) population to bridge this gap through hands-on laboratory and classroom activities. This module uses phenotypic traits, such as seed-coat colour, spike morphology, and disease resistance, to illustrate key biological concepts, including plant development, domestication, and pathogen interaction. The iTAG workflow focuses on three primary traits: (1) two-row versus six-row spikes, controlled by the domestication-related gene Vrs1; (2) hooded versus nonhooded spikes, driven by the homeotic mutation in BKn3; and (3) long versus short awns, determined by Lks2. Additionally, participants investigate resistance or susceptibility to powdery mildew, which segregates in the OWB population due to allelic variation at the Mla locus. This educational tool, developed by researchers at Iowa State University, USA, utilizes the OWB barley population due to its ease of cultivation, phenotypic diversity, and straightforward protocols for DNA extraction, PCR, and electrophoresis. These experiments have engaged thousands of students in schools across the United States & Europe. Building on the success of the Royal Society Funded Daffodil DNA Project (https://sites.dundee.ac.uk/dundee-daffodil/) and utilising existing experimental equipment, the original iTAG concept has been adapted to further inspire educators and students. With experimental resources sent to an initial cohort of schools this initiative aims to strengthen understanding of the relationship between phenotype and genotype by introducing molecular biology techniques into classroom settings.

P43: Kmer-derived haplotype detection and marker generation for breeding

Bernice Waweru, John Innes Centre, Bernice.Waweru@jic.ac.uk
Keywords: Haplotypes, K-mers, Breeding

Genetic variation is vital for plant breeding. K-mers, short DNA sequence fragments derived from genomic data, can enhance our understanding of genetic diversity. This study aims to evaluate a novel k-mer-based method for detecting haplotypes and generating haplotype-specific molecular markers for breeding, using wheat as a case study. We developed a method capable of identifying cultivar specific k-mers from raw reads of a query cultivar across a target interval. We focused on 50 kbp target regions from available genome assemblies and derived corresponding 31-mer k-mers. These reference k-mers were used to “pull out” raw reads from query cultivars of interest, which were assembled into contigs. By comparing the k-mers derived from the query cultivar contigs and the reference genome, we were able to generate a presence-absence matrix and identify unique k-mers and haplotypes using IBSpy. These k-mers should be unique to the query cultivar and specific to the target region. We tested our pipeline on two loci, the wheat yield locus (WAPO-A1) and the reduced height locus (Rht-D1). We detected known variation at both loci, including SNPs and larger deletions. Importantly, we retrieved k-mers spanning a 115-bp promoter insertion in WAPO-A1 which is absent in our original reference genome suggesting that the newly assembled query contigs were able to span across deletions. This highlights the method’s capability to detect genetic variation at specific loci and retrieve k-mers spanning across regions which are absent in the reference assembly. We are levaraging the k-mers distinguishing these haplotypes to generate haplotype-specific markers for genetic studies and marker-assisted breeding. Our k-mer based pipeline shows significant promise for identifying haplotypes and novel variations within loci associated with traits of interest. Enhanced haplotype and marker detection could improve our understanding of genetic diversity and advance marker-assisted breeding, ultimately contributing to the development of improved crop varieties.

P44. Blurring the line: blade-sheath boundaries and the extended auricle1 mutant maize leaf boundary patterning

Heather Jones, University of Edinburgh, h.jones-14@ed.ac.uk
Keywords: Maize, Leaf boundary patterning

Plant architecture is a crucial determinant of plant productivity. In cereal crops, the linear ligule and wedge-shaped auricles comprise the boundary between distal blade and proximal sheath, and are key regulators of the degree to which the blade bends away from the stem (leaf angle, LA), influencing light interception. The recessive extended auricle1 mutation disrupts this precise boundary and forms outgrowths of undulating auricle tissue along the blade. Currently, it is understood that eta1 exacerbates the phenotypes of all known P-D patterning mutants, and it is hypothesised to represent a downstream link between the KNOX and LIGULELESS pathways, linking boundary specification and tissue differentiation. This project aims to further characterise this mutant, identifying the ETA1 gene and

investigating the role of ETA1 in the blade-sheath patterning gene regulatory network. Here I will present preliminary phenotypic and mapping data for eta1 in the permissive W22 background, and discuss current work in identifying other genes involved in this network.

