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4TH INTERNATIONAL WHEAT CONGRESS



WWC

BOLOGNA - ITALY MAY 25-29, 2026

Bologna Congress Center,
Piazza della Costituzione, 4

Conference Chair

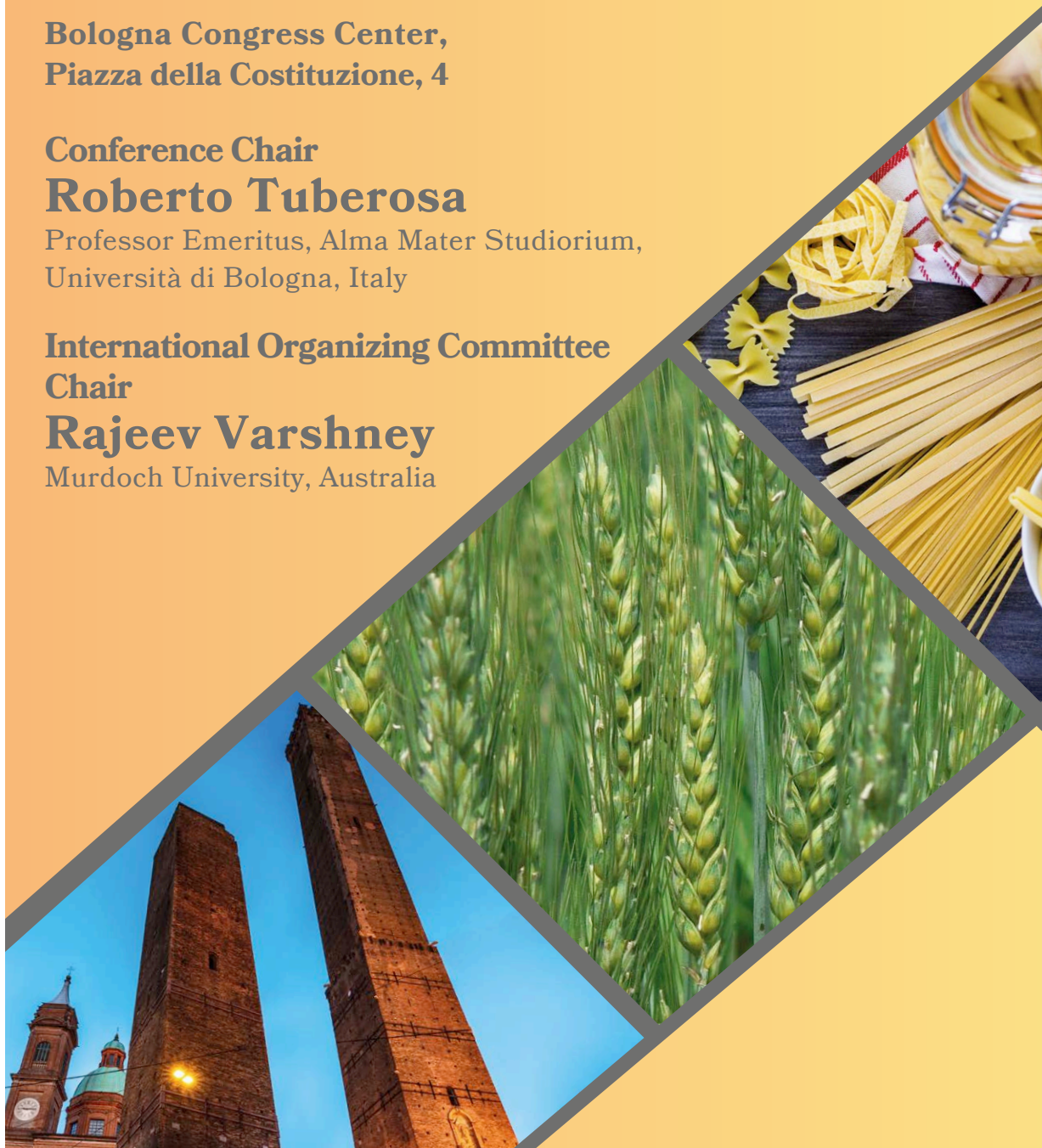
Roberto Tuberosa

Professor Emeritus, Alma Mater Studiorum,
Università di Bologna, Italy

International Organizing Committee
Chair

Rajeev Varshney

Murdoch University, Australia



ABSTRACT BOOK



Avenue media®
Conference & Expo

DAY 1 - Monday, 25 May 2026

Europa Conference Room

08:00 – 09:00	Registration of participants
09:00 - 09:30	WELCOME ADDRESSES - Francesco Lollobrigida (<i>Italian Ministry of Agriculture</i>)* - Silvia Lorenzini (<i>General Director of Agriculture, Hunting and Fishing of Emilia Romagna Region</i>) - Paolo De Castro (<i>Nomisma President, Italy</i>) - Giovanni Molari (<i>Magnifico Rettore University of Bologna, Italy</i>)* - Federico Magnani (<i>President of Accademia Nazionale Agricoltura, Italy</i>) - Roberto Tuberosa (<i>Conference Chair, Professor Emeritus, Alma Mater Studiorium, Università di Bologna, Italy</i>) - Luigi Cattivelli (<i>CREA, Italy</i>) - Rajeev Varshney (<i>IOC Chair, Murdoch University, Australia</i>) - Peter Langridge (<i>Scientific Committee Chair, Wheat Initiative</i>) <i>*invited to be confirmed</i>
09:30 - 10:10	OPENING KEYNOTES LECTURES CHAIR: Roberto Tuberosa (<i>Conference Chair, Professor Emeritus, Alma Mater Studiorium, Università di Bologna, Italy</i>)
09:30 - 09:50	Philip Pardey (<i>University of Minnesota, USA</i>) New realities of Agri-Food R&D Worldwide: Implications for varietal innovations in wheat
09:50 - 10:10	Beat Keller (<i>University of Zurich, Switzerland</i>) Pathogen-informed strategies for wheat resistance breeding
10:10 - 11:00	COFFEE BREAK
11:00 - 13:00	Session 1: ENABLING SUSTAINABLE WHEAT PRODUCTION IN A BROAD CROPPING SYSTEM. I: CROP MANAGEMENT, SOIL CONSERVATION AND HEALTH CHAIR: Pierre Martre (<i>INRAE, France</i>)
11:00 - 11:15	Moussadek Rachid (<i>INRA, Morocco</i>) Toward 1M ha of conservation agriculture in Morocco: Soils and crop resilience
11:15 - 11:30	Subbarao Guntur (<i>JIRCAS, Japan</i>) BNI-Wheats - A new category of nitrogen-efficient low-nitrifying wheat
11:30 - 11:45	Amanda de Oliveira Silva (<i>Oklahoma State University, USA</i>) Assessing wheat nitrogen use efficiency (recorded)
11:45 - 12:15	Discussion

DAY 1 - Monday, 25 May 2026

Europa Conference Room

12:15 - 13:00

SELECTED SHORT TALKS

- 12:15 – 12:19 Stefania Astolfi (*University of Tuscia, Viterbo, Italy*)
Optimizing sulfur nutrition as a driver for iron homeostasis and grain safety in durum wheat
- 12:19 – 12:23 Katharina Belt (*University of Western Australia*)
Proteome-informed breeding and management of nitrogen uptake and use efficiency across Australian broadacre wheat systems
- 12:23 – 12:27 Minely Cerón-Bustamante (*University College Dublin, Ireland*)
The wheat microbiome: Spatial and genetic drivers of bacterial and fungal communities in European wheat systems
- 12:27 – 12:31 Estienne Marie (*ARVALIS, Paris, France*)
Improving the performance of durum and winter wheat in intermediate areas of France through a combination of appropriate levers: Lessons from 10 years of system experimentation in the Syppre network
- 12:31 – 12:35 Wasihun Getahun (*Ethiopian institute of Agricultural Research, Addis Ababa, Ethiopia*)
Prospects for enhancing durum wheat productivity in Ethiopia: From field to market
- 12:35 – 12:39 Maria Hernandez-Soriano (*John Innes Centre, Norwich, United Kingdom*)
From genes to the rhizosphere: Harnessing root-microbiome interactions to improve nitrogen use efficiency in wheat
- 12:39 – 12:43 Jack Jameson (*TEAGASC, Carlow, Ireland*)
Learning from long-term data: How rotation and establishment systems have shaped winter wheat performance in a temperate Atlantic-influenced region
- 12:43 – 12:47 Ramadas Sendhil (*Pondicherry University, Puducherry, India*)
Identifying high-yield and high-profit cropping systems for sustainable wheat production in India – Evidence from nationally representative household survey
- 12:47 – 12:51 Paninder Pal Singh (*Michigan State University, United States*)
Exploring novel planting strategies for sustainable improvement in wheat yield and profits
- 12:51 – 13:00 **Discussion**

DAY 1 - Monday, 25 May 2026

Europa Conference Room

- 13:00 - 14:30 **LUNCH & POSTERS SET UP**
- 14:30 - 16:30** **Session 2: ENABLING SUSTAINABLE WHEAT PRODUCTION IN A BROAD CROPPING SYSTEM. II: PHENOMICS, ENVIROMICS, CROP MODELLING, DIGITAL AGRICULTURE**
CHAIRS: Kerstin Neumann (*Leibniz Institute of Plant Genetics and Crop Plant Research, Germany*), Nicola Pecchioni (*CREA, Italy*)
- 14:30 - 14:45 Bruno Basso (*Michigan State Univ, USA*)
Digital twins for the sustainability of cropping systems (recorded)
- 14:45 - 15:00 Andries Potgieter (*QAAFI, University of Queensland, Australia*)
The digital wheat revolution for more resilient wheat production
- 15:00 - 15:15 Jean-Pierre Cohan (*ARVALIS, France*)
Predicting wheat yield and production: Considering climate change effects
- 15:15 - 15:30 Senthold Asseng (*TUM, Germany*)
Crop model-guided traits for global adaptation to climate warming
- 15:30 - 15:45 Pierre Martre (*INRAE, France*)
Global needs for nitrogen fertiliser to improve wheat yield under climate change
- 15:45 - 16:00 **Discussion**
- 16:00 - 16:30** **SELECTED SHORT TALKS**
- 16:00 - 16:04 Shannon Baker (*Texas A&M AgriLife Research, Amarillo, United States*)
Strategically timed UAV remote sensing for robust wheat yield prediction: A multi-year study on phenology-aligned machine learning dynamics
- 16:04 - 16:08 Mariano Cossani (*SARDI-South Australian Research and Development Institute, PIRSA, URRBRAE, Australia*)
Spectral fingerprinting of wheat at early growth stages enables accurate grain yield prediction
- 16:08 - 16:12 Alexis Comar (*Hiphen, Avignon, France*)
Digitizing wheat variety testing: transitioning high-throughput phenotyping from research to regulatory infrastructure
- 16:12 - 16:16 Francesca Degan (*ARVALIS, Paris, France*)
Multi-climatic plausibility testing of nitrogen-mitigation scenarios in wheat using crop models: a benchmarking workflow for digital agronomy

DAY 1 - Monday, 25 May 2026

Europa Conference Room

- 16:16 - 16:20 Lukas Roth (*Martin-Luther-University, Halle (Saale), Germany*)
Characterizing yield through wheat's perception of chronological progression: a multi-omics plant-time warping approach
- 16:20 - 16:24 Menachem Moshelion (*The Hebrew University of Jerusalem, Rehovot, Israel*)
Synchronized plant-environment time series enable machine learning prediction of daily wheat transpiration from high-precision gravimetric lysimetry
- 16:24 - 16:28 Ehud Strobach (*Agricultural Research Organization, Rishon Lezion, Israel*)
Grain yield efficiency of dry land wheat in Israel: a high-resolution coupled crop-climate modeling approach
- 16:30 - 17:00 **COFFEE BREAK**
- 17:00 - 19:00** **Session 3: CARBON FOOTPRINT OF WHEAT PRODUCTION TO REDUCE GREENHOUSE GAS EMISSIONS: SATELLITE MONITORING OF WHEAT FARMING**
CHAIRS: Laura Ercoli (*Sant'Anna School for Advanced Studies, Italy*), Jean-Pierre Cohan (*ARVALIS, France*)
- 17:00 - 17:15 Tobias Schuhmacher (*Verband Deutscher Großbäckereien e.V., Germany*)
CO₂-footprint of the wheat value chain from farmers to mills and bakers
- 17:15 - 17:30 Netrananda Sahu (*University of Delhi, India*)
Carbon footprints and dynamics of wheat farming in India
- 17:30 - 17:45 Kenton Porker (*CSIRO - Australia*)
System synergies to build sustainable wheat yield frontiers in Australia
- 17:45 - 18:00 Tim George (*James Hutton, UK*)
Increasing sustainability of cereal crops using functional diversity
- 18:00 - 18:15 Chen Tsu-Wei (*Humboldt University of Berlin, Germany*)
Plasticity of source-sink dynamics contributes to wheat yield stability
- 18:15 - 18:45** **SELECTED SHORT TALKS**
- 18:15 - 18:19 Claudia Camplone (*University of Perugia, Italy*)
Environmental impacts of precision agriculture adoption in central Italy wheat production: A comparative LCA
- 18:19 - 18:23 Catherine Famelton (*Rothamsted Research, Harpenden, United Kingdom*)
Sucrose signalling: A new approach for reducing nitrogen inputs in wheat production?

DAY 1 - Monday, 25 May 2026

Europa Conference Room

- 18:23 - 18:27 Lukas Förter (*Justus-Liebig-University, Giessen, Germany*)
Improved carbohydrate accumulation drives wheat breeding progress and yield formation
- 18:27 - 18:31 Oorbessy Gaju (*University of Lincoln, United Kingdom*)
Phenotyping nitrogen use efficiency for a new benchmark nutrient management regime in UK farms
- 18:31 - 18:35 Vanderlise Giongo (*EMBRAPA, Passo Fundo, Brazil*)
Carbon footprint of Brazilian wheat production under contrasting farm sizes
- 18:35 - 18:39 Sendhil Ramadas (*Pondicherry University, Puducherry, India*)
Carbon footprint in wheat production: A systematic review and multi-method meta-analysis
- 18:39 - 18:44 Millicent Smith (*University Of Queensland, Brisbane, Australia*)
Breeding beyond the plot: Leveraging rotational genetics to improve wheat performance and farming system sustainability

DAY 2 - Tuesday, 26 May 2026

Europa Conference Room

09:00 - 11:00

Session 4: EXPLORING WHEAT DIVERSITY, EVOLUTION AND GENETIC RESERVOIRS

CHAIRS: Anna Maria Mastrangelo (*CREA, Italy*),
Zhiyong Liu (*Chinese Academy of Sciences, China*)

09:00 - 09:15

Weilong Guo (*China Agricultural University, China*)

Digitalizing the wheat evolution trajectories and genetic diversity

09:15 - 09:30

Tzion Fahima (*Haifa University, Israel*)

Genome-wide discovery of kinase fusion proteins for plant defense

09:30 - 09:45

Julie King (*Wheat Research Centre of Nottingham, UK*)

Genetic diversity from wheat's wild relatives

09:45 - 10:00

Satinder Kaur (*Punjab Agricultural University, India*)

Beyond the cultivated gene pool: Mining hidden genetic riches of wild germplasm

10:00 - 10:15

Elisabetta Mazzucotelli (*CREA, Italy*)

Harnessing the genetic wealth of tetraploid wheat relatives

10:15 - 10:30

Discussion

10:30 - 11:00

SELECTED SHORT TALKS

10:30 - 10:33

Matteo Bozzoli (*DISTAL, University of Bologna, Italy*)

Genetic diversity characterization of *Aegilops tauschii* wide sequenced collection to unlock useful alleles left-behind by domestication and breeding

10:33 - 10:36

Surbhi Grewal (*University of Nottingham, United Kingdom*)

Comprehensive atlas of wild relative introgressions reveals conserved introgression patterns and massive untapped diversity in wheat genebanks

10:36 - 10:39

Matthew Hayden (*Agriculture Victoria, Melbourne, Australia*)

Mapping global wheat diversity through an Australian lens

10:39 - 10:42

Max Haupt (*IPK Gatersleben, Germany*)

Genebank genomics provides a comprehensive genome diversity atlas of wheat

10:42 - 10:45

Kingsley Ikenna Ikpa-Agodo (*Tottori University, Tottori, Japan*)

Mitochondrial hybridity in *in vitro* fertilization-generated maizewheat and pearl milletwheat cybrids drive important stable phenotypic variations

DAY 2 - Tuesday, 26 May 2026

Europa Conference Room

- 10:45 - 10:48 Yael Lev-Mirom (*University of Haifa, Israel*)
Ancient grains illuminate the mosaic origin of domesticated wheat
- 10:48 - 10:51 Lorenzo Pancaldi (*DISTAL, University of Bologna, Italy*)
Comparative analysis of exome sequencing data reveals convergent selection of durum and bread wheat
- 10:51 - 10:54 Salome Lengrand (*Earth and Life Institute, Louvain-la-Neuve, Belgium*)
Long-term evolution of root architecture response to soil nitrogen management in tetraploid wheat (*Triticum durum*)
- 10:54 - 10:57 Zihao Wang (*China Agricultural University; Institute of Crop Sciences, Beijing, China*)
Digital characterization of chromosome centromeric haplotypes in polyploid wheat and their potential for breeding
- 10:57 - 11:00 Meryem Zaim (*ICARDA, Rabat, Morocco*)
Unlocking genetic diversity for climate-resilient durum wheat improvement
- 11:00 - 11:03 Amir Sharon (*Tel Aviv University*)
High-resolution genomics enables rapid gene discovery in *Aegilops longissima*
- 11:00 - 11:30 **COFFEE BREAK & POSTERS VISION**
- 11:30 - 12:30** **Panel Discussion I - SOIL AND THE RHIZOSPHERE IN WHEAT PRODUCTION: THE NEW FRONTIER FOR A SUSTAINABILITY**
CHAIRS: Laura Ercoli (*Sant'Anna School for Advanced Studies, Italy*),
Lee Hickey (*University of Queensland, Australia*)

PANELISTS: Francisca Castillo (*Neocrop Technologies, Chile*)
Maria Hernandez-Soriano (*John Innes Centre, UK*)
Eric Ober (*NIAB, UK*)
Alessandra Salvioli (*University of Torino, Italy*)+
- 12:30 - 14:00 **LUNCH**
- 14:00 - 16:00** **Session 5: WHEAT GENOMES AND PANGENOMES**
CHAIRS: Valentyna Klymiuk (*University of Saskatchewan, Canada*)
Mao Long (*Shandong Agricultural University, China*)
- 14:00 - 14:15 Marco Maccaferri (*University of Bologna, Italy*)
Tetraploid wheat pangenome to better bridge with hexaploid wheat
- 14:15 - 14:30 Luxiang Liu (*Institute of Crop Science of the Chinese Academy of Agricultural Sciences, China*)
Genome variation and breeding application of irradiation in wheat

DAY 2 - Tuesday, 26 May 2026

Europa Conference Room

- 14:30 - 14:45 Rajeev Varshney (*Murdoch University, Australia*)
Wheat pangenome 100+ and rising: Building a global haplotype catalogue
- 14:45 - 15:00 David Gilbert (*KAUST, Saudi Arabia*)
The Wheat Rchive
- 15:00 - 15:15 Adul Kader Allabdullah (*John Innes Centre, UK*)
GWAS across wheat genomes: Insights from the watkins collection
- 15:15 - 15:30 **Discussion**
- 15:30 - 16:00 SELECTED SHORT TALKS**
- 15:30 - 15:33 Emile Cavalet-Giorsa (*KAUST, Thuwal, Saudi Arabia*)
Tracing the origin of non-brittle rachis alleles in wheat
- 15:33 - 15:36 Susanne Dreisigacker (*CIMMYT, Texcoco, Mexico*)
Unlocking long-range haplotype diversity in synthetic hexaploid wheat for breeding
- 15:36 - 15:39 Cristian Forestan (*DISTAL, University of Bologna*)
From reference transcriptome to pangenome transcriptional diversity: Regulatory networks controlling kernel development in durum wheat
- 15:39 - 15:42 Kerrie Forrest (*Agriculture Victoria, Melbourne, Australia*)
An ecosystem of digital tools to solve the FAIR data problem in the pan-genome era
- 15:42 - 15:45 Weilong Guo (*China Agricultural University, Beijing, China*)
Digitalized map of homologous clusters across Poaceae species unveil the complex evolutionary trajectory of genes in Triticeae
- 15:45 - 15:48 Fei He He (*Chinese Academy of Sciences, Beijing, China*)
Genomic investigation of wheat genetic improvement: Introgression, disease resistance, and yield
- 15:48 - 15:51 Pauline Lasserre-Zuber (*INRAE, Clermont-Ferrand, France*)
The IWGSC RefSeq 3.0 and a bread wheat pangenome providing access to worldwide diversity
- 15:51 - 15:56 Kentaro K. Shimizu (*University of Zurich, Switzerland*)
10+ wheat genomes project highlights that purifying selection on deleterious variants is shaped by the interactions between subgenomes and gene expression
- 16:00 - 17:00 **COFFEE BREAK & POSTER VISION**

DAY 2 - Tuesday, 26 May 2026

Europa Conference Room

17:00 - 19:00

Session 6: WHEAT FUNCTIONAL GENOMICS

CHAIR: Eduard Akhunov (*Kansas State University, USA*)

17:00 - 17:15

Gurcharn Brar Singh (*University of Alberta, Canada*)

Genomics of novel disease resistance genes in wheat

17:15 - 17:30

Xia Lanqin (*Yazhou Bay National Laboratory, China*)

Genome editing for sustainable wheat production and population health

17:30 - 17:45

Pierre Sourdille (*INRAE, France*)

Evaluation of the fate of wild-relative introgressions in wheat

17:45 - 18:00

Huijun Guo (*CAAS, China*)

Induced mutations and application in genetic analysis of wheat yield

18:00 - 18:15

Yao Yingyin (*Agriculture University of Beijing, China*)

Deciphering the genetic basis of and-use quality in wheat

18:15 - 18:30

Discussion

18:30 - 19:00

SELECTED SHORT TALKS

18:30 - 18:33

Chiara D'Attilia (*University of Tuscia, Viterbo, Italy*)

Revealing the role of *IBH1* in brassinosteroid biosynthesis and signalling via CRISPR-Cas9 knockout in durum wheat

18:33 - 18:36

Benjamin Jaegle (*Agroscope, Zurich, Switzerland*)

K-mer-based GWAS in a wheat collection reveals novel and diverse sources of powdery mildew resistance

18:36 - 18:39

Miaomiao Li (*Chinese Academy of Sciences, Beijing, China*)

Cloning of diverse disease resistance genes from wild emmer wheat for breeding

18:39 - 18:42

Yunchuan Liu (*John Innes Centre, Norwich, United Kingdom*)

Rudimentary basal spikelet formation in wheat: The tug-of-war between vegetative and differentiation (recorded)

18:42 - 18:45

Long Mao (*Chinese Academy of Agricultural Sciences, Beijing, China*)

A TaKNOX1-TaAPO1-Rht1 feedback regulation orchestrates grain number and yield in wheat

DAY 2 - Tuesday, 26 May 2026

Europa Conference Room

- 18:45 - 18:47 Tori Millstead (*QAAFI, University of Queensland, Australia*)
Spatial transcriptomics of developing wheat seed reveals concentric gene expression zones and subgenome biased expression of key genes
- 18:47 - 18:50 Shun Sakuma (*Tottori University, Japan*)
Grain number increase 2 (gni2) improves floret fertility and enhances grain yield in wheat
- 18:50 - 18:53 Becca Testa (*John Innes Centre, Norwich, United Kingdom*)
Green be gone: Transcription factor nac3 regulates wheat senescence
- 18:53 - 19:00 **Discussion**

DAY 3 - Wednesday, 27 May 2026

Europa Conference Room

09:00 - 11:00

Session 7: INNOVATIVE WHEAT BREEDING

CHAIRS: Susanne Dreissigacker (*CIMMYT, Mexico*),
Curtis Pozniak (*University of Saskatchewan, Canada*)

09:00 - 09:20

Keynote Lecture: Eduard Akhunov (*Kansas State University, USA*)
Historical genomics of host-pathogen interaction in wheat rust pathosystem

09:20 - 09:35

Paula Silva (*INIA, Uruguay*)
Sustainable wheat production through trait discovery and pre-breeding

09:35 - 09:50

Jochen Reif (*IPK-Gatersleben, Germany*)
Innovations paving (half)-way towards hybrid wheat breeding

09:50 - 10:05

Jessie Alt (*Corteva Agriscience, USA*)
Advancing hybrid wheat through innovative breeding

10:05 - 10:20

Shuhei Nasuda (*University of Kyoto*)
Exploration of Asian wheat genetic diversity through NAM population

10:20 - 10:35

Tiwari Vijaj (*University of Maryland, College Park, USA*)
Translational research in wheat using einkorn genomics

10:35 - 10:45

Discussion

10:45 - 11:15

SELECTED SHORT TALKS

10:45 - 10:49

Filippo Bassi (*ICARDA, Rabat, Morocco*)
Genomic breeding for dryland durum at ICARDA

10:49 - 10:53

Francisca Castillo (*Neocrop Technologies, Valdivia, Chile*)
Integrative platform for accelerated development of wheat varieties via multiplex genome editing

10:53 - 10:57

Hickey Lee (*QAAFI, University of Queensland, Australia*)
An AI-guided breeding toolkit for durable multi-disease resistance in wheat

10:57 - 11:01

Takashi Okamoto (*Tokyo Metropolitan University, Japan*)
In vitro fertilization system with wheat, rice and maize gametes: Production of cytoplasmic hybrid between wheat and rice/maize across subfamily

11:01 - 11:05

Anne-Kathrin Pfrieme (*Martin-Luther-University, Halle, Germany*)
From haplotype-based QTL mapping to founder-resolved pangenomics: dissecting multi-disease resistance architecture in a wheat MAGIC population

DAY 3 - Wednesday, 27 May 2026

Europa Conference Room

- 11:05 - 11:09 Damiano Puglisi (*CREA, Italy*)
Integrating genomics, multi-trait multi-environment modeling, and multimodal deep learning frameworks for predicting yield components in Mediterranean durum wheat
- 11:09 - 11:13 Paolo Vitale (*CIMMYT, Mexico*)
Predictive breeding applications in wheat using genomics and phenomics through artificial intelligence and computer-vision
- 11:13 - 11:15 Yuan Zong (*China Agricultural University, Beijing, China*)
Wheat genome editing: From prime editing to large DNA fragment editing
- 11:15 - 11:45 **COFFEE BREAK & POSTERS VISION**
- 11:45 - 12:45** **Panel Discussion II: LIMITING PESTICIDE USE FOR A SUSTAINABLE WHEAT WITH A LOWER ENVIRONMENTAL FOOTPRINT**
CHAIRS: McNamara Louise (*Oak Park Crops Research Centre, Ireland*),
Kar-Chun Tan (*Curtin University, Australia*)

PANELISTS: Toby Bruce (*Keele University, UK*),
Nichola Hawkins (*NIAB, UK*),
Daniel Leybourne (*Agri Food and Biosciences Institute, Belfast, UK*),
Francesco Vidotto (*University of Torino, Italy*)
- 12:45 - 14:00 **GROUP PHOTO AND LUNCH aq**
- 14:00 - 19:00** **TECHNICAL TOURS**
(Meeting point at 14:00 in the Conference Hall)

DAY 4 - Thursday, 28 May 2026

Europa Conference Room

09:00 - 11:00 Session 8: DEVELOPING CLIMATE-SMART WHEAT IN THE CONTEXT OF ABIOTIC STRESSES

CHAIR: Laura Dixon (*IPK-Gatersleben, Germany*)

09:00 - 09:15

Hafssa Kabbaj (*ICARDA, Morocco*)

Genomic breeding for heat tolerance at ICARDA

09:15 - 09:30

Richard Trethowan (*University of Sydney, Australia*)

Buffering yield potential in an increasingly unstable environment

09:30 - 09:45

Daniel Miralles (*University of Buenos Aires, Argentina*)

A model based on allele combinations to predict phenology to prevent extreme weather events

09:45 - 10:00

Laura Dixon (*IPK-Gatersleben, Germany*)

The role of ambient temperatures in cereal adaptation

10:00 - 10:15

Sundeeep Kumar (*ICAR, India*)

Genomic insights into terminal heat tolerance from India's National Genebank collections

10:15 - 10:30

Discussion

10:30 - 11:00

SELECTED SHORT TALKS

10:30 - 10:33

Emily Carr (*University of Bristol, United Kingdom*)

An XTH gene modulates root exudate-substrate cohesion

10:33 - 10:36

Giulia Castorina (*CREA, Italy*)

Leveraging wild emmer wheat diversity to unlock adaptive traits to improve drought-resilience in durum wheat

10:36 - 10:39

Miles Curl (*John Innes Centre, UK*)

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

10:39 - 10:42

Seidat Oluwadamilola Dauda (*Western Sydney University, Penrith, Australia*)

Wheat's heat strategy: Linking stomatal traits, sugar dynamics, and grain omics to heat tolerance

10:42 - 10:45

Angela Juhasz (*Edith Cowan University, Joondalup, Australia*)

From root to grain: Multi-omics reveals how nitrogen, CO₂, and microbes tune wheat drought resilience and grain quality

DAY 4 - Thursday, 28 May 2026

Europa Conference Room

- 10:45 - 10:48 Zbynek Milec (*Global Change Research Institute, Brno, Czech Republic*)
Wheat responses to combined drought, heat, and elevated CO₂: Integrative morpho-physiological and transcriptomic insights under future climate scenarios
- 10:48 - 10:51 Grace Achieng Ochieng (*University of Bonn, Germany*)
Regulatory variation at TaNPF2.12 shapes nitrogen-responsive root plasticity and nitrogen use efficiency in winter wheat.
- 10:51 - 10:54 Jun Xiao (*Chinese Academy of Sciences, Beijing, China*)
Identification and functional characterization of wue and drought resilience factors in wheat
- 10:54 - 11:00 **Discussion**
- 11:00 - 11:30 **COFFEE BREAK & POSTERS VISION**
- 11:30 - 12:30** **Panel Discussion III: INTERNATIONAL COLLABORATION: CHALLENGES AND OPPORTUNITIES**
CHAIRS: Jeff Rosichan (*International Wheat Yield Partnership, USA*), Peter Langridge (*Wheat Initiative, Germany*)

PANELISTS: Maricelis Acevedo (*Cornell University, USA*), Filippo Bassi (*ICARDA, Morocco*), Richard Flavell (*John Innes Centre, UK*)
- 12:30 - 14:00 **LUNCH**
- 14:00 - 16:00** **Session 9: DISSECTING THE WHEAT-PATHOGEN AND PEST INTERACTION**
CHAIRS: Fiona Doohan (*University College Dublin*), Evans Lagudah (*CSIRO, Australia*)
- 14:00 - 14:15 Valentyna Klymiuk (*University of Saskatchewan*)
Integrative genomic approaches to resolve wheats genetic diversity for FHB resistance
- 14:15 - 14:30 Fiona Doohan (*University College, Dublin, Ireland*)
Dissecting wheat resistance to FHB and Septoria tritici blotch disease
- 14:30 - 14:45 Steven Xu (*USDA, USA*)
Breaking barriers: Ph1b-facilitated introgression of novel disease resistance genes from *Aegilops caudata*

DAY 4 - Thursday, 28 May 2026

Europa Conference Room

- 14:45 - 15:00 Wuletaw Tadesse (*ICARDA, Ethiopia*)
Accelerated wheat breeding and deployment to ensure food security in Africa
- 15:00 - 15:15 Sarrah Ben M'Barek (*Regional Field Crops Research Center Béja, Tunisia*)
Decoding wheat-fungal pathogen dynamics: Insights from durum wheat landraces
- 15:15 - 15:30 **Discussion**
- 15:30 - 16:00 SELECTED SHORT TALKS**
- 15:30 - 15:33 Natalia Arango (*King Abdullah University Of Science And Technology, Thuwal, Saudi Arabia*)
Non-host resistance genes – new sources for durable rust resistance?
- 15:33 - 15:36 Lorenzo Calzini, (*DISTAL, University of Bologna, Italy*)
Identification of candidate genes for resistance to soil-borne cereal mosaic virus in durum wheat using CRISPR-Cas9 genome editing systems
- 15:36 - 15:39 Samuel Holden (*University of Alberta, Edmonton, Canada*)
Pan-genome facilitated discovery of dominant North American stripe rust lineage's origin in somatic hybridization
- 15:39 - 15:42 Mogens Støvring Hovmøller (*Aarhus University, Agroecology, Slagelse, Denmark*)
Twenty years of global disease surveillance in wheat reveals increased vulnerability to yellow rust due to incursions of new aggressive races at regional and global scales
- 15:42 - 15:45 Chunyi Liu (*DISTAL, University of Bologna, Italy*)
Loci relevant for yellow rust resistance in a Mediterranean multi-environmental trial networks identified from the global durum genomic resource
- 15:45 - 15:48 Marion Müller (*University of Munich, Germany*)
Dual recognition of structurally unrelated mildew effectors underlies the broad-spectrum resistance of *Pm3e* in wheat
- 15:48 - 15:51 Laura Paire (*INRAE, Clermont-Ferrand, France*)
Meta-QTL analyses for better characterisation of the genetic architecture of bread wheat resistance to *Septoria tritici* blotch

DAY 4 - Thursday, 28 May 2026

Europa Conference Room

- 15:51 - 15:54 Kar-Chun Tan (*Curtin University, Perth, Australia*)
Asymmetric priority effects between co-infecting wheat pathogens undermine single-pathogen resistance
- 15:54 - 16:00 **Discussion**
- 16:00 - 17:00 **COFFEE BREAK & POSTER VISION**
- 17:00 - 19:00** **Panel Discussion IV: FROM STRAMPELLI TO INFORMED BREEDING IN A PUBLIC-PRIVATE PARTNERSHIP SCENARIO**
CHAIR: Roberto Tuberosa (*Professor Emeritus Alma Mater Studiorum, Università di Bologna, Italy*)
- PANELISTS:** Pasquale De Vita (*CREA, Italy*),
Marc Albertsen (*Ex Corteva, USA*),
Hans Braun (*ex CIMMYT, Mexico*),
José Crossa (*CIMMYT, Mexico*),
Nigussie Dechasa (*EIAR, Ethiopia*),
Xiangdong Fu (*CAAS, China*),
Guillermo Gerard (*CIMMYT, Mexico*),
Long Mao (*CAAS, China*)
- Nazareno Strampelli Award 2026 prizes**
Roberto Tuberosa (*Professor Emeritus Alma Mater Studiorum, Università di Bologna, Italy*)
Patrizia Galeffi (*ENEA, Italy*),
Stefania Masci (*University of Tuscia, Italy*)
- 19:00 - 19:10 **Presentation of IWC5 (2028)**

DAY 5 - Friday, 29 May 2026

Europa Conference Room

09:00 - 11:00	Session 10: WHEAT QUALITY, END-USE PROCESSING, NUTRITION AND HUMAN-HEALTH CHAIRS: Itria Ibba (<i>CYMMIT, Mexico</i>), Tatsuya Ikeda (<i>National Institute for Agro-Environmental Sciences in Japan, Japan</i>)
09:00 - 09:15	Francisco Barro (<i>CSICS Cordoba, Spain</i>) CRISPR/Cas strategies for high-quality, celiac disease-safe wheat
09:15 - 09:30	Nigel Halford (<i>Rothamsted, UK</i>) Agronomic and genetic approaches to reduce the risk of acrylamide formation in wheat products
09:30 - 09:45	Jan De Vries (<i>De Vries Nutrition Solutions, The Netherlands</i>) The role of wheat in a healthy and sustainable diet
09:45 - 10:00	Maria Caboni (<i>University of Bologna, Italy</i>) Whole grain and technological quality: Opportunities and challenges
10:00 - 10:15	Katherina Scherf (<i>University of Munich, Germany</i>) Proteomic insights into baking quality and wheat-related disorders
10:15 - 10:30	Discussion
10:30 - 11:00	SELECTED SHORT TALKS
10:30 - 10:34	Cristina Rodríguez-Suárez (<i>Instituto de Agricultura Sostenible, CSIC, Córdoba, Spain</i>) Mapping the landscape of carotenoid esterification in the global durum panel
10:34 - 10:38	Upendra Kumar (<i>Mahatma Jyotiba Phule Rohilkhand University, Bareilly, India</i>) Development of high dietary fiber wheat through introgression of β-glucan-rich alleles from <i>Aegilops kotschy</i>
10:38 - 10:42	Barbara Laddomada (<i>CNR ISPA, DISBA, Bari, Italy</i>) Clinical trials investigating the health-promoting effects of Svevo high-amylose products on patients affected by concomitant chronic disease and metabolic syndrome
10:42 - 10:46	Rose McNelly (<i>John Innes Centre, Norwich, United Kingdom</i>) Exploiting natural variation in starch granule size and composition in <i>Aegilops tauschii</i> to improve wheat starch

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- 10:46 - 10:50 Antonio Pescatore (*University of Florence, Italy*)
Optimizing selenium and sulphur foliar fertilization to enhance nutritional and technological quality of bread wheat
- 10:50 - 10:54 Naoto Sano (*INRAE, GDEC, Clermont-Ferrand, France*)
Pleiotropic genetic network underlying grain storage protein composition in bread wheat
- 10:54 - 10:58 Claudia Sardella (*University of Turin, Italy*)
Rheological, technological, and nutritional implications of high-amylose wheat in breadmaking
- 11:00 - 11:30 **COFFEE BREAK & POSTERS VISION**
- 11:30 - 12:30 Panel Discussion V: NOVEL NUTRITIONAL TRENDS TOWARD A HEALTHIER WHEAT-BASED DIET**
CHAIRS: Marina Carcea (*CREA, Italy*),
Jan De Vries (*De Vries Nutrition Solutions, The Netherlands*)

PANELISTS: Lorraine Brennan (*University College, Dublin*),
Silvia Folloni (*Open Fields, Italy*),
Tatsuya Ikeda (*Naro University, Japan*),
Riccardo Vecchi Lari (*Nomisma, Italy*)
- 12:30 - 14:00 **LUNCH**
- 14:00 - 16:00 Closing Session: ARE WE READY FOR DESIGNING THE FUTURE WHEAT CROP?**
CHAIRS: Sylvie Coultier (*Agriculture and Agri-Food Canada, Canada*),
Peter Langridge (*Wheat Initiative, Germany*)
- 14:00 - 14:15 Mariangela Hungria (*EMBRAPA, Brasil*)
A MicroGreen revolution empowering soil health, mitigating the emission of GHG for food production (recorded)
- 14:15 - 14:30 Brian Beres (*Agriculture and Agri-Food Canada, Canada*)
The nitrogen paradox: Feeding wheat, cutting emissions, and building resilient cropping systems (recorded)
- 14:30 - 14:45 Flavio Breseghello (*CIMMYT, Mexico*)
Is hybrid wheat a good thing for the global south?

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- 14:45 - 15:00 Ksenia Krasileva (*University of California, Berkeley, California*)
The rise of resistance: From natural diversity to precise modification of plant immune receptors
- 15:00 - 15:15 Evans Lagudah (*CSIRO, Australia*)
Embedding robust disease resistance into the architecture of tomorrow's wheat
- 15:15 - 15:30 Wolfram Weckwerth (*University of Wien, Austria*)
The holobiont concept in wheat breeding - a paradigm shift into sustainable agroecosystems
- 15:30 - 15:45 Michael Alaux (*INRAE, France*)
Use of AI in wheat databases: Overview and prospects
- 15:45 - 16:00 **Discussion**
- 16:00 - 16:30 Presentation of IWC6 (2030)**
- 16:30 - 16:45 Congress closure:**
Roberto Tuberosa (*Professor Emeritus, Alma Mater Studiorum, Università di Bologna, Italy*),
Rajeev Varshney (*Murdoch University, Australia*),
Peter Langridge (*Wheat Initiative, Germany*)

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INVITED SPEAKERS ABSTRACTS

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SHORT TALKS ABSTRACTS

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POSTERS ABSTRACTS

New realities of agri-food R&D worldwide: implications for varietal innovations in wheat

Philip Pardey ⁽¹⁾

⁽¹⁾ University of Minnesota (USA)

Abstract

Agri-food value chains around the world, including those for wheat, continue to change at a historically unprecedented pace. These changes have significant research, development and innovation (RDI) implications, not only regarding primary production (i.e., farmers, farms, and farming) but also for the pre- and post-farm components of these value chains. Drawing on newly developed global data on RDI investments and value chains, Phil will describe the nature of these changing agri-food transformation realities through an RDI lens. In so doing he will present new evidence on the profound changes in the geographical distribution of and public and private roles in agri-food R&D worldwide, highlighting the implications of all these changes for the wheat sector in general and wheat varietal innovation in particular.

Pathogen-informed strategies for wheat resistance breeding

Beat Keller ⁽¹⁾ - ***Bernasconi Zoe*** ⁽¹⁾ - ***Lukas Kunz*** ⁽¹⁾ - ***Marion C. Müller*** ⁽²⁾

⁽¹⁾ University of Zürich, Department of Plant and Microbial Biology, Zürich, Switzerland - ⁽²⁾ Technical University of Munich, Chair of Phytopathology, TUM School of Life Sciences, Freising, Germany

Abstract

Durable disease resistance in wheat increasingly depends on integrating pathogen biology into breeding strategies. While single resistance genes remain central to controlling major fungal diseases such as powdery mildew and rusts, their effectiveness is often short lived because pathogens rapidly adapt. Advances in the molecular understanding of plant-microbe interactions now reveal how both host and non-host pathogens overcome immune barriers, enabling more targeted and sustainable resistance breeding. Recent work on wheat powdery mildew illustrates these dynamics. The AvrPm8 effector gene, recognized by the wheat resistance gene Pm8, has undergone multiple independent loss of function mutations in global mildew populations once Pm8 was widely introduced with the 1RS.1BL translocation. These mutations allow the pathogen to evade recognition, explaining the rapid breakdown of Pm8 resistance. In a broad research approach to study the molecular determinants of pathogen recognition, the identification of avirulence genes corresponding to specific resistance genes has allowed us to define suitable geographical regions for the use of specific genes and gene combinations. In non-host adaptation, the example of triticale mildew which evolved through hybridization provides another example how effector diversification shapes pathogen virulence trajectories and host specialization. The AvrPm4-Pm4 interaction provides a different case of pathogen virulence evolution. Here, the avirulence effector shows little genetic diversity in the global mildew population and virulence is not conferred by a virulent effector variant. Instead, mildew evolved a suppressor specifically blocking Pm4-based cell death. Importantly, this suppressor is recognized by the Pm1a immune receptor, suggesting a breeding strategy of combining Pm4 and Pm1a-based resistance.

Together, these insights form the basis of pathogen-informed resistance breeding, an approach that integrates effector biology, population genomics, and evolutionary principles. By prioritizing resistance genes targeting multiple or functionally constrained effectors, combining genes with complementary recognition spectra, and monitoring pathogen populations for emerging virulence alleles, breeders can design resistance portfolios with improved longevity. Furthermore, this integrated approach delivers the molecular knowledge for the engineering of improved immune receptors with more diverse recognition spectra. Such strategies are essential for maintaining wheat productivity in the face of rapidly evolving and emerging pathogens and for transitioning from reactive to predictive resistance breeding.

Translational digital agronomy for durum wheat sustainability

Michele Pisante ⁽¹⁾

⁽¹⁾ University of Teramo, Department of Bioscience and Technology for Food, Agriculture and Environment, Teramo, Italy

Abstract

Durum wheat faces significant challenges globally, from adapting to climate change to the growing demand for sustainable, high-quality production from the processing industry.

To this end, advanced technological management approaches structured into Precision Digital Agriculture systems have been developed in various production areas. These systems optimize the use of production factors based on multi-source data from indirect measurements of physical parameters in the open field and real-time monitoring of crop conditions using satellite remote sensing and aerial platforms.

The recent introduction of morphological and functional imaging technologies in the laboratory, for direct, non-destructive measurements of cellular spatiotemporal dynamics related to stress biomolecules, alterations in metabolite transport, and changes in plant structure and water flow, has highlighted enormous potential. The further possibility of using imaging technologies directly in open fields currently represents the most promising prospect for translating agronomic research to early diagnostic biotic and abiotic stresses in type, and severity, for to adopt decision support systems for the application of site-specific and variable-rate precision agriculture technologies across all crop management. In the near future, functional imaging will represent the cornerstone of smart agriculture, helping to redesign new management strategies and adaptive methodological approaches for Durum wheat aimed at greater efficiency, sustainability, and eco-compatibility.

Toward 1M ha of conservation agriculture in Morocco: Soils and crop resilience

Moussadek Rachid ⁽¹⁾

⁽¹⁾ (INRA, Morocco)

Abstract pending

BNI-Wheats – A New-Category of Nitrogen-Efficient Low-Nitrifying Wheats

Guntur V Subbarao, Kishii Masahiro and Tadashi Yoshihashi

Japan International Research Center for Agricultural Sciences (JIRCAS), Tsukuba, Ibaraki, Japan.

Wheat crops consume nearly a third of nitrogen fertilizer applied to global agricultural systems. Due to uncontrolled soil-nitrifier activity, 70% of this nitrogen fertilizer applied to wheat fields is lost through nitrate-leaching and gaseous emissions of nitrous oxide, reducing nitrogen-use-efficiency and causing ecological and environmental damage. Biological nitrification inhibition (BNI) is a natural plant function where nitrification inhibitors (BNIs) are released from roots that suppress nitrifier activity to protect soil-N from being lost into larger ecosystem. Cultivated wheat-root systems do not have sufficient BNI-capacity, thus can't limit nitrate formation in the root-zone. BNI-wheats are developed by transferring the high-BNI capacity of root systems in wild-wheat (*Leymus racemosus*) (located in the short-arm of 'n' chromosome, Lr#n-SA), into modern wheats (Lr#n-SA replaces the short-arm of 3B wheat chromosome). BNI-wheats produce 3-5-fold higher BNI-activity from root systems, suppress soil-nitrifier activity, soil-nitrate formation (30-50% in the root-zone), reduce nitrous oxides emissions (about 30%). BNI-wheats require 30-50% less N-fertilizers to produce similar or better grain yields than current elite-wheats. The yield potential of BNI-wheats is about 10-12 t ha⁻¹, can have 10-20% higher grain yields (than present elite wheats). BNI-wheat technology is scalable as BNI-trait (i.e. Lr#n-SA) can be introduced into any elite-wheats (both Spring-wheats and Winter-wheats) through marker-assisted backcross breeding. Currently BNI-trait (Lr#n-SA) is being introduced into several mega-wheat varieties grown in Indo-Gangetic-Plains of India. The first BNI-wheat variety is expected to enter wheat production systems in two-three years from now. The potential for scaling BNI-wheat technology into global wheat production systems is the subject of this presentation.

Assessing wheat nitrogen use efficiency through plant nutrition approaches

Amanda de Oliveira Silva ⁽¹⁾ - ***Tony Vyn*** ⁽²⁾

⁽¹⁾ Oklahoma State University, Plant and Soil Sciences, Stillwater, United States - ⁽²⁾ Purdue University, Department of Agronomy, West Lafayette, United States

Abstract

Nitrogen (N) is one of the most significant input costs for wheat farmers, making improvements in nitrogen use efficiency (NUE; grain yield/N available) essential for reducing production expenses, minimizing environmental impact, and ensuring long-term sustainability. Effective N management in wheat is crucial not only for maximizing yield but also for maintaining grain protein concentration. However, low NUE in wheat often results from the difficulty of synchronizing N availability with plant demand under changing environmental conditions. Our previous research indicates that while some wheat varieties achieve higher nitrogen utilization efficiency (NUE; grain yield/total N uptake), this can come at the cost of reduced grain protein concentration, underscoring the need for a more integrated physiological approach to NUE improvement.

