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ASSOCIATION OF APPLIED BIOLOGISTS

MONOGRAM

CEREALS & GRASSES RESEARCH NETWORK

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

Scientific Organisers of Monogram 2026: Stéphanie Swarbreck and Kostya Kanyuka

Final Programme

Tuesday 24th March 2026

0800 **Registration Opens**

0920 **Welcome**
Stéphanie Swarbreck

0930 Session 1: Staying Ahead of the Outbreak: Biotic Threats & Defences

Chairs: Kostya Kanyuka and Nikki Walter

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

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RANK
PRIZE

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

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

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

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KWS

Thanks to KWS for sponsoring Session 1

1100-1130 **BREAK**

1130 Session 2: Cultivating Good Company: Probiotics for Plants

Chairs: Fiona Leigh & Lu Lu

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

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

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

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

1300- 1400 **LUNCH**

1400 Session 3: Beyond Yield: Grain Quality & Human Nutrition

Chairs: Carus John-Bejai and Becca Testa

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

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

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

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

1530- 1600 **BREAK**

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Wednesday March 25th 2026

0900 Session 5: Climate-Proofing Monocots: Physiology that Delivers

Chairs: Stella Edwards and Xavier Simón

0900-0940	**Elizabete Carmo-Silva, Lancaster University** Towards sustainable and temperature-resilient wheat photosynthetic productivity
0940-0955	**Miles Curl, John Innes Centre** Exploring the role of NAM-2 in delaying drought-induced senescence in wheat
0955-1010	**Dominique Hirsz, IPK-Gatersleben** Staggering towards new habits: exploring seasonality in wheat through alternative growth habits
1010-1025	**Catherine Famelton, Rothamsted Research** Dissecting interactions between trehalose-6-phosphate, nitrogen and genotype in wheat physiology
1030-1100	**BREAK**

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Thanks to RAGT for sponsoring Session 5

1100 Session 6: From Meristem to Harvest: Building the Plant

Chairs: Nikolai Adamski and Amy Newell

1100-1140	**Alex Webb, University of Cambridge** Circadian Clocks in Wheat
1140-1220	**Sarah McKim, University of Dundee** Does mother know best during grain development?
1220-1235	**Yunchuan Liu, John Innes Centre** VRT2 increases rudimentary basal spikelet formation by delaying floret development in wheat
1235-1250	**Kenan Tan, IPK-Gatersleben** Wind pollination and evolutionary innovation in grasses is driven by WAP1 enhancing pollen production and fertility
1250-1305	**Becca Testa, John Innes Centre** Green be gone: transcription factor NAC3 regulates wheat senescence

1305-1400 **LUNCH**

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

Chairs: Joshua Ham and Denis-Florentin Sfrangeu

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

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

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

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

1530-1600 **BREAK**

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

Chairs: Tally Wright and Bright Fiakeye

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

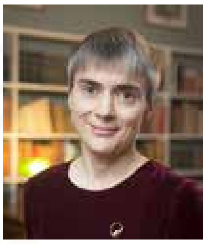
1640-1655 **Stephen Pearce, Rothamsted Research**
An expanded RHT1 allelic series enables tuneable control of wheat growth

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

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

1745- 1830 **Free Time and Drinks Reception**

1830- 1915 **Women in Crop Science and Allies Discussion Session**
Chair: Stéphanie Swarbreck



Dame Ottoline Leyser, Cambridge University

2000- late **Conference dinner at Robinson College**
Must be booked as an optional extra

Thursday March 26th 2026

0930: Session 9: Decoding Monocots: Genetics for Impact

Chairs: Miriam Schreiber and Beth Soanes

0930-1010	**Eric Ober, Niab** Navigating the GxExM landscape, and finding ways forward for crop improvement
1010-1025	**Emily Carr, University of Bristol** A sticky situation: root exudate-substrate cohesion is modulated by an XTH gene
1025-1040	**David Ashworth, James Hutton Institute** Can we develop novel algal biofertilisers from whisky co-products to produce barley sustainably?
1040-1055	**Denis-Florentin Sfrangeu, Niab** Investigating the role of the 3D soil matrix in mediating root-to-root interactions between wheat and blackgrass
1100-1130	**BREAK**
1130-1215	New Lecturer Award Winner: **Jiorgos Kourelis, Imperial College** From understanding to engineering: synthetic biology approaches to build made-to-order plant immune receptors
1215- 1230	**Monogram 2026 closing ceremony** **Stéphanie Swarbreck, Kostya Kanyuka and Elizabete Carmo-Silva**
1215-1315	**LUNCH**

1315 Resources Workshop

1315- 1445 .	**Sarah Dyer, Tally Wright and James Bedford, Niab** Ensembl plant population (see schedule on next page)
1445-1500	**Burkhard Steuernagel,** John Innes Centre Next-Gen Wheat Genomics Web Services, An initiative to update the wheat web services landscape
1500	**Meeting End**

The Ensembl Trait Mapper tool for association studies and gene discovery in plants

Presenters: Sarah Dyer (EMBL-EBI), Tally Wright (Niab), James Bedford (Niab)

Plant genomics has enabled significant enhancements for agriculture, though linking plant genes and variants to traits remains challenging. Current workflows demand expertise in bioinformatics, genetics and statistics applied through customised computational systems and hardware. The Ensembl Trait Mapper is a new web-based tool that brings population-based variant data and computational resources together in an easy-to-use interface.

This workshop will introduce you to the Ensembl Trait Mapper tool and demonstrate how it can be applied for the association of variants to plant traits. You will learn about the standardised pipeline which can be used to run genome wide association studies on your own data across a range of different crops and populations. You will explore the outputs of example phenotypes and learn how to identify variants of interest. You will see how variant coordinates can be used for gene prioritisation, and where to get more information about identified genes in the Ensembl platform.

Feedback on the tool, and how it can be applied to your work is a key part of the workshop, and we encourage you to consider your own use cases for discussion.

Learning Objectives:

- List the advantages of applying a standardised pipeline for variant association studies in plants
- Outline the features of the input file needed to run the Ensembl Trait Mapper tool
- Understand how to identify significant variants in a Manhattan plot
- Outline the ways in which GWAS results can be used for gene prioritisation and where to get more information once a gene has been identified
- Share your own views and needs with the Ensembl Trait Mapper team via feedback surveys

Timetable of the session:

Introduction to Ensembl Trait Mapper (ETM)	13:15
The standardised ETM pipeline	13:20
Exploring ETM analysis and results - guided walkthrough	13:25
Break	13:55
Gene prioritisation following an association experiment	14:10
Feedback for the ETM team	14:20
Wrap up and questions	14:30
Workshop End	14:45