P45: Comparing Root Exudate Soil Aggregation Properties in Monocots and Dicots

Emily Carr, University of Bristol, ec17981@bristol.ac.uk
Keywords: Roots, Exudates, Erosion, Soil aggregation, Rhizosphere

Earth's population is increasing rapidly, and as a result, demand for staple crops like wheat is also increasing. Despite this, recent peer reviewed research indicates that an annual total of nine million tonnes of wheat are lost globally to soil erosion – close in amount to total UK wheat production in 2020. Whilst agricultural intensification is the traditional approach to increase crop yields, it can have detrimental effects on the soil, causing degradation and desertification which exacerbates the issues facing food production. Reducing the loss of arable land is critical for the future success of agriculture, and one proposed solution is root exudates, which aggregate soil particles together and therefore improve soil structure and health. Little is known about the pathways for their release, but two candidate genes have been proposed to affect exudate composition, Xyloglucan endotransglucosylase 23 (XTH23) and ABC2 homolog 6 (ATH6). Arabidopsis mutant lines for these genes have been used for uprooting and soil binding experiments which compare the adhesive properties of the exudates. The causation of these adhesive properties have been explored using ELISAs to assess the polysaccharide composition of the exudates. Different polysaccharides have different adhesive properties, but they also have different effects on soil water retention, and this has been demonstrated using a novel experimental method which will be used to demonstrate the effect of different mutant root exudates on soil water retention. Wheat mutants for ATH6 and XTH23 have been successfully created using TILLING lines and CRISPR technology. The CRISPR lines were created internally using golden gate cloning and biolistic transformation, resulting in two different XTH23 full knockout mutant lines successfully being identified. The root exudates from these mutants will be subjected to similar experiments as the Arabidopsis mutants to investigate whether the candidate genes have similar functions in monocots and dicots.

P46: Is NAC3 a positive regulator of wheat senescence?

Rebecca Testa, John Innes Centre, becca.testa@jic.ac.uk
Keywords: Senescence, NAC3, transcriptional regulation, CRISPR/Cas9, pull-down

Senescence is the last stage in wheat development; nutrients are remobilised from the source tissues, such as the leaves, into the developing grain. Senescence regulation balances a trade-off between yield and protein content. Late leaf senescence is linked to an increase in grain yield but lower grain protein content, whilst earlier leaf senescence is associated with the reverse. Identifying transcription factors involved in regulating the timing of leaf senescence is useful, as these could be manipulated to

achieve an increase in grain protein content without hindering yield. Here, we investigate the role of NAC3, a NAC transcription factor, in regulating senescence. NAC3 was initially identified because it forms protein-level interactions with NAM-B1, a known senescence regulator. To test whether NAC3 influences senescence we have created CRISPR/Cas9 gene-edited lines. Sequencing of the T1 population identified several plants from four independent transformation events that contained edits in all homoeologs of NAC3. Additionally, two edited plants had lost the editing machinery and can be considered non-transgenic, ideal for potential field trials. nac3-edited plants showed a significant delay in peduncle senescence compared to non-edited plants. The phenotype of edited plants will be explored in more depth in the next generation. To identify additional interactors of NAC3 at the protein level we are conducting an in vitro pull-down assay. 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 will contribute to our understanding of the regulation of leaf senescence, a fundamental stage in wheat development.

P47: Unravelling the role of LIGULELESS2 in maize

Trisha McAllister[1], Ayushi Gupta[1], George Chuck[2], Edoardo Bertolini[3], Max Braud[3], Anne Sylvester[5], Andrea Eveland[3], Sarah Hake[2,4], Annis Richardson[§1,2,4]

[1].Institute of Molecular Plant Sciences, School of Biological Sciences, University of Edinburgh, Edinburgh, Scotland

[2].USDA Plant Gene Expression Center, Albany, California, USA

[3].Donald Danforth Plant Science Center, St Louis, Missouri, USA

[4].Plant and Microbial Biology, University of California Berkeley, California, USA

[5].Department of Molecular Biology, College of Agriculture, Life Sciences and Natural Resources, University of Wyoming, Wyoming, USA