To address this challenge, our research investigated plant nutrition strategies using ¹⁵N-labeled fertilizer applications as in-season phenotyping tool for wheat. We compared hard-red winter wheat genotypes with similar grain yield levels but differing protein concentrations to better understand the mechanisms driving NUE in the US Southern Great Plains. Labeled N was applied at the boot, anthesis, and soft dough stages, with biomass components sampled four days after each ¹⁵N application to track N uptake and partitioning. This approach provided a more precise evaluation of plant N status, uptake dynamics, and allocation under dryland conditions. Preliminary results suggested that ¹⁵N applications provided accurate information of current N uptake and partitioning at different wheat growth stages. By integrating physiological and management factors, this research aims to develop more efficient wheat production systems that enhance farmer profitability while promoting environmental sustainability.

Digital twins for the sustainability of cropping systems

Bruno Basso ⁽¹⁾

⁽¹⁾ Michigan State University

Abstract

Cropping systems face mounting pressure to simultaneously increase productivity, reduce environmental impact, and adapt to intensifying climate variability. Meeting these intertwined objectives at scale requires moving beyond static recommendations toward dynamic, field-specific decision support. Digital twins defined as virtual representations of agricultural fields that continuously assimilate observational data and simulate biophysical processes, offer a powerful framework for achieving this transition. Here, I describe an integrated digital twin architecture for cropping systems that links yield stability zone (YSZ), multi-source remote sensing, process-based crop modeling, artificial intelligence, and probabilistic weather forecasts to deliver site-specific, time-sensitive management guidance across millions of hectares. Application of this digital twin approach across the U.S. Corn Belt has demonstrated that variable-rate nitrogen prescriptions guided by YSZ-model-AI integration can reduce nitrogen inputs by 20–40% in low-stable and unstable zones while maintaining or increasing yield, lowering reactive nitrogen losses and the carbon footprint of grain production. Digital twins represent a transformative pathway toward climate-resilient, economically viable, and environmentally sound cropping systems, translating field-scale science into landscape-scale impact

The digital wheat revolution for more resilient wheat production

Andries Potgieter ⁽¹⁾

⁽¹⁾ (QAAFI, University of Queensland, Australia)

Abstract pending

Predicting wheat yield and production: considering additional factors to climate change is essential but challenging

Jean-Pierre Cohan ⁽¹⁾

⁽¹⁾ ARVALIS, Research & Development department, Paris, France

Abstract

Wheat yield and production are impacted by many factors in most countries around the world. Many relevant studies have been published during the last three decades to address this issue. They focused on the impact of climate change in yield, which will be a major driver of wheat production in the future. Initially they only addressed the trend evolutions of temperatures and rain events and their relationship with abiotic stress (drought, heat stress...). Then other aspects were progressively introduced like the occurrence of extreme weather events impacting the variability of yield, the role of elevated CO₂ concentration as a potential mitigating factor of wheat yield losses and, more recently, some first attempts to consider the evolution of biotic stresses. Nevertheless, an accurate assessment of the future wheat production evolution needs now to integrate some other major factors that are more challenging to address but essential to provide relevant information to farmers and agriculture stakeholders. Based on recent studies and current projects conducted in Europe, this presentation aimed to introduce how wheat yield and production predictions need now to include issues related to 1/ all biotic stresses including weeds, 2/ the economic situations of individual farms related to the international context (market prices, access to input...) and 3/ the impact of all these factors not only on yield but also on wheat surfaces which is the other determinant of wheat production. This kind of study is challenging because related data are more difficult to access and more complicated to consider in modelling. Nevertheless, adopting this approach will be essential to elaborate more relevant adaptation strategies at different scales firstly to maintain wheat production and then to increase it in the future.

Crop model-guided traits for global adaptation to climate warming

Senthil Asseng ⁽¹⁾ - ***Pierre Martre*** ⁽²⁾ - ***Heidi Webber*** ⁽³⁾ - ***Frank Ewert*** ⁽³⁾ - ***AgMIP-Wheat*** ⁽⁴⁾

⁽¹⁾ Technical University Munich, HEF World Agricultural Systems Center, Freising, Germany - ⁽²⁾ INRAE, LEPSE, Montpellier, France - ⁽³⁾ ZALF, ZALF, Müncheberg, Germany - ⁽⁴⁾ international, international, international, -

Abstract

Improving wheat (*Triticum aestivum* L.) yields to meet the projected demand for food in the future requires new approaches. A collaboration of crop modelers, physiologists, geneticists, plant breeders and system agronomists in the Agricultural Model Intercomparison and Improvement Project (AgMIP) for Wheat (AgMIP-Wheat) enabled a multi-model-ensemble-based, systematic search and evaluation of new traits for climate change adaptation. Against perceived understanding of wheat cropping systems, model simulations suggested a combination of delayed anthesis with an increased grain filling rate as possible adaptation traits for wheat to increased temperature across wheat growing regions of the world. After exploring four independent field experiments from Egypt, Italy, USA and Mexico, we identified a number of cultivars/lines which were grown along temperature transects with such trait combination, which indeed were better adapted to a warming climate. That is, these cultivars/lines yielded higher with this trait combination than other cultivars, without this trait combination, under warmer conditions. This trait combination was then introduced in a multi-model, multi-year, future climate change scenario simulation experiment across the globe. The new genotypes, with delayed anthesis and an increased grain filling rate, were in the simulation better adapted to warmer temperatures. The new genotypes could boost in the simulation, global wheat yield by 7% and protein yield by 2%, but grain protein concentration would be reduced by –1.1 percentage points. Multi-model ensembles used in a collaboration of crop modelers, physiologists, geneticists, plant breeders and system agronomists offer robust new avenues to explore novel traits to be tested in silico, before introducing these into crop breeding programs.

Global needs for nitrogen fertiliser to improve wheat yield under climate change

Pierre Martre⁽¹⁾ - **Sibylle Dueri**⁽¹⁾ - **Jose Guarin**⁽²⁾ - **Frank Ewert**⁽³⁾ - **Heidi Weber**⁽³⁾ - **Daniel Calderini**⁽⁴⁾ - **Gemma Molero**⁽⁵⁾ - **Matthew Reynolds**⁽⁶⁾ - **Daniel Miralles**⁽⁷⁾ - **Guillermo Garcia**⁽⁷⁾ - **Hamish Brown**⁽⁸⁾ - **Jean-Pierre Cohan**⁽⁹⁾ - **Jean-Charles Deswarte**⁽¹⁰⁾ - **Gustavo Slafer**⁽¹¹⁾ - **Francesco Giunta**⁽¹²⁾ - **Davide Cammarano**⁽¹³⁾ - **Roberto Ferrise**⁽¹⁴⁾ - **Thomas Gaiser**⁽¹⁵⁾ - **Yujing Gao**⁽¹⁶⁾ - **Gerrit Hoogenboom**⁽¹⁶⁾ - **Leslie Hunt**⁽¹⁷⁾ - **Kurt Kersebaum**⁽³⁾ - **Claas Nendel**⁽³⁾ - **Gloria Padovan**⁽¹⁴⁾ - **Alex Ruane**⁽²⁾ - **Amit Srivastava**⁽³⁾ - **Tommaso Stella**⁽³⁾ - **Iwan Supit**⁽¹⁸⁾ - **Peter Thorburn**⁽¹⁹⁾ - **Enli Wang**⁽²⁰⁾ - **Joost Wolf**⁽²¹⁾ - **Chuang Zhao**⁽²²⁾ - **Zhigang Zhao**⁽²³⁾ - **Senthold Asseng**⁽²⁴⁾

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Abstract

Innovations in plant breeding and agronomy have supported a linear increase in wheat yield potential since the 1960's, which has significantly contributed to global food security. However, in many regions of the world, the translation of genetic yield progress into farmers' fields is increasingly constrained by a yield gap, which in most regions is caused by low soil N availability. We will analyze improvements in grain yield that can be expected from promising new yield traits. We also quantified the amount of N that would be needed to translate an increased yield potential from these traits to higher yields in farmers' fields. First, we evaluated a multi-model ensemble (MME) of 12 wheat models at five global high-yielding field sites. We found that the ensemble captured well both the interannual yield variability and yield response to sowing date and sowing density. The MME also simulated well the yield response to new sink-source traits observed in the field at several contrasting sites. We then used our tested wheat model ensemble to quantify the yield response of improved wheat cultivars with high-yielding traits under current and climate change scenarios across 60 representative global sites and quantify yield increase with present N application rates and the amount of N-fertilizer needed to achieve full yield potential with the improved traits. Our simulations show that wheat yield could be increased with the new traits by 16% with current N fertilizer applications under both current climate and mid-century climate change scenarios. To achieve the full yield potential from the new traits, a 52% increase in global average yield under a mid-century RCP8.5 climate scenario, and simultaneously maintain grain protein concentration at the value required for bread making, N fertilizer applications would need to increase fourfold over current rates. Such increase in N fertilizer application would unavoidably lead to higher environmental impact from wheat production. New sources of N and novel solutions to improve N management reducing N fertilizer losses for high-yielding wheat crops are thus urgently needed, especially in regions where yield is already strongly limited by nutrients and where the access to fertilizer is most difficult.

CO₂ footprint of the wheat value chain from farmers to mills and bakers

Tobias Schuhmacher ⁽¹⁾

⁽¹⁾ Verband Deutscher Großbäckereien e.V., Management, Düsseldorf, Germany

Abstract

The reduction of greenhouse gas emissions has become a central challenge for the agri-food sector, particularly in staple crops such as wheat. As consumer awareness of sustainability increases, the carbon footprint of wheat-based products is emerging as a key decision factor, with a significant share of consumers willing to pay a premium for lower-emission products.

This presentation provides a comprehensive analysis of the CO₂ footprint along the wheat value chain, from agricultural production to milling and baking. Special attention is given to emission hotspots such as fertilizer use, energy consumption in processing, and logistics. The role of sustainability frameworks, such as the Farm Sustainability Assessment (FSA), is discussed as a tool for harmonizing and improving agricultural practices across environmental, social, and economic dimensions.

In addition, current industry initiatives are presented, including low-carbon fertilizers, regenerative agriculture practices, and carbon sequestration approaches. However, these measures often lead to increased costs, raising critical questions about economic viability and fair value distribution within the supply chain.

The presentation also explores innovative concepts for improving transparency and consumer communication, such as classification systems for production methods and CO₂-based labeling schemes for wheat and cereal products. While such approaches offer opportunities for differentiation and market incentives, they also pose challenges in terms of standardization, data comparability, and credibility.

Finally, the contribution outlines pathways toward a harmonized, science-based, and economically viable approach to reducing the carbon footprint of wheat products. Collaboration across the entire value chain will be essential to achieve meaningful emission reductions while ensuring the long-term sustainability of the sector.

Carbon footprints and dynamics of wheat farming in India

Netrananda Sahu ⁽¹⁾

⁽¹⁾ University of Delhi, Department of Geography, Delhi School of Economics, Delhi, India

Abstract

India's wheat sector is central to national food security, yet its carbon footprint remains poorly understood at the regional scale. The dominant gap in existing literature is a tendency to treat wheat emissions as a crop-level problem, which obscures how strongly footprint magnitude depends on the production system surrounding the crop rather than on the crop itself. This synthesis is grounded in a comprehensive body of recent literature, encompassing national spatial inventories, farm-gate carbon footprint surveys, district-scale energy assessments, process-based models, and long-term field experiments. Drawing on this evidence base, it examines where carbon burdens of wheat production are concentrated across India, which emission sources drive them, and which management transitions carry credible mitigation potential. Three drivers appear consistently across methods and regions: nitrogen fertilizer, irrigation energy, and residue management. Their relative contributions shift substantially with local production context. Reported wheat carbon footprints range from approximately 0.50 kg CO₂-equivalent per kilogram of grain in lower-intensity, less irrigation-dependent production systems of eastern India to 0.83 kg CO₂-equivalent per kilogram in Punjab, while energy and greenhouse gas intensity vary by as much as fourfold across Indian districts. Punjab, where groundwater-dependent irrigation, high nitrogen use, and residue burning combine, represents the most thoroughly documented high-footprint wheat system. Bihar and the eastern Indo-Gangetic Plains offer a structurally different and lower-emission contrast, with recent field evidence showing carbon footprint reductions of up to 78 percent under zero tillage with residue retention and nitrous oxide emission reductions of up to 16 percent through precision nitrogen management without yield loss. The central finding is that wheat's carbon footprint in India is a regional systems problem. The most credible mitigation options are already empirically established, spatially specific, and directly tied to wheat cultivation methods within its surrounding production environment.

System synergies to build sustainable wheat yield frontiers in Australia

Kenton Porker ⁽¹⁾ - ***John Kirkegaard*** ⁽²⁾ - ***Therese McBeath*** ⁽¹⁾ - ***Rick Llewellyn*** ⁽¹⁾ - ***Bonnie Flohr*** ⁽¹⁾ - ***Romulo Lollato*** ⁽³⁾ - ***Nick Poole*** ⁽⁴⁾

⁽¹⁾ CSIRO, Agriculture and Food, Urrbrae, Australia - ⁽²⁾ CSIRO, Agriculture and Food, Canberra, Australia - ⁽³⁾ Kansas State University, Wheat & Forages Production, Manhattan, United States - ⁽⁴⁾ Field Applied Research, FAR Australia, Bannockburn, Australia

Abstract

Australian wheat production has long been driven by a national aspiration to continue raising and achieving higher water limited yields. Predominantly grown in dryland systems, production occurs under some of the highest seasonal and spatial rainfall variability globally, with yields ranging from 1 to over 12 t ha⁻¹ across environments and rivalling the world's highest yielding production systems in favourable seasons. Despite higher input costs, increasing climate uncertainty, and logistical constraints, productivity per unit of water supply has continued to improve.

Agronomic and genetic innovations adopted over the past 5–10 years have increased both the yield frontier and achieved yields of Australian wheat growers. These have ranged from low cost, incremental management changes to higher input interventions requiring greater skill and coordination. In high rainfall zones, the adoption of slower developing, European derived genetics has improved the match between crop phenology and environment and enhanced disease resistance, lifting yield ceilings. In contrast, low to medium rainfall systems have been transformed through soil amelioration and engineering solutions that remove physical soil constraints and improve access to, and efficiency of, soil water. Importantly, many of these innovations demonstrate that productivity gains can align with improved profitability and sustainability outcomes, including enhanced soil natural capital, reduced reliance on pesticides, and lower emissions intensity per unit of production.

These step changes highlight the central role of agronomy in integrating new technologies into farming systems. As both emerging and longstanding constraints such as input costs, climate variability, and emissions pressures increasingly shape decision making, sustaining productivity gains will require greater collaboration across disciplines. Future progress depends on delivering scientifically robust, industry relevant farming systems programs developed in partnership with discipline experts, ensuring wheat yield growth remains both profitable and sustainable.

“Increasing sustainability of cereal crops using functional diversity”

Tim George ⁽¹⁾

⁽¹⁾ *The James Hutton Institute, The International Barley Hub, Dundee, United Kingdom*

Abstract

Enhancing the sustainability of cereal production requires a shift from uniform, high-input systems toward crops and cropping systems that exploit functional diversity. This talk explores how variation in plant traits and their genetic controls can be harnessed to improve resilience and resource-use efficiency in cereals, with a particular focus on barley. Key functional traits underpinning drought tolerance include root system architecture, osmotic adjustment, and stomatal regulation, which are controlled by complex, often polygenic networks responsive to environmental cues. Improving nitrogen use efficiency (NUE) can be addressed through traits governing root uptake capacity, internal nitrogen remobilisation, and interactions with soil microbiota, including the emerging role of biological nitrification inhibition (BNI) in reducing nitrogen losses.

The capacity of cereals to utilise organic phosphorus (P) is another critical dimension of sustainability. Traits such as root exudation of phosphatases and organic acids, mycorrhizal associations, and rhizosphere modification are discussed alongside their genetic regulation. In parallel, micronutrient efficiency—particularly for manganese (Mn)—is considered, highlighting physiological and genetic mechanisms that enable tolerance to low Mn availability in high pH or organic soils.

The presentation will highlight barley landraces as models for functional diversity, illustrating how locally adapted germplasm can combine multiple beneficial traits, including nutrient efficiency and stress resilience. By integrating trait-based approaches with advances in genomics and breeding, our work demonstrates pathways to develop cereal varieties better suited to low-input, climate-resilient agriculture. Ultimately, leveraging functional diversity offers a powerful strategy to enhance productivity while reducing environmental impacts.

Digitalizing the wheat evolution trajectories and genetic diversity with novel algorithms

Weilong Guo⁽¹⁾ - Jianxia Niu⁽¹⁾ - Xiaoming Xie⁽¹⁾ - Wenxi Wang⁽¹⁾ - Zihao Wang⁽¹⁾ - Zhe Chen⁽¹⁾ - Zhengzhao Yang⁽¹⁾ - Yongming Chen⁽¹⁾ - Yuqi Zhang⁽¹⁾ - Zhaoheng Zhang⁽¹⁾ - Lingfeng Miao⁽¹⁾ - Peng Zhao⁽¹⁾

⁽¹⁾ Wheat Genetics and Genomics Center, China Agricultural University, Beijing, China

Abstract

Entering a pan-genomic era, wheat genomic research has moved beyond a single reference to embrace the species' vast genetic diversity. We have developed a suite of novel algorithms and computational strategies to digitalize functional genomic elements in wheat, enabling high-resolution tracing of its domestication and diversification processes.

At gene level, we established a pan-genomic approach to connect emerging genome assemblies across the Triticeae tribe, culminating in the development of the Triticeae-GeneTribe (TGT) database. We further indexed homologous gene clusters (HOCs) as evolutionary units, and developed a digital framework to resolve the complex evolutionary trajectories of these clusters, deciphering the birth-death dynamics of functional genes that drive adaptive evolution.

To overcome the limitations of single linear reference, we integrated three high-quality assemblies of Chinese Spring to generate a near-perfect backbone genome (CS-NP). A pan-reference genome (WheatPanRef) was further constructed by integrating 37 high-quality assemblies, expanding the Chinese Spring reference by 4.37 Gb to a total of 18.8 Gb. The WheatPanRef is aiming to provide a unified coordinate system for variation mapping through WheatUnion.

At haplotype level, we proposed a hierarchical strategy to catalog haplotypes at both ancestral and germplasm-lineage levels based on our previously developed IntroBlocker and ggComp. A digital HapMap was built to reveal the mosaic structure of population haplotype landscape, introgression genomic blocks, and diversified centromeric haplotypes, enabling pedigree reconstruction and germplasm networking in wheat. For cost-effective genotyping, we leveraged ultra-low-coverage sequencing via CNVb to tag large copy-number variations and developed lcQTH for rapid QTL mapping by tracing parental haplotypes in mapping populations.

Toward pan-omics integration, we constructed wGRN for regulatory network inference and trait prediction, and developed PanSK uses k-mers to predict complex traits such as end-use quality. We further generated time-series transcriptomic landscapes of wheat seed and tiller development, linking phenotypic plasticity with network module dynamics, and identified a series of hub regulators.

In summary, these algorithms and resources (<https://wheat.cau.edu.cn/resources/>) collectively digitalize wheat's evolution and diversity, providing powerful tools for decoding germplasm resources and accelerating molecular breeding through pan-omics approaches.

Genome-wide discovery of kinase fusion proteins as genetic resources for plant defense

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Abstract

Domestication and modern plant breeding have eroded plant genetic diversity, making crop wild relatives the most promising source of novel R-genes for resistance breeding. Plants rely on innate immune receptors to perceive pathogen-derived signals and activate defense responses, including cell-surface receptor kinases (RKs) and intracellular nucleotide-binding leucine-rich repeat (NLR) receptors. Pathogens continually evolve countermeasures, driving an arms race that threatens global food security and highlighting the need for durable, broad-spectrum resistance.

We previously cloned the yellow rust resistance gene Yr15 (WTK1) from wild emmer wheat. Yr15 encodes a tandem kinase protein we named Wheat Tandem Kinase 1 (WTK1). Whole-transcriptome profiling showed that WTK1 rapidly reprograms defense-associated gene expression and triggers localized programmed cell death upon infection, thereby conferring effective resistance. This discovery prompted us to ask how widespread kinase-based immune architectures are across the plant kingdom.

Cloning WTK1 led to the discovery of a widespread family of tandem kinase proteins (TKPs) across the plant kingdom. TKPs are a subgroup of a broader kinase fusion protein (KFP) family that also includes Momo kinases fused with integrated domains (mKFPs) (Fahima and Coaker, Nature Genetics, 2023). Across more than 100 plant species, we identified 2,682 TKPs: over half harbor 127 distinct fused non-kinase domains (Reveguk et al., Nature Genetics, 2025). Phylogenetic analyses suggest that TKPs originated from RKs by convergent molecular evolution and may act as decoys for pathogen effectors targeting RK signaling.

Extending this framework to KFPs across 165 plant species spanning eight clades, from algae to monocots, revealed 35,582 predicted KFPs (32,545 mKFPs and 3,037 TKPs). To date, 23 Triticeae KFPs have been experimentally validated, representing 22% of all cloned Triticeae R-genes. Most functional KFPs are derived from crop wild relatives, and confer resistance to devastating diseases such as rusts, powdery mildew, and wheat blast, underscoring their value for resistance breeding. These findings establish KFPs as rich genomic resources for resistance breeding and provide a foundation for dissecting the mechanisms of kinase-based decoy immunity in plants.

Genetic diversity from wheat's wild relatives

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Abstract

Increasing the genetic diversity of wheat is key to its future production in terms of increasing yields, resistance to diseases and adaptability to fluctuations in global climate. The use of the progenitor species of wheat and its wild relatives uniquely provides a route to vastly increase the genetic variation available to wheat breeders for the development of new, superior wheat varieties.

Over 800 homozygous introgression lines, generated at the Wheat Research Centre (WRC) at Nottingham University, have been characterised using genomic in situ hybridisation, chromosome-specific KASP markers and skim-sequencing. These introgression lines have been generated from a range of wild relatives and provide a resource both to identify new sources of traits of interest such as disease resistances, flowering morphology and grain quality but also to study the genes underlying these traits of interest. The identification of the genes underlying traits of interest is being aided by the genome assemblies of wild relative species which are increasingly becoming available, including those of *Triticum timopheevii* and *Aegilops mutica* generated at the WRC.

The wild relatives of wheat are also providing routes to investigate other aspects of biology. We are using a new promotor of homoeologous recombination to increase the number of introgressions while sequencing is providing information on sites of homoeologous recombination between wheat and its wild relatives.

Beyond the cultivated gene pool: mining hidden genetic riches of wild germplasm for wheat improvement

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Abstract

Wheat (*Triticum aestivum* L.), an important staple food, provides nearly one-fifth of the calories consumed by the world's population. Over the past decades, genetic improvement has substantially enhanced wheat productivity and strengthened its resilience against numerous biotic and abiotic stresses. However, accelerating climate change, the emergence of new pathotypes, and environmental constraints continue to threaten sustainable wheat production. Harnessing novel genetic variation has therefore become a critical priority for future wheat improvement programs. Wild relatives of wheat, particularly species of *Triticum* and *Aegilops*, represent an extraordinary reservoir of genetic diversity that has remained largely untapped. At Punjab Agricultural University (PAU), Ludhiana, we maintain a rich collection of more than 1,200 wild wheat accessions representing 22 species, along with diverse germplasm developed through introgression from these wild relatives. These species serve as a goldmine of novel alleles, with individual accessions often harboring genes conferring resistance to multiple stresses. Notably, even a single wild chromosome can carry several beneficial loci, providing powerful opportunities for trait enrichment in cultivated wheat. Through wide hybridization and cytogenetic approaches, we have successfully introgressed rust resistance genes from several wild species, including *Aegilops triuncialis*, *Ae. kotschyii*, *Ae. peregrina*, *Ae. speltoides*, *Ae. lorentii*, and *Triticum monococcum*. Genomic mapping in these introgression lines revealed presence of resistance to leaf rust, stripe rust, powdery mildew and Karnal bunt in different combinations. In addition, multiple QTLs governing resistance to *Fusarium* head blight, leaf blight, and lesser grain borer, along with heat stress tolerance and improved nitrogen use efficiency, were identified from an in-house developed synthetic wheat line (*T. durum* × *Ae. tauschii*). Similarly, the introgression of a chromosome 5U of *Ae. triuncialis* into a hexaploid wheat background was found to confer resistance to powdery mildew and cereal cyst nematode, as well as enhanced drought tolerance. These findings highlight the immense potential of wild germplasm as a strategic genetic resource for wheat improvement. Integrating wide hybridization with advanced genomics and molecular mapping provides a powerful framework for unlocking this diversity and accelerating the development of climate-resilient, high-yielding wheat cultivars capable of sustaining global food security.

Harnessing the genetic wealth of tetraploid wheat relatives

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Abstract

Genetic diversity is fundamental to the discovery of novel alleles associated with agronomically important traits. Characterizing the extent and structure of genetic variation within tetraploid wheat germplasm - encompassing both wild relatives and domesticated accessions - empowers breeders to strategically select diverse sources for crop improvement. Furthermore, well-curated germplasm collections are essential for interrogating this variation and leveraging genome-wide association studies to pinpoint favorable alleles. Consequently, to support these efforts diverse reference panels which include wheat relatives have been developed, like the Tetraploid Global Collection (TGC; Maccaferri et al., 2019) and the Wild Emmer Wheat - GB collection composed of 400 accessions (WEW-GB; Mastrangelo et al., 2025).

Trait-focused subsets derived from these collections have been extensively phenotyped for yield components, disease resistance, root architecture, and drought tolerance. Specifically, the WEW-GB panel has exhibited robust resistance to select races of yellow and stem rust; these resistance loci were mapped at high resolution by exploiting the population's rapid linkage disequilibrium (LD) decay. Furthermore, this collection harbors significant allelic variation at master regulators of flowering time. Ongoing research is currently exploring wild emmer diversity to characterize water-use efficiency, stomatal morphology, and root system architecture, aimed at facilitating the targeted introgression of drought-tolerance traits into both tetraploid and hexaploid wheat backgrounds through the development of Nested Association Mapping (NAM) populations.

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Plasticity of source-sink dynamics contributes to wheat yield stability

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Abstract

Wheat grain yield emerges from complex interactions among physiological processes governing source development through photosynthesis and the subsequent remobilisation of assimilates toward grain sinks. Across developmental stages, genotype × environment × management interactions strongly influence source and sink strength and their dynamic coordination. Therefore, it is challenging to design a coherent physiological pathway shaping stable and high yield across environments. Addressing this challenge, we applied a comprehensive data-synthesis approach using a German winter wheat panel comprising 202 cultivars released between 1963 and 2018. We integrated datasets from: (i) 101 field environments with extensive measurements, including phenology, yield components, grain quality, and disease resistance; and (ii) controlled-environment experiments consisting of two greenhouse studies and seven growth chamber experiments employing manual measurements, model-assisted approaches, and high-throughput phenotyping. These experiments captured morphological, architectural, and physiological traits across phenological stages from seedling to maturity. In total, 61 source–sink-related traits were analysed. We quantified absolute and relative breeding progress across all traits, evaluated how their plasticity to environmental conditions contributed to observed genetic trends, examined signatures of selection, and compared stage-specific sensitivities of yield components to environmental variables between historical and modern cultivars. Our results show that breeding has: (i) increased plasticity in adaptive physiological traits, which underpin the plant's ability to cope with unpredictable environmental fluctuations; (ii) reduced plasticity in traits that support constitutive improvements in both source-related functions (such as light interception and light use efficiency) and sink-related traits (like spike number) across diverse environments; and (iii) enhanced yield resilience under climate change by modifying stage-specific sensitivities of yield components to short-term temperature fluctuations. These findings provide evidence that plasticity in source–sink dynamics contributes substantially to yield stability under stress conditions and highlight previously underexplored traits (e.g. stomatal traits, temperature sensitivity and photosynthetic protein turnover) and their interactions that may sustain future yield gains. Finally, we integrated breeding progress across individual source and sink traits into an interconnected physiological wiring diagram, grounded in existing conceptual frameworks, and tested the hypothesis that breeding for life-cycle plasticity in source–sink dynamics underpins the long-term improvement of yield stability in winter wheat.

Tetraploid wheat pangenome to better bridge with hexaploid wheat

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Abstract

As the donors of the AA and BB genomes of tetraploid and hexaploid wheat, these species have evolved under a range of diverse environmental conditions and pathogen pressures, making tetraploid wheat a key reservoir of genetic diversity for crop improvement.

Here, we present preliminary results from chromosome-level assemblies of 40 tetraploid wheat genomes selected from the Global Durum Wheat Genomic Resource (GDGR). These accessions were chosen to capture the full spectrum of sequence variation across wild emmer (WEW), domesticated emmer (DEW), landraces (TWL), and modern cultivars (DWC), thereby supporting both evolutionary studies and pre-breeding efforts.

As a case study, we highlight the identification of loci associated with disease resistance and spike development. These analyses provide insights into the impact of structural variation and allelic diversity, while illustrating the value of a pangenome framework for crop improvement. Importantly, we demonstrate that beneficial haplotypes derived from *Triticum dicoccoides*, *T. dicoccum*, and subspecies of *T. turgidum* can be unequivocally identified and effectively leveraged for modern breeding strategies.

In addition, the integration of short- and long-read RNA sequencing from multiple tissues across ten core accessions enabled the construction of a pan-transcriptome. This resource enhances our understanding of gene function and expression dynamics, contributing to a comprehensive atlas of gene activity in wheat.

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Genome variation and breeding application of irradiation in wheat

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Abstract

Irradiation technology for crop improvement has experienced nearly a century since 1928. According to the Mutant Variety Database of the International Atomic Energy Agency, until the end of 2025, there are 72 member countries had developed and officially released 3,502 mutant varieties across 238 species (<https://nucleus.iaea.org/sites/mvd/>). China has contributed nearly one-third of the mutant varieties developed worldwide during the same period. High-energy and heavy ion beams, characterized by the high Linear Energy Transfer (LET), exhibiting a higher Relative Biological Effect (RBE), which may induce various types of single nucleotide polymorphisms (SNPs), small insertions and deletions (InDels), and large fragment deletions in plants, making them a growing international research focus in recent years. We used wheat mutant populations derived from high-energy carbon ion beams, and detected an average of 5,585 base mutations per sample through exon capture sequencing. Compared to EMS treatment, carbon ion beams induced a higher proportion of base transversions, resulting in a greater variety of amino acid changes. Further validation in a larger population revealed that carbon ion beams induce base transition/transversion ratios ranging from 1.96 to 2.03. By integrating high-energy heavy ion beams and space mutagenesis, we developed the high-yield and widely adaptable wheat variety Lunyuan 502, which has been cultivated over 6.7 million ha, and the salt-tolerant, high-quality wheat variety Hangmai 802, currently under promotion and demonstration.

From genomes to impact: building a global wheat pangenome and haplotype catalogue for next-generation breeding

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Abstract

Bread wheat (*Triticum aestivum*, AABBDD; ~16 Gb hexaploid genome) feeds over one-third of the global population. However, its allohexaploid complexity—spanning three homoeologous subgenomes and comprising more than 85% transposable elements—has long constrained comprehensive pan-genomic characterisation. The International Initiative on PanGenome and Haplotype Catalogue in Wheat (IIPGHCW), involving partners from 14 countries, is addressing this challenge at an unprecedented global scale.

This initiative has generated two landmark datasets. First, 146 chromosome-scale, reference-grade genome assemblies have been completed, with full genome annotation achieved for all varieties (100%). These assemblies, generated using PacBio HiFi sequencing combined with Hi-C/Omni-C chromatin conformation capture, span pseudomolecule sizes of 14.2–14.8 Gb. Second, whole-genome resequencing (~15× coverage) of 1,200 diverse lines from 46 countries—organised into five panels, including the Wheat Diversity Australia Panel (338 lines), INNOVAR/European Panel (292), and Vavilov Diversity Panel (291)—has identified 63–95 million SNPs and InDels per panel relative to the Chinese Spring T2T reference genome.

Building on these resources, a graph-based wheat pangenome is under construction to capture structural variation, presence–absence variation, copy number variation, and repeat dynamics. Targeted analyses include key gene families such as the VRN/PPD, PIN, and heat-shock genes, alongside pan-genome-wide association studies (pan-GWAS) for traits including disease resistance, drought tolerance, yield stability, and grain quality. A haplotype catalogue with breeder-ready markers is being developed to enable direct translation into breeding pipelines.

In addition, collaborative efforts with Australian partners will be presented that are advancing wheat genomics and pre-breeding programs aimed at dissecting the genetic basis of key agronomic traits, including drought tolerance, heat stress response, and nitrogen use efficiency (NUE). Large-scale, multi-location field trials, conducted in partnership with Australian Grains Technologies (AGT), are generating extensive phenotypic datasets that are being integrated with genomic and physiological data. These combined resources are expected to deliver superior germplasm and robust selection tools to accelerate wheat improvement.

The wheat rchive

David Gilbert ⁽¹⁾ - ***Open Wild Wheat Consortium*** ⁽²⁾

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Abstract

The Open Wild Wheat Consortium (OWWC) is an international collaboration uniting researchers across five continents with the shared goal of developing genomically enriched resources for wheat wild relatives. Now in its third phase (OWWCiii), the consortium has generated an RNA-seq dataset for a diverse *Aegilops tauschii* panel and produced chromosome-scale assemblies using Hi-C-based scaffolding. These resources provide a comprehensive foundation for exploring the genomic architecture of resistance genes within the progenitor of the wheat D-subgenome. We have characterized resistance gene diversity across *Ae. tauschii*, revealing allelic series, lineage-specific expansions, and signatures of R gene expression.

Building on this platform, we have investigated R gene flow from wild relatives into modern bread wheat by curating a comprehensive database of over 5,000 re-sequenced accessions spanning *Triticum* and *Aegilops* species. I will discuss how we have used this resource to study the effect of speciation, domestication, and breeding bottlenecks on R gene distribution. With a particular emphasis on gene flow from the D-genome progenitor, this work provides insights into the contribution of *Ae. tauschii* to biotic stress resistance in modern wheat.

GWAS across wheat genomes: insights from the watkins collection

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Abstract

Modern bread wheat improvement has relied on a relatively narrow genetic base. Whole-genome resequencing of the A. E. Watkins landrace collection alongside diverse modern cultivars has shown that contemporary breeding programs predominantly derive from only two of seven ancestral groups, leaving substantial haplotypic and structural diversity underutilised. This diversity includes extensive gene presence-absence variation (PAV), copy number variation (CNV), and lineage-specific haplotypes that are not fully captured by conventional single-reference SNP-based genome-wide association studies (GWAS), particularly in a complex hexaploid genome.

In this work, we develop a framework for conducting GWAS across multiple wheat genomes by integrating complementary layers of genetic variation. First, SNP-based GWAS are implemented to refine QTL intervals, estimate allelic effects, and prioritise candidate genes within linkage disequilibrium blocks. Second, we establish a pan-gene CNV-GWAS framework designed to test for trait associations driven by structural and gene dosage variation. Together, these approaches aim to provide a more complete view of the genetic architecture underlying complex traits in wheat.

Using twelve high-quality hexaploid wheat genome assemblies and their gene annotations, we constructed a cross-genome pan-gene catalogue by clustering genes into orthogroups. This reference-independent representation enables association testing at the gene level and facilitates comparison of loci across assemblies, reducing coordinate dependence inherent to single-reference analyses. Gene copy number per accession is inferred from normalised read-depth estimates with genome-wide depth correction, GC adjustment, and homoeolog/paralog-aware filtering to distinguish biological absence from technical artefacts. Population structure and relatedness are modelled using LD-pruned genome-wide SNP markers within linear mixed models.

This multi-layered GWAS strategy allows detection of loci supported by SNP variation, structural variation, or both, and enables evaluation of whether dosage-sensitive genes contribute to important agronomic and wheat adaptation traits. By explicitly incorporating pan-genome diversity, this framework provides a reproducible multi-reference association strategy to interrogate underutilised ancestral variation and to translate structural genomic diversity from the Watkins collection into breeding-relevant insight.

Application of genomics to identify novel sources of disease resistance and their use in wheat breeding

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Abstract

Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), remains a major global constraint to wheat production. Stripe rust is one of the five 'priority one' diseases in Canada. Over the past few years, Cereal Breeding Lab has studied disease resistance in wheat relatives and landrace collection. In this talk, we will summarize our work on Watkins wheat landraces and genetic mapping of a novel adult-plant stripe rust resistance gene in spelt wheat cultivar CDC Silex.

(1) 297 Watkins landraces were evaluated against six diverse Pst isolates (representing six races and three predominant North American lineages) and subjected to genome-wide association analysis using high-density whole-genome resequencing data. Continuous phenotypic variation was observed across isolates, with several accessions displaying stable resistance across all lineages. Using GWAS analyses, a total of 87 QTL were identified. Ten loci co-localized with designated or cloned Yr genes and an additional 34 loci overlapped previously reported stripe rust QTL, whereas the majority did not coincide with known loci, suggesting potential novel resistance regions. Several Watkins accessions carried favorable alleles that co-localized with multiple Yr-aligned loci, identifying promising donor candidates for validation and pre-breeding.

(2) Adult-plant resistance (APR) genes provide durable, non-race-specific resistance against wheat rust diseases. We identified a novel APR locus in the spelt wheat cultivar CDC Silex that confers non-race-specific near-immune adult-plant resistance to stripe rust. The trait segregates as a single dominant gene and using BSAs mapped the locus, QYr.cbl-5D, to a single 0.31 Mb interval on chromosome 5D, confirming monogenic inheritance. Interestingly, introgression into bread wheat suppresses this resistance, suggesting the presence of a dominant suppressor factor in the bread wheat genome. We generated a scaffold-scale assembly of CDC Silex to annotate the locus and its flanking region on 5D. Within a ± 1 Mb interval flanking the QYr.cbl-5D peak, six genes were identified, of which five had no predicted function and one encodes a C2H2 zinc-finger transcription factor. Future work will aim to clone this APR and its suppressor in bread wheat. Flanking and linked SNPs from this region will enable marker-assisted selection to deploy this APR locus.

Genome editing facilitate sustainable wheat production

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Abstract

CRISPR/Cas technology enables precise modifications of DNA sequences in vivo and offers great potentials for harnessing plant genes for crop genetic improvement, speeding up the crop breeding and reshaping global agriculture. Here, we report the establishments of CRISPR/Cas (Cas9 and Cas12i) mediated single and multiplex gene editing systems in wheat, respectively. We also exhibit the creation of a series of novel germplasm including wheat high in resistant starch, nitrogen-use efficient, higher yield potential and lodging resistance, as well as wheat germplasm conferring medium/higher resistances to Fusarium head blight (FHB) and sharp eyespot, respectively. The establishment of wheat genome editing toolkits and applications of these germplasms in agricultural practice will be expected to greatly facilitate wheat functional genomics and sustainable wheat production in a global climate change context.

Keywords: Common wheat (*Triticum aestivum* L.), CRISPR/Cas, Genome editing, Toolkits, Germplasm

Genetic Dissection of End-use Quality in Wheat to Facilitate Breeding

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Wheat (*Triticum aestivum* L.) is one of the most significant staple crops, providing 20% of the calories and protein consumed worldwide (FAO, <http://faostat.fao.org>). Enhancing the end-use quality traits of wheat is a primary goal in breeding programs. Gluten proteins, which are crucial for determining end-use quality, consist of two types: polymeric glutenins and monomeric gliadins. Together, these proteins impart unique viscoelastic properties to wheat dough. However, aside from high molecular weight glutenins, the role of other seed storage proteins (SSPs) in processing quality and their application in breeding remains poorly understood. This is due to the high sequence repetitiveness, numerous gene copies, and complex structural variations associated with these proteins. In this study, we aimed to identify key genes that influence quality traits and constructed a multi-layered regulatory network underlying end-use quality. We specifically identified the γ -gliadin genes γ -1 and γ -2, along with elite alleles that play crucial roles in processing quality. We also characterized transcriptional regulators, including TaGAMYb, TaNAC019, TaCAMTA2, the histone acetyltransferase GCN5, and the transcriptional adaptor ADA2, which interact to regulate the expression of SSP genes. Additionally, we discovered two proteins, LGP1 (a gliadin) and LGP2 (a purindoline), through map-based cloning. Aberrant cleavage of the signal peptide of these two genes leads to abnormal accumulation of gluten proteins. We identified 23 SSP genes associated with end-use quality by employing k-mer-based genome-wide association studies and developed a tool called "PanSK" (Pan-SSP k-mer) for high-accuracy prediction of flour quality phenotypes based solely on SSP genotypes. Furthermore, we propose a comprehensive approach termed "WiseCookie," which integrates digital phenotyping, machine learning, and a thorough understanding of the grain-to-cookie transformation, thereby facilitating early-generation selection for breeders. These findings provide strong support for improving wheat end-use quality through the identification of key genes to enhance breeding efforts.

Key words: Wheat, End-use quality, Seed storage proteins, Regulator

Evaluation of the fate of wild-relative introgressions in the wheat genome

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Abstract

To meet human needs by 2050, bread wheat (*Triticum aestivum* L.; $2n = 6X = 42$) production needs to be significantly improved but considering the context of a sustainable agriculture. One effective approach is to better utilize the extensive but underexploited genetic resources in cereals. Disease resistance genes from wild species have been introduced into wheat, such as the rust-resistance locus *Lr37/Yr17/Sr38* (2A/2N translocation) and the eyespot resistance gene *Pch1* (7D/7Dv translocation) from *Aegilops ventricosa* (DvDvNN). These introgressed segments alter meiotic chromosome dynamics and stability by reducing the capacity of DNA exchanges (crossovers) at the introgression level. Analyses of Chinese Spring (CS), Renan (Re, harboring the two introgressions), and their hybrids (CS x Re) revealed that these latter exhibited a significantly lower fertility compared to the two parents. Cytogenetic analyses of CS, Re and CS x Re revealed that hybrids showed an increased frequency of rod bivalents and higher levels of chromosomal fragmentation, indicating disrupted meiotic chromosome configurations and reduced meiotic stability. Oligo-FISH specifically targeting chromosome 2A revealed stable ring bivalents in CS and Renan, but a mixture of ring and rod bivalents for this chromosome in hybrids, suggesting that *Ae. ventricosa* segments compromise chromosome integrity and behavior during meiosis. Interestingly, this was not the case at the level of chromosome 7D harbouring the second introgression. To our knowledge, this is the first systematic investigation of meiotic behavior involving *Ae. ventricosa* introgressions in wheat. These findings provide essential insights for optimizing alien gene introgression and improving wheat breeding strategies.

Induced mutations and application in genetic analysis of wheat yield

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Abstract

Tillering number, one of the three key components contributing to wheat yield, is an important target trait for wheat improvement. Significant progress has been made in mapping key genes and QTLs for wheat tillering. Several major genes regulating wheat tillering have been identified through methods such as homology-based cloning and map-based cloning. Mutagenesis is an important approach for creating wheat tillering germplasm. Using both high-energy heavy ion beams and EMS mutagenesis, we have isolated multiple tillering mutants. Through map-based cloning, major novel genes regulating wheat tillering were identified on chromosomes 1B and 2D, respectively. These genes regulate wheat tillering through different metabolic pathways. The discovery of these new genes and the subsequent identification of superior new allelic variations will provide new genetic resources for wheat improvement.

Historical genomics of host-pathogen interaction in wheat rust pathosystem

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Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), represents a major threat to global food security. To understand the genomic basis of host-pathogen coevolution, we conducted large-scale resistance screening of 400 genetically diverse wheat lines against 150 Pgt isolates, generating ~60,000 disease resistance scores. Our panel included landraces and cultivars from diverse geographies, revealing that modern breeding has significantly enriched wheat germplasm with resistance genes, with improved lines showing broader resistance than landraces. Consistent with the Red Queen hypothesis, modern wheat cultivars were more resistant than historical varieties, and more recently sampled Pgt isolates were more virulent than older isolates. Ancestry analysis of 223 unique resistance loci (*Sr*) identified by wheat GWAS revealed that many resistance haplotypes originated from ancient wheat lineages or wild ancestors. Breeding preferentially selected small-effect *Sr* alleles over large-effect variants, consistent with the rapid loss of efficacy of strong-effect resistance genes due to pathogen adaptation. Pgt GWAS detected ~300 significant avirulence loci (*AvrSr*) associated with resistance responses, including a strong association ($p < 1E-9$) with the known *AvrSr35* locus. *AvrSr* haplotype frequencies in the Pgt panel were consistent with a higher fitness cost of avirulence relative to virulence haplotypes. Accumulation of *AvrSr* alleles in Pgt was associated with reduced virulence. Epistatic interaction analysis between *Sr* and *AvrSr* loci identified significant interactions between 65 *Sr* haploblocks and 135 Pgt effectors. The *Sr*-*AvrSr* network included interactions of multiple *AvrSr* loci with a single *Sr* locus, as well as multiple *Sr* loci with a single *AvrSr* locus, revealing the genetic complexity underlying resistance outcomes. Our work provides insights into the genomic architecture of wheat stem rust coevolution and identifies complex interaction networks that can guide strategic resistance gene deployment and inform predictive models for sustainable disease management in wheat breeding programs.

Driving sustainable wheat production through trait discovery and pre-breeding in a public breeding program

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Abstract

Public wheat breeding programs operating in small countries with limited resources face the challenge of maintaining scientific innovation while delivering improved varieties to farmers. In such contexts, integrating external knowledge with locally generated research is essential to accelerate genetic gains and ensure the development of well-adapted cultivars. At the Instituto Nacional de Investigación Agropecuaria (INIA) in Uruguay, our breeding strategy combines pre-breeding and trait discovery approaches to enhance the resilience and performance of locally adapted wheat germplasm. Pre-breeding efforts build on advances generated by the global wheat research community. Reported markers associated with genes of agronomic interest are incorporated into the characterization of local germplasm, while newly released materials carrying valuable resistance or adaptation genes are evaluated under local conditions. When validated, these sources are used in targeted introgression and marker-assisted backcrossing programs to incorporate beneficial alleles and pyramid multiple resistance genes into elite breeding lines. Complementarily, trait discovery efforts focus on identifying the genetic basis of key agronomic traits within locally adapted germplasm. Association analyses and field evaluations are used to investigate traits such as resistance to stripe rust, fusarium head blight, plant height, and phenology, as well as their relationship with yield stability across environments. Together, these approaches illustrate how public breeding programs can leverage global knowledge while generating locally relevant discoveries, ultimately translating research into improved wheat varieties adapted to regional production systems.

Innovations paving (half)-way towards hybrid wheat breeding

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Abstract pending

Advancing hybrid wheat through innovative breeding

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Abstract

Advancing Hybrid Wheat Through Innovative Breeding

Hybrid wheat has long been recognized for its potential to deliver gains in yield stability and genetic progress; however, commercial adoption has been limited by biological and logistical challenges due to wheat plant architecture. This presentation describes an integrated breeding and hybridization platform designed to overcome these barriers and enable scalable, cost effective hybrid wheat production. Corteva's wheat breeding approach integrates efficient inbred development, rapid genomic recurrent selection, and heterotic group separation to develop hybrids. It's proprietary, patented hybridization system developed through conventional plant breeding enables consistent production of non pollen producing female parents and compatible pollen producing male parents. This hybridization system reduces land requirements for female seed production, operates across diverse genetic backgrounds, and works in all genetic backgrounds tested to date.

Hybrid seed production follows a two step process in which female parents are generated through color based seed sorting and subsequently cross pollinated with selected male inbreds. This approach allows local hybrid seed production at scale while maintaining an efficient cost of goods. Genomic selection is fully integrated to accelerate improvement of parental traits critical to hybrid seed productivity. Basic plant breeding philosophy integrated with a novel sterility system will deliver a commercially viable pathway for hybrid wheat deployment.

Exploration of asian wheat genetic diversity through nam population

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Abstract

We developed a large-scale nested association mapping (NAM) population in hexaploid wheat to enable high-resolution gene discovery and predictive breeding. This population consists of 24 biparental crosses derived from diverse Asian landraces and Japanese cultivars crossed with the common parent Norin 61, comprising 4,892 individuals and capturing underutilized genetic variation in Asian germplasm. A subset of 1,013 lines from 13 crosses was genotyped using the GRAS-Di platform, enabling the construction of high-density linkage maps. Integration of these maps produced a high-resolution consensus map that substantially improved mapping resolution compared to individual linkage maps, providing a robust framework for QTL discovery.

Using this resource, we identified previously uncharacterized loci underlying field resistance to yellow rust, demonstrating previously untapped agronomically important alleles in Asian wheat germplasm. In parallel, QTL mapping of recombination frequency revealed previously unreported genetic factors controlling recombination landscapes in wheat.

Furthermore, we developed a yield prediction model integrating time-series RNA-seq data with genotypic information. Comparisons between normal and late sowing conditions revealed that gene expression profiles immediately prior to heading consistently contributed to yield prediction in both environments, although distinct gene sets were associated with yield formation under each condition. Incorporating transcriptomic data significantly improved prediction accuracy from approximately 0.2 to 0.5 under normal sowing and from approximately 0.3 to 0.4 under late sowing, clearly outperforming genotype-only models. Collectively, our results establish this NAM population as a powerful and versatile platform for high-resolution genetic dissection and predictive breeding. By combining large-scale population design, high-density genotyping, and transcriptome-informed prediction, this study provides a foundation for next-generation wheat breeding strategies integrating genomics and functional data.

Future efforts will focus on further expanding the population and leveraging this platform to accelerate gene discovery and breeding applications in wheat.

Translational research in wheat using einkorn genomics

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Abstract

Wheat is one of the most important crops worldwide and a significant source of human calories, but it faces ongoing threats from biotic and abiotic factors. Due to a complex evolutionary history, a domestication bottleneck, and selective breeding, wheat's genetic base has been significantly reduced. To keep pace with the growing demand for production and the challenges posed by changing climatic conditions and several diseases and pests, wheat cultivars need continuous genetic improvement through the deployment of novel genes and alleles. Genome complexity and redundancy hamper the pace of gene discovery in our bread and pasta wheat. With a simple diploid cereal genome ($2n=2x=14$; ~5Gb; AA) and untapped genetic diversity in its germplasm, einkorn wheat presents an excellent model system for gene discovery and deployment for wheat improvement. Here, we outline the path for translational research in bread wheat using the einkorn wheat genomics platform. Using the integration of genomes, pangenomes, and sequence-indexed populations, along with an example of an agronomically important trait, we present an elegant platform for wheat improvement.

Genomic breeding for heat tolerance at ICARDA

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Abstract

Durum wheat production and productivity are increasingly challenged by rising temperatures, particularly in vulnerable regions such as the Senegal River Valley, where daytime temperatures during the coolest season regularly exceed 30°C. Addressing this, breeding for heat tolerance has become a central focus for ICARDA in the region.

To accelerate genetic gain, we have implemented genomic tools to identify and deploy heat tolerance loci. Through genome-wide association studies (GWAS) across three diverse panels subjected to a range of heat-stressed environments, we identified 36 loci significantly associated with heat tolerance. The corresponding SNPs were converted into Kompetitive Allele Specific PCR (KASP) markers and validated in an independent panel. Each marker explained up to 9% of the phenotypic variation for grain yield under heat stress. These markers are now integrated into genomic selection pipelines targeting the West African savannahs.

In parallel, we initiated fine mapping of a major heat tolerance QTL located on chromosome 1A, spanning an initial interval of 179 Mbp. To refine this region, 16 full-sib crosses were developed (including six semi-near isogenic lines (NILs) and 10 true-near isogenic lines) derived from progenies segregating for the QTL but sharing 51-91% genetic similarity. These lines represent the foundational material for QTL refinement. The semi-NILs and the true-NILs were phenotyped over two growing seasons under field heat stress in Senegal. Additionally, controlled heat stress was applied during flowering using plastic tunnel facilities in Morocco. A GBS-based k-mer approach was employed for genotyping. Significant markers were identified through stepwise regression, enabling the detection of tightly linked or co-located genomic regions. These k-mers were aligned to a newly assembled durum wheat reference genome to further narrow the QTL interval and identify candidate genes

Buffering yield potential in an increasingly unstable environment

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Abstract

Yield potential is vital to maintaining productivity and profitability in all wheat cropping systems globally. However, yield is significantly influenced by climate change, which affects temperature, precipitation patterns, and the frequency of extreme weather. Genetic buffering to minimise loss of yield potential is key to maintaining and even increasing productivity in future environments. We established a nationally focussed genomic selection strategy that comprised a four-tiered phenotyping platform of key field sites that included future environments, in-field heat chambers, glasshouses and ultimately national testing of selected recombinants in multi-environment commercial experiments. Double haploids were used to rapidly advance materials with high genomic estimated breeding values for validation and further recombination. This multi-tiered national strategy identified materials with adaptive plasticity for yield. They maintained and even increased yield under favourable conditions while minimizing yield losses under stress. Our experience shows that wheat productivity and profitability can be maintained as farming conditions become less favourable.

A simple model based on allele combinations to predict phenology in wheat to prevent extreme weather events

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Abstract

Crop development is crucial to crop adaptation in a specific environment. In wheat heading time and the period around that stage is critical for grains per unit area determination, being this component the most important for explaining grain yield variations. One of the target of a plant breeding program is to deliver germplasm for specific environments or sets of environments. The prediction of phenology using molecular markers for adaptation genes is an attractive alternative to screen large number of varieties for their adaptation to multiple environments. Using this information, wheat critical period can be identified for a particular environment, hence these models could be used to select the allele combinations that would result in heading times within a low-risk window with optimum growing conditions. One of the objectives of our group was to calibrate a prediction model using the allelic characterizations for wheat main developmental genes combined with the principal environmental drivers that affect wheat life cycle, to accurately predict wheat heading date. A dataset with a total of 49 Argentine wheat cultivars and two recombinant inbred lines was chosen to cover a wide range of allelic combinations for major vernalization, photoperiod, and earliness per-se genes. The model was validated using independent data from an Argentine wheat trial network that includes sites from a wide latitudinal range. Ultimately, using this gene-based model, simulations were made to identify optimal gene combinations (ideotypes) × site combinations in contrasting locations. The selected model accurately predicted heading date with an overall median error of 4.6 days. This gene-based crop model for wheat phenology allowed the identification of groups of gene combinations predicted to head within a low-risk window and can be adapted to predict other phenological stages based on accessible climatic information and publicly available molecular markers, facilitating its adoption in wheat-growing regions worldwide. We developed an open-source web model named CRONOTRIGO (CRONOWHEAT in English) based interface that allows portable phenological prediction in real-time (available at <https://cronogentrigo.agro.uba.ar>) and enables a free access (previous registration) through various platforms such as a desktop, laptop or mobile.

The role of ambient temperatures in cereal adaptation

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Abstract

Environmental signals regulate many aspects of plant growth and adaptation. Understanding how these signals influence important yield component traits is essential to develop germplasm which is robust to unusual and rapidly changing environments. Our research focusses on dissecting how temperature and photoperiod intersect to control floral related development. We are interested in identifying the molecular genetic factors which regulate the integration of these environmental signals using both controlled chamber and field experiments. Here I will present our recent advancements in understanding the regulation of tiller development and spike architecture with respect to environmentally sensitive genetic factors.

Towards climate-smart wheat: genomic insights into terminal heat tolerance from india's national genebank collections

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Abstract

Abiotic stresses, particularly drought and heat, pose major constraints to wheat (*Triticum aestivum* L.) productivity and threaten global food security. Heat stress is especially damaging as it accelerates grain filling, reduces grain weight, and leads to significant yield penalties. To elucidate the genetic architecture underlying heat tolerance, a genome-wide association study (GWAS) was performed using a diverse panel of 2,457 wheat genotypes comprising Indian landraces, CIMMYT breeding lines, cultivars, and released varieties. The panel was evaluated across three agro-climatic locations in India (BISA-Ludhiana, Jabalpur, and Samastipur) over two cropping seasons (2021-2023) under both timely- and late-sown conditions. Phenotyping was conducted for 15 agro-morphological and physiological traits, including grain yield, plant height, heat susceptibility index, and normalized difference vegetation index (NDVI) at multiple growth stages. Genotyping was carried out using a 35K SNP array. Population structure analysis classified the panel into six distinct subpopulations, with subpopulation 2 representing nearly 40% of the genotypes and largely consisting of Indian landraces, thereby contributing substantially to the observed genetic diversity. GWAS was implemented in GAPIT using three multi-locus models, leading to the identification of 52 significant marker-trait associations (MTAs) distributed across 16 chromosomes. Functional annotation of genomic regions underlying these MTAs revealed 60 putative candidate genes associated with heat stress responses, including genes involved in photosynthesis (chlorophyll a-b binding protein), oxidative stress regulation (flavin-containing monooxygenase), and stress-mediated growth and development (auxin-responsive protein). Haplotype analysis using the genehapR package identified nine distinct haplotypes across key candidate genes. Gene expression analysis further indicated that 10 genes were highly upregulated under stress conditions, with one gene exhibiting the highest fold-change (10.68), suggesting a pivotal role in heat stress adaptation. This key gene was further studied through haplo-pheno analysis, particularly for heat susceptibility index (HSI) and grain yield, to evaluate its allelic variation, phenotypic effects, and breeding potential. The superior haplotypes associated with HSI and improved grain yield were identified as valuable donors and are proposed for introgression into elite breeding lines through marker-assisted breeding to enhance heat tolerance while maintaining high yield potential.

Integrative genomic approaches to resolve wheats genetic diversity for FHB resistance

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Abstract

Fusarium head blight (FHB) is a devastating fungal disease - primary causal agent *Fusarium graminearum* - that affects numerous crops, including wheat, worldwide. It is one of the most serious threats to wheat production, leading not only to reductions in total yield but also to significant economic losses due to grain downgrading caused by the accumulation of mycotoxins, such as deoxynivalenol (DON). Genetic resistance is the most effective strategy for controlling FHB; however, sources of resistance are limited and remain understudied due to the complexity of resistance expression and the hemibiotrophic nature of the pathogen.

Tall wheatgrass *Thinopyrum elongatum* (2n=14, E genome) is a wild wheat relative from the tertiary gene pool, known to carry the major resistance locus *Fhb7-7E* on its 7EL chromosome arm. Here, we demonstrate that introgression of a distal portion of 7EL, carrying the *Fhb7-7E* locus and embedded within a *Th. ponticum* 7el1L segment, onto the 7AL arm of four Canadian durum cultivars and breeding lines resulted in enhanced FHB resistance under both controlled and field conditions. All introgression lines showed significant improvements in FHB resistance, although the phenotypic expression of resistance varied depending on the genetic background.

To investigate plant-pathogen interactions, we employed multilevel integrative genomic approaches. First, we generated a reference-quality whole-genome assembly of one introgression line using PacBio HiFi and Omni-C technologies to characterize introgression size and identify potential genes associated with FHB resistance. In addition, we conducted an RNA-seq time-course experiment using sample collected from the introgression line and its recurrent parent. RNA-Seq analysis revealed differentially expressed genes associated with early-stage infection, resulting in slowdown of symptom development and the spread of infection. The identified genes are aligned to the introgression region from the generated reference genome assembly to identify potential candidate genes associated with FHB resistance. Together, these results provide valuable insights for FHB resistance breeding.

Dissecting wheat resistance to FHB and Septoria tritici blotch disease

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Abstract

Our research is focused on understanding how cereals, pathogens and the microbiome interact, in order to enhance disease control. Our research on Fusarium head blight (FHB) and Septoria tritici blotch (STB) has revealed novel gene pathways associated with disease resistance in wheat. For example, our studies of a novel wheat gene, TaFROG, led to the identification of several genes that can improve FHB resistance. Our studies of the wheat genome identified genomic hotspots associated with FHB resistance, i.e. regions enriched in genes responsive to FHB disease and hence potential disease resistance genes. Ongoing work is assessing the relationship between wheat, *F. graminearum* and the wheat head microbiome. Based on our completed oat x FHB x microbiome studies, we know that specific microbial assemblages are associated with low levels of toxin production by Fusaria. Thus, we question whether the same thing occurs in the wheat x FHB x microbiome interactions. For STB disease, transcriptomics identified genes associated with STB resistance, a genome wide association study of a panel of elite genotypes identified candidate genes associated with basal resistance in wheat and a multi-omics study, including transcript-wide association analysis, differential gene expression analysis and e-QTL analysis highlighted a small number of genes associated with STB susceptibility. Ongoing studies are assessing the interplay between wheat, STB and the microbiome of wheat. The outputs of our research clearly show FHB and STB diseases are underpinned by evolutionary divergent machinery and that the microbiome can shape the plant-pathogen interactions.

Breaking barriers: preferential allosyndetic introgression of novel disease resistance genes from structurally rearranged *aegilops caudata* genome

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Abstract

Gene introgression from wild relatives is a powerful strategy for modern wheat improvement, yet its success primarily depends on recombination between homoeologous chromosomes. Although ph1b- induced homoeologous recombination has been widely exploited, the influence of chromosomal rearrangements on introgression outcomes remains poorly understood. Here, we show that large-scale chromosomal rearrangements can redirect recombination to the chromosomes under different homoeologous groups and drive preferential allosyndetic introgression between non-homoeologous chromosomes or chromosome arms from *Aegilops caudata*, a wild wheat relative whose C genome contains extensive structural rearrangements, into wheat. Using a wheat chromosome 6A monosomic-induced 6AS•6CL Robertsonian translocation combined with ph1b-induced recombination, we generated 17 independent recombinants carrying the stem rust resistance gene Sr69 from chromosome arm 6CL; six of them also conferred resistance to powdery mildew. Unexpectedly, 16 of 17 (94.1%) recombinants resulted from exchanges with wheat group-7 chromosomes rather than the homoeologous group-6 chromosomes. Comparative sequence and marker analyses identified a 67-Mb rearranged interval on 6CL that is syntenic with telomeric regions of the long arms of wheat group-7 chromosomes, with sequence similarity strongly predicting translocation frequency. Physical and optical mapping delimited introgression sizes from 20.5 to 123.1 Mb. Recombination within the rearranged interval produced compensating 7A/6C, 7B/6C, and 7D/6C translocations, whereas recombination outside this region generated non-compensating 6A/6C exchanges. Localization of Sr69 to a 20.5-Mb interval enabled identification and validation of a novel NLR gene underlying Sr69-mediated stem rust resistance. Consistently, the powdery mildew resistance gene Pm7C, previously transferred from chromosome arm 7CL into wheat 7DS, resides within a 177-Mb rearranged 7CL region syntenic with a 187-Mb region of wheat 7DS. These findings demonstrate that structural rearrangements can redirect ph1b-induced meiotic recombination and determine introgression pathways. As high-quality genome assemblies become available for wild relatives, this work provides a framework for accessing underexploited genetic diversity embedded within highly rearranged genomes for wheat improvement.

Accelerated wheat breeding and scaling to ensure food security in Africa

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Abstract

The wheat breeding program at ICARDA deployed Accelerated Wheat Breeding Scheme (AWBS4) using combination of classical and molecular approaches to develop high yielding genotypes with resistance to abiotic and biotic stresses. AWBS4 involves elite x elite crosses (simple crosses, F1top crosses), generation advancement using speed breeding facilities, two cycles of generation advancement in the field (winter and summer seasons), marker assisted selection followed by key location phenotyping of stage 1 and stage 2 trials. The scheme enables to increase efficiency, genetic gain and shorten the breeding cycle. It takes only 4 years from crossing to distribution of elite genotypes to national programs through international nurseries. Yield levels of the top yielding elite spring bread wheat genotypes ranged up to 6t/ha at Wadmedani station of Sudan under extreme heat stress, 4 t/ha at Merchouch station of Morocco under terminal moisture stress (180 mm) and 11 t/ha at Sids station in Egypt under optimum conditions. Annually, ICARDA distributes 300 elite spring bread wheat genotypes to its partners through international nurseries. In the last 10 years alone, more than 75 bread wheat varieties of ICARDA origin have been released by National Agricultural Research System (NARS) in the CWANA and SSA regions. Significant marker trait associations have been identified and used for marker assisted selection. Scaling of heat tolerant wheat varieties in SSA particularly in Ethiopia, Nigeria and Sudan has shown huge potential of wheat production in these countries. In Ethiopia, irrigated wheat production expanded from almost zero in 2018 to more than 2 million hectares in 2024 setting the beginning of wheat green revolution. Deployment of heat tolerant wheat varieties along with improved crop management practices at scale could potentially transform wheat production and ensure food security in Africa.

Key words: Africa, Breeding, Food Security, Scaling, Wheat

Decoding wheat–fungal pathogen dynamics for resilient crops: insights from durum wheat landraces

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Abstract

Tunisia, a major durum wheat producer and a secondary diversification region for the crop, faces escalating challenges due to climate change and intensifying fungal pathogens pressure. Diseases like Septoria tritici blotch (STB) and tan spot, pose increasing threats, with stem rust re-emerging sporadically. The limited availability of resistant cultivars and heavy reliance on fungicides further increase these production risks. Amid this growing pressure, Tunisian and Mediterranean durum wheat landraces represent a valuable but underutilized genetic resistance resource.

Building on the STB precision phenotyping platform established in 2015 in collaboration with CIMMYT and Tunisian research institutions, over 150,000 wheat accessions have been screened across two disease hotspot locations. In parallel, comprehensive datasets on disease dynamics, pathogen diversity, and resistance profiles have been generated. This multi-layered pipeline has since been expanded beyond STB to include both tan spot and wheat stem rust diseases.

For tan spot, a collection of Tunisian landraces was phenotyped for resistance under field conditions and genotyped using the 90K SNP array. Genome wide association study (GWAS) analysis identified several marker-trait associations (MTAs), highlighting eight Tunisian landraces, including Mahmoudi, as particularly promising donors for resistance.

For stem rust, race phenotyping confirmed the predominance of the Sicily race (Clade III-B) in Tunisia, along with Clades IV-F and IV-B. Seedling assays using a collection of Mediterranean durum wheat accessions, revealed that only 9.4% of accessions exhibited resistance across all tested races, including Ug99, underscoring the urgent need for resistance introgression and highlights the value of resistant landraces. Within this context, the OpenDurumGPT consortium with the support of GetGenome recently sequenced the full genomes of two Tunisian landraces, Mahmoudi and Chili, iconic for cultural and genetic resource significance. This effort will accelerate the discovery of candidate genes linked to fungal disease resistance. Overall, this work, which integrates precision phenotyping, GWAS, and genomics, demonstrates how combining insights into host genetic diversity and pathogen virulence dynamics can provide a scalable roadmap for developing resilient wheat cultivars to address evolving fungal threats across the Mediterranean and West Asia and North Africa (WANA) regions.

CRISPR/Cas strategies for high-quality, celiac disease-safe wheat

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Abstract

Strategies based on the CRISPR/Cas system for obtaining high-quality wheat safe for individuals with celiac disease focus on the precise modification of complex gluten gene families to eliminate immunogenic epitopes while preserving the essential technological and nutritional properties of the grain. Initial efforts utilized CRISPR/Cas9 to induce targeted mutations in alpha-gliadin genes, specifically focusing on the region encoding the highly immunogenic 33-mer peptide, which allowed for the editing of up to 35 out of 45 identified genes and a reduction in immunoreactivity of approximately 85%. Recent advancements have expanded this approach through multiplex editing to simultaneously target gamma- and omega-gliadin gene clusters, resulting in wheat lines with total gluten content reductions as high as 97.7%. A significant technological milestone involves the use of paired sgRNAs and Cas9 or Cas12a nucleases to precisely excise immunogenic complexes, enabling their replacement with non-toxic synthetic DNA templates that improve digestibility by introducing new enzymatic cleavage sites. The success of these strategies relies on natural biological compensation mechanisms, where the decrease in gliadins is balanced by an increase in High Molecular Weight Glutenin Subunits (HMW-GS), which are critical for maintaining dough elasticity and baking quality. Furthermore, this protein restructuring offers significant nutritional benefits, including an increase in the content of the essential amino acid lysine, which is typically limited in conventional wheat. Finally, integrating these genome-editing tools into doubled haploid (DH) platforms enables the stable and rapid fixation of modified traits into elite wheat varieties, facilitating the production of non-transgenic, immune-safe lines in a single generation.

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Agronomic and genetic approaches to reduce the risk of acrylamide formation in wheat products

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Abstract

Acrylamide is a carcinogenic processing contaminant that forms from free (non-protein) asparagine and reducing sugars (predominantly glucose, fructose and maltose) 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 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 cv. Cadenza. Mutations in the A, B and D genome TaASN2 genes have also been produced by chemical mutagenesis and stacked to produce a total TaASN2 knockout of cv. Claire. We have also assessed the effect of a natural deletion of B genome TaASN2. In field trials, the CRISPR lines show significant (up to >90%) reductions in free asparagine concentration and a concomitant decrease in acrylamide formation in heated flour, biscuits and bread, especially after toasting. These genetic approaches 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 attempting to add a high lysine trait to the low asparagine wheat using cisgenics. The work is being conducted during a period of rapid change in regulations governing genome edited crops in the UK, culminating in the Genetic Technology (Precision Breeding) Act (March 2023), and its associated secondary legislation (March 2025). The UK started processing applications to market precision bred organisms (PBOs; GE crops with no transgene present) in November 2025. The EU is also moving to change its regulations on GE crops through the development of its New Genomic Techniques legislation. The acrylamide issue in cereal products is the subject of the ACRYRED COST Action (<https://acryred.eu/>).

The benefit of whole grain pasta for a healthier diet

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Abstract

As worldwide interest in gut health and metabolic wellness intensifies, basic foods are under increased examination. Pasta, a cherished culinary staple, should not be disregarded. Substituting refined pasta with 100% whole grain alternatives is among the most significant, although undervalued, measures for achieving a healthy diet. Comparing the nutritional profiles of refined “white” pasta and whole grain pasta demonstrates a large enhancement in dietary fiber, resistant starch, B vitamins, minerals and bioactive phytochemicals. The complete grain matrix—comprising bran, germ, and endosperm—impedes carbohydrate breakdown, resulting in more stable blood glucose levels, extended satiety, and enhanced gut bacteria diversity, all without necessitating calorie monitoring. Data from epidemiological and intervention research additionally associates frequent consumption with diminished risk factors for cardiovascular disease, type 2 diabetes, and colorectal cancer.

Whole grain and technological quality: opportunities and challenges

Maria Fiorenza Caboni (1)

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Abstract

Wheat and wheat-based products are widely consumed for their nutritional value, versatility, and long shelf life. The European Food Safety Authority, welcomes the definition applies to whole grains stated by the American Association of Cereal Chemists: "WG consist of the intact, ground, cracked or flaked caryopsis, whose principal anatomical components (starchy endosperm, germ and bran) are present in the same relative proportions as they exist in the intact caryopsis". While nutritionists recommend consuming whole-grain products for their health benefits, this is complicated by the potential deterioration of the lipid fraction found in the germ. These lipids are rich in unsaturated fatty acids and other bioactive molecules such as tocopherols and plant sterols. The lipid fraction, however, whilst representing a resource, also poses a critical issue: indeed, the grinding process itself inevitably promotes the activation of lipolytic enzymes. This activation causes an increase in free fatty acids, which, particularly when in a low-humidity environment where contact with oxygen is inevitable, are more prone to oxidation. The quality of the fat content in flour significantly affects the shelf life of cereal-based products, such as breadsticks. The susceptibility of fat to rancidity becomes more critical when the processed products are required to have a medium to long shelf life, as is the case with breadsticks. Although this type of product is formulated using a stable, high-quality fat, its shelf life is influenced by the small amount of fat present in the flour.

Wheat proteomic insights into baking quality and wheat-related disorders

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Abstract

As a primary global food crop, wheat serves as a fundamental source of dietary carbohydrates, proteins, fiber, B-vitamins, and minerals for human nutrition. However, wheat also counts as one of the major food allergens and causes celiac disease and non-celiac gluten sensitivity in predisposed individuals. The storage proteins of the wheat kernel, known as gluten proteins, have a dual role in determining both breadmaking performance and being the trigger of celiac disease and allergy. Gluten proteins are a complex mixture of ω -, α - and γ -gliadins as well as high- and low-molecular-weight glutenin subunits (HMW-GS and LMW-GS). Their quantities depend on both the cultivar and the growing conditions, and the relative composition is associated with end-use properties.

Qualitative and quantitative analysis is usually performed on wheat flour fractions using reversed-phase or gel permeation high-performance liquid chromatography with UV detection, but this method cannot capture single proteins or specific peptides.

This is where high-throughput untargeted and targeted proteomics come in to provide insights into gluten protein composition at the molecular level. In the context of baking quality, we established a targeted liquid chromatography tandem mass spectrometry (LC-MS/MS) method to quantitate eleven gluten protein groups based on selected marker peptides. Linear correlations with baking quality traits showed weak to moderate associations between six groups and grain protein content, sedimentation value, and wet gluten content. Bread volume was only weakly to moderately correlated, primarily with HMW-GS Dy10. Regarding wheat-related disorders, we identified 494 celiac disease-active peptides across five wheat species using untargeted proteomics to better understand their respective immunoreactive potential. There was a significant variation between species, with spelt having the greatest diversity of epitopes and einkorn possessing the lowest variety but higher concentrations of specific reactive sequences. Further work will integrate both untargeted and targeted workflows for marker peptides related to baking quality and to wheat-related disorders to get more comprehensive insights and assess protein expression variability across a larger diversity of species and cultivars.

A MicroGreen revolution improving soil health, mitigating the emission of greenhouse gases and contributing to food and nutrition security

Mariangela Hungria ⁽¹⁾ - Marco Antonio Marco Antonio ⁽¹⁾

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Abstract

The transition toward sustainable agricultural systems requires innovative strategies to increase productivity while reducing environmental impacts. Microbial-based technologies, particularly plant growth-promoting microorganisms (PGPM), are emerging as key components of a “MicroGreen Revolution,” offering viable alternatives to conventional chemical inputs. Nowadays, Brazil has global leadership in the use of bio-inputs to replace chemical fertilizers, but this is the result of more than seven decades of research, industrial development, and extension activities. Brazil is today the first producer and exporter of soybeans, which has been possible only due to the use of nitrogen-fixing elite strains of *Bradyrhizobium* that can fulfill all N requirements of the most productive genotypes. Estimates indicate that in 2025, 85% of the soybean farmers practiced annual inoculation, resulting in economic benefits of about US\$27 billion and avoiding the emission of 260 million tons of CO₂-equivalents. The use of bio-inputs in grasses is more recent, dating from 2009/10, with *Azospirillum brasilense* strains Ab-V5 and Ab-V6, with the capacity of nitrogen fixation ? although far lower than in the soybean ? but also with the ability of synthesizing phytohormones, increasing root growth dramatically, and improving nutrient use efficiency and water uptake. In maize, inoculation with Ab-V5 and Ab-V6 improves nitrogen use efficiency, allowing reductions of up to 25% in N-fertilizer without yield penalties. Inoculation was adopted on 10.22 million ha cropped to maize in the last crop season, and estimates of saving 25% of N-fertilizers result in an economic benefit of US\$276 million and mitigation of 1.87 million tons of CO₂-equivalents. Consistent results have also been obtained with wheat inoculated with strains Ab-V5 and Ab-V6. The Brazilian experience demonstrates that microbial inoculants are scalable, applicable across farming systems, and capable of contributing to global food and nutrition security. Expanding their adoption in wheat production represents a promising pathway toward more sustainable and efficient agricultural systems worldwide.

The nitrogen paradox: feeding wheat, cutting emissions, and building resilient cropping system

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Abstract

Aside from water, nitrogen (N) is the most important yield-limiting factor, and most expensive input, in global wheat production. Fertilizer prices have surged, and now exponentially, because of geopolitical conflict. While N use efficiency is paramount for on-farm ROI, N losses into the atmosphere and belowground raise awareness to the goal of reducing the environmental footprint of wheat systems. These intersecting pressures define the nitrogen paradox: the same input that drives yield and grain protein is also a major source of cost, emissions, and elevated business risk for wheat-based farming systems. This presentation synthesizes insights from multi-year, multi-environment wheat systems research to illustrate how the Genotype $\times$ Environment $\times$ Management (G $\times$ E $\times$ M) framework can reconcile these competing objectives. Case studies include the 20/20 project, a pilot study designed to test if reductions to management intensity by 20% could be offset by alternative practices and biological inputs so yield is maintained or even enhanced by 20%. While early, these findings underscore the potential for certain biologicals such as compost teas to attain the 20:20 tradeoff and reduce reliance on synthetic N, while others are either cost-prohibitive or lack efficacy. Other case studies include cultivar-specific N management for winter wheat systems in the USA Wheat Belt where genetic variance within an N management context reveals potential for cultivar-specific N prescriptive practices to enhance system NUE. The final case study from the Canadian prairies is used to argue that a balance with meeting global demand for wheat while concomitantly reducing greenhouse gas emissions (GHG) are not necessarily incompatible goals as enhanced efficiency forms of N show potential for the reduction of GHG's. Advances in individual technologies are of little benefit until they are melded into resilient G $\times$ E $\times$ M systems that will flourish in the field under unpredictable conditions. For example, optimized management enabled a 21-year-old cultivar to outperform the newest genetics available, emphasizing that breeding gains are maximized only when paired with agronomic strategies that unlock expression. These insights show how integrated agronomy can transform the nitrogen paradox into a pathway toward climate-smart, economically viable, and resilient wheat production systems.

Is hybrid wheat a good thing for the global south?

Flavio Breseghello ⁽¹⁾

⁽¹⁾ CIMMYT, Global Wheat Program, Texcoco, Mexico

Abstract

Our talk examines whether hybrid wheat can be a beneficial innovation for the Global South, using the HyBread Project as a case study aimed at delivering high yielding, disease-resistant hybrid wheat to East Africa and South Asia. We outline the biological and breeding foundations of the effort, including a patented blue aleurone male sterility system and early priorities such as identifying quick wins, establishing heterotic groups, and promoting allogamy ability of parents. The first hybrids are expected to reach field evaluations in the target environments in 2028. Hybrid wheat is framed as a potential breakthrough, defined as achieving a 25% yield advantage over current varieties, within ten years, through a combination of sustained genetic gains in inbred parents and hybrid vigor expressed as yield potential and stability, stress tolerance, and disease resilience. We depict two extreme, yet possible outcomes of hybrid introduction to the market: i) hybrids as catalysts for productivity, market development, and improved livelihoods, or ii) hybrids as a source of dependency, market concentration, and loss of farmers' trust on science and breeding. Key technical, agronomic, socioeconomic, and market questions that will determine outcomes are discussed. To manage risks, we propose a champion–challenger model in which inbred varieties remain the benchmark while hybrids compete transparently on performance in real production environments, ensuring farmers' choice, evidence-based decisions, and continuous improvement in any scenario. The conclusion emphasizes that the success of hybrid wheat in the Global South will depend on a multidisciplinary scientific approach, sustained public sector support, and growing private sector engagement. Maintaining strong inbred breeding pipelines alongside hybrid-focused breeding schemes will ensure that wheat hybrids will only dominate the market in the Global South if they are a proven good thing for small farmers.

From natural diversity to engineering disease resistance in wheat

Kyungyong Seong ⁽¹⁾ - Rakesh Kumar ⁽¹⁾ - China Lunde ⁽¹⁾ - Wei Wei ⁽¹⁾ - Daniil Prigozhin ⁽²⁾ - Sophie C. Sent ⁽³⁾ - Lorena Parra ⁽¹⁾ - McCree Tang ⁽¹⁾ - Brandon Vega ⁽¹⁾ - Amanda Dee ⁽¹⁾ - Isabel Saur ⁽³⁾ - Ksenia Krasileva ⁽¹⁾

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Abstract

Plant disease resistance includes a remarkable spectrum of diversity across genomes, transcriptional regulation, and protein structures. Natural diversity in plant immune receptors represents not only a record of host-pathogen coevolution, but also a practical foundation for engineering improved disease resistance in crops. A key enabling tool is availability of contiguous and well annotated genomes. We have recently assembled a blueprint for such analyses in wheat, a tetraploid wheat cultivar Kronos, which now has an integrated chromosome-scale reference genome and annotation resource built to support functional genomics. The Kronos platform brings together extensive mutant, transcriptomic, and phenotypic datasets, including approximately 3,000 exome-capture and promoter-capture datasets, while resolving previously inaccessible coding and regulatory variation as well as over 1,000 manually curated NLR immune receptors. This work provides the genomic and analytical infrastructure needed to identify, interpret, and mobilize natural and induced diversity in wheat immune receptors and other genes of interest. In parallel, we utilized an example wheat resistance gene Sr50 to demonstrate how natural diversity and computational biology can be combined to engineer receptor function. Sr50 is a wheat NLR that recognizes the stem rust effector AvrSr50, but pathogen escape can occur through natural effector variation, including a single surface-exposed substitution. Building on structure-guided engineering, iterative modeling, docking, and mutagenesis we redesigned Sr50 variants with resurrected recognition of the AvrSr50 escape form, providing a framework for countering pathogen adaptation through rational NLR engineering. Together, our studies define a translational path from diversity-informed theory and genomic resource development to rational immune receptor engineering for more durable crop resistance.

Embedding robust disease resistance into the architecture of tomorrow's wheat

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Abstract

Over several decades, substantial global effort has been directed toward the identification and deployment of diverse resistance (R) genes across the wheat gene pool for crop improvement. From a functional and applied standpoint, the key attributes of resistance are the magnitude of protection against economically significant disease and the durability of that protection across environments and time. Molecular dissection of wheat R genes has revealed considerable mechanistic diversity, encompassing classical immune receptors as well as non-canonical resistance determinants that collectively contribute to the observed phenotypic outcomes.

Conceptual foundations of resistance durability are encapsulated by two enduring principles. H. Flor's gene for gene framework highlights the evolutionary vulnerability of single resistance specificities to pathogen virulence mutations, while Roy Johnson defined durable resistance as that which "has remained effective in a cultivar during its widespread cultivation for a long sequence of generations or period of time in an environment favourable to a disease or pest." These principles continue to underscore the need for resistance strategies that mitigate selective pressure on pathogen populations. Any molecular strategy aiming to deliver durable resistance in future wheat cultivars must explicitly integrate these foundational insights.

In this context, the CSIRO team and collaborators have developed a gene stacking platform that exclusively employs naturally occurring wheat coding and regulatory sequences to assemble multiple resistance genes into a single, genetically linked locus. By generating cisgenic, polygenic resistance configurations, this approach enables coordinated expression of stacked genes while simplifying inheritance and deployment through breeding pipelines. The integration of such cisgenic resistance stacks into the genomic architecture of next generation, precision bred wheats provides a molecularly robust framework for achieving enhanced durability of disease resistance.

The holobiont concept in wheat breeding - a paradigm shift into sustainable agroecosystems

Wolfram Weckwerth ⁽¹⁾

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Abstract

The holobiont concept-recognizing the host plant and its associated microbiome as a single evolutionary and functional unit-has gained traction in plant sciences as a powerful paradigm for sustainable crop improvement [1]. In wheat (*Triticum aestivum* L.), this integrated framework underscores the dynamic interplay between plant genotypes, environmental conditions, root exudate-driven microbiome assembly, and emergent traits such as nutrient use efficiency, stress resilience, and disease resistance. Recent multi-omics advances, especially panomics [2], now make it feasible to dissect and harness this complexity in breeding programs. Here, we review the holobiont concept, its application in wheat breeding, and the natural variation of wheat root exudate metabolomes and their downstream influence on rhizosphere function [3].

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Use of AI in wheat databases: overview and prospects

Michael Alaux ⁽¹⁾ - ***Mario Caccamo*** ⁽²⁾ - ***Sarah Dyer*** ⁽³⁾ - ***David Edwards*** ⁽⁴⁾ - ***Keywan Hassani-Pak*** ⁽⁵⁾ - ***Taner Sen*** ⁽⁶⁾

⁽¹⁾ INRAE, University Paris-Saclay, Versailles, France - ⁽²⁾ NIAB, -, Cambridge, United Kingdom - ⁽³⁾ EMBL-EBI, -, Cambridge, United Kingdom - ⁽⁴⁾ -, University of Western Australia, Perth, Australia - ⁽⁵⁾ Rothamsted Research, -, Harpenden, United Kingdom - ⁽⁶⁾ USDA-ARS, UC Berkeley, Albany, United States

Abstract

In the frame of the Wheat Information System expert group of the Wheat Initiative, we share our experiences and practices of using AI, including LLMs, in our wheat databases.

This presentation will provide an overview of the various application of AI in some of the most internationally renowned wheat databases: EnsemblPlants (EMBL-EBI), GrainGenes (USD-ARS), GnpIS (INRAE-URGI), KnetMiner (Rothamsted Research) and at the Centre for Applied Bioinformatics (University of Western Australia), among others.

The presentation will introduce the main prospects for the coming years, which promise to be a game changer for wheat research.



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SECTION 1

Enabling sustainable wheat production in a broad cropping system: I crop management, soil conservation and health

Optimizing sulfur nutrition as a driver for iron homeostasis and grain safety in durum wheat

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Abstract

Sustainable wheat production in diverse cropping systems relies on the precise management of nutrient interactions to maximize resource use efficiency. While iron (Fe) and sulfur (S) are often treated as independent inputs, their metabolic pathways converge on specific hubs that dictate plant performance. This study employed a factorial modulation of S and Fe in hydroponically grown durum wheat to determine how sulfur availability hierarchically controls the plant's ability to acquire and utilize Fe.

The findings reveal that S status functions as a regulatory bottleneck for Fe homeostasis, determining biomass allocation and the transcriptional activation of both sulfate transporters and Fe-acquisition genes. At the center of this interaction lies a root metabolic hub dominated by citrate and S-related metabolites such as O-acetylserine, cysteine, and methionine. Correlation networks indicate that this citrate-centered module is essential for coordinating the internal transport of iron, meaning that inadequate sulfur nutrition effectively "locks" the plant's ability to manage its Fe stores regardless of Fe availability in the soil.

Beyond growth, the modulation of S nutrition plays a critical role in food safety. Under S-limited conditions, especially when coupled with low Fe, nitrogen metabolism is rerouted, leading to a significant accumulation of free asparagine. This shift has profound implications for the broad cropping system, as high asparagine levels in the grain are the primary precursor for acrylamide formation during industrial processing. Consequently, integrated Fe-S management emerges as a vital strategy for enabling sustainable production that balances high nutritional density with the safeguarding of food safety standards. These results provide a metabolic blueprint for optimizing wheat cultivation by tuning shared nutrient hubs to support both environmental sustainability and consumer health.

Proteome-informed breeding and management of nitrogen uptake and use efficiency across Australian broadacre wheat systems

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Abstract

Improving nitrogen (N) use efficiency (NUE) is central to enabling sustainable wheat production in Australian broadacre farming systems, where variable rainfall, low soil fertility and increasing climate stress constrain crop performance. As one of the world's major wheat exporters, it is important to balance high and reliable grain production with sustainable fertiliser inputs and environmental impacts. Western Australia, in particular, represents a challenging production environment that mirrors conditions expected to become more widespread under climate change. Combining the breeding for NUE in different environments with analysis of nitrogen-management responses in wheat crops provide a valuable foundation for developing resilient, low-input management strategies and matching these strategies to varieties best suited to specific environments.

Here, we present a multi-location analyses of protein-level responses in wheat that capture both genotype-dependent and environment-specific N signatures, reflecting underlying differences in N acquisition, remobilisation and partitioning to grain. Inorganic and organic N fertiliser types, biostimulants, and their amounts and timing of application varyingly influence these responses. This has allowed tracking of elite lines and wheat breeding populations grown under contrasting fertiliser regimes, N input levels and/or soil management practices across Australian broadacre systems. Our studies integrate agronomic measurements of nitrogen uptake and NUE with molecular protein profiling of post-anthesis flag leaves, developing grain and harvested grain. Across sites, fertiliser strategies and cultivars, we observed reproducible shifts in grain protein allocation associated with N supply and utilisation efficiency. Importantly, key protein markers consistently respond to N input across environments, highlighting their potential as molecular indicators of N status and fertiliser responsiveness. The data informs active breeding programs for NUE in Western Australia and management practises related to N application.

By linking wheat protein profiles with agronomic performance, this work establishes a framework for developing protein-based nitrogen response signatures. These signatures could support future prediction tools to guide NUE breeding, optimise fertiliser inputs, improve system-level nitrogen use efficiency and inform decisions on matching the right varieties and fertiliser strategies to specific environments. Overall, the datasets demonstrate how integrating breeding and management trials with molecular phenotyping can enable more precise, climate-resilient nutrient management in broadacre wheat systems.

The wheat microbiome: spatial and genetic drivers of bacterial and fungal communities in european wheat systems

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Abstract

The wheat microbiome is a key component of sustainable and resilient wheat production systems. Rather than assembling randomly, microbial communities are shaped by interactions between plant genotype, environmental conditions, and crop management. Yet, the collective impact of these factors on root and rhizosphere microbiomes under field conditions remains poorly understood. During the 2023-2024 growing season, we analysed bacterial and fungal communities associated with eight bread wheat (*Triticum aestivum*) varieties grown under two nitrogen input levels (sustainable and optimal) across three European locations (France, Ireland, and Italy). Roots and rhizosphere soil were sampled at crop maturity, and microbial communities were characterized using high-throughput amplicon sequencing. We evaluated microbial alpha diversity using observed richness and the Shannon index, and assessed community composition using Bray-Curtis dissimilarities, PERMANOVA, and partial redundancy analysis (pRDA). Clear compartment- and taxon-specific patterns emerged. In roots, bacterial richness and Shannon diversity were mainly driven by geographic location, with additional genotype-by-site interactions, while nitrogen input had little effect. In contrast, bacterial diversity in the rhizosphere responded to wheat genotype, site and nitrogen level, indicating greater sensitivity of rhizosphere communities to both host and management. Fungal richness in roots was primarily associated with wheat genotype, whereas rhizosphere fungal richness was influenced by genotype, site, and nitrogen input. Fungal Shannon diversity in both compartments was largely structured by geographic location. Bray-Curtis-based PERMANOVA showed that bacterial community composition in both roots and rhizosphere was strongly shaped by geographic location, with smaller but significant effects of nitrogen input and marginal effects of wheat variety. In contrast, fungal community composition across both compartments was more closely associated with wheat genotype than with site. Partial RDA further indicated that wheat genotype and plant functional traits, such as grain protein content and test weight, explained a small but significant fraction of bacterial community variation after accounting for site effects. We also identified specific microbial genera that correlated with root versus rhizosphere soil compartments, suggesting compartment-specific microbial associations. These findings highlight the potential to combine targeted breeding with optimized nitrogen strategies to steer wheat-associated microbiomes in ways that support more sustainable crop production.

Improving the performance of durum and winter wheat in intermediate areas of France through a combination of appropriate levers: lessons from 10 years of system experimentation in the Syppre network

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Abstract

Agriculture must succeed in reconciling food and energy production and conservation of the environment. This requires a shift towards new production systems, based on both ecological intensification and technical innovations, adapted to local conditions and manageable by farmers. To address this issue, the French technical institutes on arable crops ARVALIS, Terres Inovia and ITB launched in 2015 Syppre®, a collaborative project which brings together French national and regional stakeholders. The Syppre experimental network is implemented in five platforms that are representative of France's major regions for arable crop production: Picardie, Champagne, Berry, Lauragais and Béarn. Since 2016, each platform has been testing at least two systems, a reference one, representative of local farming practices, and an innovative system, more diversified, co-designed with local stakeholders to meet a multi-performance objective defined as follows: profitability and productivity greater than or equal to that of the reference with improved environmental performance. After 10 years of experiments, several innovative cropping systems have seen improvements in the technical and economic performance of their main crops, particularly durum wheat and winter wheat. In clay-limestone slopes susceptible to erosion in Lauragais, the cropping system and nitrogen fertilization management enable the production of 6.5 t/ha of durum wheat with 120 kg/ha of nitrogen and 13.5% protein, i.e. 80 kg/ha less nitrogen than our control. This contributes to significantly improving the carbon footprint of durum wheat. In plain area with limited potential, the performance of winter wheat have been improved thanks to the effective management of grass weeds enabled by the diversification of the cropping system with spring crops (sunflower, millet), in comparison with the winter wheat in the reference cropping system (rapeseed - winter wheat - barley). The lower pressure of autumn grass weeds leads to higher yields while reducing the herbicide TFI, especially for the wheat following the two spring crops. Consequently, the wheat in the innovative system achieves a higher margin than the wheat in the reference system. These results show the importance of combining levers at the cropping system scale in combating factors that limit crop performances, with wheat benefiting particularly from this approach.

Prospects for enhancing durum wheat productivity in ethiopia: from field to market

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Abstract

Ethiopia, as the largest wheat producer in sub-Saharan Africa, holds significant potential to enhance its durum wheat sector, which currently accounts for 25-30% of national wheat cultivation predominantly by smallholder farmers in the highlands. Despite favorable agro-ecological conditions, rich genetic diversity in landraces, and recent advances in improved varieties, durum wheat productivity remains low due to biotic stresses—especially wheat stem rust and *Fusarium* head blight—abiotic challenges exacerbated by climate change, weak seed systems, low-input traditional farming practices, and inefficient market linkages. The sector also suffers from inadequate post-harvest infrastructure, limited mechanization, and fragmented value chains, leading to underutilization of local production and reliance on imports for processed durum wheat products. This review highlights Ethiopia's untapped genetic and agronomic potential, institutional capacities, and growing market demand as foundations for transforming durum wheat production and value addition. Strategic interventions focusing on accelerated genetic improvement, integrating landrace diversity with modern breeding tools, climate-smart agronomic practices, strengthened seed systems, mechanization, and market development are critical. Policy reforms, capacity building, and multi-stakeholder coordination are essential to foster private sector engagement, improve farmer livelihoods, and enhance food security. Mainstreaming climate resilience and establishing comprehensive national strategies will position Ethiopia as a competitive player in the global durum wheat market, promoting sustainable agricultural growth and rural development.

From genes to the rhizosphere: harnessing root-microbiome interactions to improve nitrogen use efficiency in wheat

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Abstract

Crop root traits that shape rhizosphere microbial communities represent an important but largely unexplored mechanism for improving soil fertility and crop resilience in intensively managed agricultural systems. The A.E. Watkins collection of bread wheat landraces contains extensive genetic diversity that has remained largely untapped in modern breeding. Whole-genome resequencing has grouped these landraces into seven ancestral groups (AGs), providing a framework to investigate how wheat genetic diversity influences rhizosphere microbiome assembly.