[§]Current location

trisha.mcallister@ed.ac.uk

Keywords: Development, Leaf, Maize, Boundaries

Life on earth is marked by an incredible diversity in form and function, but how this diversity is defined and coordinated throughout development remains a fundamental question in biology. Organ shape poses a particularly attractive target for crop improvement given that it can profoundly influence plant productivity. A crucial element in shape determination is the formation of boundaries between and within organs. These boundaries are defined during the earliest stages of development, when meristematic cells begin differentiating into distinct domains. Determination and maintenance of these domains influence growth patterns within the primordia to direct how an organ will be shaped. However, the regulatory networks underlying domain patterning and boundary specification and how they are modified to generate morphological diversity remain unknown. In maize, the BZIP transcription factor LIGULELESS2 (LG2) is thought to have a key role in defining boundaries between domains in different organs. lg2 mutants lack a clear boundary between the leaf sheath and blade, the tassel has fewer branches, and there are defects in bract formation. How LG2 functions during the development of these

different organs and specifies boundaries is unclear. To address this, we are combining transcriptomic and proteomic data to build the regulatory network that LG2 acts in. Through comparing regulatory networks between organs we hope to identify both core components, providing insight into how boundaries may be specified and maintained in growing organs, and key organ-specific changes that may be responsible for morphological differences.

P48: Gene Regulatory Networks Driving Wheat Spike Architecture Through Meristem Transitions

Ella Penny, John Innes Centre, ella.penny@jic.ac.uk
Keywords: Wheat inflorescence architecture, GRNs, development, modelling

The architecture of wheat inflorescence is characterised by the repeating arrangement of floral structures (spikelets) long the main axis (spike). The inflorescence can therefore be described as series of initiation of [Leaf + Meristem] units. The shape and patterning of spikelets are defined by the branching transitions that meristems in the developing spike undergo, ending in floral identity. These transitions are governed by gene regulatory networks (GRNs). Recently, Backhaus et al. (2022) showed opposing expression gradients of two interacting gene families, SEPALLATA (SEP) and SHORT VEGETATIVE PHASE (SVP), which have opposing expression gradients that influence spikelet formation. A computational model based on interactions between SEPs and SVPs successfully explained the typical lanceolate shape of wheat spikes but falls short in replicating phenotypes observed in certain mutants, such as vrn1ful2ful3, which exhibit altered meristem transitions. Long et al. (2024) further demonstrated spatially coordinated gene expression gradients, showing differences in meristems before visible shape changes are observed. This project aims to unravel the underlying mechanisms that determine inflorescence shape. We will focus on the GRNs that coordinate wheat spike development through meristem transitions to describe inflorescence architecture. Our hypothesis is that the GRNs introduce delays in the system that give rise to desynchronised development across the spike. We are modelling the GRNs using ordinary differential equations (ODEs). By iteratively introducing and testing new regulatory interactions within the ODE framework, we compare model outputs against the original SVP/SEP model to identify plausible mechanisms underlying these delays. Our goal is to use the timing of these transitions from the GRNs to drive a spatial model of branching. We will expand existing models by integrating the [Leaf + Meristem] concept and exploring the impact of both established and novel gene networks on meristem transitions and leaf states.

P49: DEDAL: An Open-Source Cloud-Based Solution for Drone Phenotyping

Miguel Gonzalez Sanchez, John Innes Centre, miguel.gonzalez-sanchez@jic.ac.uk
Keywords: Drones, Phenomics, Cloud-Computing, Plant-Health , Open-Source

This work introduces DEDAL (Distributed Ecosystem for Drone Analytics in Life-sciences), a cloud-based solution hosted at the John Innes Centre (JIC) and designed to support the UK crop genetics community in processing and phenotyping drone data. The increasing affordability of high-capability drones has made them a valuable tool for assessing plant health, yet extracting scientific insights from

these devices remains challenging. Key barriers include the high cost of proprietary software licenses, the hardware requirements for data processing, and the complexity of integrating open-source solutions and community best practices. DEDAL addresses these challenges by providing a tailored cloud-based platform for UK academics. Built on a robust OpenNebula infrastructure, DEDAL offers two core services: (1) processing raw drone data using OpenDroneMap to generate orthomosaics and plant health indices, which users can view, download, and analyse further; and (2) hosting specialised environments for open-source tools like FieldImageR, enabling the extraction of vegetation indices, plot height, and other phenotyping metrics from processed orthomosaics. Future developments aim to enhance DEDAL's capabilities by integrating AI models for advanced phenotyping tasks, such as yield estimation and disease scoring. The current resources available far exceed those of a single workstation, and if DEDAL proves to be a popular resource, plans are underway to expand computational and storage capacity, including the potential addition of GPUs to meet growing demand. For more information, visit dedal.jic.ac.uk.