We have investigated whether wheat genetic lineage predicts rhizosphere microbiome recruitment under field conditions. Eighty-one landraces representing the seven AGs and two elite cultivars were grown in replicated field plots, and rhizosphere soil was collected at plant maturity. Bacterial and archaeal communities were characterised using 16S rRNA amplicon sequencing, and differences in microbiome composition, differential abundance, predicted functional potential, and microbial association networks were analysed across genotype groups.

Rhizosphere microbiome composition reflected the genetic structure of the wheat population. Elite cultivars showed highly similar microbial recruitment to landraces belonging to AG2 and AG5, the groups genetically closest to modern breeding material. In contrast, five ancestral groups genetically distant from elite cultivars displayed distinct microbiome assemblies. These differences included shifts in alpha and beta diversity, altered abundances of taxa involved in nitrogen and carbon turnover, and changes in the structure of microbial co-occurrence networks. Notably, several distant AGs exhibited reduced abundance of ammonia-oxidising archaea and associated nitrification functions, alongside enrichment of taxa involved in organic matter decomposition and nutrient cycling.

Network analyses further indicated genotype-specific restructuring of microbial associations, including shifts in hub taxa and interaction patterns linked to nitrogen and carbon metabolism. These findings demonstrate that wheat genotype influences not only microbiome composition but also the ecological organisation of rhizosphere microbial communities.

Together, our results provide field-based evidence that wheat genetic diversity shapes the assembly of the rhizosphere microbiome. Landraces from ancestral groups not widely used in modern breeding appear to harbour root traits that selectively recruit or suppress key microbial taxa. Harnessing these traits in breeding programmes may offer new opportunities to optimise nutrient cycling, enhance nitrogen-use efficiency, and improve soil productivity in sustainable cropping systems.

Learning from long-term data: how rotation and establishment systems have shaped winter wheat performance in a temperate atlantic-influenced region

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Abstract

Crop rotation and establishment system choice are critical for sustainable wheat production in Ireland's high-yielding Atlantic-influenced climate. This study draws on 12 years of data (2014-2025) from the Teagasc Knockbeg long-term experiment near Carlow, Ireland, evaluating establishment systems (plough - 225 mm, shallow plough - 150 mm, min-till - 150mm, strip-till - 175 mm [replaced by direct drill in 2021]) and rotations contrasting continuous winter wheat (WWC) with winter wheat after winter oats (WWO) and winter oilseed rape (WWOSR, replaced by spring beans, WWB, in 2023).

Long-term climate normals (1991-2020) indicate a mean annual temperature of 9.8 °C, a 9.6 °C mean seasonal difference (winter - summer mean temperature) and annual precipitation of ~850 mm, supporting high yield potential under rainfed conditions.

Across all systems, wheat after break crops yielded significantly higher than WWC, which averaged 9.91 t/ha (2014-2022) and 9.42 t/ha (2023-2025). For 2014-2022, break crop effects were significant in 7 of 9 years, with mean gains of +16.9% for WWO and +19.0% for WWOSR. For 2023-2025, gains were +16.2% for WWO and +20.0% for WWB, with significance in 2 of 3 years. Yield advantage varied widely (-0.3% to +40.3%), driven by seasonal conditions around establishment.

Establishment system effects were significant in 7 of 12 years, with some non-plough systems often yielding less than plough systems: strip-till was lower in 4 of 7 years, min-till in 2 of 12, and direct drill in 2 of 5.

System × break crop interactions were not significant overall, indicating rotational benefits persist across systems. Plough-based systems delivered the largest absolute gains, though benefits were evident across all systems except where heavy rainfall occurred at establishment.

Direct comparisons among break crops revealed no consistent winner overall: WWO and WWOSR performed similarly in 2014-2022, while WWO and WWB were comparable in 2023-2025. A single exception occurred in 2025, when WWB surpassed WWO in direct-drill.

In conclusion, break crops provide robust, meaningful yield advantages for winter wheat across all establishment systems, though system choice influences absolute yield levels. Rotational diversity remains essential to support resilience and productivity under increasing climate variability.

Identifying high-yield and high-profit cropping systems for sustainable wheat production in india - evidence from nationally representative household survey

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Abstract

Sustainable wheat production mandates cropping systems that balance high productivity and economic viability with efficient resource use. Identifying the most efficient cropping system that includes wheat for high productivity and high returns is essential amidst rising input costs and climate variability. In the milieu, an attempt has been made to assess a cropping system that delivers the highest wheat yield and profit, addressing sustainable production goals. Using the latest round of nationally representative Situation Assessment Survey data on wheat-farming households (n=14981), which contains comprehensive information on inputs used, costs and returns across India, this research evaluates the potential of wheat-based cropping systems. Cross-tabulation and gross margin analysis were employed to quantify profitability by comparing gross returns (yield x price) with paid-out costs. The results were also tested for their statistical significance. Our analysis indicated a substantial variation in yield and profit levels across cropping systems and regions. At the national level, the yield of wheat was higher (1295.91 kg/acre) in the rice-wheat system, whereas the profits were highest (INR 26753.53 per acre) in the millets-wheat system. Among wheat-growing states in India, significant variation was noticed. The yield was highest in Tamil Nadu (2667 kg/acre) under the millets-wheat cropping system. In terms of profit, it was highest under the oilseeds-wheat system (INR 46371 per acre) in the non-capital region of Delhi. A regional pattern also emerged, with north-western states registering higher yields and profits. Further, a regression tree approach was used to identify the socio-economic factors that determine the yields and profits. The analysis indicated irrigation as a major determinant. Our study concludes that yield and profit can be maximised through a diversified and region-specific cropping pattern. Policy efforts should focus on incentivising diversified rotations, promoting soil-health farm operations, and encouraging region-specific systems for ensuring sustainable and profitable wheat production.

Exploring novel planting strategies for sustainable improvement in wheat yield and profits

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Abstract

Improving winter wheat (*Triticum aestivum* L.) planting strategies for better crop establishment and canopy development are crucial for sustainable improvement in yield and profits. Wheat is traditionally sown using a low-precision grain drill, which can result in uneven stand and canopy, leading to lower yield potential. Research is lacking in evaluating agronomic practices that can lead to optimal canopy structure and maximize radiation interception as well as its use efficiency across production environments. Field trials were conducted at multiple locations in the Great Lakes Region over the last decade to evaluate the importance of seed placement accuracy and row spacing, optimal seeding rate and seeding time, and varietal canopy architecture (planophile vs erectophile varieties). Variables studied included seeding depth and plant spacing, tiller production and canopy development, radiation interception and use efficiency, tiller angle across varieties, yield components, and final yield. Data from small-plot trials showed that wheat planted with precision planter in narrow rows (13 cm) improved seeding uniformity compared to drill (19 cm rows) and led to 3-32% yield increase. Precision planting exhibited an 8-33% yield increase over grain drill at 4 out of 8 on-farm site-years, likely due to more precise seed placement in narrow rows leading to more heads ha⁻¹. Yield and profits were maximized when planting soon after the hessian-fly safe date for the region, and progressively increasing seeding rate as planting was delayed minimized yield losses. Planophile canopies showed wider tiller angle (23.6°) compared to erectophiles (17.8°) and had greater light interception but lower use efficiency. Varieties with erect canopies maximized yield under high yield environments provided by narrow row spacings and early plantings, while planophile varieties provided high and stable yield under lower yield environments such as wider rows (>19 cm). Overall, our results from on-farm and small-plot trials have demonstrated that wheat yield and profits can be enhanced by improving seed placement accuracy, use of narrow row spacing, timely planting and lowering seeding rates, and matching variety canopy type to the production environment.

SECTION 2

Enabling sustainable wheat production in a broad cropping system: II phenomics, enviromics, crop modelling, digital agriculture

Strategically timed UAV remote sensing for robust wheat yield prediction: a multi-year study on phenology-aligned machine learning dynamics

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Abstract

Accelerating genetic gain in wheat breeding requires high-throughput phenotyping (HTP) to overcome labor-intensive bottlenecks and subjectivity associated with traditional field assessments. Unoccupied Aerial Systems (UAS) are a transformative HTP tool, providing a non-destructive, scalable platform to capture crop development with high spatial and temporal resolution across thousands of experimental plots. Accelerating genetic gain in wheat breeding requires high-throughput phenotyping to overcome labor and subjectivity constraints in field evaluation. Selecting optimal flight timing and predictive models is critical to ensure consistency across seasons. This study optimized UAV flight timing for wheat yield prediction by evaluating multi-year vegetation indices (VIs), including Normalized Difference Vegetation Index (NDVI), Normalized Difference Red Edge Index (NDRE), and Excess Green (ExG), aligned using Days Relative to Heading (DRH). Data from ten flights per year during the 2018-2021 growing seasons were used to assess predictive accuracy of machine learning models, including XGBoost, Ridge Regression, Random Forest, ExtraTrees, Partial Least Squares Regression, and Neural Networks. To address seasonal differences in planting date and sampling intervals, VIs were synchronized using DRH. Models were trained on 2018-2020 data and validated using an independent 2021 dataset. To enhance model explainability and ensure the reliability of the results, feature importance was evaluated over 100 iterations to identify the most consistent phenological window for yield prediction. XGBoost, ExtraTrees, and Random Forest achieved the lowest prediction errors (RMSE = 6.03 bu ac⁻¹; NRMSE = 9.59%, RMSE = 6.1 bu ac⁻¹; NRMSE = 9.7, RMSE = 6.58 bu ac⁻¹, NRMSE = 10.47%) and showed negligible performance change in 2021 (Δ RMSE = -0.12 bu ac⁻¹), indicating robust out-of-year generalization. VIs at +1 DRH were the most critical predictors, underscoring the importance of canopy condition during early grain filling and senescence for yield estimation. Concentrating UAV flights at heading therefore provides a resource-efficient approach for accurate yield prediction. Within the tested production environments, this framework supports high-throughput selection by identifying temporally stable canopy-yield relationships and optimizing UAV flight timing to reduce operational redundancy and cost.

Digitizing wheat variety testing: transitioning high-throughput phenotyping from research to regulatory infrastructure

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Abstract

Over the past two decades, high-throughput phenotyping (HTP) has transformed wheat research, enabling large-scale trait analysis and accelerating genetic gain through phenomic prediction. However, its integration into official variety testing—the regulatory backbone of varietal registration and seed certification—remains limited. Accurate, reproducible, and scalable phenotyping continues to rely predominantly on manual visual assessments, which are labor-intensive, operator-dependent, and difficult to harmonize across sites, years, and regulatory authorities. This gap represents a major barrier to the full operational deployment of digital phenotyping.

We present the validation and regulatory adoption of a handheld high-throughput phenotyping system (Literal, HIPHEN) for automated wheat head counting under official field trial conditions. The system integrates standardized RGB-NIR image acquisition and three-dimensional reconstruction, enabling automated, reproducible measurements at plot scale. Validation was conducted under Bundessortenamt (German Federal Plant Variety Office) conditions across seven trials in Germany, including 79 plots and 12 highly contrasting cultivars. Protocols involved repeated acquisitions totalling 22 images per plot and reference manual counts (10 per plot). Performance was assessed using agreement metrics (R^2 , RMSE), repeatability analysis, and consistency of cultivar ranking across sites.

Results demonstrated strong agreement with reference measurements, high repeatability, and robust ranking stability, confirming both scientific validity and operational feasibility. Based on these outcomes, the Bundessortenamt formally integrated the system into its official wheat phenotyping protocols. This represents a critical milestone, marking the transition of handheld HTP from experimental research tool to regulatory measurement infrastructure.

We will discuss the validation pathway, operational integration, and implications for scaling digital phenotyping across traits, platforms, and regulatory systems. Alignment with emerging international frameworks, including the 2024 EPPO digital phenotyping guidelines, provides a foundation for harmonized, FAIR-compliant phenotyping. This transition opens the path toward a fully digitized, standardized, and scalable global variety testing system.

Spectral fingerprinting of wheat at early growth stages enables accurate grain yield prediction

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Abstract

Breeders' selection, optimal farm management decisions, and supply chain planning require reliable yield forecasts. Although many yield prediction approaches rely on climatic and environmental information, their accuracy at early stages of the growing season remains limited, constraining their practical value for timely decision-making. In most cases, crop modelling and remote sensing approaches applied early in the season do not provide sufficiently accurate predictions to support management interventions or strategic planning.

In this study, we evaluated the potential of wheat spectral fingerprinting to predict grain yield at early growth stages. A total of 1,272 grain yield observations (ranging from 0.2 to 5.5 t ha⁻¹) were collected across multiple sowing times, nitrogen rates, cultivars, and locations in South Australia. Biomass samples were collected at growth stage DC 31, and spectral signatures were obtained using an ATR-FT-IR spectrometer. Of the total dataset, 603 plots were used for model calibration and 619 for independent validation.

The spectral fingerprint at DC 31 explained 83.75% of the variability in grain yield in the calibration dataset (RMSEE = 0.496 t ha⁻¹). Independent validation yielded an R² of 0.76 with an RMSEP of 0.63 t ha⁻¹, demonstrating strong predictive capacity at an early growth stage.

The proposed model predicts yield with greater accuracy than most currently available tools at comparable growth stages, without requiring extensive environmental or management inputs. This approach has potential applications in regional supply chain planning, optimization of breeding program resource allocation, and more precise nitrogen requirement estimation based on early-season yield predictions.

Multi-climatic plausibility testing of nitrogen-mitigation scenarios in wheat using crop models: a benchmarking workflow for digital agronomy

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Abstract

Sustainable nitrogen (N) management in cereals demands models that deliver robust, reproducible and agronomically plausible responses across environments. This work is conducted within the EU project NutriBudget, which develops next generation nitrogen budgeting tools for sustainable crop and soil management across Europe. We present a scenario-benchmarking and plausibility framework built on the CHN crop model and tailored to digital agronomy and enviromics. The study evaluates 26 mitigation scenarios (grouped into 13 measures: reduced-N levels, optimized fertilization, organic amendments, cover crops, tillage, residue retention, pH correction proxy, biochar) across five contrasting climatic contexts (Atlantic, Boreal, Continental, Mediterranean, Mountain) using standardized C/N inputs and harmonized management calendars.

For each climate × scenario combination (n = 130), daily outputs over a crop rotation were aggregated by crop into consistent mass-balance diagnostics: inputs (mineral fertilizer, organic sources, soil supply, deposition), outputs (crop uptake, leaching, volatilization, denitrification), surplus and balance. Scenario effects were quantified relative to a control in absolute and percentage terms with 95% confidence intervals. This enables screening of direction, magnitude and uncertainty, and supports relevant modelling questions: prediction under variability, enviromic sensitivity, decision-support readiness.

Results show stable, climate-sensitive patterns. Reduced-N (CRN1-5) yields monotonic decreases in surplus/balance with effect sizes modulated by climate. Organic amendments display coherent positive N inputs and improved uptake, strengthened by slurry incorporation. Cover crops produce climate-dependent benefits, highest where growth windows are longer. pH correction and biochar exhibit plausible but more uncertain responses, highlighting priority areas for model refinement. In a subset with observations, the framework reproduces treatment ranking and effect direction, supporting model-data consistency and the transferability of insights.

We propose this plausibility-first workflow as a scalable building block for digital support systems: (i) it stress-tests mitigation portfolios before calibration, (ii) it reveals climate-specific sensitivities for targeted design, and (iii) it streamlines the transition to validation with field datasets and future sensor/data-fusion. By combining crop modelling, enviromic stratification and rigorous uncertainty diagnostics, the approach advances resilient N management for wheat systems.

Characterizing yield through wheat's perception of chronological progression: a multi-omics plant-time warping approach

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Abstract

Understanding crop performance across diverse and shifting environmental conditions is essential for addressing global food security challenges. Crop production systems are governed by three primary components: plant genetics (G), environmental conditions (E), and management practices (M). In breeding and variety evaluation contexts, management is typically optimized and held constant, focusing attention on the interaction between genetics and environment, commonly expressed as $P = G \times E$, where P represents the observed phenotype.

Modern molecular techniques enable comprehensive genetic characterization at the genome scale, while publicly available weather data from governmental open data initiatives provide detailed environmental information. However, a fundamental mismatch exists between data scales: while genetic markers and environmental time series usually comprise >100k data points, multi-environment trial (MET) datasets to characterize phenotypes typically contain fewer than 10k observations. This creates a classic high-dimensional, low-sample-size scenario that complicates system modelling.

Field phenotyping technologies offer a solution by generating time-resolved phenotypic measurements $P(t)$, representing the cumulative effect of genetic and environmental interactions over time (t), where $P(t)$ is defined as the integral from 0 to t of $G \times E(\tau) d\tau$. These technologies can produce datasets exceeding 150k data points, aligning phenotypic data volume with genetic and environmental datasets to enable robust empirical modelling.

Yet, specific approaches that can handle such multi-modal data are yet sparse. Here, we introduce Plant Time Warping (PTW), a deep learning approach that integrates image time series, genetic markers, and environmental variables to model genotype-specific physiological responses to temperature and vapor pressure deficit. PTW outperforms conventional genomic prediction approaches when predicting yield across 48 European year-locations in previously unobserved environments. The model successfully captures nonlinear growth dynamics that vary with developmental stages and reveals distinct response signatures linked to yield performance and stability.

These response patterns support both historical analysis and future yield projections, establishing a framework for site-specific variety selection and breeding programs. By unifying phenomic, genomic, and environmental data streams, our approach offers significant potential for advancing climate adaptation research in agriculture, particularly in addressing the challenge of predicting crop performance under novel environmental conditions.

Synchronized plant-environment time series enable machine learning prediction of daily wheat transpiration from high-precision gravimetric lysimetry

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Abstract

Accurate prediction of crop water use is essential for climate-smart breeding and crop modelling under increasing heat and drought stress. Data-driven approaches, including machine learning, are becoming central to digital agriculture, yet their reliability depends critically on the availability of high-quality physiological training data that capture dynamic plant-environment interactions.

Here we integrate functional phenotyping based on high-precision gravimetric load-cell lysimetry (PlantArray) with continuous atmospheric sensing to model daily whole-plant transpiration. Across seven growing seasons and 48 experiments conducted in two semi-controlled greenhouses, plant physiological signals and environmental variables were recorded every 3 minutes (up to 480 measurements per day) for 269 plants monitored over 3-4 weeks each.

The resulting dataset spans Mediterranean summer and winter crops, including tomato, wheat, and barley, and comprises more than 3.6 million synchronised plant-environment observations. Whole-plant weight dynamics were directly converted to daily transpiration and paired with meteorological drivers including temperature, relative humidity, vapour pressure deficit, radiation, and daily light integral, together with plant-level descriptors such as plant type, substrate, and biomass estimated from predawn net weight following drainage to field capacity.

Machine learning models including Decision Tree, Random Forest, XGBoost, and Neural Networks were trained to predict daily transpiration. Random Forest and XGBoost showed the best generalisation, achieving $R^2 = 0.89$ in cross-validation and $R^2 = 0.82$ in independent holdout experiments. Feature attribution consistently identified ambient temperature as the dominant environmental driver, with plant biomass providing a key complementary predictor.

These results demonstrate that continuous paired monitoring of plant physiology and environment can generate reliable functional labels for machine learning. Such datasets enable robust prediction of crop water use and provide a scalable physiological framework for wheat-focused modelling, quantitative stress analysis, and future integration with imaging-based phenotyping pipelines.

Grain yield efficiency of dry land wheat in Israel: a high-resolution coupled crop-climate modeling approach

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Abstract

Wheat provides approximately 25% of global calorie consumption, yet production in dryland regions remains highly vulnerable to climatic variability. In regions such as the Eastern Mediterranean, spring wheat is primarily rain-fed, leading to significant year-to-year yield fluctuations. As climate change intensifies water scarcity and global food demand rises, developing site-specific crop management strategies is imperative. This study employs a high-resolution (3 km²) coupled modeling framework, integrating the Weather Research and Forecasting (WRF) model with the Noah-MP-Crop model, to simulate wheat growth and land-atmosphere feedbacks. By accounting for the bidirectional interactions between the regional climate and annual crops, the model provides a robust assessment of yield and water use efficiency (WUE). Following calibration against commercial spring wheat data in Israel, the coupled model was executed over a 30-year period, demonstrating a strong correlation between model predictions and recent field observations. Our results reveal a critical non-linear relationship between soil moisture, yield, and WUE. Specifically, we identified a threshold where water stress exceeding 30% can trigger a rapid decline in potential yield. Soil texture analysis indicated that while clayey soils offer greater resilience to moisture variability, sandy soils can outperform them under severe water stress when other agroclimatic conditions are optimal. These findings underscore the necessity of climate-informed, site-specific management. We conclude that the strategic selection of cultivars and soil-specific management, guided by coupled regional models, can substantially improve wheat yield efficiency and food security under future climate projections.

SECTION 3

Carbon footprint of wheat production: toward a reduction of greenhouse gas emissions

Environmental impacts of precision agriculture adoption in central Italy wheat production: a comparative LCA

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Abstract

The agricultural sector globally accounts for 22.3% of greenhouse gas emissions, 70% of freshwater consumption, and 24% of land use. This issue, combined with global population growth and the resulting increase in food demand, poses a risk to the entire food system. Thus, there is an urgent need to develop new cultivation techniques that focus not only on sustainability but also on efficiency.

In this context, smart and precision agriculture have been developed as strategies that use technological systems, such as variable-rate application and prescription maps, automatic implement control, Global Navigation Satellite System (GNSS) antennas, and aftermarket Topcon systems, to enable site-specific interventions. These approaches seek to reduce the use of agricultural inputs without affecting crop yields. Therefore, this study aims to identify and quantify the differences in environmental impacts between conventional and precision agriculture systems.

The analysis considers two consecutive three-year cycles (2019-2021 and 2022-2024) of soft wheat production on the same farm located in Umbria, Italy, thereby ensuring consistent pedoclimatic conditions. A conventional farming system was adopted during the first period, whereas precision agriculture practices were implemented in the second. To quantitatively assess the environmental implications of this transition between farming systems, a life cycle-based approach was employed.

The study applies the Life Cycle Assessment (LCA) methodology in accordance with ISO 14040-44 using the ReCiPe 2016 Endpoint (H) impact assessment method and the Ecoinvent 3.12 database to evaluate environmental impacts. This methodology was selected because it not only accounts for system inputs, but also relates them to production and land use, providing a comprehensive evaluation of overall environmental sustainability. The functional unit selected for the study is 1 ton of harvested soft wheat. Referring to the selected functional unit, the results show that the transition from conventional to precision agriculture led to a significant improvement in environmental performance, with an overall impact reduction of approximately 40%. Major reductions were observed in impact categories such as human toxicity, ecotoxicity, and water consumption. These improvements were achieved not only through a reduction in input use but also through changes in input composition, resulting from better adaptation to the adopted technologies.

Sucrose signalling: a new approach for reducing nitrogen inputs in wheat production?

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Abstract

Increasing nitrogen fertiliser use has contributed to yield gains in wheat but has led to increased environmentally damaging NO emissions. We urgently need to improve nitrogen use efficiency (NUE) without compromising productivity, given that wheat provides approximately 18% of global caloric intake. Understanding the metabolic and signalling processes that underpin grain filling under reduced nitrogen inputs is paramount to reducing NO emissions.

During grain filling, sucrose remobilised from vegetative tissues is converted into starch in the developing grain. Trehalose-6-phosphate (T6P) acts as a key signal of sucrose availability and promotes starch biosynthesis, however, its interaction with nitrogen supply during wheat yield formation remains poorly characterised.

We previously developed a light-activated T6P biostimulant that transiently elevates endogenous T6P levels and has been shown to increase grain yield and protein content in field-grown wheat. Preliminary evidence further suggests that T6P application may enhance nitrogen uptake. Building on this work, we investigate the hypothesis that nitrogen availability and genetic background modulate wheat responses to T6P across physiological and molecular scales.

Using contrasting wheat genotypes and nitrogen regimes, we assess the effects of T6P on carbon allocation, nitrogen uptake, and grain composition. This work aims to clarify the integration of carbon signalling and nitrogen nutrition in wheat and to evaluate the potential of T6P-based interventions to improve NUE under agronomically relevant conditions.

Improved carbohydrate accumulation drives wheat breeding progress and yield formation

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Abstract

Analysis of European winter wheat varieties released since the 1960s revealed a steady yield increase through breeding, driven by improvements in sink-related traits and particularly the number of grains per spike as the key sink trait. However, because yield formation depends on complex source-sink interactions throughout the entire vegetation period, investigating source-related traits is essential for a comprehensive understanding of yield progress in wheat breeding.

The accumulation of stem water-soluble carbohydrates (SWSC) is a key determinant of source capacity after the transition to generative growth and plays an important role in yield formation. To evaluate SWSC concentration in the context of genotype × environment interactions, 50 well-characterized elite European winter wheat varieties representing five decades of breeding progress were grown in a field trial with two irrigation treatments (rainfed and additional irrigation). In addition to yield and yield components, plant samples were collected at four developmental stages (flag leaf, anthesis, milk/dough stage, and maturity) to investigate temporal SWSC dynamics under abiotic stress conditions and their relationships with yield and spike traits. Spike samples collected at harvest were phenotyped in detail for floret and kernel number per rachis node, as well as kernel weight and length.

The results showed a steady increase in SWSC concentration, mirroring the historical improvement in yield with the year of variety registration. Furthermore, SWSC concentration was negatively correlated with the number of kernelless florets per spike, and both traits were associated with the year of variety release. These findings suggest that the improved yield performance of modern varieties is related to enhanced source capacity, improving grain filling efficiency and resulting in fewer kernelless florets per spike.

We therefore propose that SWSC was a key source-related factor contributing to historical yield progress in winter wheat breeding and that its improvement facilitates more effective grain filling in modern varieties. Ongoing validation through additional sample analyses and multi-location field trials aims to provide deeper insight into the complex genotype × environment interactions influencing SWSC dynamics and yield performance, particularly under abiotic stress or reduced-nitrogen conditions.

Phenotyping nitrogen use efficiency for a new benchmark nutrient management regime in UK farms

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Abstract

Agriculture accounts for 10% of UK GHG emissions, with nitrogen (N) and nitrous oxides forming 83% of UK field emissions. Driving productivity by increasing nitrogen use efficiency (NUE, proportion of applied and soil N recovered in grain) offers considerable opportunity to mitigate climate impacts whilst reducing production costs. Determining nitrogen rates for cereals is challenging and farmers need real-time interactive recommendations to accurately target nitrogen applications. An ongoing NUE profits project consisting of 9 partners funded by Innovate UK aims to developing a novel nutrient management tool that targets robust 25% increases in NUE for UK wheat. Two field seasons were conducted in 2024 (Dyson farming) and 2025 (University of Lincoln) on three levels of N on winter wheat variety Extase. Measurements of physiological, agronomical and remote sensing traits were collected over two seasons at the two sites. Nitrogen (N) application rate has a significant effect on NUE ($P < 0.05$) and grain yield ($P < 0.05$). Results of an NUE trial in 2024 showed that at low (50 kg/ha), medium (110 kg/ha) and high (220 kg/ha) N application levels, NUE was at 66.4, 61.5 and 43.4 kg DM/kg N respectively. Similarly in 2025, at low (80 kg/ha), medium (160 kg/ha) and high (240 kg/ha) N levels, NUE was 67.4, 42.3 and 34.8 kg DM/kg N respectively. In both 2024 and 2025, grain yield was highest at the high N level (12.5 and 9.5 t DM/ha) compared to medium (10.3 and 8.1 t DM/ha) and low level (6.4 and 7.5 t DM/ha). Nitrous oxide (N₂O) emission measurements in 2025 also showed similar temporal flux patterns but a non-linear dose-response across the three N levels, with annual emissions of 0.46, 0.61 and 0.65 kg N₂O-N/ha at low, medium and high N levels, respectively. Soil moisture was the dominant control on N₂O emissions as pulse-fluxes were often observed following rainfall events rather than fertiliser applications. Data collected will be integrated into a crop model with data assimilation and machine learning to predict N requirement with the outcome of making nitrogen use efficiency measurements the new benchmark from which farmers utilise nitrogen providing more profit, and environmental gains.

Carbon footprint of Brazilian wheat production under contrasting farm sizes

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Abstract

The increasing global demand for food has driven the intensification of agricultural production, characterised by higher input use, expanded mechanisation, and increased pressure on land resources, resulting in higher greenhouse gas (GHG) emissions. Wheat is one of the most widely cultivated cereal crops worldwide and plays a central role in global food security. In Brazil, the recent expansion of wheat cultivation highlights the need for robust assessments of its environmental performance. Life Cycle Assessment (LCA) is a well-established approach for quantifying environmental impacts and identifying emission hotspots in agricultural systems. This study aimed to quantify the carbon footprint of Brazilian wheat production and to compare emission profiles between large and small farms to identify key mitigation opportunities. The assessment followed a cradle-to-farm gate approach, using a functional unit of 1 hectare of wheat cultivation. Primary data were collected from 61 farms located in the southeastern and central-eastern mesoregions of Paraná State, southern Brazil, encompassing farm sizes ranging from 7 to 697 hectares and a total cultivated area of approximately 202,600 hectares. All farms operated under no-tillage systems combined with crop rotation. Input use and field operations were obtained through structured interviews with farmers. Greenhouse gas emissions were calculated using the BRcalc method, with field emissions estimated in accordance with IPCC guidelines and NO_x emissions based on literature values. The global warming potential (GWP100) was quantified using SimaPro software and the Ecoinvent® database. The carbon footprint of wheat production was estimated at 1,915.9 kg CO₂-eq ha⁻¹ for large farms and 2,053.9 kg CO₂-eq ha⁻¹ for small farms. Field emissions were the dominant contributors, accounting for approximately 60% of total emissions in both systems, followed by emissions associated with nitrogen fertilizer production. These results highlight nitrogen management as the main leverage point for reducing emissions in wheat production systems. Overall, the findings indicate that improving nitrogen use efficiency and increasing productivity are key strategies for reducing the carbon footprint of Brazilian wheat production.

Carbon footprint in wheat production: a systematic review and multi-method meta-analysis

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Abstract

Carbon footprint estimation is crucial for understanding environmental impact and policy formulation. In this context, we systematically reviewed 422 articles indexed in Scopus on carbon footprint in wheat production, including 141 articles (33.4%) with quantitative data for meta-analysis. Analysis was conducted using Python with pandas, scipy, and matplotlib. Due to limited variance reporting (0.7% of complete data), we used three complementary approaches: vote counting (n=59), percentage synthesis (n=75, 142 values), and qualitative analysis (n=81). Interventions at the farmers' field included nitrogen/fertiliser application (n=52), farm management practices (n=32), irrigation (n=15), crop rotation (n=8), and organic amendments (n=7). Our analysis indicated that vote counting showed a 59.3% reduction, whereas its counterpart registered a 40.7% increase (p=0.19). Mean carbon footprint change was 34.55% (SD=44.58%), with the highest success rates for general practices (75%), followed by organic amendments (60%). Further, high heterogeneity indicates context-dependent outcomes. In our analysis, nitrogen/fertiliser management had the strongest evidence (63 values). Findings reveal mitigation potential, but also highlight the critical need for standardised variance reporting in agricultural life cycle literature. Our study concludes that this review underscores the urgent need for targeted mitigation strategies in wheat that address the major emission drivers within wheat production systems. By integrating insights from diverse methodologies, it provides a robust foundation for advancing low-carbon agricultural practices and informing policy decisions aimed at reducing the overall environmental footprint.

Breeding beyond the plot: leveraging rotational genetics to improve wheat performance and farming system sustainability

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Abstract

Wheat productivity and profitability in rainfed systems depend not only on within-crop genetic gain but also on the performance of preceding rotation crops. Grain legume crops provide critical disease breaks and contribute nitrogen through symbiotic fixation (SNF), yet crop improvement programs typically optimise crops in isolation rather than for their effects on subsequent wheat. Accelerating wheat yield and quality while improving system sustainability requires breeding strategies that explicitly consider these rotational effects.

We quantified how genetic variation in mungbean influences subsequent wheat performance. A mini-core panel of 300 mungbean accessions was grown in replicated field plots, followed by a single wheat variety planted in the same locations. Wheat yield exhibited moderate broad-sense heritability when analysed as a function of the preceding mungbean genotype, ranging from 2.51-3.49 t/ha. Integrated analyses of mungbean traits, soil nitrogen dynamics, soil physicochemical properties, and rhizosphere microbiomes highlighted potential biological drivers underpinning these responses. Haplotype mapping in mungbean detected genomic regions associated with wheat yield and grain quality, suggesting that rotational effects are genetically tractable.

Building on this proof-of-concept, we propose incorporating “acceptor traits” in wheat breeding programs, such as early vigour, nitrogen uptake efficiency, and root architecture, that respond positively to preceding pulse genotypes. By combining rotational selection with wheat breeding, this approach can improve yield stability while reducing fertiliser inputs and lowering reliance on pest and disease sprays, offering measurable sustainability and carbon footprint benefits. Breeding wheat not only for its own genetics but for its capacity to benefit from optimized rotations represents a new frontier in sustainable crop improvement.

SECTION 4

Exploring wheat diversity, evolution and genetic reservoirs

Genetic diversity characterization of *Aegilops tauschii* wide sequenced collection to unlock useful alleles left-behind by domestication and breeding

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Abstract

Aegilops tauschii, the diploid progenitor of the D subgenome of hexaploid wheat (*Triticum aestivum* L.), is a key reservoir of genetic diversity and a source of valuable alleles left-behind due to strong bottleneck consequent of wheat domestication. We characterized the phenotypic diversity for plant architecture and root traits of 242 *A. tauschii* accessions from the Open Wild Wheat Consortium (OWWC), all supported by whole genome resequencing. The panel includes the highly differentiated L1 (Turkey-Afghanistan-Central Asia) and L2 (southwestern Caspian Sea) lineages, the latter involved in wheat domestication. Plant developmental and architecture traits (phenology, growth habit, tillering, spike morphology, anthocyanin accumulation, shoot and root biomass) were assessed in a two-years field trial conducted in Cadriano (BO), Italy (2019/20 and 2020/21). Root system architecture (RSA) was assessed under controlled conditions by growing pre germinated seedlings on filter paper sheets placed on polycarbonate plates soaked in modified Hoagland solution. Roots were imaged to quantify root growth angle, primary and total root length, root diameter, root network area, and lateral root density and length. A k mer based GWAS (Gaurav et al. Nat. Biotechnol. 2022), identified high resolution QTLs for multiple traits: senescence (chr3, chr7), heading date (chr2, chr7), flag leaf length (chr4, chr7), elevation angle (chr2, chr4, chr5), peduncle length (chr2, chr7), root length (chr2, chr3, chr7), lateral root density and length (chr2, chr6, chr7) and root growth angle (chr3). The very low average linkage-disequilibrium (in a range of 50 kb-2 Mb) was key to localize the MTAs to very few candidate genes, annotated using orthologues from wheat, rice and *Arabidopsis thaliana*. Furthermore, for prioritized candidate genes, a detailed gene network analysis was performed using *Triticum aestivum* cv Chinese Spring v1.1, highlighting the involvement of further genes involved in root development and morphology (chr2D), cellular differentiation and auxin related pathways (chr5).

Overall, the study reveals extensive phenotypic and genetic variation in *A. tauschii* and its strong potential to provide beneficial alleles for improving root architecture and adaptive agronomic traits in wheat.

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Comprehensive atlas of wild relative introgressions reveals conserved introgression patterns and massive untapped diversity in wheat genebanks

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Abstract

Wild relative introgressions introduce genetic variation from related species into wheat, supplying traits that enhance adaptation, resilience, and yield. However, it remains unclear whether introgression patterns reflect random historical events or conserved strategies shared across germplasm types and time.

We present a comprehensive comparative analysis spanning historic and modern wheat: the Watkins landrace collection (827 accessions), the IPK winter wheat panel (760 accessions), and 221 modern elite cultivars including the 10+ wheat lines. Using chromosome scale assemblies from Chinese Spring RefSeq v2.1 and 20 wild relative species, combined with low coverage whole genome resequencing of these lines (1x), we systematically detected introgression blocks at 1 Mb resolution across all 21 chromosomes and identified 4,020 unique patterns across 1,808 accessions.

Despite contrasting germplasm types, temporal periods, and geographic origins, all datasets display strikingly conserved patterns. Five wild species dominate the introgression landscapes: *Aegilops tauschii*, *Triticum monococcum*, *Triticum timopheevii*, *Aegilops ventricosa*, and *Triticum urartu*, collectively accounting for more than 70% of detected introgressions. Genome-wide distributions mirror one another across subgenomes (approximately A: 43%, D: 41%, B: 16%), with conserved chromosomal hotspots on chromosomes 1D, 2D, 6A, and 7A. Notably, introgression density converges at 42 to 44 per accession across most lines, while elite modern cultivars and the 10+ lines show a higher mean of 47 wild relative introgressions, indicating that breeders are consistently retaining wild derived alleles, knowingly or not. Yet substantial diversity remains untapped. In the Watkins panel, 2,074 introgressions representing 68.6% of ancestral group specific patterns were lost during modern breeding. In the IPK panel, 1,217 introgressions representing 53% occur only in plant genetic resources (PGRs) and never entered breeding pipelines. Cross-panel comparisons reveal that of Watkins' lost diversity, only 30% persists in European PGRs, while 70% represents truly lost from contemporary germplasm. Conversely, 586 IPK specific patterns were never observed in the Watkins collection. In total, 2,512 deployment ready introgressions remain available across genebanks in these landraces and PGRs.

These results demonstrate that independent breeding systems conserved complementary subsets of ancestral diversity and provide a strategic framework to mobilise genebank introgressions for climate resilience and yield improvement.

Genebank genomics provides a comprehensive genome diversity atlas of wheat

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Abstract

To meet the challenges of the 21st century and ensure the sustainability of wheat production, breeders are seeking beneficial genetic variation to improve modern breeding germplasm. Today, ex situ genebanks are the most important reservoirs available to study and deploy genetic variation of wheat genetic resources for crop improvement. The genotyping of global wheat germplasm collections in recent years has prepared the ground to embark on this endeavor. Here, we present a comprehensive overview of a wheat genome diversity atlas on the basis of genotyping-by-sequencing data of the IPK wheat germplasm collection that was generated within the GeneBank3.0 (GB3.0, Genomics-based exploitation of wheat genetic resources for plant breeding) project, as well as further next generation sequencing datasets (DARtseq) of the AGENT (Activated GENEbank NeTwork) and SeeD (Seeds of Discovery) projects, mapped onto the Chinese Spring V2.1 reference assembly. This dataset includes genotypes of domesticated wheat species as well as wild wheat relatives, and represents a total of 117,738 genebank accessions. Within the combined dataset we observed differences in marker densities attributable to different sequencing strategies. To leverage private and overlapping markers between data subsets we performed genotype imputation in 74,455 *T. aestivum* genotypes for 142,736 informative markers. Imputation accuracy was very high based on random marker masking. To further demonstrate the usefulness of the imputed, high density marker set we performed genome-wide associations scans (GWASs) with genebank legacy phenotypes for the traits flowering time, heading date, plant height and thousand kernel weight. GWAS was conducted using both the original and imputed marker sets across ten genebank environments, multiple genetically distinct *T. aestivum* populations, and two GWAS models, resulting in a total of 423 analytical scenarios. These scenarios highlighted 610 marker trait associations (MTAs) and pinpointed 360 genomic regions, 125 of which emerged in more than one scenario. Further work will elucidate the biological function of these genomic regions in a meta-analysis focusing on MTAs that were detected repeatedly across populations and/or environments as well as on pleiotropic interactions, thus adding a new layer of phenotypic causation to the wheat diversity atlas.

Mapping global wheat diversity through an Australian lens

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Abstract

The Australian Grains Genebank (AGG) holds one of the world's largest wheat collections. Through the AGG Strategic Partnership - a five year, \$30M initiative transforming the AGG into a bio-digital resource centre - these accessions have been characterised using imputation-enabled SNP arrays and DArTseq. Digital tools developed through the Partnership now make it possible to view AGG wheat diversity within a global genomic context and assess how well major international whole genome resequencing and pan-genome datasets represent the diversity required for Australian wheat improvement.

Comparisons with genotyped CIMMYT, ICARDA and IPK genebank accessions reveal that the AGG captures much of the world's wheat diversity at the macro level. However, aligning AGG wheat diversity with major global resequencing and pangenome datasets exposes a striking gap: the diversity most relevant to Australian breeding is sparsely represented in international sequence resources. This highlights the need for targeted whole genome resequencing and reference quality assemblies for AGG accessions central to Australian wheat improvement.

The completed genotypic characterisation of the AGG wheat collection, combined with the Partnership's digital tools, has also enabled a detailed assessment of accession duplication within the AGG and across global genebanks. We found that 38% of AGG accessions have at least one close match at $\geq 99.8\%$ genetic identity, consistent with patterns reported in other genotyped genebanks. This finding has led to changes in conservation management practices that have improved AGG operational efficiencies. Similar, cross-genebank comparisons uncovered widespread near-identical and duplicate accessions, a finding supported by accession passport data analysis. These findings raise broader questions about the structure and distribution of global wheat diversity across genebanks and the long-term conservation strategies required to manage it effectively.

Here, we share key insights from such analyses and show how the AGG's digital tool ecosystem can help researchers and breeders unlock the full value of its plant genetic resources for wheat crop improvement.

Mitochondrial hybridity in in vitro fertilization-generated maizewheat and pearl milletwheat cybrids drive important stable phenotypic variations

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Abstract

Phenotypic variation and its heritable components are central to understanding how cytoplasmic diversity influences agronomic performance in crop species. In this study, we evaluated phenotypic diversity and broad-sense heritability across a 114-panel of wheat cybrids (incorporating mitochondria derived from maize or pearl millet) generated through in vitro fertilization, alongside IVF-derived and normally propagated wheat cv. "Felder" controls. Multi-environment field evaluations conducted over two years captured variations in plant height, total biomass, grain yield, chlorophyll content, developmental timing, and spike architecture. Linear mixed models fitted using Restricted Maximum Likelihood (REML) enabled variance partitioning into genetic (G), environmental (E), and genotype-by-environment (GxE) interaction components within an unbalanced field design (alpha lattice). Significant phenotypic variation among lines ($p < 0.001$) was observed across traits, showing clear differences between the wheat cybrids and the parental Felder control, indicating that alien mitochondrial backgrounds can modulate trait expression. Broad-sense heritability estimates (H^2) were consistently moderate to high across traits ($H^2 = 0.659-0.911$), indicating substantial genetic contributions to phenotypic variation. Biomass, grain yield components, plant height, and developmental timing traits exhibited particularly high heritability ($H^2 \geq 0.809$), whereas traits such as spike number and chlorophyll content showed comparatively lower but still substantial heritability ($H^2 = 0.659$ and 0.766 , respectively). Narrow 95% confidence intervals further supported the robustness of these estimates across years. The strong contribution of line variance across traits highlights the functional importance of mitochondrial-nuclear interactions in shaping agronomic phenotypes. Collectively, these results demonstrate that mitochondrial hybridity generates stable and heritable phenotypic diversity in wheat cybrids, supporting cytoplasmic engineering as a complementary strategy for crop improvement.

Ancient grains illuminate the mosaic origin of domesticated wheat

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Abstract

This study illuminates the evolutionary trajectory of domesticated wheat through the genomic analysis of 3,000-6,000-year-old grains excavated in the southern Levant. Our results identify these specimens as an early domesticated form closely related to wheat accessions from Ethiopia, the Arabian Peninsula, and India. Genomic evidence supports our multi-stage model of wheat domestication, centered on the genetics of the non-shattering spike, a key trait requiring mutations in both the TtBtr1-A and TtBtr1-B genes. These mutations likely arose independently in northern and southern wild populations, respectively. The foundational event of domestication was therefore the hybridization of these two populations, which united the required mutations to create the first truly domesticated wheat. Remarkably, our data suggests this hybridization occurred at least twice, giving rise to distinct domesticated lineages. Following this event, subsequent diversification occurred, revealing that these ancient grain lineages subsequently acquired advantageous traits through gene flow from local wild emmer populations. Together, these findings redefine wheat domestication as a prolonged dynamic, and regionally interconnected process, showing how a foundational hybridization event was independently achieved multiple times and then continuously diversified by human-led dispersal and subsequent local adaptation.

Comparative analysis of exome sequencing data reveals convergent selection of durum and bread wheat

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Abstract

Wheat (*Triticum* spp.) is a crucial cereal crop with two dominant species, tetraploid durum wheat (*T. turgidum* ssp. *durum*, BBAA genome) and hexaploid bread wheat (*T. aestivum* ssp. *aestivum*, BBAAADD genome). Their evolutionary history is complex and influenced by the process of domestication started in the Fertile Crescent during the Neolithic era. While durum wheat derived from wild (*T. turgidum* ssp. *dicoccoides*) and domesticated tetraploid emmer (*T. turgidum* ssp. *dicoccum*) through two main rounds of domestication, bread wheat is the result of a hybridization plus whole-genome duplication between domesticated emmer and wild goatgrass (*Aegilops tauschii*).

To evaluate the effect of convergent selection between durum and bread wheat throughout domestication and the gene flow contribution from wild germplasm, we merged two exome-capture datasets consisting of 253 tetraploid and 640 hexaploid accessions, obtaining 837,177 SNPs distributed within the A and B sub-genomes.

Reduction in nucleotide diversity (DRI) was observed during wheat domestication, affecting approximately 13% (1.3 Gbp) of cultivated tetraploid genome (0.6 Gbp during the first round and 0.7 Gbp during the second). Notably, a rough 40% (0.5 Gbp) of these reduced-diversity blocks were observed also in hexaploid wheat, most of them (0.4 Gbp) connected with emmer domestication. In addition, 0.2 Gbp of shared blocks show strong signals of differentiation (*Fst*) and co-localize with pivotal domestication loci such as *Br1-B1* and *Q* locus.

Remarkably, 64% (1,0 Gbp) of the total blocks are in the A sub-genome, while only 0.6 Gbp are in the B sub-genome, suggesting a differential role of the two sub-genomes in wheat domestication.

Furthermore, *fd* statistic revealed an extensive contribution of wild emmer in the A and B sub-genomes of bread wheat landraces, with 0.7 Gbp showing signals of introgression and harbouring crucial adaptation genes (e.g. *VRN-A1*, *PPD-A1*).

These findings show that domestication caused a significant diversity reduction in the cultivated wheat germplasm and that convergent selection of cultivated *Triticum* spp. is mainly due to a limited set of genes mainly located in the A sub-genome. In addition to that, gene flow from wild emmer had a fundamental impact on cultivated hexaploid wheat, contributing to its environmental adaptation.

Long-term evolution of root architecture response to soil nitrogen management in tetraploid wheat (*Triticum durum*)

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Abstract

Soil nitrogen (N) is a resource under intense competition among neighbouring plants, a condition that likely exerted persistent evolutionary pressure on wheat root-system architecture (RSA). In contrast, modern crop breeding in the past century has largely relied on management practices that minimize interspecific competition. As a consequence, adaptive root traits relevant under competitive or low-N environments may have been left behind. The current shift in agricultural policies toward more sustainable and environmentally responsible production systems now demands a re-evaluation of breeding targets, with renewed emphasis on root traits that enhance resource-use efficiency under reduced inputs.

In a first study, we examined how anthropogenic selection and agronomic management have shaped the development of the root system throughout and since the domestication of tetraploid wheat. To this end, we used a durum wheat pangenome collection of 125 accessions representing the full diversity of *Triticum turgidum* species, including wild emmer (22), domesticated emmer (36), *T. timopheevi* (4), *T. turgidum* landraces (23), and modern durum (31) and bread wheat (8). These materials were selected to ensure a comprehensive geographical and evolutionary representation.

In a second experiment, we investigated the genetic determinants of RSA in a contemporary, globally sourced diversity panel of durum wheat cultivars, including 218 cultivars and advanced lines. Our aim was to quantify the heritability of key root architectural traits, their plasticity under varying nitrogen conditions and a set of newly derived model-based variables associated with soil N capture.

The two collections have been grown under contrastingly low- and high- N in an aeroponics high-throughput root phenotyping platform where high-resolution images of the whole root system were captured every two hours for three weeks. The resulting collection of images has been analyzed using semi-automated software based on morphological image analysis functions to estimate emission, elongation rate and direction of seminal roots and density, elongation rate and direction of lateral roots. We then use virtual avatars of each genotype to simulate soil N dynamics in the soil-crop system with the final aim to derive novel parameters of N-uptake dynamics by crops, capturing its dependency on environment and management.

Digital characterization of chromosome centromeric haplotypes in polyploid wheat and their potential for breeding

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Abstract

In polyploid wheat, ultra-long recombination-suppressed regions around chromosome centers are a major structural feature of the genome. These regions contain large numbers of genes and include the centromere, a key chromosomal structure influencing recombination behavior, making them important for wheat improvement. Recent studies identified multiple chromosome centromeric ancestral haplotype groups (centAHGs) in polyploid wheat. These haplotypes, inherited from wild tetraploid wheat, average more than 100 Mb in length, show substantial divergence among groups, and have remained highly linked during evolution. However, whether finer-scale haplotypic structures exist within centAHGs, and how such structures affect agronomic traits and recombination frequency, remain unclear.

To address these questions, we integrated whole-genome resequencing data from nearly 2,000 wheat accessions worldwide and developed a fine-scale centromeric haplotyping framework for the systematic identification and cataloging of centromeric haplotypes. We further combined multi-year, multi-environment phenotypic data to evaluate haplotypic effects on important agronomic traits, and used multiple RIL populations to assess the effects of parental haplotype combinations on recombination frequency.

Our results revealed a two-layer nested genetic architecture in chromosome centromeric regions. In total, we identified 47 centAHGs and 2,741 finer-scale centromeric haplotypes (centHaps), revealing substantially greater genetic diversity within these regions than previously recognized. This diversity appeared to be shaped primarily by genetic differentiation rather than recombination. Significant differences in genetic effects among centAHGs were detected for multiple agronomic traits, including grain weight and leaf length, and some centAHGs showed stable effects on multiple traits across environments, suggesting their potential value in breeding. Notably, progeny derived from parents carrying identical centAHGs exhibited approximately 1.5-fold higher recombination frequencies, indicating that parental centAHG matching is associated with higher recombination frequency and may accelerate the introgression of favorable alleles into elite cultivars. Overall, our study identifies chromosome centromeric haplotypes as a previously underappreciated component of wheat genomic architecture and provides a basis for their digital characterization, effect evaluation, and future application in genomics-assisted breeding.

Unlocking genetic diversity for climate-resilient durum wheat improvement

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Abstract

Durum wheat is a cornerstone of Mediterranean agriculture and cuisine, yet its resilience and productivity face increasing challenges from climate change and shifting production environments. Stabilizing yields under those conditions requires identifying and deploying new, resilient and diverse genetic resources. This work presents two comprehensive approaches to mobilizing genetic resources under two projects called AGENT and BOLD. Within the AGENT initiative, historical phenotypic data from 43,293 wheat accessions were curated issued from a global network between 9 European and ICARDA genebanks. Precision subsets from each genebank served as training population for genomic selection, enabling the prediction of genomic breeding values (GEBVs) and supporting more informed selection by breeders. The BOLD initiative emphasized participatory assessment and targeted use of diversity. 46 elites lines derived from crosses with crop wild relatives (CWR) were evaluated in multi-environment trials in Morocco and other partner countries. Interestingly, These CWR-derived lines outperformed commercial checks across most sites, showing 11-48% yield gains alongside improved disease resistance to some rusts, rot root and Hessian fly, and several quality traits. Participatory trials with Moroccan farmers identified preferred lines for varietal release and commercialization based on agronomic performance and farmer priorities.

P125 - High-resolution genomics enables rapid gene discovery in *aegilops longissima*

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Abstract

Harnessing the genetic diversity of wild wheat relatives is becoming increasingly critical as global agriculture faces biotic and abiotic stresses driven by climate instability. *Aegilops longissima*, a diploid wheat wild relative, harbors a rich reservoir of unexplored agriculturally relevant alleles with strong potential to bolster wheat adaptability to these challenges. To enable efficient utilization of *Ae. longissima* genetic diversity, we developed an integrated platform for accelerated trait discovery that includes an *Ae. longissima* annotated, chromosome-scale long-read reference genome, 10x whole-genome sequenced diversity panels, a comprehensive gene expression atlas, and a high-resolution SNP- and k-mer-based association mapping pipeline tailored for large, structurally dynamic wild-relative genomes. We demonstrated the power of this framework by rediscovering known rust-resistance genes and subsequently identifying multiple novel loci associated with rust resistance, heading time, and root depth. Candidate genes underlying each trait were validated in transgenic wheat lines, underscoring the platform's power to rapidly and accurately pinpoint loci underlying key adaptive traits. Our results not only enable the identification of novel genes for agriculturally important traits, but also demonstrate the scalability of the system for unlocking adaptive variation from wild wheat germplasm, positioning *Ae. longissima* as a highly accessible and valuable resource for wheat improvement.

SECTION 5

Wheat genomes and pangenomes

Tracing the origin of non-brittle rachis alleles in wheat

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Abstract

The domestication of wheat is an event that shaped the history of humanity, and its effects continue to impact our society today. Understanding the complex roots of its origin is not only important for reconstructing the past, but also for fully characterizing this mosaic-origin genome for crop improvement. One of the key steps in domestication is the mutation of the TtBTR1 genes, which results in the non-brittle rachis phenotype.

The discovery and characterization of a third independent loss-of-function mutation raises new questions about wheat domestication. Two of these questions—where and when the mutations occurred—can now be addressed thanks to the availability of a large panel of wild emmer whole-genome sequencing data. Here we present an in-depth spatio-temporal analysis of the three Ttbttr alleles, revealing that these mutations occurred independently in three wild emmer populations within a timeframe predating the advent of agriculture, and explaining why these questions have been so debated in previous studies. This study illustrates how cutting-edge genomic analyses can help answer longstanding questions about domestication and evolution whose answers were long thought to be lost to time.

Unlocking long-range haplotype diversity in synthetic hexaploid wheat for breeding

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Abstract

Synthetic hexaploid wheat (SHW) captures novel genetic diversity from tetraploid and diploid progenitors providing a valuable resource for improving yield potential, stress tolerance, disease resistance, and nutrient-use efficiency in bread wheat. Over the past three decades, CIMMYT has led the development and deployment of SHW, with synthetic-derived lines (SDL) comprising 20% of top performers in international yield trials. Therefore, we aim to characterize the genomic structure of SHW and quantify the contribution of wild-derived haplotypes to the performance of SHW and its elite derivatives.

Specifically, we address three questions, i) what is the average genetic contribution of the *Ae. tauschii* parent across selected SDL? ii) are specific genomic regions from the *Ae. tauschii* parents consistently retained, or is parental contribution randomly distributed? and iii) do retained genomic regions show trait associations?

We performed whole genome re-sequencing (WGS) of 150 SHW and 145 SDL. To overcome limitations reference-based alignment and SNP calling when analysing crop wild relatives, we applied IBSPy, a k-mer based approach, to detect long-range haplotype blocks absent from current wheat references. By integrating publicly available *Ae. tauschii* genomic resources with chromosome-scale assemblies from wheat pangenome projects, we generated high-resolution haplotype maps.

Preliminary results identified large *Ae. tauschii*-specific haplotype blocks across the genome in SHW, some of which were retained in SDL, although haplotype inference was highly sensitive to donor representation. For example, WGS from an *Ae. tauschii* Lineage 2 donor identified identical-by-state region (>99.95% similarity) on chromosome 4D in the SDL Chuanmai 42. This region is maintained in other SDL and contains a yield-associated QTL. Similarly, the Lineage 1 reference genome TA10171 revealed lineage-specific segments on chromosomes 1D, 4D, 5D, and 7D. TA10171 carries the stem rust resistance gene *SrTA10171* effective against Ug99-related races, highlighting the untapped breeding potential of Lineage 1 diversity.

From reference transcriptome to pangenome transcriptional diversity: regulatory networks controlling kernel development in durum wheat

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Abstract

Kernel development is a major determinant of grain yield and quality in durum wheat (*Triticum turgidum* ssp. durum), yet the regulatory architecture underlying this process remains not completely understood. Here we combine high-resolution transcriptomics and pangenome resources to characterize the gene regulatory programs controlling kernel development in tetraploid wheat.

We first generated a detailed developmental expression atlas in the reference cultivar Svevo, profiling transcript abundance across eight stages of kernel development. Time-resolved transcriptome analysis enabled the reconstruction of gene co-expression networks and the identification of regulatory modules associated with key developmental transitions. Several transcription factors belonging to MYB, AP2/ERF and NAC families emerged as candidate master regulators coordinating pathways related to storage compound accumulation, hormone signalling, and cellular differentiation during grain formation.

To investigate how these regulatory programs vary across genetic backgrounds, we extended the analysis to ten accessions representing the diversity captured by the tetraploid wheat pangenome project. RNA-seq profiling across four kernel developmental stages revealed both conserved and genotype-specific transcriptional programs. Pan-transcriptome analysis classified expressed genes into core, shell, and cloud categories, highlighting substantial expression variation across genotypes. Notably, genes involved in carbohydrate metabolism, hormone signalling, and transcriptional regulation, together with seed storage protein encoding genes displayed pronounced genotype-specific expression patterns.

By integrating developmental transcriptomics with pangenome diversity, this work provides new insights into the regulatory networks controlling kernel development and identifies candidate genes and pathways underlying agronomically relevant traits. These results demonstrate the power of combining reference transcriptome analyses with pangenome-scale approaches to dissect complex developmental processes in crop species.

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An ecosystem of digital tools to solve the FAIR data problem in the pan-genome era

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Abstract

Wheat genetics research in the pan-genomics and big-data era has unprecedented potential to deliver major advances in short timeframes. New genetic, genomic and pan-genomic resources are being published at a rapid pace, with public repositories growing exponentially. However, key challenges remain in how to incorporate these resources effectively - not only in terms of access to specialist bioinformaticians, data scientists and computing infrastructure, but also in knowing how to extract value from the sheer volume and diversity of data available.

The Australian Grains Genebank Strategic Partnership has developed an ecosystem of digital tools designed to address these challenges in novel and practical ways. These include Pretzel, for visualisation and interactive exploration of genetic and genomic data; Brioche, which focuses on solving data interoperability; Genolink, for integrating and working with genebank passport data; and additional tools with complementary capabilities. While each tool was created for a specific purpose, they have been designed to interoperate, enabling users to connect information and functionality across multiple data types.

Although FAIR (Findable, Accessible, Interoperable, Reusable) data principles guided development, the tools are particularly powerful in addressing interoperability, one of the most difficult FAIR components to implement effectively. They enable genotype data to be re-phased onto new reference genomes, integration of datasets from diverse genotyping platforms, comparative analyses across genomes and pan-genomes, and linkage to research and breeder knowledge. Together, these tools lower the barrier to working with large-scale data - supporting tasks ranging from basic data access for non-bioinformaticians to complex biological queries requiring multi-layered data integration.

This presentation will demonstrate how this digital tool ecosystem has been applied to real-world questions in wheat research connected to the Australian Grains Genebank, highlighting its value for accelerating discovery and breeding outcomes.

Digitalized map of homologous clusters across poaceae species unveil the complex evolutionary trajectory of genes in triticeae

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Abstract

Gene birth-death dynamics are primary drivers of genomic plasticity and phenotypic innovation, providing traits crucial for plant adaptation. However, resolving fine-scale evolutionary trajectories within local genomic neighborhoods remains a formidable computational challenge at the pan-genus scale, particularly for polyploid Triticeae species where frequent tandem duplications obscure traditional homology. Previously, we established a homology inference strategy incorporating gene collinearity to connect 108 genome assemblies across the Triticeae tribe, resulting in the Triticeae-GeneTribe (TGT) database (<http://wheat.cau.edu.cn/TGT/>). Building upon this foundation, we present a pan-genus evolutionary analysis spanning 25 Poaceae species. By developing GoldMiner, a novel computational framework that utilizes homologous gene clusters (HOCs) as fundamental evolutionary units, we systematically traced gene birth-death dynamics with unprecedented precision. Processing 248 diploid genome partitions, we constructed a digitalized pangenomic map indexing over 5 million HOCs to reconstruct their origins, duplications, and losses across seven discrete evolutionary phases. Our analysis reveals that more than half of newborn HOCs is derived from the expansion of existing clusters rather than de novo origination. In Triticeae, the emergence of these new HOCs coincides with historical climatic fluctuations and is significantly enriched in abiotic stress response and defense pathways. Compared to related grasses like rice and maize, nearly two-thirds of Triticeae HOCs (62.49%) underwent massive lineage-specific expansions, particularly nucleotide-binding leucine-rich repeat (NLR) immune receptors. Gene loss also serves as a potent adaptive strategy. Our HOC tracking indicates that the loss of specific regulatory clusters, such as those negatively regulating salt stress, likely facilitated Triticeae ecological specialization. Meanwhile, genomic redundancy generated by wheat polyploidization buffers HOC loss, directly contributing to widespread copy number variations (CNVs) in modern germplasm. We also decoded the complex seed storage proteins (SSPs) super-cluster, revealing dual-scale dynamics of stable inter-HOC formation coupled with explosive intra-HOC diversification of gliadins across specific subgenomes. These results establish a digitalized atlas of grass gene evolution, providing a strategic framework for the precise resolution of gene cluster evolution. To democratize access to these resources, we provide the waGOLD platform for real-time exploration of pan-genus HOC evolutionary trajectories (<http://wheat.cau.edu.cn/TGT/waGOLD/>).

Genomic investigation of wheat genetic improvement: introgression, disease resistance, and yield

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Abstract

Genetic introgression has played a pivotal role in the domestication and genetic improvement of wheat. Introgression: Population-level genomic analyses reveal that approximately 15% of the common wheat genome is derived from wild emmer wheat. When considering introgressions from a broader range of donors, about 20% of the genes in a typical wheat cultivar can be classified as introgressed fragments. Gene expression analysis of these introgressed segments indicates a general trend: genes involved in primary metabolic processes tend to exhibit reduced activity, whereas those associated with stress responses show significantly enhanced activity. Disease Resistance: Powdery mildew is a major disease affecting wheat production. Utilizing introgressions from wild relatives to confer resistance in cultivated varieties represents an environmentally friendly control strategy. However, the co-evolution between wheat and the powdery mildew pathogen often leads to the rapid breakdown of resistance genes. To decipher this host-pathogen interaction, we developed a bidirectional GWAS strategy. This approach allows for the dissection of the interaction mechanisms between wheat and the pathogen at a population level. Our findings indicate a positive correlation between powdery mildew resistance and the number of resistance genes present in a genotype. Nevertheless, whether this gene stacking phenomenon is directly driven by breeding selection requires further validation, given that yield enhancement remains the paramount objective in wheat breeding. Yield: Through the calculation of epistatic effects between haplotype blocks, we identified network modules controlling yield traits. These modules comprise numerous independent genomic loci and can be conceptualized as epistatic complexes - combinations of alleles with tight synergistic interactions that have been forged under long-term breeding selection. The existence of these epistatic complexes may explain the often-observed genetic background dependency of superior alleles.

The IWGSC RefSeq 3.0 and a bread wheat pangenome providing access to worldwide diversity

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Abstract

To face the increasing impact of unpredictable climate variations on yield, there is an urgent need to accelerate crop breeding. Targets of cultivar improvement are changing and a wider genetic diversity has to be explored to sustain yields meeting global demand. In bread wheat, most genetic diversity is held within landrace accessions that were locally adapted over thousands of years by traditional farming prior to modern agriculture. While today's commercial cultivars contain only a fraction of this available gene pool, landraces remain a key reservoir for adaptive traits. The IWGSC Wheat Diversity Project addresses this critical need by providing platinum-quality genomes of 12 landraces that represent the worldwide diversity of bread wheat¹ (*Triticum aestivum* L. $2n = 6x = 42$, AABBDD). In addition, the project provides an improved community reference, Chinese Spring, to be released as IWGSC CS RefSeq v3.0, using state-of-the-art technologies and annotations³, ensuring trackable mappings to prior versions² of this essential resource. Multiple pangenome graph approaches are available to characterize the foundational diversity present in these genomes. This presentation focuses on one approach wherein one graph per chromosome was built across each of the 13 genomes using the Minigraph-Cactus pipeline⁴. Through these graphs, an all-against-all transfer of gene annotation was performed using GrAnnot5 resulting in an accurate and comparable pangenome annotation. Applications of this graph includes characterization of the core, shell and cloud genomes that shape this diversity reservoir, and potentially harbor targets of breeding such as genes controlling adaptive traits. This method is also advantageous in the exhaustive detection of structural variations (SNP, CNV, INDEL) by mapping, that can improve the performance of association studies and genomic selection, departing from typical reference-based analyses. Leveraging this wheat pangenome will help to improve our understanding of genome evolution dynamics and to characterize more exhaustively diversity panels at key agronomic loci.

10+ wheat genomes project highlights that purifying selection on deleterious variants is shaped by the interactions between subgenomes and gene expression

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Abstract

The genome-wide pattern of purifying selection on deleterious variants has attracted broad interest in breeding and evolutionary biology. Compared with diploid species, much less is known about purifying selection in polyploid bread wheat, in which duplicated homoeologs may exhibit functional redundancy. Here, we examine the pattern of polymorphisms and the combined effects of both subgenome and gene expression on estimates of purifying selection using the de novo annotated assemblies and pan-transcriptome data of the 10+ Wheat Genomes Projects. Cultivars of the 10+ Wheat Genomes Projects are known to encompass many segregating introgressed chromosomal segments from other species. Purifying selection was detected after filtering chromosomes harboring segregating foreign introgression, consistent with the effectiveness of hybrid breeding in wheat. Interestingly, strong purifying selection is observed in the category of genes that are highly expressed in root tissues and located in the D-subgenome, which is thought to have contributed to range expansion after allopolyploidization. We suggest that the combination of expressed tissues and subgenomes will inform the target of future wheat breeding to mitigate the effect of deleterious variants. We also examined genome-wide correlations of nucleotide diversity and Tajima's D between homoeologs. These correlations in bread wheat were as low as those observed in the natural polyploid *Arabidopsis kamchatica*. This suggests that each homeolog tends to experience distinct evolutionary trajectories in both natural and domesticated polyploid species.

SECTION 6

Wheat functional genomics

Revealing the role of IBH1 in brassinosteroid biosynthesis and signalling via CRISPR-Cas9 knockout in durum wheat

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Abstract

Durum wheat (*Triticum turgidum* ssp. *durum*) is a cornerstone crop of the Mediterranean agroecosystems, where increasing environmental stresses threaten yield stability. Brassinosteroids (BRs) are key phytohormones regulating plant development and stress responses, yet their regulatory networks remain only partially elucidated in polyploid cereals. This study investigates the functional role of IBH1, a transcription factor involved in BR signalling, in the durum wheat cultivar Svevo.

CRISPR-Cas9 knockout lines targeting both IBH1 homeoalleles were generated and advanced to the T₂ generation. Sequence and structural analyses revealed that single-nucleotide deletions caused frameshift mutations leading to severe disruption of the DNA-binding domain and protein-protein interaction interfaces, strongly supporting a complete loss-of-function scenario. In silico three-dimensional modelling further indicated pronounced conformational alterations, particularly in the protein encoded by homeoallele IBH1-A1.

Functional characterization of edited lines highlighted a clear regulatory role of IBH1 in the BR pathway. Expression profiling of genes involved in BR biosynthesis and signalling at seedling and second-leaf stages revealed significant transcriptional reprogramming compared with null segregants.

These molecular changes were associated with consistent phenotypic effects, including an overall increase in thousand-kernel weight linked to elongated kernel morphology across edited lines.

Ongoing analyses aim to integrate hormone profiling with root system architecture and nutrient uptake. Brassinosteroid levels are being quantified by HPLC at the second-leaf stage, identified as a phase of peak IBH1 activity, while hydroponic experiments coupled with WinRhizo-based phenotyping are being used to assess root traits and their relationship with micro- and macronutrient accumulation. Overall, this study provides novel insights into the role of IBH1 in coordinating brassinosteroid signalling and yield-related traits in durum wheat, highlighting its potential as a target for improving crop performance under changing environmental conditions.

K-mer-based GWAS in a wheat collection reveals novel and diverse sources of powdery mildew resistance

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Abstract

Wheat landraces and cultivars stored in gene banks worldwide represent a valuable source of genetic diversity for discovering beneficial genes critical for agriculture increasingly constrained by climate change. We assembled and genotyped, using DArTseq technology, a panel of 461 accessions representative of the genetic diversity of Swiss wheat material. The collection was evaluated for powdery mildew resistance at the seedling stage with 10 different wheat mildew isolates, and under field conditions over two consecutive years. To find new sources of mildew resistance, we developed a K-mer-based GWAS approach using multiple reference genomes. Compared to approaches based on single reference genomes, we unambiguously mapped an additional 25% of K-mers by using multiple reference genomes including *Triticum aestivum* as well as four progenitor genomes. Our approach outperformed classical GWAS based on SNP-based arrays. As proof of concept, we re-discovered the resistance genes Pm1, Pm2, and Pm4 and further found novel loci associated with mildew resistance. In total, we detected 34 resistance loci in the seedling stage, of which, 7 corresponded to known Pm genes. Furthermore, we identified a region associated with adult plant resistance to wheat mildew, which was only detected by K-mer analysis and not with GWAS approaches using SNPs. The described non-reference-based approach highlights the potential of integrating multiple wheat reference genomes with K-mer GWAS to harness the untapped genetic diversity present in germplasm collections.

Cloning of diverse disease resistance genes from wild emmer wheat for breeding

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Abstract

Crop wild relatives harbor abundant natural variation conferring disease resistance that can be exploited for crop improvement. Our team has long been dedicated to cloning disease resistance genes from wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*, WEW), the wild ancestor of modern tetraploid and hexaploid wheats, for wheat disease resistance improvement. In recent years, we have isolated five powdery mildew resistance genes from WEW via map-based cloning: Pm41 (Li et al. 2020 New Phytol), MIWE18/MIIW172 (Wu et al. 2021 Plant Biotechnol J), Pm26/MIIW170 (Zhu et al. 2025 Nature Genet), Pm36/MI3D232 (Li et al. 2024 Nature Commun), and PmWR183 (Zhang et al. 2025 Nature Commun). Among these, Pm41 and MIWE18/MIIW172 encode canonical coiled-coil, nucleotide-binding site, leucine-rich repeat (CNL) resistance protein; Pm26/MIIW170 is conferred by a genetically linked atypical NLR pair TdCNL1/TdCNL5; PmWR183/Pm68 is controlled by an adjacent NLR pair PmWR183-NLR1 and PmWR183-NLR2; while Pm36 encodes a tandem kinase with a C-terminal transmembrane domain (WTK7-TM). Race-specificity assays showed that these five resistance genes are effective against over 90% of Chinese *Blumeria graminis* f. sp. *tritici* isolates across major wheat-growing regions. Notably, Pm36 conferred immunity or high resistance against all 104 isolates tested, indicating broad-spectrum disease resistance. Geographical analysis revealed that these powdery mildew resistance genes were present at very low frequencies exclusively in WEW populations, yet entirely absent in domesticated emmer, durum, and hexaploid wheat, highlighting their significant potential as untapped genetic resources for wheat breeding. Furthermore, those genes have been successfully introgressed into Chinese elite wheat varieties by combining backcrossing and marker-assisted selection to develop novel germplasm with pyramided disease resistance and superior agronomic performance. These disease-resistant lines have been distributed to over 200 institutions and individual breeders across China for wheat breeding.

Rudimentary basal spikelet formation in wheat: the tug-of-war between vegetative and differentiation

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Abstract

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

A TaKNOX1-TaAPO1-Rht1 feedback regulation orchestrates grain number and yield in wheat

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Abstract

The Green Revolution boosted wheat yields through the introduction of semi-dwarfing Rht-B1b alleles, but further genetic gains in intrinsic yield potential, particularly through increasing spikelet number per spike (SPS), remain a major challenge. Here, we identify TaKNOX-B1, a class I KNOX transcription factor, as the causal gene underlying a major SPS quantitative trait locus on chromosome 4B through genome-wide association study. A natural missense mutation (Leu⁸⁴ to Phe⁸⁴) in TaKNOX-B1 alters protein conformation, disrupts its repression by the DELLA protein Rht-B1b, and is associated with increased SPS and positive selection in modern breeding. We demonstrate that TaKNOX1 directly activates transcription of TaAPO1, a known regulator of inflorescence architecture. Remarkably, TaAPO1 protein competes with TaKNOX1 for binding to Rht-B1b, thereby liberating TaKNOX1 from DELLA-mediated inhibition and creating a self-reinforcing positive feedback loop that amplifies the output of both regulators during spike development. Pyramiding elite haplotypes of TaKNOX-B1 and TaAPO-B1 synergistically enhances grain number and yield per spike. Our discovery of the TaKNOX1-TaAPO1-Rht1 feedback module reveals a molecular mechanism that integrates meristematic activity and DELLA signaling to sculpt wheat inflorescence architecture, providing a powerful genetic framework for breeding high-yielding wheat varieties.

Spatial transcriptomics of developing wheat seed reveals concentric gene expression zones and subgenome biased expression of key genes

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Abstract

Gene expression of developing seeds drives essential processes such as nutrient storage, stress tolerance and germination. However, the spatial organisation of gene expression within the complex structure of the seed remains largely unexplored. Here we report the use of the STOmics spatial transcriptomics platform to visualise spatial expression patterns in the wheat (*Triticum aestivum*) seed at the critical period of grain filling in mid-seed development. We analysed >4,000,000 spatially resolved transcripts, across multiple tissue domains, and identified gene expression clusters linked to eight functional cellular groups. Notably, our analysis characterised four distinct clusters within the endosperm, appearing in concentric layers from the inner to outer regions of the grain, and identified novel marker gene candidates for the clusters found. We further investigated known tissue-specific genes and identified subgenome biased expression for the genes puroindoline-B, metallothionein protein, and α -amylase/subtilisin inhibitor. These findings provide new detail about gene expression across and within different functional cellular groups of the developing seed and demonstrate that spatial transcriptomics could further our understanding of subgenome differences in polyploid plants.

Grain number increase 2 (GNI2) improves floret fertility and enhances grain yield in wheat

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Abstract

Wheat is one of the most important food crops, providing 20% of calories and proteins. By 2050, wheat demand is expected to increase by 70% due to the global population increase. To meet these requirements, raising wheat grain yield sufficiently and sustainably must be of the utmost priority. Wheat inflorescence architecture determines grain number and affects final grain yield. Here, we present the cloning of all homoeo-loci for the number of grains per inflorescence in tetra- and hexaploid wheat. The identified homoeo-genes encode a homeodomain-leucine zipper class I transcription factor named Grain Number Increase 2 (GNI2). GNI2 is the closest paralog of GNI1, which is already characterized in wheat. Triple-knock-out lines of GNI2 generated by CRISPR-Cas9 in a bread wheat genetic background produce significantly more grains per spike, thereby enhancing grain yield under semi-field conditions and high-density planting. Using long-read sequencing analysis for natural variation of GNI2s revealed a set of four homoeo-allelic haplotypes. When paired with the favorable reduced-function allele of gni-A1105Y in bread wheat, grain yield was enhanced by about 5-7% under high-input farming and by 10-15% under low-input conditions, highlighting their potential to boost productivity across diverse farming environments. Moreover, we demonstrate that GNI2s act as growth modulators and work additively in root and shoot tissues while concurrently extenuating local floral growth via senescence-related transcriptional signatures. When combined, GNI1 and GNI2s affect floral growth and fertility through modulating source-sink relations and harvest index. Our study provides clear evidence that exploring floral degeneration in temperate cereals in greater detail is a seminal path towards improving floret fertility and grain yield in wheat.

Green be gone: transcription factor NAC3 regulates wheat senescence

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Abstract

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

We are investigating the role of NAC3, a NAC transcription factor, in regulating senescence using CRISPR/Cas9 gene-edited lines. Over two successive generations of phenotyping in the greenhouse, *nac3* CRISPR mutants show delays in reaching senescence of 3-4 days for the flag leaf and 1-6 days for the peduncle. Furthermore, NAC transcription factors are known to act as heterodimers. To identify additional interactors of NAC3 at the protein level we are conducting an in vitro pull-down assay. Preliminary results identify several novel transcription factors as candidate interactors of NAC3, which will be verified using yeast 2 hybrid assays. This will reveal how NAC3 fits into the transcriptional regulation of wheat senescence and may identify new candidates involved in senescence regulation.

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

SECTION 7

Innovative wheat breeding

Genomic breeding for dryland durum at ICARDA

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Abstract

Durum wheat is a staple and industrial food of many dryland farming systems. ICARDA breeding program has delivered since 1977 germplasm adapted to these farming systems achieving over 150 varieties released in 23 developing countries. The rate of genetic gain in dryland system was assessed in an historical set to reveal an average of +0.9% per year. However, to meet the challenge of climate change and demographic increase, this rate had to be doubled in the past decade. The novel inclusion of accelerated re-cycling via genomic selection and the use of "speed breeding" to F4 resulted in a steep increase to 1.5% per year. In addition, the continuous inclusion of novel genetic diversity for target traits remains a key strategy of ICARDA to adapt germplasm to harsh conditions. The identification and validation of markers associated with key loci is also fundamental to deliver germplasm adapted to stresses. For instance, the average water productivity across moisture stressed environments was estimated at 5.1 kg ha⁻¹ mm⁻¹, but the inclusion of the positive alleles at three loci on chr. 1B, 2A and 7B generated an average of + 2.2 kg ha⁻¹ mm⁻¹. Further, three loci on chr. 3A, 3B and 7B associated to root angle provided +12% yield advantage when field tested under terminal drought stress. Similarly, two loci on chr 1A and 3B resulted in +17% grain yield under severe heat stress tested along the Senegal River. The discovery and inclusion into breeding of these and other alleles will be discussed. Overall, the ICARDA program has integrated the latest genomic and breeding methodologies to double its rate of genetic gain under the harshest climatic conditions, but we continue to need the support of the whole community to continue to do so.

Integrative Platform for Accelerated Development of Wheat Varieties via Multiplex Genome Editing

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Abstract

Wheat is essential for global food security, yet its improvement is hindered by low regeneration rates, genotype-dependent transformation, and long generation times that delay breeding progress. To address these challenges, we used Neotrait Engine®, an integrated platform combining: (i) Neomics Miner® for candidate gene discovery, (ii) speed breeding to shorten generation cycles, and (iii) Genome Editing (GE). This enabled a robust, reproducible, and accessible transformation platform for seven commercial wheat varieties from Chile and Argentina, effectively reducing genotype dependency.

Neotrait Engine® has been applied to two case studies: high-fiber wheat with improved dietary fiber content while maintaining baking quality, and drought-tolerant wheat developed through rapid iteration cycles to enhance performance under water stress.

With Neomics Miner®, genes were prioritized based on annotated functions, orthologs, expression profiles, gene ontology, and homoeolog characteristics. Speed breeding enabled 8-10-week generation cycles of wheat, reducing breeding rounds. For multiplex editing, efficient gRNAs were selected using predicted on-target activity, secondary structure, chromatin accessibility, and genomic context. Polycistronic gRNA arrays were assembled into plasmids harboring Cas9 and a hygromycin marker. Incorporation of the GRF4-GIF1 gene fusion significantly improved regeneration across elite genotypes. Edited plants were obtained within ~8 weeks, and confirmed mutations across wheat's three subgenomes were shown to be fixed and heritable.

Regulatory agencies in Chile and Argentina classified the high-fiber GE wheat generated through this platform as non-GMO, enabling field trials and commercial advancement under conventional breeding regulations. This is the first CRISPR-edited wheat approved in the Americas and the second worldwide, marking a major milestone for precision breeding.

Overall, this work presents a streamlined and scalable workflow for rapidly developing healthier, more resilient, and sustainable wheat varieties. The integration of gene discovery, accelerated growth, and multiplex editing, supported by a favorable regulatory landscape, provides a powerful framework to address nutritional and climate challenges.

An AI-guided breeding toolkit for durable multi-disease resistance in wheat

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Abstract

Wheat production faces persistent pressure from multiple fungal diseases, each capable of causing severe yield losses. Resistance to a single disease is challenging, typically governed by combinations of loci with environment-dependent effects. Breeding for resistance to multiple diseases simultaneously compounds this complexity enormously: breeders must identify and stack favourable alleles across dozens of genomic regions, account for genotype-by-environment interactions, and do so across thousands of candidate lines, a combinatorial problem that becomes intractable using conventional approaches. AI-guided tools to translate genomic information into actionable breeding decisions are urgently needed.

Here, we describe the development and application of such a toolkit, centred on haplotype-based genomics and demonstrated through multi-disease resistance case studies in wheat. The toolkit integrates three core components: (i) definition of genome-wide haploblocks via linkage disequilibrium partitioning; (ii) estimation of haplotype effects using local genomic estimated breeding values (local GEBVs), enabling identification of regions with the largest and most consistent effects across environments; and (iii) an AI-driven optimal haplotype selection algorithm, powered by a genetic algorithm, to select optimal parents and guide long-term breeding simulations.

We demonstrate the toolkit through case studies using the Vavilov wheat diversity collection and the Australian 'OzWheat' panel, genotyped with whole-genome SNP markers and phenotyped across multi-environment trials in Australia and Ethiopia. Multi-trait haplotype characterisation across leaf rust, stripe rust, stem rust, crown rot, tan spot, and *Septoria nodorum* blotch revealed significant genetic correlations and identified pleiotropic haploblocks, four influencing all six diseases simultaneously, demonstrating potential to stack multi-disease resistance in a single breeding effort. For stripe rust, genotype-by-environment interaction analysis separated haplotypes governing average resistance from those conferring cross-environment stability, with AI-driven selection achieving superior long-term genetic gains over conventional truncation selection. Finally, an introgression fitness index paired with a genetic algorithm enabled selection of optimal donor parents, prioritising favourable resistance haplotypes while preserving elite genomic backgrounds. Selected crosses are being advanced through speed breeding, enabling multiple generations per year to rapidly pyramid resistance haplotypes into elite germplasm. Together, these tools provide breeders with practical, AI-driven decision support to accelerate the development of wheat varieties with durable, broad-spectrum disease resistance.

In vitro fertilization system with wheat, rice and maize gametes: Production of cytoplasmic hybrid between wheat and rice/maize across subfamily

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Abstract

In vitro fertilization (IVF) system is emerging as a new breeding technology for transferring genetic materials from distantly related species into the target crops, as IVF system serves as a bridge between sexual crossing and somatic hybridization. Cross-pollination dependent hybridization between intergeneric or inter-subfamily combinations often results in unsuccessful fertilization/embryogenesis due to pre- and/or post-fertilization barriers. In addition, cytoplasmic genome hybridization is rare due to maternal transmission of cytoplasmic organelles. Meanwhile, somatic hybridization involves fusing somatic protoplasts from different species, resulting in hybrid cells that contain nuclear and cytoplasmic genomes from both parents. However, in the majority of monocotyledonous plants including wheat, regeneration from protoplasts remains either unattainable or inefficient. The IVF system in angiosperms involves a combination of three basic microtechniques: (i) the isolation and selection of male and female gametes, (ii) the fusion of pairs of gametes, and (iii) single-cell cultures, and complete IVF system has been established in wheat, maize and rice. The IVF systems can be applied to generate new genotypes and/or hybrids, as gametes isolated from different species can be fused to produce distantly related hybrid zygotes beyond the reproductive barrier, and the combination and number of gametes for electro-fusion can be adjusted according to the species and ploidy of interest.

Recently, through IVF with isolated wheat and rice gametes, we produced allopolyploid rice-wheat hybrid zygotes that developed into wheat cytoplasmic hybrids (cybrids) with rice-wheat hybrid mitochondria. In addition, wheat cybrids with maize-wheat hybrid mitochondria have also been recently created in our laboratories. These wheat cybrids across subfamily largely expand the variations in nucleus-cytoplasm (NC) relationship as well as cytoplasmic genome, and the variations in the NC relationship/combination are relevant from both agricultural and evolutionary perspectives. In the congress, we will explain how the novel wheat cybrids have been created toward new wheat breeding.

From haplotype-based QTL mapping to founder-resolved pangenomics: dissecting multi-disease resistance architecture in a wheat MAGIC population

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Abstract

Stripe rust (*Puccinia striiformis*, YR) and Fusarium head blight caused by *Fusarium culmorum* (FHB) are major challenges to wheat production worldwide. While YR can cause severe yield losses under epidemic conditions, FHB reduces both yield and grain quality and leads to mycotoxin contamination. Although numerous resistance genes have been described, many race-specific resistances are rapidly overcome, emphasizing the need for durable, quantitatively inherited resistance deployed into elite breeding material. The winter wheat MAGIC population WM-800, derived from eight European cultivars, provides enhanced allelic diversity and recombination for dissecting complex traits in a breeding-relevant context. Across multiple environments, WM-800 was phenotyped for YR resistance, FHB susceptibility, plant height, and anther extrusion. High broad-sense heritabilities ($H^2 \approx 0.92$ for stripe rust; >0.80 for FHB and developmental traits) enabled robust haplotype-based genome-wide association analyses. Phenotypic BLUEs were estimated across multiple environments using linear mixed models, and 27,000 genome-wide SNP markers were organized into founder-informed haploblocks to capture linkage disequilibrium structure. Marker-trait associations were identified using cross-validated multiple regression models.

Eight QTL for YR resistance were identified on chromosomes 2B, 3A, 4A, 4B, 5A and 7B, including two potentially novel loci, jointly explaining ~59% of the genotypic variance. Founder-specific allele effect estimation revealed a major resistance allele contributed by cv. Tobak and an accumulation of favorable haplotypes in cv. Bernstein. FHB resistance displayed a strong triangular relationship with plant height and anther extrusion. The semi-dwarfing genes *Rht-B1* and particularly *Rht-D1* acted as major pleiotropic regulators, increasing FHB susceptibility while reducing plant height and anther extrusion. Nevertheless, semi-dwarf lines with moderate FHB tolerance indicated compensation through additional minor-effect QTL.

To further resolve the molecular basis of founder-specific resistance haplotypes, chromosome-scale long-read assemblies of the eight founders are currently being established within the MAGIC-Pangenome project. Their integration with haplotype-based quantitative analyses will enable the resolution of structural variation within major resistance intervals and provide a translational framework for informed allele stacking in durable multi-disease resistance breeding.

Integrating genomics, multi-trait multi-environment modeling, and multimodal deep learning frameworks for predicting yield components in mediterranean durum wheat

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Abstract

In the context of increasing climatic variability across Mediterranean agroecosystems, durum wheat (*Triticum durum* Desf.) breeding requires predictive frameworks capable of generalizing genotype performance across heterogeneous heat and drought environments. This study combines allele-informed genomic modeling, multi-trait multi-environment (MTME) modeling, and multimodal deep learning (MM-DL) to improve genomic prediction (GP) of morpho-phenological and yield-related traits.

A diversity panel of 186 genotypes was evaluated across multiple sowing x season combinations under Mediterranean field conditions. Functional allelic variation at major adaptive loci (Vrn-A1, Ppd-A1, Ppd-B1, and Rht-B1) was characterized to identify adaptive allelic combinations, whereas genome-wide association analysis was performed to identify genomic regions associated with phenological development and plant architecture. Incorporating allelic combinations and GWAS-derived markers as fixed effects significantly improved single-environment (SE) and multi-environment (ME) GP accuracies for morpho-phenological traits beyond marker-only models. To explicitly model genotype x environment interaction and inter-trait dependence, MTME models were implemented to jointly analyze yield components and morpho-phenological traits across environments. By exploiting genetic and residual covariance structures, MTME consistently outperformed SE, ME, and multi-trait (MT) approaches. Under cross-validation schemes simulating unobserved genotype-environment combinations (CV2), prediction accuracies reached $r = 0.86$ for spike length (SL) and $r = 0.78$ for grain number per spike (GN). Building upon this structured statistical framework, a MM-DL architecture was implemented, integrating genome-wide markers (genomic), environmental covariates (enviromic), and near-infrared spectroscopy (phenomic). Model performance was evaluated using a leave-one-environment-out strategy to simulate prediction in unseen seasons and sowing conditions. Multimodal models consistently outperformed genomic-only approaches. A stable hierarchy of trait predictability was observed: SL > number of spikelets per spike (NS) > grain weight per spike (GW) > spike weight (SW) > GN. Architectural traits showed higher cross-season stability (r up to 0.71-0.80), whereas environmentally sensitive traits such as GN exhibited greater gains from multimodal integration.

Overall, integrating biologically informed genomic effects, covariance-structured MTME modeling, and MM-DL provides a unified predictive framework that strengthens selection decisions and accelerates genetic gain under Mediterranean climate uncertainty.

Predictive breeding applications in wheat using genomics and phenomics through artificial intelligence and computer-vision

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Abstract

Predictive breeding (PB) based on genomic selection (GS) and phenomic selection (PS) has gained substantial attention in wheat breeding over the past decade. However, several bottlenecks, such as the lack of standardized analytical pipelines and limited predictive ability for complex traits, still constrain its large-scale implementation in breeding programs. In this research, we evaluated practical PB applications integrating genomics, high-throughput phenotyping (HTP), artificial intelligence (AI), and computer vision across three case studies.

First, we predicted yellow rust (YR) severity using unmanned aerial vehicle (UAV)-derived HTP data combined with genomic markers, comparing conventional statistical models and AI-based frameworks. Second, we assessed the added value of UAV-derived HTP within a sparse phenotyping design for grain yield prediction. Third, we implemented a smartphone-based computer-vision framework to estimate plot-level yield and its components.

For YR severity, predictive ability increased markedly when HTP-derived data were used compared with genomic markers alone. For example, support vector regression (SVR) improved from 0.35 (markers only) to 0.87 (wavelengths only). While conventional statistical models showed robust performance, AI-based approaches frequently achieved superior predictive accuracy. In the sparse phenotyping framework, integrating genomic and phenomic information improved grain yield prediction compared with genomic data alone, reaching predictive abilities of up to 0.60, even when HTP data were unavailable for target individuals. Additionally, computer-vision models based on smartphone videos successfully predicted yield components, showing significant correlations with yield-related traits, although further validation is required.

These proof-of-concept studies demonstrate the practical potential of integrating genomics, phenomics, and AI-driven approaches into wheat breeding pipelines. Such strategies can reduce labor-intensive disease scoring, improve the precision of grain yield prediction, and enable rapid estimation of yield components across thousands of lines, ultimately enhancing breeding efficiency, improving decision-making, and increasing genetic gain in wheat breeding programs.

Wheat genome editing: from prime editing to large DNA fragment editing

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Abstract

Wheat is a staple crop, and maintaining or increasing its yield is crucial for global food security. However, its allohexaploid nature and functional gene redundancy pose major challenges for effective and precise genetic improvement. Although CRISPR/Cas9 has been widely used, it primarily generates gene knockouts, limiting its application for diverse agricultural needs. Prime editing (PE) enables precise base substitutions and small insertions/deletions, but its efficiency in polyploid wheat is extremely low, precluding the generation of stable mutants.

Here, we systematically optimized the PE system by engineering the pegRNA, reverse transcriptase, and fusion protein architecture, establishing an enhanced system (ePPEplus) that dramatically improves prime editing efficiency in hexaploid wheat. This platform enables simultaneous precise editing of up to eight genes in a single transformation, providing a robust tool for functional genomics and trait stacking. Building on ePPEplus, we developed DualPE, a strategy for seamless manipulation of large DNA fragments (kb to Mb scale). By generating a pair of inverted 3' DNA flaps via PAM-out targeting at both ends of a chromosome segment, DualPE achieves precise, scarless deletions, replacements, and inversions in both monocot (wheat) and dicot (tobacco and tomato) plants, expanding the scope of precise genome engineering to complex structural variations.

To facilitate user access, we developed WheatTarget, the first integrated webserver for guide RNA design tailored to different wheat subgenomes. It supports knockout, base editing, prime editing, large-fragment editing, and multiplex editing, and also recommends editing vectors and provides efficiency analysis tools. This work provides a versatile technology suite for precise genome editing in polyploid crops, offering new strategies for genetic enhancement and breeding.

SECTION 8

Developing climate-smart wheat in the context of abiotic stresses

An XTH gene modulates root exudate-substrate cohesion

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Abstract

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

Leveraging wild emmer wheat diversity to unlock adaptive traits to improve drought-resilience in durum wheat.

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Abstract

Increasing climate variability, characterized by rising temperatures, prolonged dry periods, and unpredictable precipitation patterns, poses a major threat to agricultural productivity. Durum wheat (*Triticum turgidum* subsp. *durum*) is a strategic crop for Mediterranean agriculture, where increasingly frequent and severe drought episodes undermine yield stability. Developing climate-smart varieties requires exploiting the extensive genetic diversity across tetraploid germplasm, particularly its wild progenitor, the wild emmer wheat (WEW, *T. turgidum* subsp. *dicoccoides*). WEW, from the full Fertile Crescent, is promising to be integrated into breeding pipelines to enhance drought resilience and water-use efficiency (WUE).

An in-depth phenotypic characterization of 18 WEW accessions, utilized as parentals to develop a NAM population with the cultivar Svevo, has been carried out under both well-watered and water-deficient conditions. This study aims to identify key physiological traits associated with drought tolerance and to select the most promising WEW genotypes suitable for durum wheat improvement.

Stomatal-related traits, central to WUE and drought adaptation, such as stomatal density and stomatal conductance, were assessed using high-throughput imaging with a handheld digital microscope and Licor porometer, respectively. Substantial natural diversity in stomatal density and distinct stomatal responses to drought emerged across WEW genotypes. Additional traits measured at maturity, including biomass, tiller number, and plant height, revealed significant reductions under water deficit, confirming the sensitivity of these components to drought stress. Nonetheless, several WEW accessions displayed stable performance and favourable trait combinations under stress, indicating the presence of valuable adaptive alleles.

Overall, these results provide the essential foundation required to select the best-performing NAM subpopulations for upcoming advanced phenotypic and genomic analyses in large-scale field experiments in multiple locations. This robust characterization will enable the future application of targeted and untargeted genomic analyses to precisely identify the key determinants of drought tolerance. This integrated approach is set to accelerate the development of climate-smart durum wheat varieties capable of sustaining productivity under increasingly challenging abiotic stress scenarios.