P50. Hyperspectral imaging for grain protein content and its uniformity – a combined GWAS and transcriptomics approach.

Thomas E. Welch, University of Nottingham, thomas.welch1@nottingham.ac.uk
Keywords: Wheat, Protein, GWAS, NAM, Transcriptomics, RNA-seq

Grain protein content (GPC) is a critical determinant of wheat grain quality, influencing end-use applications, milling efficiency, and product quality. GPC is a primary economic driver for farmers, with high GPC harvests commanding premiums and substandard harvests suffering discounts. Furthermore, the degree of grain-to-grain variance of GPC can have a substantive impact, individual grains have the potential to enhance or drag-down the overall quality of a batch. Nitrogen supply is the most manageable determinant of GPC for growers, but its utility is constrained by cost volatility and environmental concerns. Future progress in improving GPC will therefore largely be made by breeding genetically improved cultivars. Successful selective breeding requires reliable quantitative trait loci (QTLs), which for GPC are hard to detect in association studies due to it being a highly quantitative trait, influenced by a small number of major-effect genes and numerous small-effect genes acting additively. Our aim is to identify genes important for the control of GPC and its within cultivar uniformity. Given the inherent challenges of this aim, we will use a two front approach, genomic and transcriptomic. A genome wide association study (GWAS) will be conducted using the enhanced diversity and resolution of a large nested-association mapping (NAM) population. High-throughput phenotyping of GPC can be achieved using a Hyperspectral imaging method. Whereby statistical modelling is used to estimate GPC of each grain sample from its absorbance of light at the near-infrared spectral range. In conjunction, a time-course RNA-seq study is being conducted, whereby within grain gene-expression changes will be compared between carefully chosen wheat varieties (differing markedly in their GPC and GPC-uniformity) at key post-anthesis growth stages. Ultimately, likely candidate genes for selective breeding may be pinpointed as those which undergo noteworthy gene expression changes in our RNA-seq assay, and fall within significant QTLs we detect in our GWAS.

P51. Metabolomic and transcriptomic profiling reveals Tef's adaptive strategies under drought stress

Baharehsadat Haddadi1, Manfred Beckmann1, Fiona Corke2, John Doonan2, Luis A. J. Mur1,* and Aiswarya Girija3,*
DLS, Aberystwyth University, 2National Plant Phenomics Centre, 3IBERS, Aberystwyth University. bah13@aber.ac.uk, * joint project coordinators
Keywords: Tef, Drought, Metabolomic, Transcriptomic, gluten-free

Tef (Eragrostis tef), a gluten-free cereal rich in nutrition, protein, fibre, vitamins, and minerals, offers a good alternative for individuals with gluten intolerance, such as those with celiac disease. Despite its resilience as a crop, understanding tef's response to drought stress is crucial due to the potential limitations drought can impose on its final yield. As an orphan cereal, research on tef remains limited. Therefore, investigating its molecular responses to drought stress is crucial for developing drought-tolerant varieties with improved yield and quality. This advancement could also support in expanding the innovation for new gluten-free cereal-based products meeting both food security and sustainable agriculture in a changing climate. This study aimed to screen and characterised the response of diverse tef genotypes to drought stress. Three-week-old seedlings of four tef genotypes (cv.s Alba, Ent, Tsedey and Manyi) were subjected to sever drought (15 % SWC) and well-water control (65% SWC) for 4 and 8 days at the National Plant Phenomic Centre. Both metabolomic and transcriptomic profiling revealed that sugars and proline accumulated significantly in response to drought stress. Moreover, drought stress significantly altered phenylpropanoid metabolism across tef genotypes. Flavonoid levels generally decreased, except in Alba, which exhibited an initial increase in flavonoid accumulation at 4 days, followed by a decline at 8 days. A notable shift towards increased production of cell wall-associated metabolites was observed. Within the jasmonic acid (JA) pathway, linoleic acid levels increased while JA accumulation decreased under drought. Transcriptomic analysis revealed upregulation of cuticular-related genes, suggesting a potential diversion of lipid metabolism towards cutin biosynthesis. In conclusion, these findings suggest that production of lignin and cuticular compounds contributes to cell wall strengthening and increased hydrophobicity, showing significant drought adaptive mechanism in tef.