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

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Abstract

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

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

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

Wheat's heat strategy: linking stomatal traits, sugar dynamics, and grain omics to heat tolerance

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Abstract

Rising temperatures threaten global wheat (*Triticum aestivum*) production, reducing grain yield and quality in a crop feeding over 2.5 billion people. Despite growing awareness of heat stress impacts, the mechanistic links between stomatal architecture, source-sink sugar dynamics, and grain-level metabolic and lipidomic responses across genotypes differing in heat tolerance remain poorly understood.

We screened 319 wheat genotypes under glasshouse and field conditions, assessing physiological performance, yield, stomatal structure, and leaf sugar accumulation. Tolerant (H-199), moderately sensitive (H-031), and susceptible (H-161, H-165) lines were selected for integrated metabolomic and lipidomic profiling, and QTL mapping identified genomic regions associated with stomatal traits and heat resilience. Heat stress induced genotype-stratified stomatal, metabolic, and lipidomic responses. Tolerant lines maintained yield through robust stomatal architecture and limited sugar buffering, while susceptible lines showed elevated grain lipid accumulation. Key stomatal QTLs were mapped to chromosomes 3A, 3D, and 4A. H-199 upregulated stress-protective metabolites (quercetin 3-O-pentoside, trans-resveratrol, and 1,5-anhydrosorbitol) alongside lipidomic upregulation of kaurane and suppression of vicine and germacrone, indicating coordinated antioxidant and osmotic protection. H-031 displayed a jasmonate-mediated response, upregulating methyl dihydrojasmonate and epigallocatechin with suppression of protocatechuic acid and phytosphingosine-1-phosphate. Susceptible varieties showed upregulation of linoleic acid, cinnamic acid, and docosanoic acid with lipidomic downregulation of phytol and germacrone, reflecting compromised membrane homeostasis. KEGG enrichment highlighted phenylpropanoid biosynthesis, flavone and flavonol biosynthesis, linoleic acid metabolism and flavonoid biosynthesis as key heat-responsive pathways differentiating tolerant from susceptible genotypes.

These findings reveal integrated structural, metabolic, and lipidomic markers of heat tolerance, offering actionable genomic and biochemical targets for breeding climate-adaptive wheat with improved yield stability and grain quality.

From root to grain: multi-omics reveals how nitrogen, CO₂, and microbes tune wheat drought resilience and grain quality

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Abstract

Plant's available nitrogen status, atmospheric CO₂ concentration and soil microbiome composition interact to modulate plant drought responses, yet their combined effects on grain yield and grain composition remain poorly characterised. Here, four bread wheat cultivars grown across two consecutive seasons (2022-2023) at the INRAE field-trial site in Clermont-Ferrand, France, under four treatment combinations - contrasting water supply and CO₂ levels with differing soil nitrogen levels to simulate current and future agroclimatic scenarios. Using quantitative and targeted proteomics, metabolomics and micronutrient composition analysis of the harvested grains, we investigated how water availability and atmospheric CO₂ concentration combinedly affect grain protein concentration and composition. We identified substantial treatment-driven changes in grain protein accumulation, with water availability as the primary driver, further modulated by CO₂ concentration and soil nitrogen availability in a cultivar-dependent manner. Drought stress primarily altered proteins associated with nitrogen allocation, osmotic adjustment and energy metabolism, indicating a shift in nutrient reservoir reserves toward grain filling. Elevated CO₂ levels, by contrast, shifted the plant carbon-nitrogen-sulphur balance, increasing proteins levels related to nutrient uptake and energy metabolism, prioritising plant growth over stress defence. In parallel, targeted metabolomics profiling of central carbon pathway metabolites revealed shifts in osmolyte and vitamin production, production and scavenging of reactive oxygen species and hormonal signalling, each closely associated with rhizosphere microbiome composition and nitrogen availability. Phenomics data, including root N and C levels measured across several developmental timepoints, heading and flowering dates, yield components, biomass partitioning, grain nitrogen and end-use quality measurements, were integrated with proteomics, metabolomics and microbiome profiling of the rhizosphere and bulk soil across all four conditions using a multiomics integration approach. The multi-omics integration analysis revealed cultivar-specific molecular signatures, indicating that protein-yield trade-off under drought stress is environmentally plastic rather than genetically fixed, mitigated by atmospheric CO₂, soil N levels and soil microbiome.

Wheat responses to combined drought, heat, and elevated CO₂: integrative morpho-physiological and transcriptomic insights under future climate scenarios

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Abstract

Climate change increases the frequency and severity of environmental stresses such as drought and high temperature, which strongly threaten crop productivity. At the same time, rising atmospheric CO₂ concentrations generally stimulate photosynthesis and may, under certain conditions, alleviate some of the negative impacts of abiotic stress. In our study, we assessed the morpho-physiological and transcriptomic responses of bread wheat (*Triticum aestivum* L.) to drought (D), elevated temperature (eT), and elevated CO₂ (eC), applied individually, in dual combinations (eT+D, eC+D, eC+eT), and in a combined treatment involving all three factors (eC+eT+D). The combined eT+D treatment caused the strongest declines in plant growth and yield, whereas eC consistently improved water-use efficiency across treatments. Transcriptome analysis showed pronounced changes in gene expression under multiple stress conditions, with over-representation of pathways related to hormone signalling and photosynthesis. Several transcription factor families, including MYB, NAC, and WRKY, along with putative marker genes, exhibited differential regulation among treatments. Co-expression network analysis identified gene modules correlated with important traits such as shoot biomass and grain yield, underscoring the role of stress-responsive signalling mechanisms. Together, our results provide insights into wheat responses to combined climate-related stresses and highlight potential molecular targets for breeding climate-resilient varieties.

Regulatory variation at TaNPF2.12 shapes nitrogen-responsive root plasticity and nitrogen use efficiency in winter wheat

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Abstract

Nitrogen (N) is a major determinant of wheat productivity, and improving nitrogen use efficiency (NUE) remains essential to reduce fertilizer inputs and environmental impact. TaNPF2.12, encoding a putative nitrate transceptor, was identified to coordinate root growth NUE under contrasting nitrogen supply. A promoter SNP located 88 bp upstream of the start codon (–88 T/C) defines two haplotypes, with the T allele associated with enhanced root elongation under low N and the C allele conferring reduced root plasticity and lower NUE.

These findings led us to propose a model in which promoter variation at TaNPF2.12 modulates nitrogen-responsive root development through interaction with the nitrate assimilation pathway via NIA1. Validation in 54 independent wheat lines evaluated across two field seasons confirmed the stability of the –88 promoter effect across genetic backgrounds and environments. Promoter analysis revealed that the –88C allele introduces a canonical GCCCORE motif, suggesting potential AP2/ERF-mediated regulation; yeast one-hybrid assays are being used to assess DNA-protein interactions at this site. A second coding-region SNP showed no phenotypic effect, suggesting that regulatory rather than structural variation underlies the observed differences.

Genetic crosses between T and C allele genotypes showed that F1 hybrids largely phenocopied the T allele parent, with divergence in root growth becoming evident early under low nitrogen. This early divergence prompted temporal RNA sequencing of the hybrids to characterize broader molecular changes associated with the growth response. Root architectural and anatomical analyses, together with C/N quantification in roots and shoots, were consistent with this pattern, with F1 hybrids closely resembling the T parent. Time-course expression profiling of TaNPF2.12 and NIA1 in F1 hybrids was also consistent with the proposed functional relationship between these genes.

Together, these findings indicate that natural regulatory variation at TaNPF2.12 contributes to nitrogen-responsive root plasticity in winter wheat.

Keywords: Nitrogen use efficiency; root growth, TaNPF2.12; promoter SNP; ERF transcription factors; winter wheat

Identification and functional characterization of WUE and drought resilience factors in wheat

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Abstract

Improving wheat drought resilience and water use efficiency (WUE) is critical for sustaining productivity under increasing water scarcity. Here, we integrate GWAS, eQTL, population-transcriptome analysis, and Summary-data-based Mendelian Randomization (SMR), followed by functional validation using indexed EMS mutants, to systematically identify WUE regulators. GWAS across water conditions in 228 accessions identifies 73 QTLs for WUE-traits. Transcriptome profiling of 110 diverse accessions reveals 28 drought-responsive modules. eQTL mapping uncovers 146,966 regulatory variants, including condition-specific hotspots associated with key drought-related pathways. Integrative analysis underscores 85 high-confidence candidate genes, notably TaMYB7-A1. Overexpression of TaMYB7-A1 enhances photosynthesis, WUE, root development, and grain yield under drought condition by activating TaPIP2;2-B1 (water transport), TaRD20-D1 (stomatal regulation), and TaABCB4-B1 (root growth), reflecting reduced water loss and improved physiological resilience. In addition, a stable WUE and Grain Number Per Spike (GNPS) associated locus on chromosome 2B led to the identification of TaVDCC, which encodes a voltage-dependent calcium channel subunit localized to the endoplasmic reticulum and plasma membrane. CRISPR/Cas-mediated editing confirmed that TaVDCC modulates calcium signaling, drought resilience, and yield-related traits. TaVDCC interacts with TaCCP1 to form a functional calcium-channel complex, with distinct haplotypes exhibiting differential calcium signaling activity. Collectively, these findings provide mechanistic insights and valuable genetic resources for precision breeding of drought-resilient, water-efficient wheat.

SECTION 9

Dissecting the wheat-pathogen and pest interaction

Non-host resistance genes - new sources for durable rust resistance?

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Abstract

The tight co-evolution between cereal crops and rust fungi has led to a pronounced host specialization, with one rust species generally only infecting one cereal host. Understanding the molecular principles that govern these non-host resistance mechanisms may provide new sources of durable resistance across cereal species.

Previously, we had identified orthologous lectin receptor kinases (LecRKs) from domesticated and wild barley that mediate non-host resistance to leaf rust. Through biochemical, proteomic, and structural analyses, we show these receptors interact with a highly conserved class of rust-derived glycoside hydrolases (GHs), triggering a cell death response. Notably, we found that some rice LecRKs perceive stem rust-derived GHs, indicating that this molecular perception mechanism is conserved across cereal species. Transgenic expression of one rice LecRK in the wheat cultivar Fielder enhanced resistance to wheat stem rust, demonstrating the feasibility of transferring non-host immune receptors across cereal species to improve wheat disease resistance.

Together, these findings reveal previously uncharacterized recognition specificities within cereal LecRKs. The successful transfer of rice LecRK-mediated immunity into wheat highlights the potential of exploring naturally occurring receptor variants to possibly engineer durable and broad-spectrum resistance in wheat and other crops.

Identification of candidate genes for resistance to soil-borne cereal mosaic virus in durum wheat using CRISPR-Cas9 genome editing systems

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Abstract

Soil-Borne Cereal Mosaic Virus (SBCMV) significantly reduces wheat yield and grain quality. Because natural resistance mutations are rare, developing genetic resistance through New Genomics Techniques represents the most sustainable strategy to protect crops and support rising food demands. This work aims to identify and biologically characterize SBCMV resistance genes in durum wheat. In hexaploid wheat, resistance is provided by the combined action of Sbm1 (5D) and Sbm2 (2B), whereas in durum wheat Sbm2 is the only major locus known to confer resistance.

A GWAS performed on the UNIBO Durum Panel refined the Sbm2 region to a 2.661 Mb interval (0.2 cM) containing 93 genes. RNA-Seq analysis comparing resistant and susceptible cultivars further reduced the candidates to ten differentially expressed genes. Among these, seven were prioritized based on expression profiles and gene ontology as the strongest candidates for virus resistance. The Svevo reference genome carries the resistant Sbm2 alleles, making it a suitable genotype for functional validation through gene editing.

For knockout validation, plasmid vectors carrying multiple CRISPR-Cas9 gRNAs were assembled using Golden Gate cloning. The efficiency of each gRNA/Cas9 editing system was tested in leaf protoplasts from resistant Svevo plants, and mutations at target sites were confirmed through NGS amplicon sequencing. Additionally, screening of 2000 M4 Svevo EMS lines identified seven mutants with strong susceptibility, providing complementary allelic variants for validation of candidate genes.

Currently, binary vectors containing Cas9, GRF-GIF morphogenic genes, and high-efficiency gRNAs are being used for Agrobacterium-mediated transformation of Svevo immature embryos. Phenotypic analysis of regenerated plants will clarify the function of the seven candidate genes and determine their effective involvement in SBCMV resistance in durum wheat.

Acknowledgements: This work has been funded by Ministry of Agriculture, Food Sovereignty and Forests through the project "Tecnologie di Evoluzione Assistita per le filiere agroalimentari Italiane (TEA4IT)" - sub-project "Tecnologie di Evoluzione Assistita per le filiere agroalimentari Italiane: Messa in campo di piante TEA di Cereali a paglia (TEA4IT_Cer) (DM IMPEGNO N. 586237 del 31_10_2025).

Pan-genome facilitated discovery of dominant North American stripe rust lineage's origin in somatic hybridization

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Abstract

Wheat stripe rust, caused by *Puccinia striiformis* formae specialis tritici (Pst) is a perennial and endemic threat to cereal production worldwide, incurring monetary costs in prevention and yield reduction. Outside the Himalayan region the fungus has not been observed reproducing sexually, despite being characterised extensively over the past 100 years by researchers in many countries. Instead, Pst circulates as numerous rapidly evolving clonal lineages termed PstS0, PstS1, etc. up to PstS18. Scientific research into the adaptability and evolutionary history of the fungus has recently been revolutionised by chromosome conformation capture (CCS) phased genome sequencing which can analyse each of the two dikaryotic haploid genomes independently. Here we describe the first North American *P. striiformis* pan-genome, comprising 24 Pst and 3 *P. striiformis* f.sp. *hordei* genomes from samples taken in North America including five phased assemblies using CCS, and with the remaining assemblies scaffolded using their fully phased clonal relative. We identify the origin of the predominant North American Pst lineage; PstS18, as a somatic hybridization event between the older African-derived lineage PstS1 and another unknown lineage based on a shared identical haplotype. As well as identifying gene families which distinguish haplotypes on a trans-lineage and trans-species level, we also show ongoing gene family loss and expansion in clonal lineages after their emergence which may account for their notorious flexibility in virulence type. We finally categorize all the haploid sub-genomes in our collection and in previously published phased Pst assemblies as belonging to one of 10 haplotypes split into two global haplotype groups, acting as a platform for further investigation of the distribution of Pst haplotypes worldwide.

Twenty years of global disease surveillance in wheat reveals increased vulnerability to yellow rust due to incursions of new aggressive races at regional and global scales

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Abstract

Consistent and coordinated efforts in wheat yellow rust surveillance involving more than 400 people, and 50 countries on six continents, have demonstrated a surprising level of connectivity between yellow rust populations on different continents, despite previous reports about significant divergence between geographically separated populations in Asia, Africa, Europe and the Americas. Our conclusions are based on more than 4000 *Puccinia striiformis* f.sp. *tritici* (Pst) samples characterized by the Global Rust Reference Center in Denmark using simple sequence repeat (SSR) markers. The use of time and georeferenced sampling information, same genotyping methodology throughout the entire period of study, database driven management and visualization of results, and modelling studies investigating the plausibility of wind-dispersal along hypothesized dispersal routes, allowed us to conclude the following: i) at least twelve cases of inter-continental spread of Pst, ii) seven cases with major impact on disease epidemics in recipient areas, i.e., resulting in significant changes in pathogen populations/widespread yield losses, and/or dramatic impact on wheat breeding programs of global relevance, iii) windborne dispersal as well as human-mediated transport were likely involved in particular dispersal events. Airborne spore dispersal was plausible between the Middle East and East Africa as well as Europe. Detections of prevalent clonal groups Pst6, Pst11, and Pst16 in East Africa after previous detections in Central/South Asia support the previously proposed Rift Valley pathway for rust fungi. Available data indicates that direct dispersal along this pathway is unlikely, but stepwise transmission cannot be excluded due to low sampling intensity in critical areas on the Arabian Peninsula and the Horn of Africa. Our study stresses the urgent need for continued and coordinated crop pathogens monitoring across borders. Only global efforts will enable prevention and control of pathogens that represent major challenges for food security. Long-term support by multiple funding sources is highly acknowledged: Bill and Melinda Gates Foundation, UK Foreign, Commonwealth & Development Office, European Union's Horizon 2020 research and innovation programme, Strategic Danish Research Council, Danish Ministry of Food, Agriculture and Fisheries, and Jordbruksverket (Sweden). The work of Marcel Meyer was funded by the Deutsche Forschungsgemeinschaft.

Loci relevant for yellow rust resistance in a Mediterranean multi-environmental trial networks identified from the global durum genomic resource

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Abstract

Yellow rust (YR), caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is a major global wheat disease. We screened the Global Durum Genomics Resources across 13 field environments (Mediterranean region, Argentina, California), evaluating 500 durum wheat cultivars (DWC) and 1,123 *T. turgidum* ssp. *landraces* (TWL). In cultivars, higher resistance characterized lineages from Italy, CIMMYT '60/'70/'80, and ICARDA-temperate; North America-France, INRAE evolutionary populations, and ICARDA-dry were more susceptible. GWAS detected eight major loci on 1A, 1B (three QTLs), 4B, 5A, 5B, and 7B. The strongest, QYr.ubo-1B.1, mapped to a 3.4 cM (~167 Mb) interval, was significant in seven environments, and explained 15.81% of multi-environment variance. QYr.ubo-1B.2 and QYr.ubo-7B.1 were each detected in four environments, explaining 5.49% and 10.64% of variance, and mapped to 4.0 Mb and 2.1 Mb intervals, respectively. In landraces, resistance was enriched in populations from the Horn of Africa (*T. aethiopicum*), Balkans (*T. turgidum turgidum*), Eastern Europe-Transcaucasus (*T. carthlicum*), Egypt-Cyprus-Iberia (*T. durum*), and North Africa (*T. durum africanum*), while *T. durum syriacum* and *T. turanicum* were more susceptible. GWAS identified nine major loci on 1B, 2A, 2B, 4B, 5A, 5B, 7A, and 7B. QYr.ubo-1B.3 explained 7.68% of variance and co-localized with QYr.ubo-1B.2 within 0.4 Mb (effective in seven environments). QYr.ubo-7B.1 had the highest variance explained (9.37%) and was effective in eight environments. Projection of known loci suggested overlaps: QYr.ubo-1B.1 with Yr64/Yr65/Yr24/Yr26/YrCH42; QYr.ubo-1B.3 with Yr29; QYr.ubo-7B.1 with Yr67 (=YrC591).

KASP® markers were developed for allele tagging: for QYr.ubo-1B.1, IWB74353 ("C") and IWB31756 ("T"); for QYr.ubo-7B.1, IWB71291 and IWB21717 (resistance associated with allele "T").

In-silico expression highlighted candidates. For QYr.ubo-1B.1, TraesCS1B02G181600 (TaAbc1)—linked to ROS-mediated HR—was overexpressed under infection; its silencing reduced HR. For QYr.ubo-7B.1, candidates included an NBS-LRR (TraesCS7B02G462000), paired NLRs (RGA4/RGA5), and genes linked to LHY and WRKY TFs implicated in immune/ROS defenses.

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Dual recognition of structurally unrelated mildew effectors underlies the broad-spectrum resistance of Pm3e in wheat

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Abstract

The wheat Pm3 locus provides race-specific resistance against the wheat powdery mildew fungus. It occurs as an allelic series of at least 17 functional alleles encoding distinct NLR-type intracellular immune receptors with the ability to recognize secreted avirulence (AVR) effectors with an RNase-like structure. Comprehensive comparison of individual Pm3 NLRs has been hampered in part by the presence of background effects in respective donor lines and by the limited knowledge of corresponding AVR effectors of which only three, AvrPm3a/f, AvrPm3b/c and AvrPm3d have been molecularly isolated. We used transgenic wheat lines expressing individual Pm3 alleles to comparably test their recognition spectrum towards a global wheat powdery mildew collection of more than 90 isolates covering all major wheat growing areas worldwide. We show that the Pm3d and Pm3e alleles, differing by three and two amino acids from the non-functional allele Pm3CS respectively, provide broad-spectrum resistance against the global pathogen diversity and identify underlying AVR factors. We demonstrate that Pm3d recognizes two highly similar RNase-like AVRs, encoded by gene paralogs. In contrast, Pm3e detects two structurally diverse AVRs: one shared with Pm3d, the other originating from a large, uncharacterized protein family with a novel structural fold. We identified individual amino acid polymorphisms in the LRR domain of Pm3d and Pm3e NLRs that determine recognition specificity towards their respective AVRs. Lastly, we demonstrate that Pm3d and Pm3e resistance activities can be combined through NLR engineering. We conclude that the broad-spectrum resistance of Pm3d and Pm3e alleles is based on their ability to each recognize two AVR factors, thereby reducing the chance for gain-of-virulence mutations in the wheat mildew pathogen to evade NLR recognition. Our study furthermore demonstrates that Pm3 NLRs can recognize structurally diverse AVR effectors and are amendable to NLR engineering thereby highlighting their potential for durable wheat protection.

Fornisci il tuo feedback su BizChat

Meta-QTL analyses for better characterisation of the genetic architecture of bread wheat resistance to septoria tritici blotch

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Abstract

Among the numerous diseases impacting wheat production, Septoria tritici blotch (STB) caused by the fungus *Zymoseptoria tritici* remains one of the most prevalent and difficult to control. Genetic improvement of wheat cultivars for STB resistance is crucial but very little is known about the diversity of resistance sources present in French cultivars, thus limiting the selection efficiency on this trait. To identify QTL involved in STB resistance in French cultivars, we applied two meta-analysis approaches, one compiling data from all QTL studies referenced in the literature including those on French cultivars, and the other exploiting historical STB data from French variety trials.

We reanalysed data from 16 interval mapping studies (QMAP) and eight genome-wide association studies (GWAS), defining 185 and 189 QTL across 64 and 48 distinct environments, respectively. We developed a novel meta-analysis framework allowing the integration of QTL from both QMAP and GWAS into a single meta-QTL analysis. This approach identified 35 meta-QTL distributed across 15 of the 21 bread wheat chromosomes, including 23 meta-QTL detected in three to 19 environments. After projection onto reference genomes, ten meta-QTL with interval sizes below five megabases revealed candidate genes possibly involved in resistance.

In parallel, we analyzed an historical database including 651 French wheat varieties evaluated from 2019 to 2024 in 396 trials, with available climate data and recorded sowing dates, heading dates, and STB severity scores. Through a decision-tree mixed-model analysis, trials were classified into eight mega-environments (ME) based on climatic conditions and disease pressure. This classification increased the population size from, on average, 30 varieties per trial to 118 per ME, thus enabling GWAS analyses. Ongoing work including GWAS on adjusted STB means within each ME and subsequently meta-GWAS to identify QTL associated with STB resistance in French germplasm will be presented.

Together, these complementary approaches will contribute to a new reference map of QTL controlling STB resistance, especially in French wheat cultivars providing valuable knowledge to support breeding for enhanced resistance to this major wheat disease.

Asymmetric priority effects between co-infecting wheat pathogens undermine single-pathogen resistance

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Abstract

Wheat leaves in the field are rarely infected by a single pathogen — yet resistance breeding programmes continue to evaluate cultivars against pathogens in isolation. Here, we show that this approach may be systematically selecting for cultivars that are vulnerable in the presence of multiple co-infecting pathogens. *Parastagonospora nodorum* and *Pyrenophora tritici-repentis* are fungal pathogens that cause septoria nodorum blotch and tan (syn. yellow leaf) spot of wheat, respectively. Both pathogens frequently co-infect wheat in the field. Using a newly developed digital PCR method across natural field surveys, inoculated field trials, and controlled environment experiments, we found that the majority of symptomatic field infections involved both pathogens simultaneously, and that host resistance effective against each pathogen alone was compromised under co-infection. Critically, we demonstrate that infection outcome is determined not just by which pathogens are present, but by the order in which they arrive. When *P. tritici-repentis* establishes first, disease and biomass of both pathogens increase significantly, even in resistant hosts. When *P. nodorum* establishes first, subsequent *P. tritici-repentis* colonisation is strongly suppressed regardless of host genotype. Field trial data suggest the *P. tritici-repentis*-priority scenario reflects what occurs in natural systems. To our knowledge, this is the first documented case of asymmetric priority effects overcoming host resistance in a plant pathosystem. These findings have direct implications for resistance breeding: cultivar selection under single-pathogen challenge may not necessarily capture the interaction dynamics that govern disease outcomes in the field. We advocate for disease complex screening as a necessary component of durable resistance development in wheat.

SECTION 10

Wheat quality, end-use processing, nutrition and human-health

Development of high dietary fiber wheat through introgression of β -glucan-rich alleles from *aegilops kotschy*

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Abstract

Global incidences of type-II diabetes and cardiovascular diseases are increasing rapidly and one of the practical mitigation strategies includes inclusion of cereal dietary fibres, particularly β -glucan and arabinoxylan in daily diet. While wheat forms the most important staple diet in the world, the dietary fibre content in conventional wheat varieties were found to contain only ~0.7% β -glucan on average, far below the 2% recommended threshold of daily dietary fibre requirement. Therefore, we explored a panel of 478 germplasms including secondary and tertiary gene pools of wheat for high grain β -glucan among which *Aegilops kotschy* (accession AK-3790), emerged as exceptional genetic resource, exhibiting β -glucan levels up to 3.73% and arabinoxylan up to 10.34%. Therefore, to transfer high dietary fiber trait into bread wheat background, a cross was made between HD3086, WH1105 and *Aegilops kotschy* (AK-3790), which resulted in a derivative line UPHAU3 containing 7U chromosome of *Aegilops kotschy*. The introgression of 7U chromosomes was verified with marker-assisted selection and genomic in situ hybridization. However, UPHAU3 had high grain β -glucan but low yield and incidence of stripe rust. To overcome these limitations, two systematic backcrossing programs were conducted with recurring parents WH1105 and HD3086, followed by generation advancement. Selected BC2F2:3 progenies achieved remarkable β -glucan enhancement, with line BC2F2:3 23-5 attaining 1.76% grain β -glucan, an 88% increase over conventional wheat varieties while retaining rust resistance and yield at par with HD3086. The resulting biofortified wheat lines offer a sustainable solution for enhancing dietary fibre intake and addressing nutritional security in wheat-consuming populations globally.

Clinical trials investigating the health-promoting effects of Svevo high-amylose products on patients affected by concomitant Chron's disease and metabolic syndrome

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Abstract

The amylose-amylopectin ratio has profound effects on starch properties impacting not only wheat technological quality, but also human health. Higher amylose content is associated with reduced starch digestion resulting in a lower postprandial plasma glucose response and improvement of postprandial metabolism. In this work, we set up a randomized controlled clinical study to evaluate the metabolic effects of durum wheat-based foods rich in amylose. Two diets were compared: one comprising Svevo high amylose wheat-based foods (pasta: 100 g/die, crackers: 20 g/die and biscuits: 25 g/die), and a control diet including the same type and quantity of wheat-based products but made using traditional Svevo semolina. The two dietary interventions were tested over 12 weeks on patients affected by concomitant symptoms of inflammatory bowel disease and metabolic syndrome. Several inflammatory markers and metabolic parameters were monitored every six weeks to measure Skeletal muscle mass (SMI) index, nutrition risk screening (MUST), Crohn's disease activity index (CDAI), means of anthropometry, bioelectrical impedance vector analysis (BIA). Moreover, patient's feces were collected at the beginning of the study and the end to assess variation in the microbiota composition as depending on the dietary intervention. The results showed that the high amylose diet was associated with a higher tendency to reduce circulating markers associated with metabolic syndrome including cholesterol, glycemia and triglycerides, together with the fat mass. The group of patients who received the high amylose wheat products showed a significant improvement of intestinal-related functions, improvement of muscle mass/SMI index and reduction of malnutrition, improvement of stool consistency (Bristol index), reduction of daily evacuation number, thus resulting in a significant improvement in the quality of life of patients.

Exploiting natural variation in starch granule size and composition in *Aegilops tauschii* to improve wheat starch

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Abstract

Wheat endosperm starch is of huge commercial importance, providing up to 25% of calories in our diets, whilst also having key roles in the production of paper, biodegradable polymers and pharmaceuticals. Starch granules are composed of amylopectin and amylose, and in grains of the wheat there are two different types of granules: large, lenticular A-type granules and small spherical B-type granules. The size distribution and composition of starch granules has a strong influence on grain quality and the end uses of starch, but the genetic control of these traits remains poorly understood.

Here we have characterised endosperm starch in a diversity panel containing 117 accessions of *Aegilops tauschii*, the progenitor of the wheat D genome. We discovered huge variation in starch granule size distributions within the panel, which exceeds that observed in domesticated wheat. This large intraspecies variation has been exploited in a genome wide association study (GWAS). We identified five previously uncharacterised loci associated with granule number, and a further five regions associated with granule size. We identified candidate genes within these loci and one of these encoded for Limit Dextrinase (LDA), a starch debranching enzyme. Excitingly, the role of LDA in starch granule formation had not previously been explored, so we investigated this in *Ae. tauschii* and wheat. We discovered two LDA variants with increased enzymatic activity which were prevalent in *Ae. tauschii* accessions with large B-type granules. However, complete elimination of LDA in tetraploid wheat caused only minor effects on endosperm starch granules. Together, this suggests that gain-of-function mutations in LDA influence B-type granule formation. Our work therefore highlights the potential of *Ae. tauschii* to discover novel alleles and new gene candidates which can be used to extend to our mechanistic model of A-type and B-type granule formation in wheat. Furthermore, we propose that the loci identified here could be integrated into wheat breeding programs to reintroduce starch granule traits which have been lost during domestication, and improve grain quality by modulating starch granule size.

Optimizing selenium and sulphur foliar fertilization to enhance nutritional and technological quality of bread wheat

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Abstract

Micronutrient malnutrition remains a major global concern, partly due to the inherently low micronutrient concentration of staple crops such as bread wheat (*Triticum aestivum* L.). In parallel, wheat production systems are increasingly required to improve technological quality and nutritional value without penalizing grain yield. Foliar fertilization with selenium and sulphur (S) represents a promising agronomic strategy to enhance mineral bioavailability, modulate protein composition, and reduce anti-nutritional compounds, particularly under rainfed Mediterranean environments. A two-year field experiment (2020-2022) was conducted in Tuscany, Italy, using a split-split-plot design under rainfed conditions. Two bread wheat cultivars differing in genetic background and technological traits, the modern 'Bologna' and the old 'Sieve', were evaluated. Five Se rates (0, 2.57, 5.14, 10.27, and 20.54 g ha⁻¹ as sodium selenite) were applied at flowering or watery ripe stage, while three S rates (0, 3.2 and 6.4 kg S ha⁻¹ as wettable sulphur) were applied at booting. Grain yield, protein concentration and fractions (gliadin and glutenin), starch content, free asparagine, phytic acid, mineral concentrations, phytic-acid-to-mineral molar ratios, and dough rheological parameters were determined. Data were analyzed using mixed-effects linear models to assess genotype, Se, S and interaction effects. Grain yield was primarily driven by genotype and seasonal conditions, with no significant yield penalties associated with Se or S applications. Protein concentration was largely genotype-dependent, with a moderate response to increasing Se rates. Selenium application reduced free asparagine and phytic acid concentrations, leading to lower phytic-acid-to-Se, -Cu, -Fe, -Mn and -Zn molar ratios, suggesting improved potential micronutrient bioavailability. Sulphur supply did not significantly alter total protein content but markedly shifted protein composition by decreasing gliadin and increasing glutenin fractions, thereby improving the gliadin-to-glutenin balance. Free asparagine was strongly influenced by S fertilization and further reduced by Se, particularly under adequate S availability. Overall, targeted foliar Se and S applications enhanced grain nutritional and technological quality without compromising yield. Although genotype remains the dominant factor shaping productivity and quality traits, strategic micronutrient management provides an effective tool to develop nutritionally improved and quality-oriented wheat production systems under rainfed Mediterranean conditions.

Mapping the landscape of carotenoid esterification in the global durum panel

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Abstract

High carotenoids levels in wheat grain improve both nutritional quality and the visual appeal of durum wheat-derived products such as pasta or semolina. These pigments, responsible for the desirable yellow colour of the grain, occur either in free form or esterified with fatty acids. Esterification has been associated with increased carotenoid accumulation and stability, being a promising target trait for wheat breeding. Indeed, carotenoid esters exhibit greater retention during storage in durum wheat and throughout the bread-making process. XAT-7A1, the gene responsible for esterification in durum wheat belongs to the dispensable genome, as it is not annotated in the durum wheat reference genome and has so far been identified only in a small number of landraces in a Spanish germplasm survey.

The Global Durum Panel (GDP), an internationally curated collection of 1,011 tetraploid wheat genotypes, provides an excellent resource for identifying novel sources of the XAT-7A1 gene worldwide. To explore this, an initial screening of 230 GDP landraces was performed using a diagnostic marker for XAT-7A1, developed by our group and converted into a KASP assay. This analysis identified 48 lines carrying XAT 7A1 haplotypes: 22 Type I/II and 26 Type III. Subsequent HPLC analysis confirmed the presence of carotenoid esters in all Type I/II lines and their absence in Type III lines and in genotypes lacking XAT 7A1, giving 100% selection accuracy.

Furthermore, several landraces displayed remarkably interesting esterification profiles: some accessions showed up to 55% esterification of total carotenoids, while others exhibited a higher proportion of diesters relative to monoesters. These XAT 7A1 variants represent valuable genetic resources for enhancing carotenoid esterification and stability.

Finally, an emerging geographical pattern can be observed among landraces carrying XAT-7A1 gene. Type I/II haplotypes are mainly distributed across the Mediterranean-Anatolia-Iran region, whereas Type III haplotypes occur predominantly in Ethiopia, the Arabian Peninsula, and North Africa. This distribution broadly reflects the classical dispersal routes of durum wheat, corresponding to the Western-Mediterranean and the Eastern-Southern diffusion routes, respectively.

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Pleiotropic genetic network underlying grain storage protein composition in bread wheat

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Abstract

Grain storage protein (GSP) composition underlies end-use quality in bread wheat and is a complex quantitative trait influenced by multiple protein fractions and quantification scales (e.g., grain weight- or flour protein-based normalization). To dissect its genetic architecture, we reanalyzed 30 GSP-related traits measured on 181 wheat accessions using single-trait GWAS followed by a multi-trait framework. Single-trait GWAS identified numerous QTLs enriched in known GSP structural gene regions, but association patterns varied depending on protein types and scales, highlighting the limitations of single-trait approaches. To integrate effects across traits and scales, we performed multi-trait GWAS, identifying 258 candidate SNPs enriched in coding regions. Functional annotation of genes near these SNPs (within ± 15 kb) indicated enrichment for structural GSP components, chromatin regulation, and transcriptional control. These loci were further refined through gene expression filtering, linkage disequilibrium consolidation, and trait-based association criteria, yielding 76 high-confidence SNPs. Network and clustering analyses based on the effect size and direction of these 76 SNPs revealed five SNP clusters with distinct pleiotropic effect patterns on specific protein groups. We further performed principal component analysis (PCA) on the six major GSP components (high and low molecular weight-glutenin subunits, $\alpha\beta$ -, γ -, $\omega 1,2$ -, and $\omega 5$ -gliadins) in the same 181 accessions, obtaining principal component axes capturing major variation in GSP composition. To clarify the relationship between the PC axes of GSP composition and the pleiotropic SNP clusters, we calculated, for each accession, a cluster-specific SNP score defined as the proportion of minor alleles carried within each SNP cluster. Significant correlations were observed between the SNP scores and the PC scores. Importantly, the five pleiotropic SNP clusters were validated in an independent panel of 55 accessions with GSP compositional data computed using a different normalization scheme. Three SNP clusters consistently showed significant associations with the major axes of GSP variation. SNPs within clusters exhibited highly conserved effect directions, supporting their robustness as core genetic modules and highlighting their potential as genetic markers for GSP composition. Together, these results establish a multi-trait framework for dissecting compositional traits and reveal pleiotropic SNP modules shaping the genetic architecture of GSP composition in bread wheat.

Rheological, technological, and nutritional implications of high-amylose wheat in breadmaking

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Abstract

In recent years, wheat genotypes with a modified amylose-to-amylopectin ratio have been developed to enhance the functional and nutritional quality of cereal-based foods. High-amylose (HA) wheat, with amylose contents ranging 40-80% of total starch compared to 20-30% in conventional cultivars, is of interest due to its enrichment in the derived products in resistant starch (RS), which is associated with reduced postprandial glycemic response. However, the technological performance of HA wheat remains a major limitation for its application in breadmaking.

In this study, a conventional bread wheat cultivar (Cadenza) and an amylose-rich mutant line (HA), derived from the same genetic background using the TILLinG (Targeting Induce Local lesions in Genome) procedure, were cultivated during 2022-23 in Northwest Italy. The genotypes were evaluated under two nitrogen (N) strategies, a control fertilized during the vegetative growth stages and a late N application (40 kg N/ha at booting). The effects of the genotype and the late N fertilization on flour composition, dough rheology, and bread physicochemical and nutritional quality were assessed.

Marked compositional differences were observed between genotypes. HA exhibited lower starch content and significantly higher amylose, protein, ash, and arabinoxylan levels. These differences strongly influenced dough rheological behavior: HA doughs showed higher water absorption (+50%), lower storage (-18%) and loss (-25%) moduli, and complex viscosity (-19%), reflecting higher extensibility and a less rigid dough structure. HA breads displayed -25% specific volume and 1.3-fold higher crumb hardness, with reduced cohesiveness and springiness. During storage, crumb hardness of Cadenza increased, but remained similar in HA loaves. This was confirmed by the increasing values of Cadenza apparent melting enthalpy over time, indicating a greater degree of amylopectin reordering. All HA breads were significantly enriched in RS and met the criteria for RS-related health claims (15% RS of total starch vs. 2% in the control). Late N fertilization had only minor effects and was more relevant for the control.

The results highlight the nutritional potential of HA wheat while confirming technological constraints. Breeding strategies aimed at improving breadmaking suitability within high-amylose genetic backgrounds are required to improve the baking performance and support the development of nutritionally enhanced products.

1

***INVITED SPEAKERS
ABSTRACTS***

2

***SHORT TALKS
ABSTRACTS***

3

***POSTERS
ABSTRACTS***

P1 - Activating genomic resources to decipher biological nitrification inhibition (bni) in wheat

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Abstract

Biological nitrification inhibition (BNI) holds promise as a mechanism to improve fertilizer use efficiency and reduce nitrogen losses in cereal crop production systems. BNI is the natural ability of certain plants to produce exudates from their roots that suppress soil nitrification. Cultivated wheat (*Triticum aestivum*) exhibits limited BNI activity, but *Leymus racemosus*, a wild relative of wheat, has demonstrated high BNI capacity. International efforts have transferred a large region of a *L. racemosus* chromosome (Lr#N-SA = T3BL.3NsbS) that controls BNI activity into wheat, replacing the short arm of chromosome 3B through conventional breeding. Near-isogenic lines (NIL) with and without the translocation were developed into the genetic backgrounds of the CIMMYT elite wheat cultivars ROELF and MUNAL. Our aim is to decipher the gene(s) involved in BNI activity in these wheat genetic backgrounds. To that end, we generated long-read, chromosome-scale pseudomolecule assemblies using 30x genome coverage PacBio HiFi sequencing and Hi-C data for the two BNI+ NILs and their wheat recurrent parents. In addition, we have started annotating the genome assemblies using predictive and evidence-based strategies, with the intent of developing robust markers to support marker assisted selection and to identify high priority candidate genes for functional analysis of BNI activity in wheat. These genomic resources will improve our underlying understanding of BNI activity to accelerate targeted breeding of this trait for more climate-resilient wheat production.

P2 - Evaluating genotype-by-treatment interactions in hexaploid and durum wheat under combined water and nutritional stresses

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Abstract

Background: Climate change challenges wheat production, highlighting the need to optimize Water Use Efficiency (WUE) and fertilization strategies. This study, part of the WheatSecurity Project, investigates genotype and biostimulant interactions on wheat responses under combined drought and reduced nitrogen (N) stress.

Methods: Two experiments were conducted on PlantArray (PA) phenotyping platform to evaluate Genotype $\times$ Environment $\times$ Management (G $\times$ E $\times$ M) interactions by crossing different genetic backgrounds (G) with drought stress (E) and varying nitrogen/biostimulant protocols (M). In the PA-SSP six hexaploid wheat (*T. aestivum* ssp. *compactum*) landraces were evaluated under a medium N input (40% of the common field dose) to isolate the effects of the biostimulant (EKOseed microbial fertilizer) under drought. In the PA-TD experiment the behaviour of nine durum wheat (*Triticum durum*) cultivars under a drastically reduced N regime (15%) supplemented with a biostimulant was compared against higher N input (75%), both under drought stress. Physiological parameters including Dry Weight, Cumulative Transpiration, and WUE, were assessed via ANOVA and Tukey's HSD.

Results: PA-SSP experiment revealed two response strategies: i) Active Resilience where the biostimulant increased biomass and WUE despite drought (e.g., GB_111) and ii) Passive Downsizing: where genotypes reduced growth and consumption as a survival mechanism. In PA-TD experiment, the biostimulant acted as a physiological buffer enabling a 60% reduction in nitrogen input without compromising biomass in most durum cultivars. Across both experiments, analysis of the critical soil water content ($\bullet$ Crit) showed that the biostimulant (in most of the genotypes) modulates hydraulic strategies by triggering an earlier decline in transpiration, improving resilience during hydration phase transitions.

Conclusions: Our phenotyping protocol successfully identified specific resilient strategies and demonstrated that biostimulant efficacy depends on the genetic background. When paired with compatible genotypes, these products can significantly reduce synthetic nitrogen requirements while maintaining or improving water productivity under adverse climatic conditions. The outstanding performance of the GB_111+biostimulant combination highlights the importance of G $\times$ E $\times$ M interactions in sustainable agriculture; further research is now required to confirm the obtained result and dissect the genetic basis and the molecular pathways responsible for this favourable interaction, aiming to integrate these traits into future breeding programs.

P3 - A comparison of innovation systems to enable public-private collaboration in wheat breeding

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Abstract

Fully realizing the value of research investments in wheat breeding at the farm gate requires actors across government, academia, farm groups, and the private sector to work cohesively. Public investment in agricultural research in Canada has fallen 21% over the past decade (Gulab & L'hermie, 2025). This has shifted the innovation pipeline increasingly towards the private sector. In addition to research and variety development, networks, funding structures, and policy frameworks can incentivize or disincentivize collaboration within a sector, subsequently impacting how efficiently new varieties are produced and commercialized.

Understanding how other jurisdictions have structured their breeding systems can inform strategies for Canada to move forward. This “whole-of-system” approach is captured in the concept of Agricultural Innovation Systems (AIS). Effective collaboration across the system is a defining feature of productive AIS's. Networks, funding structures, and policy frameworks can incentivize or disincentivize collaboration within a sector.

Drawing on in-person and virtual interviews, field tours and author observations, this study examines the different aspects of agriculture innovation systems needed to capitalize on research investments in wheat breeding across public and private sectors. The study includes observations from eleven countries including: Australia, Canada, the United States, the Netherlands, Brazil, Kenya, Rwanda, and the United Kingdom. Our results show that clear governance, sustainable funding, well-resourced extension, and an enabling regulatory environment all contribute to successful variety development and adoption.

P4 - Genetic differences in wheat nitrogen use efficiency are explained by radiation interception under contrasting nitrogen availabilities

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Abstract

The enhancement of nitrogen use efficiency (NUE) is a critical challenge for crop production to minimise the environmental impact. Therefore, high NUE genotypes are a clue to wheat breeding. To this aim, the objective of this study was to identify key traits associated with NUE under contrasting nitrogen availabilities.

A field experiment was conducted over two seasons in the high-yielding environment of Valdivia, Chile. We evaluated two wheat genotypes from the CIMMYT's Wheat Association Mapping Initiative (WAMI) population: ATTILA/3*BCN*2///BAV92 (ATTILA) and WBLL1*2/KUKUNA (WBLL1), contrasting in NUE from a previous assessment (26.9 and 43.2 g g⁻¹ for ATTILA and WBLL1, respectively), plus a Chilean wheat cultivar (Pantera-INIA), included as a local control. Wheat genotypes were sown under two contrasting nitrogen (N) availability levels: a control without N fertilization and a fertilized treatment supplying 300 kg N ha⁻¹. The experiment was arranged in a split-plot block design, where the main plot was assigned to the nitrogen availability level and the subplots to genotypes in three blocks. Except for N treatments, the experiment was carried out under optimal crop management. Data were analysed using ANOVA.

On average, across growing seasons, GY in the control treatment for Attila, Wbll, and Pantera were 964, 1203, and 1354 g m⁻², and under fertilization 1257, 1372, and 1396 g m⁻², respectively. As expected, grain yield (GY) showed a strong association ($R^2 = 0.95$) with aboveground biomass; meanwhile, harvest index (HI) did not ($R^2 = 0.03$, $p = 0.63$). The dynamics of aboveground biomass accumulation were modelled using a four-parameter logistic model, which exhibited a high degree of association ($R^2 = 0.94-0.98$). Among the determinants of biomass production (i.e., radiation interception, radiation use efficiency, and associated traits), the intercepted radiation (IR) revealed differences ($P < 0.05$) within treatments. Furthermore, N treatments affected leaf area index (LAI) across combinations of seasons, genotypes, and nitrogen treatments, while the specific leaf weight (g cm⁻³) was not ($P > 0.05$) affected by nitrogen treatments, either among genotypes or between seasons. Consequently, these results provide insights into key traits associated with NUE and helpful tools for wheat breeding.

P5 - From maximum to economically optimal yield and quality: nitrogen management strategies for winter wheat in flanders, belgium

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Abstract

Winter wheat is a major arable crop in Flanders (Belgium), supported by well-established cultivation practices. However, increasingly stringent nitrogen (N) fertilisation regulations and strong price fluctuations for both grain and mineral fertilisers challenge the economic viability of winter wheat production. This raises the question of whether current production systems should target maximum yield or rather an economically optimal yield under reduced N inputs, and how modern winter wheat varieties respond to such strategies.

Over three consecutive growing seasons (2023-2025), three project partners conducted field experiments to evaluate the effects of different crop management strategies. The primary focus was on the response of multiple winter wheat varieties to a wide range of N fertilisation levels (0-250 kg N ha⁻¹), based on soil analyses and fertilisation advice for maximum yield. In addition, during the 2023 and 2024 seasons, the potential of biostimulants, e.g. containing the nitrogen-fixing bacterium *Methylobacterium symbioticum*, and a foliar fertiliser (N-leaf), supplying nitrogen, sulphur, and magnesium, was assessed under reduced N input scenarios. Economic analyses were performed using prevailing market prices for wheat and fertilisers to compare the cost efficiency of maximum versus economically optimal yield strategies.

Results showed that grain yield response plateaued at relatively moderate N rates (from approximately 150 kg N ha⁻¹), despite advisory recommendations of around 210 kg N ha⁻¹ and a calculated maximum yield at 223 kg N ha⁻¹. Based on yield response and economic calculations, the economically optimal N rate was estimated at 179 kg N ha⁻¹. Grain quality analyses indicated that protein content kept increasing, even above optimal and recommended N gift, important for the cultivation of baking wheat.

Biostimulant application had no significant effect on grain yield, although a slight increase in protein content was observed, corresponding to a marginal N equivalent (≈ 1.2 kg N ha⁻¹). Application of N-leaf resulted in an estimated N equivalent of 37 kg N ha⁻¹ based on yield response, but effects varied substantially across sites.

P6 - Effect of biostimulant application at different growth stages on wheat grain morphology

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Abstract

Wheat (*Triticum aestivum* L.) is one of the most important cereals for human consumption. Improving grain yield and quality sustainably remains a key challenge under increasing environmental and agronomic constraints. In this context, biostimulants are obtaining attention as tools to enhance crop performance, although their effectiveness strongly depends on the growth stage at application and genotype-specific responses. This research investigated the impact of biostimulant application at three key growth stages - booting (BS), stem elongation (SES), and heading (HS) - both individually and in combination (BS+SES+HS), using two winter wheat genotypes (Essekerka and Eminentia), to assess effects on morphological traits. To quantify these effects, 1000 kernel weight, grain area, width, length, and circularity were measured using digital image analysis.

Biostimulant application significantly enhanced grain morphological traits in both genotypes, depending on growth stage and genotype. In Eminentia, all biostimulant treatments resulted in a significant increase in 1000 kernel weight compared to the control, indicating high responsiveness across developmental stages. In contrast, Essekerka exhibited a significant increase in 1000 kernel weight primarily when biostimulants were applied at HS and in the combined BS+SES+HS treatments, highlighting a more stage dependent response. Grain area and width increased significantly in both genotypes, while grain length showed a genotype-specific increase, most notably following HS application. Grain circularity tended to decrease after biostimulant treatments, suggesting slight shape modifications associated with increased grain size and weight.

The results indicate that the HS is critical for biostimulants application to maximise grain weight and size, while combined applications across multiple growth stages can further enhance grain yield related traits depending on genotype. These findings emphasise the importance of optimising biostimulant strategies according to wheat developmental stages and genetic background, and support their potential integration into sustainable wheat production and breeding programs.

Keywords: *biostimulants, growth stage, grain morphology, wheat*

P7 - Enhancing durum wheat drought resilience and soil fertility through microbial biostimulants and wheat-clover intercropping systems

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Abstract

Climate change is increasingly affecting agricultural systems, particularly in the Mediterranean region, where rising temperatures and severe drought events contribute to land degradation and desertification. At the same time, intensive agricultural practices based on the extensive use of synthetic fertilizers, pesticides, and frequent tillage have accelerated soil degradation and erosion.

Triticum durum is a fundamental component of Mediterranean agroecosystems and is known for its adaptability to diverse environments. However, its productivity is increasingly threatened by water scarcity, which limits plant growth and yield and may also increase susceptibility to diseases. The adoption of regenerative agricultural practices is therefore essential to maintain soil fertility, improve crop resilience, and ensure long-term food security.

In this context, this study explores the application of regenerative agronomic practices to enhance wheat performance under drought conditions. Specifically, a wheat-clover intercropping system was tested to improve soil water dynamics, promote beneficial plant-plant interactions, reduce disease pressure, prevent soil erosion, and enhance long-term soil fertility. In addition, a microbial-based biostimulant containing mycorrhizal fungi and Trichoderma spp. was tested as a strategy to support soil biological activity and nutrient availability.

Different durum wheat genotypes with contrasting levels of drought tolerance were evaluated to investigate plant-plant interactions within the wheat-clover intercropping system under both well-watered and drought stress conditions. The effects of intercropping were assessed through biochemical, physiological, and morphological analyses.

To evaluate the efficacy of the microbial biostimulant, the formulation was applied to plants grown under greenhouse conditions simulating field environments with controlled drought stress. A phenotyping platform was used to monitor plant growth and biomass accumulation, water status and water-use efficiency, photosynthetic performance, stress and senescence indices, and yield-related traits. In addition, a metabarcoding analysis is planned to characterize the wheat root-associated microbiome.

Preliminary results indicate that intercropping affects wheat genotypes differently, influencing biomass production and nutrient uptake. Furthermore, the microbial biostimulant promoted plant growth and physiological performance, suggesting that the presence of mycorrhizal fungi and Trichoderma can help mitigate the negative effects of drought stress while supporting soil health.

P8 - Bread wheat varietal mixtures enhance yield stability and grain quality in variable environments

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Abstract

Varietal mixtures offer a promising approach to enhance cereal system resilience under climate change. This study evaluated the yield and technological quality of binary and ternary bread wheat mixtures compared with single-variety plantings across three contrasting environments (favorable, semi-arid, and mountainous). Sixteen single-variety plantings, 10 binary, and 8 ternary mixtures were conducted over two growing seasons (2023-2024 and 2024-2025) using a randomized complete block design with three replications. Grain yield and key quality traits, thousand-kernel weight, test weight, protein content, gluten strength were evaluated. The results showed that binary mixtures achieved an average yield gain of +3.0% while ternary mixtures exhibited high yield stability and environmental adaptability across contrasting conditions. Nearly half of ternary combinations (48%) showed positive yield gains, with the best-performing mixture (Ibtissam+Khadija+CCBT185) achieving remarkable gains up to +70% and maintaining an average performance of +13.9% across all tested environments. Stability analysis revealed that ternary and binary mixtures exhibited significantly enhanced yield stability compared to single varieties, reflecting superior environmental adaptation and resilience to variable climatic conditions. Technological quality was maintained or slightly improved in varietal mixtures: thousand-kernel weight and test weight were comparable to single varieties ($p>0.05$), while protein content increased by 1.0% in binary mixtures and 2.1% in ternary mixtures. The results show that varietal mixtures improve yield stability and grain quality by combining complementary varieties, thereby increasing resilience to climatic variability. These findings highlight the potential of varietal mixtures as a climate-smart strategy for bread wheat production.

Keywords: Bread wheat, Varietal mixtures, Grain yield, Grain quality, Stability, Resilience.

P9 - Fragmented consensus: industry challenges in defining sustainable wheat

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Abstract

Evolving, operational definitions of sustainability are needed to accommodate both shifting social expectations and diverse stakeholders' perspectives. With a focus on the US wheat value chain including breeders, agronomists, input suppliers, growers, millers and bakers, and consumers we used expert elicitation and network analysis to show stakeholders had an a priori, partial consensus on abstract goals (e.g. "economic viability", "social responsibility"), but sector-dependent metrics of sustainability. From a baseline of fragmented and vague consensus, stakeholders used quadrant analysis to collectively identify technologies with low adoption and potential to improve sustainability, and co-constructed a strategy to develop an operational label for sustainable bread including a clear, shared definition of sustainability; promoting consumer education; and spread of economic incentives for sustainability across sectors. Our insights from the wheat value chain in the US can be useful in other agricultural industries and jurisdictions.

P10 - The yield and quality of winter wheat grain under different sowing and nitrogen management strategies: a case study in northeastern poland

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Abstract

The aim of the study was to assess the impact of sowing strategies and spring nitrogen (N) fertilization rates on the technological quality of winter wheat (*Triticum aestivum* L.) grain, including milling quality, protein complex characteristics, and enzyme activity expressed as the falling number. The grain was obtained from a small-area field experiment conducted between 2018 and 2021 at the Agricultural Experimental Station in Bałcyny, northeastern Poland. The experimental factors included sowing date (early, delayed by 14 days, and delayed by 28 days), sowing density (200, 300, and 400 live grains m⁻²), and split spring N fertilization (40 + 100, 70 + 70, and 100 + 40 kg ha⁻¹) applied at BBCH stages 22-25 and 30-31. A sowing delay of 14 and 28 days increased the bulk density (by 1 and 1.5 percent points (%p), respectively), vitreousness (by 3 and 6%p, respectively), and total protein content of grain (by 1% and 2%, respectively). A sowing delay of 14 days increased grain hardness (by 5%), the flour extraction rate (by 1.4%p), and the falling number (by 3%) while also decreasing grain uniformity (by 1.9%p). In turn, a sowing delay of 28 days increased the wet gluten content of grain (+0.5-0.6%p) and improved the quality of the protein complex in the Zeleny sedimentation test (+1.5%). An increase in sowing density from 200 to 300 live grains m⁻² led to a decrease in grain uniformity, the total protein content and the wet gluten content of grain. A further increase in sowing density decreased grain vitreousness (by 1.4%p). The grain of winter wheat fertilized with 40 and 100 kg N ha⁻¹ in BBCH stages 22-25 and 30-31, respectively, was characterized by the highest hardness (64.7), vitreousness (93%), flour extraction rate (73.9%), total protein content (134 g kg⁻¹ DM), wet gluten content (36%), and Zeleny sedimentation index (69 mL).

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P11 - Conservation agriculture for sustainable wheat production under the soil-climate conditions of Uzbekistan

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Abstract

Wheat is a strategic crop for food security in Uzbekistan, where production is increasingly challenged by soil degradation, declining organic matter, water scarcity, and climate variability. Conservation agriculture (CA) offers a promising pathway to address these constraints while sustaining productivity and soil health. This abstract synthesizes knowledge and practical experience gained through participation in the Wheat Training for Uzbekistan 2025 program organized by the International Maize and Wheat Improvement Center (CIMMYT), with a focus on adapting CA principles to the agro-ecological conditions of Uzbekistan.

The training provided hands-on exposure to key CA practices, including zero or reduced tillage, crop residue retention, diversified cropping systems, and precision mechanization for wheat establishment. Field and laboratory studies demonstrated that CA improves soil physical properties by reducing bulk density and compaction, enhancing aggregate stability, and increasing water infiltration and moisture retention. Improved soil biological activity and nutrient cycling were also observed, supporting healthier root development and improved nitrogen use efficiency in wheat systems.

For Uzbekistan's arid and semi-arid environments, CA-based wheat production is particularly relevant. Direct seeding of wheat using zero-till drills or residue-managing seeders can reduce soil disturbance, conserve limited soil moisture, and enable timely sowing after previous crops. Residue retention helps mitigate erosion, moderates soil temperature, and suppresses weed emergence, while integrated weed management remains essential for sustainable adoption. CA-compatible machinery and custom hiring services are critical to ensure accessibility for farmers and to support large-scale implementation. Expected outcomes of adopting conservation agriculture in Uzbekistan include improved soil health, increased water-use efficiency, stable or enhanced wheat yields, reduced production costs, and lower environmental footprints. In the long term, CA can strengthen climate resilience, enhance carbon sequestration, and contribute to sustainable intensification of wheat-based systems. The experiences gained through CIMMYT training highlight the strong potential of conservation agriculture as a science-based and practical approach for sustainable wheat production in Uzbekistan.

P12 - Growth dynamics and nitrogen utilization characteristics of a wheat line with biological nitrification (BNi) inhibition capacity

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Abstract

Biological nitrification inhibition (BNi), whereby plant roots suppress soil nitrification and potentially alter nitrogen availability, has been proposed as a promising trait for improving nitrogen (N) use efficiency in wheat-based cropping systems. However, the physiological basis underlying yield performance of BNi-enabled wheat under different N environments remains unclear. In this study, we investigated the yield, growth, N uptake, and N assimilation characteristics of a BNi-enabled wheat line and its parental line through field experiments in Hokkaido, Japan, complemented by hydroponic experiments with contrasting N forms. In the field trials, the BNi wheat generally exhibited poorer early growth and produced fewer ears, suggesting limited tiller establishment during early developmental stages. Nevertheless, when sufficient number of ear was established, the grain yields of BNi wheat could be comparable to the parental line, indicating a high potential source capacity to support the grain development. Notably, the BNi wheat maintained higher nitrogen uptake during the late growth stages despite lower nitrate reductase activity, suggesting a distinctive imbalance between nitrate reduction capacity and whole-plant nitrogen uptake, which is atypical for upland crops generally regarded as nitrate-preferring. In hydroponic culture, however, the plant growth followed the order in nitrate-only > mixed ammonium-nitrate > ammonium-only treatments, indicating that ammonium did not work as the growth promoter in both genotypes. These field and hydroponic results indicated that the superior late-stage nitrogen uptake observed in BNi wheat was unlikely brought through a preference for direct ammonium uptake. It could result from utilization of gradual supplying ability of nitrate over an extended period, potentially due to reduced nitrification in the rhizosphere. These could bring the slow early growth and the enhanced later growth in which nitrogen uptake and biomass accumulation were maintained in BNi wheat. Under the cool climate in of Hokkaido, these characteristics in BNi wheat could not always show as higher yield advantage. It is useful to develop the suitable cultivation practices through which BNi-enabled wheat could improve the performances in early growth performance and subsequent sink establishment.

P13 - Integrated biological and chemical control strategies for the management of mycotoxin contamination in wheat cropping systems under different tillage regimes

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Abstract

Cereals are the main global food source, and wheat is the leading crop by cultivated area. Current European strategies promote conservative and regenerative agriculture, encouraging the reduction of agronomic input, including the transition from conventional (CT) to minimum tillage (MT) to reduce emissions, costs and soil erosion. However, MT increases fungal inoculum due to previous crop residue occurrence on the soil surface, and therefore the wheat infection of *Fusarium* Head Blight (FHB) agents and the contamination of mycotoxin, particularly deoxynivalenol (DON). As cereal cropping systems increasingly shift toward conservative agriculture and reduced use of chemical pesticides, this study aims to evaluate the use of biological control agents (BCAs) as a preventive strategy to limit the severity of fungal diseases and the contamination by regulated mycotoxins (deoxynivalenol and zearalenone) as well as emerging mycotoxins (moniliformin and enniatins).

A four-year split-plot field experiment was carried out with soil tillage (CT vs MT) as main factor and the following fungal control treatments as sub-factor; untreated control, BCA application on soil at the stem elongation stage (*Trichoderma asperellum* and *T. gamsii*), chemical fungicide (F) application at wheat flowering, and their combination (BCA+F). In both tillage conditions, BCA application increased grain yield compared to untreated plots (+7%), while BCA+F provided the highest yield (+26%) and test weight (+5%). On average, MT increased FHB incidence by 35% and DON contamination by 151% compared to CT. For both soil tillage, BCA reduced FHB incidence and DON contamination (-10%), while fungicide showed a higher effect in MT (-63%) compared to CT (-50%). In MT, DON was 14% lower for BCA+F than F alone, while in CT no significant differences were detected between F and BCA+F.

In MT conditions, BCA could represent a viable alternative or complement to chemical fungicide strategies, reducing the production of FHB agents inoculum and resulting in a lower sanitary risk. Further studies are required to identify the most effective biological control agents and optimize their application in accordance with environmental and agronomic conditions.

P14 - From multi-omics to breeding: adaptive mechanisms of wheat under combined nutrient and water stress

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Abstract

Wheat productivity is often limited by drought and nutrient deficiency, particularly in Mediterranean environments. Enhancing nitrogen use efficiency (NUE) and drought tolerance requires deeper insight into the molecular regulation of nitrogen metabolism under stress. This study compared tetraploid (Svevo) and hexaploid (Chinese Spring) genotypes integrating phenotypic, metabolomic, and transcriptomic approaches.

Plants were grown in controlled lysimeter systems under seven treatments combining nitrogen (N), phosphorus (P), and water (W) deprivation. Physiological traits (chlorophyll content, photosynthesis, biomass), leaf elemental composition, metabolic profiles (amino acids, soluble sugars, phenolics, flavonoids), grain quality parameters, and RNA-seq-based transcriptomics were evaluated.

Responses were genotype- and stress-specific. Svevo was highly sensitive to combined N-P deficiency and W-N interactions, exhibiting accelerated senescence and reduced chlorophyll and biomass. Chinese Spring was more sensitive to water stress alone. Nitrogen supplies alleviated P deficiency effects, underscoring the importance of nutrient balance. Chlorophyll content differed between cultivars during early vegetative growth under W and W-P treatments. In Svevo, stomatal conductance varied significantly during early grain development under W+N and P-only treatments. Biomass trends were similar overall, though modulated by N availability. Protein content responded to treatments in both cultivars; dry gluten remained stable in Svevo but varied in Chinese Spring.

Correlation analyses showed positive associations between biomass, photosynthetic efficiency, and grain quality traits, even under stress. In contrast, phenolic and flavonoid accumulation, indicative of stress defence, was negatively correlated with growth and quality, suggesting a trade-off between defence and productivity.

RNA-seq profiling revealed numerous differentially expressed genes (DEGs) under combined stresses, including both shared and stress-specific regulatory networks. Many DEGs were common to both genotypes, though regulation patterns varied with stress combinations. In Chinese Spring, upregulated genes included both treatment-specific and commonly induced genes, indicating partially convergent pathways. In Svevo, functional enrichment highlighted overexpression of genes involved in metabolic processes, including carboxylic and fatty acid metabolism, reflecting extensive metabolic reprogramming. Integrating physiological and transcriptomic data provides a comprehensive view of nitrogen metabolism under abiotic stress. Identified genotype-specific strategies and candidate genes represent valuable resources for breeding wheat with improved NUE and stress resilience.

This study was conducted within the PRIN2022-PNRR WheatSustain project.

P15 - Thinking outside the row - investigating alternate spatial arrangements in wheat cropping

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Abstract

Maintaining equal distance between neighbouring wheat plants through alternate spatial arrangements can increase radiation interception and radiation use efficiency, and potentially alleviate detrimental plant responses to intraspecific competition. Just as the convention of evenly spaced crop rows was popularised with the 18th century invention of the horse-drawn seed drill, alternative spatial arrangements for crops will soon be practical with the advent of the automated age. Hexagonal (hex) planting arrangement places plants equidistant from each other, with the six closest neighbours to any one plant forming a hexagon around it. For the same density, hex arrangements allow greater distance from neighbouring plants compared to conventional drill rows, particularly at wider (0.25-0.36 m) row spacing common in Australia. In the first of a multi-year field experiment, the responses of four genotypes of varying competitive ability were investigated in standard row and hex arrangements at densities of 100 and 36 plants m⁻². Genotypes chosen were aligned in phenology, with two cultivars with known differences in response to intraspecific competition, and two sibling research lines that differ in height (semi-dwarf and double dwarf). Precise positioning of each plant was achieved through customised seed tape, with the density confirmed by plant counts and measurements post emergence.

Hex arrangements had greater NDVI from 90 days after sowing to flag leaf emergence. At flag leaf emergence, the 100 plants m⁻² hex arrangements had more green leaf dry matter and were intercepting more light than standard row treatments. Hex arrangements had a higher growth (305 vs 270 g/m² of total dry matter) from flag leaf to anthesis (assumed to be the critical period for yield determination), with greater spike dry matter (234 vs 217 g/m²) and stem dry matter (462 vs 427 g/m²) at anthesis. Yields for two of four genotypes were 16% higher at 100 plants m⁻² in the hex arrangement compared to the standard arrangement, with no genotype suffering a yield penalty at any density in the hex arrangement. These results demonstrate the potential benefits of alternative spatial arrangements in wheat cropping, which could set a new paradigm when combined with next-generation precision sowing machinery.

P16 - From knowledge to practice: the economic assessment of improved varieties adoption in the case of wheat

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Abstract

Since the establishment of the National Wheat Breeding Program, Morocco has made significant progress in developing new wheat varieties adapted to the edaphic and climatic conditions of its main agroecosystems. Initially, breeding efforts focused primarily on yield improvement and disease resistance, reflecting the country's post-independence priorities. Over time, however, the program has evolved toward a more integrated approach that considers environmental, economic, social, and technological dimensions. Issues such as production costs, grain quality, farmers income, and gender inclusion have gained increasing importance in recent years. This study aims to analyze the process of technology transfer related to new wheat varieties through the perceptions and experiences of researchers, policymakers, and producers. Special attention is given to the genetic traits of improved varieties and gender, particularly the role of women in developing and implementing national wheat breeding program. The research approach is based on multi-stakeholder workshops, household survey and econometric models, they represent favorable, less favorable and semi-arid regions. Three target platforms were identified by the project's team that represent different agrosystems. Advanced statistics methods and Cobb-Douglas model will be used to investigate the determinant of knowledge transfer and simulate the impact of improving knowledge flow among actors and inform policy makers about the urgent need to develop a national wheat certified seed alliance to improve communication and collaboration between stakeholders and the national wheat breeding program. As a legal instrument, the expected output of this research will contribute to better understanding communication mechanisms, reinforce knowledge flows and to inform on inclusive and effective agricultural innovation policies in Morocco's wheat sector.

Keywords: *Wheat, Technology transfer, Knowledge, Gender, Innovation*

P17 - A multidimensional framework for selecting soft wheat varieties in dryland environments integrating productivity, nitrogen use efficiency, stability and economic performance

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Abstract

Wheat production in dryland and semi-arid environments is strongly constrained by climatic variability and limited availability of agricultural inputs, particularly nitrogen. Identifying varieties that combine high productivity, efficient nitrogen use and stable performance across environments is therefore essential to improve the sustainability and resilience of wheat-based cropping systems.

This study proposes a multidimensional analytical framework to support the selection of soft wheat varieties by integrating agronomic performance, nitrogen use efficiency (NUE), yield stability and economic indicators. The framework was applied to 33 bread wheat varieties evaluated across six environments in Afghanistan (three locations × two growing seasons). Field trials were conducted under irrigated conditions using a randomized complete block design with three replications. Grain yield, straw yield, thousand kernel weight, grain protein content and NUE components were measured and analysed.

To assess varietal performance and environmental responses, linear mixed models were used to partition the effects of genotype, environment and genotype × environment interaction. Yield stability was evaluated using AMMI analysis and Wricke's ecovalence index. Nitrogen use efficiency was further decomposed into uptake efficiency, translocation efficiency and grain yield per unit of grain nitrogen. An economic indicator, the Net Nitrogen-adjusted Margin (N_{NaM}), was developed to integrate yield, grain protein-based market price, straw value and nitrogen input costs. A multiple linear regression model was then used to identify the main drivers of economic performance.

Environmental effects explained more than 80% of the variability in yield-related traits, highlighting the strong influence of environmental conditions on wheat productivity. Grain yield ranged from 3.7 to 6.15 t ha⁻¹ across varieties, while nitrogen uptake efficiency varied between 0.41 and 0.72. The regression model explained 96.5% of the variability in N_{NaM}, indicating that nitrogen uptake efficiency and straw yield were key determinants of economic performance.

A composite index integrating productivity, NUE, stability and economic indicators enabled the ranking of varieties and identified genotypes combining high yield potential, resource-use efficiency and stable performance across environments. This integrative framework provides a scalable tool for varietal evaluation and decision support in wheat production systems under resource-limited and climate-variable conditions.

P18 - Sensory profiles of wheat: Suitability for resilient production and consumer acceptance

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Abstract

Reducing external inputs to crop production while preserving sensory quality is essential for advancing environmentally friendly food systems and meeting consumer demands. This study assessed the sensory characteristics of 29 diverse wheat genotypes, representing 11 genetic backgrounds, comprising wheat-rye introgression lines, *Triticum carthlicum*, and modern cultivars, using a standardized food model (wholegrain porridge) assessed by Quantitative Descriptive Analysis (QDA) across 13 sensory attributes. The impact of reduced inputs was examined by cultivating genotypes in conventional and organic environments. Modern cultivars were associated with sweetness, sturdiness, and mild odour and flavour profiles, whereas rye introgressions and *T. carthlicum* exhibited more intense graham and rye odours, bitterness, and umami taste. Conventional cultivation resulted in higher odour and flavour intensities ($P < 0.005$), while organic cultivation enhanced sweetness and texture with reduced bitterness. For example, graham and rye odours showed higher mean intensities under conventional conditions (e.g. ~39 vs ~35 and ~35 vs ~32, respectively). Grittiness was slightly higher under conventional cultivation ($P < 0.05$), whereas sturdiness remained unaffected. Principal component and cluster analyses revealed environment-specific genotype groupings, but 2R/2D remained high, 1R/1D low across environments. Strong positive correlations were observed among odour and flavour traits ($r = 0.65-0.88$) and among grittiness, bitterness, and umami ($r = 0.68-0.83$), while sweetness correlated negatively with grain-like flavours ($r = -0.42$ to -0.70). Canonical correlation analysis demonstrated a significant interdependence between pre-ingestive and ingestive traits. Overall, genotype-specific sensory responses indicate that low-input cultivation leads to differentiated, rather than uniform, sensory outcomes, offering opportunities to align sensory quality with sustainable wheat production.

P19 - Remote sensing -based evidence from farmers' fields on how wheat benefits cropping systems

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Abstract

Spring and winter wheat provide and gain benefits when included in diversified crop rotations. This was evident based on the method [1] developed to estimate pre-crop values for farmers' fields by using Sentinel 2 -images. Legacy effects differ depending on previous and subsequent crops used in rotations, as well as prevailing farm and weather conditions [2]. Therefore, becoming aware of the legacy effects is challenging for farmers. Wheat covers in total >200.000 ha, i.e. ~10 % of cultivated land area in Finland. Due to climate warming cultivation of both spring and winter wheat has expanded from their original south-western production region towards more northern and inland areas [3,4]. Wheat is often cultivated in the prime field parcels of a farm, where also other valued break-crops can be grown. As an average spring wheat and winter wheat provided legacy effects of ca. 6–8 % for peas, 2–5 % for faba beans, 5–6 % for oil crops, and 3 % for sugar beet [1]. On the other hand, legacy effects of grain legumes were 9 %, oil crops 8 %, sugar beet 10 %, and potatoes 6 %, perennial grasslands and other cereals 5 % for spring wheat as a subsequent crop. The productivity benefits of other cereals were 4 %, oil crops 9 %, and grain legumes 11 % for winter wheat. Winter wheat has lower cultivation area due to overwintering risks and less species used as previous crops. These results from farmers' fields highlight the immediately realized, two-way legacy benefits of including wheat in rotations when compared to monotonous wheat sequencing. In addition, there are likely other long-term sustainability impacts that are not reachable with this method.

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[3] Peltonen-Sainio, P. & Jauhiainen, L. 2020. <https://doi.org/10.1007/s10113-020-01682-x>

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P20 - Perennial wheat and perennial cereals: grain and forage yield

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Abstract

Perennial grain crops are emerging as promising alternatives to conventional annual cereals, offering the potential to produce food while maintaining continuous living cover and enhancing agroecosystem resilience. Perennial wheat (*Triticum X Tynopirum*), kernza, and perennial cereal rye (*Secale cereale X S. strictum*) represent leading candidates for dual-purpose systems that provide both grain and high-quality forage. Although breeding programs have advanced these crops in recent years, comparative evaluations of forage and grain yields of breeding lines across species under field conditions are still unknown.

Fourteen Kernza populations from The Land Institute (TLI) and the University of Minnesota (UMN) breeding programs were planted in autumn 2024 using a randomized complete block design with four blocks in two locations in Wisconsin, USA. Planting took place on September 12 at a seeding rate of 11.2 kg/ha. In addition, seven perennial wheat lines from TLI and Washington State University (WSU) breeding programs, along with one perennial cereal rye line from the UMN breeding program, were planted in a randomized complete block design with three blocks at the West Madison research station. Seeding rates for the TLI and WSU perennial wheat lines and the perennial cereal rye were 86.3, 61.7, and 56.0 kg/ha, respectively. In summer 2025, grain and forage were harvested, dried and weighed. Perennial cereal rye was harvested on July 18. Kernza and wheat were harvested on July 29.

Kernza forage (6.64 t/ha) and grain (0.80 t/ha) yields did not differ by program across locations, but there were differences among populations, being MN2201 the highest-yielding population for both forage (7.99 t/ha) and grain (0.94 t/ha). Perennial wheat forage (7.28 t/ha) and grain (2.87 t/ha) yields did not change with program. The perennial cereal rye produced a higher grain yield (5.67 t/ha) than perennial wheat from TLI (1.85 t/ha) and was those from WSU (3.89 t/ha), while also greater forage yield (12.4 t/ha) than the perennial wheat. The top-performing perennial wheat line was CS14PHR21 (WSU), with forage and grain yields of 9.92 t/ha and 5.62 t/ha, respectively. The strong grain and forage performance of the perennial cereals highlights the potential as dual use crops.

P21 - Timing matters: sowing date modulates winter wheat agronomic optimum plant density

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Abstract

Winter wheat (*Triticum aestivum* L.) yield is influenced by sowing date, which interacts with genotypes and management practices to determine the agronomic optimum plant density (AOPD). Understanding how sowing date affects AOPD across genotypes and management conditions can inform decisions to maximize yield and resource use efficiency. This study evaluated the effect of sowing date on winter wheat AOPD under varying environments, nitrogen rates, seeding rates, and genotypes. Field experiments were conducted across three environments in Kansas during the 2025-26 season. A hierarchical multilevel split-plot design was implemented, with sowing date (Early, Optimum, and Late) as the whole-plot, nitrogen rate (0 or 225 kg ha⁻¹) as the subplot, seeding rate (100 or 300 seeds m⁻²) as the sub-subplot, and genotype (DoubleStop CL+, Bob Dole, WB4699, and KS Hatchett) as the sub-sub-subplot. Plant density was measured in a 1-meter sampling area per plot. Nitrogen fertilization increased tillers, spikes, and grain yield by 26%, 25%, and 17%, respectively. Sowing date (as day of year) significantly affected all variables except plant population. Raw data and posterior distributions suggested that early sowing dates increased grain yield by 3.4-2.8 Mg ha⁻¹. Posterior AOPD estimates from the hierarchical Bayesian model were higher for early than late sowing (42 vs. 37 plants m⁻²). Raw data shows penalties from late sowing on yield in high-yielding environments ($r^2 = 0.54$). Across environments, delayed sowing reduced both yield potential and AOPD, suggesting that yield losses cannot be fully compensated by increasing plant density or nitrogen rate. Elastic-net regression identified available water at sowing, cumulative fall precipitation, and growing degree days as the main environmental predictors of AOPD. These results suggest that sowing date interacts with management practices to influence AOPD and yield potential, providing an initial step toward actionable insights for optimizing winter wheat production under variable environmental conditions.

P22 - Enhancing spring wheat adaptation in Northern Sweden through early maturity, yield potential and quality improvement

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Abstract

Spring wheat (*Triticum aestivum* L.) is an important crop in Sweden, and its improvement in northern Swedish growing conditions remains challenging owing to short seasons, temperature variability, and the need to maintain baking quality. Breeding northern-adapted genotypes that combine early maturity with acceptable baking-related quality and favourable grain traits is therefore a priority for resilient production and crop diversification. In this study, 245 spring wheat genotypes were evaluated during 2024-2025 under northern Swedish field conditions based on multi-trait phenotyping of phenology, grain physical characteristics, processing quality indices, and amino acid composition. Field evaluations have revealed wide genetic variations in adaptation and quality traits. Several genotypes combined early development with promising end-use quality, showing significant grain protein content (17.0-18.3%), high Zeleny sedimentation values (67-70 mL), and high Falling Number (327-390 s), indicating stable starch functionality and reduced risk of pre-harvest sprouting. Selected genotypes also demonstrated high thousand-kernel weight (up to 46.6 g) and high litre weight (up to 84.2 kg hL⁻¹), contributing to good grain filling under short-season conditions. Across the 2024 dataset, the same genotypes reached early maturity (days to maturity: 88-95) while maintaining higher protein and good-quality indices, indicating that reduced growth duration occurred without clear penalties to end-use performance under high-latitude conditions. In 2025, the top-performing genotypes combined a protein content of 15.8-18.5% with early development (days to heading 55-59 and days to maturity 92-97), demonstrating the possibility of selecting early genotypes while maintaining baking-related quality. Amino acid profiling across both seasons showed a stable gluten-associated pattern, dominated by glutamic acid (27.6-32.6% of crude protein) and proline (9.8-11.4%). Essential amino acids, such as lysine (2.23-3.12%), methionine (1.39-1.68%), and tryptophan (1.05-1.39%), showed moderate but exploitable variation, indicating the potential to improve nutritional balance alongside technological performance. These results identify northern-adapted spring wheat genotypes that combine early maturity, good baking quality, and favourable grain traits, providing valuable breeding material for high-quality wheat production in northern environments.

P23 - Optimizing wheat agronomic inputs in the humid Midsouth region of the United States

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Abstract

Wheat has historically been considered a secondary crop in the humid Midsouth region of the United States, in part due to complications integrating it into the cotton (*Gossypium hirsutum*, L.) production system. Recent shifts away from cotton and into grain (most notably, *Glycine max*, L.) along with substantial increases in observed wheat yield have increased interest in the commodity. There are currently two distinct management approaches to the crop; producers typically fall either within the high-input, high-risk, high productivity category or the low-input, low-risk, marginal productivity category. Research trials conducted by the University of Tennessee evaluating seeding rates, foliar fungicides, nitrogen rates, nitrogen timings, foliar insecticides, and growth regulators have been conducted to maximize the return on investment of each input. Results have suggested seeding rates should target a minimum plant stand of 1.2 million plants per acre. Fall applications of nitrogen have not provided significant yield gains, as early season demand is typically met with available nitrogen. Total nitrogen applications between 90 and 120 lb per acre typically optimize returns. Proactive applications of foliar fungicides targeting leaf diseases rarely provide a return. Applications of foliar fungicides targeting *Fusarium* Head Blight occasionally provide a return. Seed treatments of an inexpensive insecticide and a foliar application of an insecticide targeting prevention of spread of Barley Yellow Dwarf Virus by aphids almost always provide a positive return on investment. Finally, results suggest growth regulators should target areas which lodge if a return on investment will be realized. By optimizing the selection of inputs, risk associated with producing wheat in the humid Midsouth region of the United States will be minimized.

P24 - Evaluating planting strategies and varietal canopy architecture for maximizing winter wheat yield

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Abstract

Improving winter wheat (*Triticum aestivum* L.) planting strategies for better crop establishment and optimal canopy architecture are crucial for achieving greater yields. Grain drills are typically used to plant wheat, which can result in uneven plant stand and canopy development, leading to lower yields. To address these issues, we conducted field trials in Hickory Corners and Lansing, MI during the 2024-2025 seasons to evaluate the performance of a custom-built precision planter (with row spacings of 13, 25, and 38 cm) against a conventional seed drill (with 19 and 38 cm row spacing). Two planophile and two erectophile varieties were tested under these five row spacing systems. Additionally, a second field trial was conducted using an erectophile variety to compare optimal seeding rate using a precision planter (13 cm rows) and a conventional drill (19 cm rows), with four seeding rates ranging from 0.98 to 3.95 million seeds ha⁻¹. Our results showed an increasing trend in wheat yield with narrower row spacings ($p < 0.05$), with greatest yield observed in 13 cm spacing (8,178 kg ha⁻¹). Planophile varieties achieved 80% canopy coverage in 13, 19, and 25 cm row spacing, while 38 cm rows never reached closure. Planophile canopies showed wider tiller angle (23.6°) compared to erectophiles (17.8°) and had greater light interception at multiple heights within the crop canopy. Precision planter reduced variability in seed depth ($p=0.02$) compared to the drill. Furthermore, plant population to achieve maximum yield was lower for precision planter (2.54 million plants ha⁻¹) compared to the conventional drill (> 4 million plants ha⁻¹). Overall, our results demonstrated that wheat yield can be enhanced by improving seed placement accuracy, reducing row spacing, and optimizing seeding rate for varieties with differing canopy architecture.

P25 - Restorative biostimulants as a strategic tool for drought resilience and resource efficiency in durum wheat systems

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Abstract

As climate change intensifies drought frequency across the Mediterranean basin, the sustainability of durum wheat production, a cornerstone of regional agriculture, is increasingly threatened. Developing adaptive management strategies that maintain yield stability under water scarcity is a global priority for broad cropping systems. This study investigates a paradigm shift in crop management, moving from traditional stress prevention toward an active metabolic recovery approach. We evaluated the efficacy of a novel biostimulant containing glycine betaine, vaterite, and *Pseudomonas protegens*, with a specific focus on optimizing application timing to maximize resource use efficiency. To identify the most effective intervention window, the treatment was applied either as a preventive measure before stress onset or as a restorative measure following drought exposure in drought-sensitive durum wheat seedlings. While drought severely inhibited growth, triggered oxidative damage through MDA accumulation, and disrupted nutrient ionomics, our results demonstrate that the biostimulant's impact is highly time-dependent. While pre-stress application showed only tissue-specific effects, the post-stress restorative strategy emerged as the superior approach for enabling sustainable production. This intervention successfully rescued the plants by restoring shoot biomass to control levels, effectively reversing the growth-stunting effects of the drought period. This recovery was driven by a sophisticated coordination of physiological and molecular mechanisms. The biostimulant enhanced root architecture and maintained ionic homeostasis, ensuring the plant's continued ability to access soil resources. At the molecular level, a significant downregulation of stress-responsive genes, including TdDHN15.3, TdDRF1 and TdSHN1, indicated a profound alleviation of stress perception and a rapid return to vegetative growth. These findings shift the agronomic paradigm from simple stress avoidance to active recovery, offering a timing-optimized strategy to bolster the resilience of cereal production. By focusing on restorative application, this approach provides a scalable, precision-agriculture solution for safeguarding wheat productivity and food security in increasingly arid environments.

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P26 - Primer crops to improve wheat productivity in high soil strength sandy soils

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Abstract

High soil strength (HSS) is a widespread constraint in Australian sandy soils, restricting root growth and limiting crop access to subsoil water and nutrients. Although deep tillage can reduce HSS and increase yields, initial benefits are often inconsistent across soil types and landholders observe soil reconsolidation between 1 to 5 years post ripping, depending on location. High soil strength at depth in the soil profile limits the crops access to subsoil water that is critical for crop production in low and variable rainfall environments.

To determine whether different primer crops could modify soil conditions and improve subsequent wheat productivity, three field experiments were established across contrasting sandy soil environments: (1) Western Australia - a deep sand classified as an Arenosol; (2) South Australia - a shallow sand over deeper calcareous sand classified as a Tenosol; and (3) Victoria - a sand over dense clay subsoil classified as a Sodosol. In the first year, treatments followed a factorial design combining deep ripping (40-60 cm) or no ripping with four regionally relevant crop species representing contrasting root systems (e.g., lupin or faba bean, canola, tillage radish, wheat). In the second year, all plots were sown to wheat in WA and SA to quantify legacy effects of ripping and primer crop choice. Measurements included soil strength profiles, rooting depth, soil water extraction and wheat grain yield.

Across the sites, results showed that wheat consistently benefited from being sown after break crops, with the strongest effects occurring after tillage radish or legumes. In contrast, the benefits of deep ripping varied strongly with seasonal conditions and soil type.

P27 - Impact of fungicide strategies on yellow rust (*Puccinia striiformis*) and yield in winter wheat cultivars in Belgium

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Abstract

The control of yellow rust (*Puccinia striiformis*) remains a key challenge in winter wheat production, requiring optimized fungicide strategies adapted to varietal susceptibility. This study evaluated the effect of different fungicide programs on yellow rust incidence and grain yield in two winter wheat cultivars under Belgian conditions.

A field experiment was conducted at the UGent-HOGENT experimental farm (Bottelare, Belgium) on a homogeneous sandy loam soil. Two cultivars were included: 'Johnson' (resistant) and 'Campesino' (susceptible). Six fungicide schemes, including an untreated control, were applied at different timings between late April and the end of May 2022. The trial followed a randomized block design.

Yellow rust severity was assessed at multiple time points, alongside yield and quality parameters. Drone-based imagery was used to derive vegetation indices and canopy characteristics. Statistical analyses were performed using ANOVA and Kruskal–Wallis tests.

A strong varietal effect was observed: 'Johnson' showed no symptoms, while 'Campesino' exhibited significant infection. Fungicide treatments significantly reduced disease severity in 'Campesino', with the most intensive program providing the best control. The untreated control consistently showed the highest infection levels. Late-season disease severity was strongly negatively correlated with yield. Vegetation indices also showed negative relationships with disease, although not always significant.

These results highlight the importance of combining resistant cultivars with targeted fungicide strategies, and demonstrate the added value of remote sensing for disease monitoring.

P28 - Optimizing disease management and economic performance of winter wheat through varietal choice, application timing and variety mixtures under Flemish conditions

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Abstract

Control of leaf and ear diseases in cereals in Flanders is crucial to achieve stable and profitable yields. Effective disease management requires insight into seasonal disease pressure, varietal susceptibility, and weather conditions. Variety choice is a key preventive measure and strongly determines disease development and the need for fungicide applications. Since each treatment entails a cost, the final economic return depends on how much disease can be tolerated without compromising yield. Over several years, Inagro conducted research focusing on variety choice, use of variety mixtures, number of fungicide applications, and optimal timing. The objective was to obtain practical, directly applicable results for farmers.

In one series of trials, two winter wheat varieties with contrasting disease tolerance were sown and treated with fungicide schemes ranging from extensive to intensive. Application timing varied between flag leaf-1 and flag leaf stages. In addition, an On-Farm Experiment (OFE) was conducted in which four varieties were grown both as pure stands and as an equal mixture.

Results showed that the disease-susceptible variety responded more strongly to fungicide treatments, with yield increases up to 19% compared to untreated plots. The tolerant variety showed a more limited response, with a maximum yield increase of 8%. In seasons with moderate disease pressure, a single well-timed fungicide application in combination with a tolerant variety resulted in the highest economic return. The OFE with winter wheat mixtures, consisting of four genetically diverse but similarly maturing varieties, showed comparable crop development and slightly lower yields than the varietal average. However, disease pressure was reduced. The main benefits of mixtures were risk spreading and improved yield stability, particularly in years with high disease pressure.

Future disease management of disease in winter wheat will rely more on combination of methods. As suggested in this abstract variety choice, intensity + timing of applications and variety mixtures can offer tailor-made solutions for farmers.

P29 - A high tillering QTn.mst-6B allele can increase productive tillers and yield under high-biomass spring wheat cultivars grown in rainfed environments

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Abstract

A greater gain in bread wheat production will sustain global economics and food security. The goal of the project is to deploy useful alleles to increase yield potential and stability from US public wheat breeding programs into CIMMYT's elite spring wheat high-biomass germplasms. Two CIMMYT cultivars were selected primarily based on their high grain yield and high biomass traits, which also demonstrated resistance or tolerance to biotic and abiotic stresses in various environments. The two cultivars were "Baj #1" and "Kingbird #1." These cultivars carry a high spikelet number per spike (SNS) allele for a major gene, WAPO-A1. A high-yielding Montana spring wheat cultivar, "Vida," was used as the donor parent for a high-tillering QTn.mst-6B allele in the CIMMYT lines through backcrossing. Near-isogenic Lines (NILs) with different allele combinations of WAPO-A1 and QTn.mst-6B were developed and used to test additive effects on yield component traits. The high-tillering QTn.mst-6B allele was also backcrossed into two Montana-adapted spring wheat cultivars, "DuClair" and "McNeal." The Baj#1/Vida and Kingbird/Vida NILs were evaluated from 2021 to 2024 in Sonora, Mexico (early winter-sown; latitude: 27° 20' N; irrigated conditions) and Montana, USA (spring-sown; latitude: 45° 47' N; rainfed conditions). All other entries were only evaluated in Montana. Across environments in Sonora, productive tiller number, biomass, and grain yield did not show significant differences between the NILs carrying the low and high tillering alleles in both Baj#1/Vida and Kingbird/Vida backgrounds. The spikelet number per spike increased in the NILs that contain the high SNS WAPO-A1 allele. In Montana, similar results for the WAPO-A1 and QTn.mst-6B allele effects on traits were observed in Kingbird/Vida NILs. However, the Baj#1/Vida NILs carrying the high-tillering QTn.mst-6B allele showed increased productive tiller number and improved grain yield under rainfed environments.

P30 - Productivity and identification of high-yielding genotypes of perennial grain crops in rainfed farming conditions of South-Eastern Kazakhstan

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Abstract

In 2023-2024, field experiments were conducted in the foothills of southeastern Kazakhstan under rainfed conditions to assess grain yield and identify high-yielding genotypes of perennial wheat (TLI series) and intermediate wheatgrass (*Thinopyrum intermedium*). Particular attention was paid to quantitative yield indicators and the selection of the best genotypes demonstrating stable or significantly increasing productivity.

Weather conditions in 2024 were more favorable than in 2023, resulting in a significant increase in grain yield for most of the studied genotypes. Among perennial wheat varieties, the TLI-21F3-805 genotype demonstrated the highest yield potential and the strongest positive response to improved moisture management, with grain yield increasing from 23 g/m² in 2023 to 546 g/m² in 2024, representing the largest increase among all genotypes studied. The TLI-21F3-810 and TLI-21F3-816 genotypes also demonstrated stable yield growth: from 143 to 300 g/m². In contrast, the local check winter wheat variety Steklovidnaya 24 showed a decrease in yield from 494 to 411 g/m², indicating less adaptability to various hydrothermal conditions. Intermediate wheatgrass demonstrated a strong productivity boost in the second year. In the first year, grain yields ranged from 1 to 12 g/m², but in 2024, they increased significantly to 53-173 g/m². The highest yields were recorded for genotypes TLI-704 (up to 173 g/m²) and TLI-801 (up to 160 g/m²), which were identified as the most promising genotypes. These genotypes combined increased productive tillering (up to 1090 stems/m²) with improved grain formation. Overall, the results highlight a significant genotype-year interaction and confirm that TLI-21F3-805 among perennial wheat, as well as TLI-704 and TLI-801 among intermediate wheatgrass, are the most productive and environmentally resilient genotypes in the semi-arid conditions of southeastern Kazakhstan. These selected genotypes represent valuable breeding material for perennial grain crops with increased grain yield potential, which can be introduced into production.

P31 - The effects of strigolactone on the tiller formation in wheat

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Abstract

Strigolactones (SLs) are plant hormones that regulate diverse developmental processes and environmental responses. They are also known to be root-derived chemical signals that regulate symbiotic and parasitic interactions with arbuscular mycorrhizal fungi and root parasitic plants, respectively. Since the discovery of the hormonal function of SLs in 2008, there has been much progress in the SL research field. In particular, a number of breakthroughs have been achieved in our understanding of SL biosynthesis, transport and perception. Strigolactones are a structurally diverse class of plant hormones that control many aspects of shoot and root growth. Strigolactones are also exuded by plants into the rhizosphere, where they promote symbiotic interactions with arbuscular mycorrhizal fungi and germination of root parasitic plants in the Orobanchaceae family. Therefore, understanding how strigolactones are made, transported, and perceived may lead to agricultural innovations as well as a deeper knowledge of how plants function. In this study, GR24 was applied to the wheat leaves during 5-leaf and 7-leaf stage to investigate the effect of GR24 on the formation of the wheat tiller. We observed that the GR24 addition decreased the tiller number while the leaf number was not impacted. At the same time, the length of the born tillers was reduced after spraying the GR24. The formation percentage of the fertile tillers was found to increased due to the unfertile tillers was inhibited by the GR24. The GR24 induced the reduction of cis zeaxanthin either in leaf or in axillary buds of wheat in 7-leaf stage. The ratio of IAA/CZ and ABA/CZ in wheat leaf was increased compare with the control values. Taken together, the application of GR24 could significantly inhibit the occurrence of the axillary buds of wheat, which could be a effective methods to inhibit the occurrence of unfertile tillers and facilitate the fertile-tiller formation before overwinter stage.

P32 - Slow-release nitrogen fertilizer optimizes the vertical distribution of root systems and soil nutrients in the middle and later stage of wheat

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Abstract

Nitrogen (N) input is crucial for increasing soil nutrients and improving crop root architecture. Slow-release N fertilizer has been expected to regulate soil nutrient supply in the middle and later growth stage of wheat, but its effect on root architecture and soil nutrients and their interactions remains unclear. The self-made root canal-soil column system was used to investigate the effects of sulfur-coated urea (SCU), urea (U) and compound fertilizer (CF) on the vertical distribution of wheat root and soil nutrients. The vertical distributions of root length, length density and dry weight in 0–90 cm soil layer increased first and then decreased after booting. Compared with U and CF treatment, SCU treatment increased the total root length by 26.16% and 29.60%, and increased the total root dry weight by 24.24% and 38.05% at the maturity stage, respectively. The dry weight per unit length in 40–90 cm soil layer in SCU treatment was higher than that in U (+17.23%) and CF (+11.85%) treatment. SCU treatment significantly increased the alkali-hydrolyzed N content in 0–40 cm soil layer at the maturity stage, but showed no significant difference in 40–90 cm soil layer with U and CF treatment. SCU application was conducive to the synergism of soil alkali-hydrolyzed N content and root distribution, which not only increased N supply in topsoil and avoided N leaching into deep soil, but also increased the root growth, contributing greatly to delaying root senescence in the later growth stage and improving grain yield.

P33 - DiPredict - AI based optimization of selection under drought stress in wheat breeding

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Abstract

Wheat (*Triticum aestivum* L.) is one of the leading crops globally. Abrupt changes in the climate are causing concerns for its production. Drought stress is becoming increasingly prevalent - Saxony-Anhalt in Germany is particularly affected due to the rain shadow of the Harz mountains in the Central German dry region. Simultaneously, advances in technological, statistical and computational domains have opened avenues for sustainable crop improvement. With DiPredict, a research network has been established in Saxony-Anhalt that sets the course for future-oriented, digitalized plant breeding in times of climate change and its associated challenges. The research network includes Martin Luther University Halle-Wittenberg, Anhalt University of Applied Sciences, the Julius Kühn Institute, Institute for Resistance Research and Stress Tolerance, Quedlinburg and the breeding company RAGT 2n S.A.S. with its wheat breeding station in Silstedt. The focus of DiPredict is to promote digitalization in agriculture through AI-based optimization of selection under drought stress in wheat breeding. For this, a diversity panel of 50 relevant bread wheat genotypes has been selected that will be screened for agronomically interesting traits regarding their response to drought at multiple drought-prone locations across multiple years. Unmanned aerial vehicles (UAVs) with various types of sensors such as RGB, hyper-/multispectral, thermal, and LiDAR will be used to capture sensor data in high-throughput to predict the traits of interest for wheat research and breeding. A novel hyperspectral FTIR imager will also be used onboard of a survey aircraft to collect data from all field trials. In addition, the PlantArray system (Plant-DiTech) will be used for an automated functional phenotyping of the same genotypes under control and drought conditions to collect detailed data on transpiration dynamics and water use efficiency. By applying the same sensor techniques in the controlled PlantArray experiments and in field trials, we aim to identify proxies that allow improved phenotyping for water use efficiency related traits in the field. This way the knowledge gathered for the 50 reference genotypes will be extrapolated to thousands of plots in breeding nurseries to close the gap between research and breeding for the targeted use of UAVs to develop drought-tolerant cultivars.

P34 - Use of non-supervised clustering to classify wheat phenology

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Abstract

The achievement of Sustainable Development Goals 2 (Zero Hunger) and 8 (Decent Work and Economic Growth) has highlighted precision agriculture, specifically digital farming, as a key tool for increasing food production and optimizing resource use. To achieve these two objectives, the use of georeferenced yield maps to train final yield production models is especially popular in literature. The relevance of these prediction models can be understood from two perspectives: early prediction models for planning corrective site-specific management, and late prediction models for forecasting the total production of a crop. To implement these models, the most common approach is the use of machine learning and deep learning algorithms, along with meteorological data, reflectance data, and other physiological measurements of the crops. However, to train a robust model that is applicable to different locations, a large dataset is required, with data available from various growing seasons and geographical areas. In this sense, the homogenization of the datasets is essential, as understanding the plant cycle at each moment of modeling will enable better training of the model and its application to other datasets. Other studies have employed this homogenization method by collecting data at the field level, using the phenological stage or Growing Degree Days. With big datasets, those methods are not viable. In response to this, the use of the spectral signature of crops during their growing cycle could be employed to determine their phenology. In this manner, non-supervised clustering methods have been employed to categorize the spectral signature of winter wheat into distinct groups. Clustering can distinguish four different groups of spectral behavior, two of which are easily distinguishable and key for modeling: the vegetative active phenological stages (tillering and stem elongation) and the senescence of the wheat crop. In this sense, clustering has the potential to classify some of the phenological stages of the wheat crop, allowing for the homogenization of datasets necessary to train early and late-season prediction yield models.

P35 - Image-based classification of cereal breeding trial plots in Martonvasar

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Abstract

The application of modern remote sensing methods not only forms the foundation of precision agriculture, but also contributes to more sustainable production, improves the accuracy of yield estimation, and supports well grounded economic decision making.

Although the technology has great potential, its application faces several challenges. The use of sensors in agriculture is still limited due to their high cost, and image analysis and processing—together with the large datasets and complex environmental information—require sophisticated analytical approaches.

The ENVI software, as one of the most widely used image processing and analysis tools, is a key instrument for processing satellite and drone imagery, especially when the goal is to examine crop conditions, developmental differences, or the differentiation of species and varieties.

Our aim was to determine whether species (wheat, barley, triticale, and durum wheat) and varieties could be distinguished from one another using ENVI classification methods at the ZD49 growth stage, when the crop stand is still free from biotic and abiotic stress and has not yet reached heading or flowering. We also examined what the classification results would show one month later, at a stage when some plots were already affected by disease (ZD69-71).

The barley variety 'MV Initium' and the winter wheat variety 'MV Toborzo' could be identified using ROIs; these genotypes have significantly earlier heading and maturity times, and achieved error matrix values above 90% in the MLC classification at the ZD69-71 stage. Their distinguishability is therefore linked to their developmental stage. The nearly completely yellow leaf canopy of the winter wheat variety 'MV Taller' resulted from yellow rust infection, and the program identified other plots affected by similar abiotic or biotic stress as belonging to this variety. This phenotypic appearance confirms that field validation is an indispensable part of phenotyping, as it allows us to determine whether the reduction in leaf chlorophyll content was caused by biotic rather than abiotic stress (such as soil patches).

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P36 - Combining genomics, phenomics and phenotyping analysis to better characterize durum and bread wheat varieties under multi-environmental trials

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Abstract

Enhancing cereal productivity can be effectively supported by integrating advanced genomics with high-throughput phenotyping (HTP), particularly when applied to well-structured germplasm collections. In this framework, UNIBO and its partners contributed to two EU-funded projects, INNOVAR-H2020 and WheatSecurity, aimed at characterizing large durum and bread wheat panels using genomics and UAV-based phenotyping. The overarching objective was to strengthen DUS (Distinctness, Uniformity and Stability) and VCU (Value for Cultivation and Use) procedures while assessing variety performance under contrasting nitrogen and biostimulant applications. Two panels of 250 European durum and bread wheat varieties were evaluated across 13 environments over three growing seasons. Subsets of 16 durum and 12 bread wheat genotypes were further tested under different nitrogen management and biostimulant treatments. Both panels were genotyped using the Illumina iSelect 90K SNP array and monitored through UAV-based HTP across nine key developmental stages. UAV imaging enabled the extraction of more than 20 vegetation indices related to biomass accumulation, photosynthetic efficiency, senescence, disease symptoms, and yield potential. These indices were also used to estimate dynamic traits such as ground coverage, biomass growth, nitrogen uptake, chlorophyll content, and senescence rates. Several UAV-derived traits showed strong correlations with heading and maturity dates, frequently outperforming traditional visual scoring. On the molecular side, haplotype-based analyses improved genetic characterization and enabled haplotype-level GWAS. Integrating ground-based traits with UAV-derived indices identified numerous genetic determinants (QTLs) associated with conventional and innovative phenotypes, including biomass development, yield, NDVI, and senescence-related indicators. Differences in the ability to detect QTLs and $G \times E \times M$ interactions between tetraploid durum and hexaploid bread wheat were also explored. Overall, combining UAV-based phenotyping with genomic analyses provides a robust framework to support and enhance varietal evaluation, increasing the objectivity, accuracy and scalability of DUS and VCU assessments.

Acknowledgements. Research was supported by H2020 FP7 "INNOVAR - Next generation variety testing for improved cropping on European farmland" and "WheatSecurity - Identification and sustainable deployment of wheat genetic diversity to enhance the resilience and security of the SusCrop- ERA-NET European food supply."

P37 - NIRS-based models in wheat breeding: potential and challenges!

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Abstract

Near-infrared spectroscopy (NIRS) provide rapid and non-destructive measurements that capture information related to grain composition and quality traits. In wheat breeding programs, these spectral data offer opportunities to explore relationships between grain composition traits, such as protein content, and complex agronomic traits including grain yield.

In this study, we evaluated the potential of NIRS-based phenomic data to support grain yield prediction in winter wheat using both single-trait and multi-trait prediction approaches. A multi-year dataset including phenotypic records, protein content measurements, and NIRS spectra was analyzed using several statistical and machine learning models. Spectral data were preprocessed using different treatments and used to construct hyperspectral similarity matrices for phenomic prediction.

Prediction performance was assessed using cross-validation and forward prediction scenarios reflecting practical breeding conditions. In addition, multi-trait models incorporating protein content were evaluated to investigate whether exploiting trait correlations could improve prediction of grain yield.

P38 - Development of a decision support system for precision agriculture in soria: from uncertainty to variable rate-nitrogen prescription maps in wheat fields.

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Abstract

Advanced agronomic systems are facing a critical challenge: ensuring global food security for a growing population while reducing the environmental impact of intensive production. In this context, sustainability has become both an agronomic and economic necessity, driven by rising energy costs and volatility in the fertilizer market. Wheat (*Triticum aestivum*) is a vital crop for food sovereignty in Europe, particularly in Spain. However, its production is subject to significant regulatory pressures. Initiatives such as the European Green Deal and the Farm to Fork strategy have set ambitious targets for reducing nutrient pollution, compelling producers—especially those in Nitrate Vulnerable Zones—to significantly optimize the use of agrochemicals. Nitrogen is the most critical limiting factor for crop yield and flour quality. However, its management is complex. Inefficient application not only leads to economic losses for farmers but also causes environmental harm, such as the leaching of nitrates into aquifers and the emission of nitrous oxide (N₂O), an important greenhouse gas. Despite these risks, conventional management practices often use uniform applications, overlooking the natural variability within fields. Precision agriculture has emerged as a technological solution to address this variability. Research shows that substituting uniform management with variable rate applications can optimize input use while maintaining yield and significantly reduce environmental impact by lowering residual nitrates in the soil.

Despite the availability of precision agriculture machinery, its practical implementation is hindered by agronomic challenges, such as the difficulty of interpreting data and the lack of compatibility between different systems. Farmers view these challenges as significant barriers to adoption. Therefore, there is an urgent need for tools that can translate the vast amounts of available information into actionable agronomic decisions. A Decision Support System based on ad hoc software developed is proposed as a solution that integrates complex data to generate accurate recommendations while simplifying the handling of uncertainty. This system aims to provide clear guidance to facilitate the successful adoption of Precision Agriculture.

P39 - Characterizing wheat gxe interactions via factor analytic models and climate covariates for cross performance prediction in unobserved environments.

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Abstract

The digital transformation of plant breeding relies on the effective integration of historical phenotypic data with high-dimensional environmental and genomic information. A significant challenge in contemporary genomic selection is modelling complex genotype-by-environment (GxE) interactions within unbalanced, large-scale breeding pipelines. This study implements a factor analytic (FA) linear mixed model framework to leverage ten years (2016 - 2025) of historical yield data from a national Australian bread wheat (*Triticum aestivum* L.) breeding program. A multi-environment trial (MET) analysis was conducted on the national network of early-generation field trials with integrated high-density parental genomic data and progeny pedigree matrices. To define the environmental drivers of GxE, we combined latent factors derived from the FA model with explicit meteorological covariates. This multi-layered approach establishes genetic and environmental connectivity across disparate regions, years, and stages of breeding cycle, refining additive genetic effect estimations and improving predictive accuracy for cross performance in unobserved environments. The aim of this research was to predict yield of crossing populations to identify specific parents or ancestral lineages that are primary drivers of GxE sensitivity within in each regional breeding program/mega-environment.

The model framework specifically overcomes the data fragmentation and selection bias inherent in large-scale commercial breeding programs. It handles partial replication, where not every genotype is grown in every environment, by leveraging the factor analytic framework to borrow information across the trial network. Simultaneously, the model accounts for the Bulmer effect by allowing for heterogeneous genetic variances across selection stages. This transition from a constant variance assumption ensures that the iterative depletion of genetic diversity is quantified, leading to more accurate breeding value estimations. Preliminary results demonstrate the model's utility in identifying ancestral lineages that drive GxE sensitivity. Our findings suggest a complex relationship between intra-population genetic variance and environmental plasticity, where specific ancestral lineages, parents and genomic regions predictably govern the trade-off between yield stability and environmental plasticity in their progeny. These results provide a scalable statistical framework for utilizing legacy breeding data in predictive crop modelling to optimize future selection strategies and characterize the environmental sensitivity of elite wheat germplasm.

P40 - Temporal qtl mapping of canopy height using UAV-based phenotyping in bread wheat

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Abstract

Plant height is a key adaptive trait in bread wheat (*Triticum aestivum* L.), integrating genetically regulated developmental processes with environmental responsiveness. However, most genetic studies rely on static, end-of-season measurements, which limit the resolution needed to detect stage-specific gene effects. Here, we combined multi-season RGB-UAV phenotyping with dynamic GWAS and QTL mapping to dissect the temporal genetic architecture of canopy height in bread wheat under Mediterranean field conditions. Field trials were conducted over three growing seasons in southern Italy using an elite diversity panel and a recombinant inbred line (RIL) population. Digital canopy height (DCH), derived from UAV imagery, showed strong agreement with ground measurements ($R^2 = 0.89-0.98$), validating the robustness of the high-throughput phenotyping platform. Temporal GWAS and QTL mapping identified hundreds of significant genomic regions and revealed a clear developmental sequence of genetic effects. A notable finding was the identification of a “genetically silent window” during the tillering stage (BBCH 20-29), when vertical elongation temporarily paused to facilitate axillary development, rendering height-associated markers transiently undetectable. Following this plateau, a sequential activation of major adaptive genes was observed: *Vrn-A1* and *Ppd-A1* regulated early vegetative-to-reproductive transitions, followed by the dominant influence of the dwarfing genes *Rht-B1* and *Rht-D1* during rapid stem elongation. Growth-rate metrics modeled using P-splines exhibited greater temporal sensitivity than absolute canopy height, capturing genetic signals earlier in development. Candidate gene prioritization identified a core regulatory backbone of 24 genes, including NAC and WRKY transcription factors associated with meristem stability and nutrient remobilization.

Together, these results establish DCH as a dynamic trait encoding the timing of key developmental transitions. This work provides a quantitative framework for integrating temporal canopy architecture into genomic breeding strategies aimed at enhancing yield stability under climate variability. Ongoing analyses using artificial intelligence are further refining the temporal resolution of phenological modeling, with promising preliminary results for genomic prediction of late-season phenology based on early-stage UAV and environmental data. Preliminary genomic prediction results for late durum wheat phenology, using early-stage information derived from NIR spectra data and environmental covariates, indicate relatively high predictive accuracy.

P41 - Explainable AI uncovers genomic regions associated with wheat yield prediction within a multimodal deep learning model

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Abstract

Explainable AI uncovers genomic regions associated with wheat yield prediction within a multimodal deep learning model

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Food security is a critical challenge with the projected increase in the world's population. As a staple crop for over one third of the population, efforts to support wheat (*Triticum aestivum* L.) breeding are vital to sustain this rapid growth. With the rise of artificial intelligence (AI), the use of machine learning models to predict wheat yield based on singular forms of data have been common, however few studies implement both genotypic data from single nucleotide polymorphisms (SNPs) and phenotypic image data captured by unmanned aerial vehicles. Furthermore, the use of explainable AI software in detailing the decision-making behind yield predictions in these models has potential to be explored considerably further. In this study, a multimodal neural network is proposed that incorporates both SNPs and multispectral image bands as inputs, and is then analysed with the explainable AI software Shapely Additive Predictions (SHAP). Compared to the baseline statistical model, the SNP- only network and image-only network, the multimodal network is the best performing model with an R2 value of 0.84, improving upon the unimodal models by 10%, 49% and 21% respectively. Across models, SHAP analyses revealed both individual SNPs and chromosomes of interest, with defined regions within chromosomes 7A & 7D showing strong influence in yield predictions. SHAP also highlighted regions of interest in the image models, indicating that areas such as canopy boundaries have a strong impact on wheat yield prediction.

P42 - Managing for upside in a variable climate: envirotyping wheat yield frontiers

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Abstract

Profitability in broadacre wheat cropping systems in Australia's low to medium rainfall zones depends on the ability to capture water-limited yield potential (WLYP), particularly the upside available in favourable seasons. In wheat, yield potential is largely determined during the critical period from late stem elongation to flowering, yet the crop conditions governing this window are shaped much earlier through emergence timing, canopy development, water supply, nitrogen availability, and stress exposure. This creates a central challenge for agronomy: yield-defining decisions must be made before seasonal outcomes are known. Here, we integrate envirotyping, crop modelling, and field experimentation to define profitable yield frontiers and identify adaptive agronomic principles that improve upside capture while limiting downside risk. Using process-based simulations across representative low- to medium-rainfall wheat environments, we characterised the timing, frequency, and intensity of water, heat, and frost stress relative to crop phenology. These stress patterns were linked to multi-site experiments evaluating sowing time, early crop establishment, nitrogen supply, and canopy development under contrasting starting plant-available water (PAW) and seasonal trajectories. Results show that alignment of crop growth with favourable critical-period conditions dominates yield outcomes. High starting PAW increases the value of early establishment and expands upside potential, whereas low PAW constrains system responsiveness and shifts yield control to in-season rainfall. Once sowing opportunity is missed, the scope to recover yield potential later in the season is limited. Adaptive agronomy was most effective when used to support robust early system set-up rather than to compensate for lost potential. Envirotyping provides a powerful framework to guide these adaptive decisions and benchmark profitable yield frontiers under increasing climate variability.

P43 - Scaling law links plant growth variation to grain yield in wheat stands

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Abstract

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 195 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 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.

P44 - Genomic prediction in wheat: using random regression models for stability with genotype-specific phenology derived environmental covariates

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Abstract

Wheat (*Triticum aestivum* L.) is a critical cereal crop for global food security, yet its productivity is increasingly threatened by climate change. Sustaining and improving wheat yields under future climate scenarios will require cultivars with enhanced resilience to environmental extremes and variability. This study evaluated two genomic prediction strategies aimed at increasing climate resilience through improved prediction of yield stability and genotype performance across environments.

First, we assessed a random regression-based genomic prediction approach for yield stability, examining the impact of the number of environments, environmental variance, and data balance using three multi-environment trial datasets from wheat, barley, and oats. Second, we tested a genomic prediction strategy incorporating enviromics data within a random regression framework using environmental covariates. These models were compared with GBLUP and GBLUP models incorporating genotype-by-environment interaction through factor-analytic variance-covariance structures, using phenomic, genomic, and enviromic data from 1,683 genotypes evaluated across 71 environments and characterized by 45 phenology-derived environmental covariates.

Training sets including at least 15 environments were required to achieve high predictive ability for yield stability; however, strategic selection of environments had a greater influence on prediction accuracy than simply increasing their number. This demonstrates the potential of random regression models to identify stable genotypes earlier in breeding pipelines and to guide more resource-efficient stability testing schemes. Additionally, random regression models using environmental covariates outperformed GBLUP by 52-124% in predictive accuracy and performed within 15% of factor-analytic models. At least one random regression model achieved higher predictive ability in more than 90% of environments when predicting new, un-phenotyped conditions—a scenario in which factor-analytic models cannot be used.

These results highlight the value of enviromics-informed random regression models for predicting genotype performance in new or untested environments with high accuracy, making them promising tools to support the development of climate-resilient wheat cultivars.

P45 - Applications of drone-based high-throughput phenotyping in wheat variety evaluation

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Abstract

Crop variety selection strongly influences yield, quality, input requirements, and environmental impact, making variety testing essential for wheat production. Recent advances in crop sensing technologies offer new opportunities to improve the efficiency, objectivity, and precision of variety evaluation. Unmanned aerial vehicles (UAVs) enable rapid, high-resolution assessment of large field trials across space and time. We evaluated protocols for the acquisition and analysis of RGB, multispectral, and thermal UAV imagery, complemented by RGB time-lapse imaging and ground-based sensors, to enhance the accuracy and throughput of trait assessment. The study was conducted over three growing seasons (2021-2023) in Swiss winter wheat variety trials, including more than 30 registered European varieties and candidate lines for the Swiss recommended list.

Traits assessed included early vigor, leaf area index, canopy temperature, biomass, chlorophyll and nitrogen content in the biomass, plant height, senescence, maturity, and grain yield. Plant height, soil cover as a proxy for early vigor, and canopy temperature were estimated accurately and consistently, whereas leaf area and biomass remained more challenging. For canopy temperature, a mixed-model approach incorporating temporal and geometric covariates substantially improved measurement consistency and genotype specificity compared with conventional orthomosaic-based methods.

Overall, this study establishes robust UAV-based protocols for high-throughput field phenotyping of key agronomic traits, with direct applicability to variety testing, breeding programs, and field crop research.

P46 - Relationships between UAV-derived vegetation indices, grain yield and plant height in wheat genotypes across growth stages and seasons

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Abstract

Remote sensing and vegetation indices derived from unmanned aerial vehicles (UAVs) provide a powerful tool for assessing crop performance under field conditions. The objective of this study was to evaluate the relationships between multispectral vegetation indices and grain yield and plant height of wheat across different growth stages and growing seasons. The field experiment was conducted as a randomized complete block design with 20 wheat genotypes in two replications during the 2022/2023 and 2023/2024 growing seasons. Standard agronomic practices were applied, and plot size was 5 m². UAV-based multispectral imaging was performed using the DJI Phantom 4 Multispectral platform. UAV data were collected from March to June 2023 (six surveys) and from March to June 2024 (five surveys), covering key growth stages of winter wheat: tillering, stem elongation, heading, flowering, grain filling and full maturity. Vegetation indices NDVI, GNDVI and NDRE were calculated from multispectral imagery. Orthomosaics and index maps were generated using Pix4D Fields software. Correlation analyses between vegetation indices and grain yield and plant height were conducted using Minitab. The results revealed pronounced seasonal differences in the strength and timing of relationships between vegetation indices and agronomic traits. In the 2022/2023 season, grain yield showed a significant correlation only with GNDVI (0.489*) at the late grain filling stage, while plant height exhibited significant and highly significant correlations with NDVI (0.588**), NDRE (0.574**) and GNDVI (0.639**) predominantly during the tillering stage. In contrast, during the 2023/2024 season, grain yield demonstrated significant and highly significant correlations with vegetation indices. Highly significant correlations were observed at the stem elongation stage with NDVI (0.593**), NDRE (0.657**) and GNDVI (0.703**), at the heading stage with NDVI (0.580**) and NDRE (0.594**) and with NDRE (0.601**) at the late grain filling stage. NDVI and NDRE remained significantly correlated with yield during later growth stages. No significant correlations were detected between vegetation indices and plant height in the 2023/2024 season. These findings confirm that the predictive potential of vegetation indices for wheat yield and plant height is strongly influenced by environmental conditions and phenological timing, highlighting the importance of multi-year UAV-based assessments in wheat breeding programs.

P47 - Precision phenotyping of transpiration profiles and vegetation indices reveals importance of early response to drought in winter wheat

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Abstract

Drought, as one of the most prevalent abiotic stresses, imposes significant yield losses on wheat production. Identifying drought-tolerant and water-saving genotypes is therefore important for wheat breeding programs. Water use efficiency (WUE) is a key physiological trait for maintaining biomass production under drought conditions. In this study, a non-destructive and gravimetric phenotyping system (PlantArray) was used to evaluate diurnal transpiration profiles as well as WUE and physiological behaviour of 19 winter wheat genotypes under well-watered and drought stress conditions. Drought stress, defined as 35% soil water capacity, was applied at third leaf stage (BBCH13) for four weeks. Afterwards, plants were exposed to a recovery phase for ten days by restoring the soil water capacity to 70%. Throughout the entire growing period, the facility recorded pot weight at three-minute intervals enabling precise quantification of transpiration traits. Additionally, vegetation indices (VIs) were measured using ScanCorder (Compolytics). Finally, aboveground biomass was harvested at the end of the experiment to determine dry weight and calculate WUE. Drought stress significantly ($p < 0.001$) increased WUE of the genotypes, primarily due to reduced daily transpiration rates of up to 60%. This reduction was correlated with stomata conductance ($r = -0.24$, $p < 0.05$) and decreased canopy stomatal conductance. The water-saving genotypes exhibited early sensing of drought stress by regulating canopy stomatal conductance, whereas the water-spending genotype showed limited stomatal regulation under stress. Genotypes showed variation in their response to drought and the subsequent recovery phase. The water-saving genotypes sensed drought early but recovered slowly, whereas the water-spending genotypes responded late but recovered quickly. Early drought sensing appeared to exert a greater impact on biomass accumulation than rapid recovery, highlighting the importance of timely physiological response under drought. More than 140 VIs were assessed during the drought phase, and several of them including NDRE and MSRNir showed significant correlations with WUE i.e. $r = 0.35$ ($p < 0.01$) and $r = 0.34$ ($p < 0.05$), respectively. These results indicate that selected VIs could be used to develop predictive models for WUE estimation in future applications.

P48 - Phenome-Emphasis - the French plant phenomic infrastructure

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Abstract

Since 2012, Phenome-Emphasis has developed high-performance infrastructure that enables the characterisation of hundreds of plant varieties and thousands of plants under various climatic and agroecological scenarios, including drought, elevated atmospheric CO₂, high temperatures, low input levels and crop mixtures. This infrastructure comprises four controlled-environment facilities for in-depth analysis of leaf and root development; two semi-controlled field facilities, one of which is equipped with a free-air CO₂ enrichment system and both of which have rainout shelters; and three large open-field facilities. All of these facilities are equipped with climate sensors and imaging tools, such as the Phenomobile, drones, hand-held sticks and IoT devices, for the architectural and functional analyses of individual plants or plots. Two additional complementary facilities focus on metabolomic and structural measurements associated with experiments on phenotyping platforms. The infrastructure develops tools and methods to support trait extraction from images and organise data for multiple applications, with the aid of artificial intelligence and modelling. These innovations can be co-developed with technology SMEs and are accompanied by training programmes aimed at a wide audience. Phenome-Emphasis coordinates several projects, including the European Infra-Tech project PHENET, and is the French node of the European EMPHASIS infrastructure. Phenome-Emphasis installations and services are accessible to public and private partners alike through a transparent access mode. Between 2020 and 2025, Phenome-Emphasis annually provided access over 110 times, published more than 20 papers, and provided training to over 220 people.

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P49 - UAV image-based high-throughput phenotyping for wheat breeding: from single rows to yield plots

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Abstract

Wheat breeding programs require accurate phenotyping across plot sizes, from single rows to multi-row yield plots, and UAV multispectral imaging offers a promising high-throughput approach. However, on densely planted single-row plots, canopy closure, intertwined neighboring plots, and limited ground visibility make both plot segmentation and digital terrain model (DTM) estimation considerably harder than on yield plots. The objective of this work was to develop a UAV-based phenotyping approach for single-row wheat plots and to assess relationships between small plot and yield plot phenotypes. Field trials were conducted at the University of Saskatchewan Crop Development Centre over two years (2024-2025) at two locations, evaluating 20 wheat genotypes in single-row plots (32 replicates per genotype; 1,280 total plots, 0.40 m by 0.24 m) with nearby yield trials (3 replicates per genotype, 1 m by 5 m), with destructive sampling at four growth stages (Zadoks 39, 59, 87, and post-maturity) providing ground-truth for eight traits: height, plant count, above-ground biomass, spikes per plant, seeds per spike, seeds per plot, grain yield, and harvest index (HI). Across two years, HI values from single rows and yield plots were strongly correlated at the genotypic level ($r = 0.87-0.93$), confirming that small plots capture genotypic rankings despite greater spatial variability; other small plot and yield plot phenotype relationships were also assessed. A Python-based package was developed that extracts 14,179 engineered features from multispectral imagery and structure-from-motion point clouds, integrating spectral indices, point cloud features, and novel interaction terms. On single rows, height prediction achieved $R^2 = 0.84$, while above-ground biomass prediction achieved $R^2 = 0.753$ (RMSE ≈ 24 g), validated across 20 random data splits; interaction features combining geometric properties with spectral indices showed the strongest correlations with biomass. This work demonstrates that UAV-based phenotyping can be extended to plot scales smaller than previously attempted, predicting traits that are themselves predictive of yield plot performance.

P50 - High-throughput stomatal phenotyping provides novel selection targets for stress-resilient wheat

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Abstract

Phenotyping stomatal traits and their developmental plasticity across environments is time-intensive but critical for improving water-use efficiency and photosynthesis in climate-resilient crops. Robust assessment requires large genotypic panels and systematic screening of both upper and lower leaf surfaces under constant conditions (growth chamber) and fluctuating conditions such as greenhouse and field environments. Here, we used a high-throughput handheld microscope (ProScope HR5; 400× magnification) to acquire 19,165 images from 60 wheat cultivars grown in growth chamber, greenhouse, and field conditions. Images were collected from the third, sixth, and flag leaves, and from both leaf surfaces. We developed an accurate pipeline using 521 training images considering the wide phenotypic diversity among cultivars and leaf surfaces, and was validated on 718 independent images. The pipeline enabled quantification of 14 stomatal traits related to size, deviation, maximum conductance, and spatial patterning. Specifically, we: (1) estimated trait heritability across environments, (2) assessed the effects of light, temperature, drought, and nitrogen on stomatal traits and their plasticity across leaf surfaces, and (3) evaluated genetic diversity and breeding progress. Notably, stomatal density, width, length, width-length ratio, size, stomatal cover area, divergence, and maximum conductance showed high heritability (0.75-0.94) across growth chamber and field conditions under contrasting light and temperature regimes. Stomatal traits of third leaves under controlled environments reliably predicted flag leaf traits in the field (lower surface: $r = 0.70$; upper surface: $r = 0.64$). Across environments, the upper leaf surface exhibited higher stomatal density (21-36%), cover area (10-17%), and maximum conductance (19-37%), indicating greater contribution to transpiration and cooling. In contrast, the lower surface showed more consistent spatial patterning (23-39%), potentially facilitating efficient CO₂ diffusion. Notably, cultivars characterized by high stomatal density and small stomatal size showed significant differences in water-use efficiency between well-watered and drought treatments in the greenhouse. Moreover, breeding has increased the percentage of stomatal area on both leaf surfaces. Overall, integrating high-throughput stomatal phenotyping into breeding programs provides robust selection targets and paves the way for developing climate-resilient cultivars with optimized gas exchange and water-use efficiency.

P51 - From imagery to selection: advancing wheat breeding with UAV-based high-throughput phenotyping

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Abstract

Among the various activities involved in a breeding program, phenotyping is a core process, as it drives the selection of superior candidates. The use of uncrewed aerial vehicle (UAV) imaging enables the rapid collection of large amounts of phenotypic data, particularly with spectral information and digital surface models, supporting scalability in large breeding pipelines. A major challenge is to obtain accurate data that effectively assists indirect selection, trait prediction and decision-making. In this context, we evaluate the application of high-throughput phenotyping using uncrewed aerial vehicles in wheat breeding. The study was conducted in four experimental areas in the state of Rio Grande do Sul, Brazil, in 2025. The trials included early-, preliminary- and late-stage yield trials, evaluating plant height, above-ground biomass and early vigor. Additionally, plot quality was assessed by incorporating image-derived ground coverage as a fixed covariate in yield estimation models. Results demonstrated strong potential UAV-based phenotyping. For plant height, Pearson's correlation between UAV-derived and ground-measured data ranged from 0.36 to 0.82. For biomass, the relationship between UAV-derived plant height and ground-truth biomass showed correlations of 0.47 and 0.76 across two trials. Early vigor was predicted using a categorical model, achieving overall accuracies of 61 and 62%. Regarding plot quality, incorporating ground coverage as a fixed covariate reduced residual variance and altered genotype ranking in yield analyses, with the covariate being highly significant in the model ($p < 0.001$). These findings demonstrate the practical applicability of UAV-based high-throughput phenotyping in large-scale wheat breeding programs.

P52 - AI-based system to support sustainable agriculture and cereal supply chain

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Abstract

A meta-analysis of cereal (barley, bread and durum wheat) varieties cultivated in the Mediterranean area from 2013 to 2023 has been carried out to collect data of yield, quality and disease resistance, together with management and environmental conditions, to serve as agronomic knowledge basis of the CERERE (Cereals REsiliency REvolution for agile supply chain management in the Mediterranean) project (PRIMA Programme 2023 - Section 1 - Food Value-chain 2023 - Topic 1.3.1 (RIA). This information represents the ground truth for a resilient farming intelligence as it served as input to assess the accuracy and the performance of a prototype based on IoT-sensors for Smart Farming developed in the frame of the project, for monitoring crop health, soil conditions, weather and environmental conditions, water and nutrient management and other useful factors to forecast the expected crop yield. It has been already validated at the laboratory level. Data collection in real time is possible after sensors installation in a one-year trial at CREA in Foggia, that is in course with up to 10 durum and bread wheat varieties adapted to Mediterranean conditions. The comparison between data manually evaluated and those gathered from sensors could give an indication on their functioning.

Moreover, an AI-based recommendation system is being developed to support farmers and smallholders to make informed choices in view of response to potentially disruptive supply/distribution vulnerabilities of the cereal supply chain. In an initial case study, a CATBoost regressor model was trained using the historical agronomic knowledge base collected to provide evidence-based recommendations on varietal selection, by incorporating parameters such as geographic location, management practices, and environmental conditions. This specialized engine complements the generic reasoning capabilities of an LLM-based intelligent orchestrator, delivering tailored suggestions through a conversational interface. This setup enables farmers and smallholders to engage in a direct dialogue with the system, allowing them to seek clarifications or explore 'what-if' scenarios regarding this decision-making problem. This approach lays the foundation for a tailored, adaptive support system that evolves through user interaction, ensuring personalized guidance for the resilient management of the cereal supply chain.

P53 - Satellite-derived nitrogen nutrition index for precision fertilization in durum wheat: agronomic, economic and environmental performance

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Abstract

Improving nitrogen (N) management in wheat systems is essential to enhance nitrogen use efficiency while reducing environmental impacts and production costs. Precision fertilization based on remote sensing technologies provides new opportunities to match N supply with crop demand, but long-term assessments integrating agronomic, economic and environmental outcomes are still limited.

This study evaluated satellite-based variable-rate N fertilization strategies in durum wheat over four consecutive growing seasons (2018-2022) in a Mediterranean environment in central Italy. Four fertilization approaches were compared: a conventional uniform N rate (Flat), two NDVI-based variable-rate strategies (NDVIH and NDVIL), and a nitrogen nutrition index approach (NNI) derived from Sentinel-2 imagery.

Vegetation indices (NDVI, EVI2 and MCARI) were used to estimate crop biomass and nitrogen status and to generate prescription maps for site-specific fertilization. Agronomic performance, grain quality parameters, nitrogen fertilizer use efficiency (NfUE), economic returns and carbon footprint were assessed.

Across the four growing seasons, the NNI-based strategy reduced nitrogen fertilizer application by approximately 12% compared with the conventional uniform fertilization without negatively affecting grain yield. Average grain yields ranged between about 5.3 and 5.9 t ha⁻¹ across treatments, with no significant differences among fertilization strategies. Despite the reduced N input, the NNI approach consistently achieved the highest nitrogen fertilizer use efficiency, reaching values up to about 96% on average and exceeding 100% in one season, indicating improved utilization of soil nitrogen reserves. In addition, the NNI strategy improved economic performance by significantly lowering fertilization costs and increasing the rate of return compared with the other fertilization approaches. Social costs associated with nitrogen fertilization were substantially reduced under the NNI treatment, while the carbon footprint of grain production decreased by approximately 7.6% (about 20 g CO₂-eq kg⁻¹ grain) compared with the conventional uniform fertilization. NDVI-based strategies showed intermediate or inconsistent responses and generally did not outperform the NNI approach.

Overall, the results demonstrate that satellite-derived NNI represents an effective decision-support tool for precision nitrogen management in durum wheat. Integrating remote sensing with variable-rate fertilization can improve nitrogen use efficiency and economic returns while reducing the environmental footprint of wheat production systems.

P54 - Evaluation of photosynthetic traits across various hexaploid wheat genotypes

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Abstract

Wheat is one of the most economically and nutritionally significant crops since it is a staple food for millions of people globally. Recent researches indicate that increasing photosynthetic efficiency is crucial for enhancing production, abiotic stress tolerance, nutrient-use efficiency, and overall crop sustainability. As a result, modern wheat breeding and physiological improvement programs currently place a strong emphasis on photosynthetic traits. It is now widely accepted that improving these traits is a calculated way to boost output and adaptability to changing environmental conditions. As a result, increasing photosynthetic efficiency has emerged as a major goal in the advancement of wheat breeding and agricultural improvement in general. In this study, sixty hexaploid wheat genotypes were assessed at the ICAR-Indian Institute of Wheat and Barley Research, Karnal, India, during two consecutive crop seasons (2021-2022 and 2022-2023). A dibbler was used in the field studies to guarantee consistent plant establishment, and spacing. A wide range of physiological, morphological, anatomical, biochemical, and yield-related characteristics associated with photosynthetic efficiency were used to evaluate the genotypes. Physiological evaluations included gaseous exchange measures using IRGA, and other photosynthesis associated traits like PSII activity, NDVI, flavonoid content, Nitrogen Balance Index (NBI), and Chlorophyll Content Index. Anatomical characteristics includes stomatal length, stomatal breadth, stomatal density, and interveinal distance. Morphological characteristics comprised leaf area, specific leaf area (SLA), and specific leaf weight (SLW). Grain yield (GY) and related yield components were included in yield characteristics. To the best of our knowledge, this is the first exhaustive studies on photosynthesis in Indian wheat genotypes. The overall analysis indicates that, large variation exists for all study traits among genotypes and further, there is large scope for complementing different photosynthesis associated traits. Different trait specific and superior genotypes across measured traits were identified for trait complementation in Indian wheat breeding programmes. These standout genotypes serves as valuable resources for breeders seeking to develop high-yielding and resilient wheat varieties for sustainable wheat production and strengthening global food security.

P55 - Magnetic resonance imaging (MRI) for wheat grain phenotyping and beyond

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Abstract

Comprehensive seed screening is crucial for breeding and biotechnology. However, most screening tools only offer limited characterisation, focusing on either grain composition or morphometry (shape, length and width). We have now introduced a novel tool that combines nuclear magnetic resonance imaging (MRI) with deep learning algorithms, named MRI-Seed-Wizard. The main advantage of this tool is that it can examine inner organs and tissues, such as the endosperm, embryo or aleurone, thereby providing non-invasive access to features of inner grain architecture that would otherwise be hidden. In the case of wheat, for example, we can reliably detect over 20 traits, many of which are inaccessible using conventional techniques, including X-ray computed tomography. We also provide advanced MRI protocols that allow for the rapid, simultaneous assessment of hundreds of seeds, enabling high sample throughput. The MRI-Seed-Wizard tool can now routinely be used for wheat and barley, and is currently extended to be applicable to other crops.

Notably, MRI can be used not only for structural imaging of grains, but also to visualise the tissue-specific distribution of lipids, water and metabolites in living, developing or germinating seeds. For example, it can be used to visualise sucrose distribution and uptake into the grain. In conclusion, using the most versatile imaging modality, MRI, opens up new perspectives in wheat phenotyping and crop improvement.

P56 - Cross-sensor phenotyping reveals key traits for yield-based drought tolerance in wheat

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Abstract

Drought stress poses a major threat to wheat (*Triticum aestivum* L.) productivity, particularly in northern European agroecosystems where even moderate water deficits during critical growth stages can drastically reduce yield. To improve phenotyping for drought resilience, we evaluated six wheat genotypes with contrasting tolerance mechanisms using a multi-sensor framework that combined hyperspectral, multispectral, thermal, and fluorescence measurements under controlled tunnel conditions. Spectral data were pre-processed through interpolation, derivative analysis, and principal component analysis (PCA), and correlated with agronomic traits including yield, plant biomass, and thousand-grain weight. Drought induced clear agronomic penalties, with plant biomass and grain yield exhibiting significant variety-dependent responses, allowing ranking of genotypes by yield stability. Thermal imaging (ΔT) and hyperspectral water-status indices (NDWI, MSI, WI, WBI, NMDI) provided the strongest drought-control separation and were highly predictive of yield loss (ΔT $R^2 \approx 0.84$; WI $R^2 \approx 0.78$). Fluorescence-based metrics revealed photoprotective responses (increased ΦNPQ , decreased $\Phi PSII$), complementing thermal and spectral indicators, but were less robust predictors of yield penalty at single-date sampling. Multispectral vegetation indices showed moderate sensitivity but were often redundant with other sensors. Cross-sensor analysis highlighted that yield-based drought tolerance is best captured by combining thermal stress proxies, water-status spectral indices, and red-edge functional indices (VOG2, fAPAR), whereas fluorescence and greenness metrics add mechanistic context. Despite limited replication, this study demonstrates the utility of simultaneous multi-sensor monitoring to detect drought stress, interpret physiological responses, and identify trait combinations most informative for wheat breeding programs. These findings provide a framework for high-throughput phenotyping of drought resilience and guide the selection of genotypes with stable performance under water-limited conditions.

P57 - A lightweight semi-automated framework for wheat spike segmentation and spike-level phenotyping

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Abstract

The number and morphology (size and weight) of the spikes per unit area are one of the yield components and among the most important phenotypic traits that determine the yield of wheat. However, the comprehensive analysis of these traits remains challenging, particularly in complex field canopies where accurate spike-level phenotyping is hindered by occlusion, appearance variability, and the limited availability of large-scale instance-level annotations. Recent advances in deep learning, particularly single-stage detectors such as YOLO-based instance segmentation models, offer promising solutions for extracting phenotypic information from visual data with relatively low computational cost.

In this study, we evaluate the YOLOv11x model for wheat spike segmentation using a dataset collected with an RGB camera at the CREA Research Centre for Cereal and Industrial Crops. The dataset consists of 3,900 wheat images in JPG format, each with a resolution of 4000 × 3000 pixels. To facilitate automatic mask-to-polygon conversion, segmentation label generation, visual verification, and dataset expansion, we propose a lightweight pseudo-labelling framework with graphical user interface (GUI) support. The proposed framework integrates YOLO-based instance segmentation with pseudo-labelling to efficiently construct large-scale instance-level datasets and enable reliable estimation of key spike traits, including spike number and spike size, for scalable image-based phenotyping under complex field conditions.

Experimental results demonstrate that incorporating weights obtained from ablation models and optimizing hyperparameters (momentum factor and Initial learning rate) significantly improves segmentation performance. Precision increased from 82.43% to 85.52%, F1-score improved from 80.84% to 85.02%, and mAP50 increased from 85.33% to 90.33%. These improvements enable more accurate spike segmentation, leading to more reliable spike counting and spike size estimation. A strong correlation was observed between coverage and total spike area ($R^2 = 0.92\%$). This result suggests that the feature extraction pipeline correctly identifies the area covered by wheat spikes in each image and that the segmentation outputs can be reliably used for spike-level phenotyping tasks, wheat breeding and research. Future research will focus on developing multi-model deep learning architectures for feature extraction and integration, aiming to combine complementary representations from different models to improve wheat phenotyping and strengthen genotype-phenotype relationship analysis.

P58 - Differential antioxidative and molecular responses among winter wheat genotypes: implications for precision crop management

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Abstract

Climate change has increased the risk of biotic stress by expanding pathogen populations, intensifying disease outbreaks, and enabling diseases to spread to new regions. Various fungal infections account for approximately 20% of the yearly global wheat grain yield and quality deterioration. Fusarium species, causing Fusarium head blight (FHB), are listed among the top 10 most significant wheat pathogens worldwide. This study aimed to evaluate genotype-specific antioxidative and molecular responses to FHB in resistant and susceptible winter wheat genotypes, to support precision breeding strategies and improve decision-making in sustainable wheat production systems. This was achieved by determining disease impact on the antioxidative and molecular responses of wheat spikes to FHB under controlled conditions. Susceptible genotype significantly increased H₂O₂ content in response to artificial infection. Increased reduced glutathione (GSH) levels and significantly increased oxidized glutathione (GSSG) concentrations in susceptible genotype despite increased glutathione reductase activity might indicate that GSSG has not been successfully reduced. Furthermore, increased GSH consumption could also be a consequence of GSH participation in direct or the indirect removal of reactive oxygen species (ROS) in wheat cells, as well as in maintaining other antioxidants in a reduced state. Contrarily, resistant genotype showed no significant changes, suggesting a more effective antioxidative response. Since glutathione S-transferase maintained high activity levels in resistant genotype, it can be assumed that this enzyme not only plays an important role in ROS scavenging, but also in detoxifying Fusarium mycotoxins. The induction of nonexpressor of pathogenesis-related genes 1 (NPR1) and pathogenesis-related (PR) genes is a primary mechanism by which salicylic acid affects the immune response to pathogens. Thus, genes encoding PR1, PR3, and PR5 proteins were upregulated in all studied genotypes in response to artificial inoculation. The expression of the NPR1 gene was significantly upregulated only in the resistant genotype. Since molecular and antioxidative responses linked to FHB resistance are potential biomarkers for precision breeding and genotype-specific crop management, integrating them into decision-support systems can improve cultivar placement and early disease risk assessment, supporting precision and sustainable agriculture by minimizing the need for fungicide and lowering environmental impact.

P59 - Integrating OJIP kinetics and gas exchange traits to screen for drought tolerance in wheat

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Abstract

Wheat (*Triticum aestivum* L.) is facing increased productivity threats from drought incidents due to the ongoing climate change. Also, in temperate regions, e.g. in Sweden, wheat production has been detrimentally affected during specific years, e.g. 2018 and 2023, by long drought periods within the crop development period. Thus, reliable phenotypic indicators are needed for augmented selections within breeding for drought tolerance, to improve genotypic resilience. The present study aimed to delineate the fast kinetics of leaf chlorophyll fluorescence (OJIP) and gas exchange traits as selection criteria for drought stress tolerance in wheat. A total of 20 spring and 32 winter wheat genotypes were evaluated under control (irrigated) and natural drought (rainfed) conditions at three different locations in Sweden viz., Helgegården, Öland and Alnarp. Leaf OJIP kinetics and gas exchange traits were recorded at anthesis stage and grain yield was measured at physiological maturity. Analysis of variance inferred significant variation in early OJIP and gas exchange traits between treatments, genotypes and locations with significant interactions between the sources. OJIP were increased under drought, inferring closed reaction centers. Correlation analysis indicated drought induced disruptions in electron transport through PSII leading to reduced yield. Natural drought resulted in a significant reduction ($P < 0.01$) of maximum quantum yield of PSII, efficiency of electron movement beyond QA and Quantum yield beyond QA with a concomitant reduction in performance index (40%), indicating significant impairment of photochemical efficiency. However, energy absorption per reaction center (17%) and trapped energy per reaction centre (7%) were increased under natural drought conditions, with marginal change in electron transport flux per reaction center (3%), indicating the impediment in electron transport beyond PSII under natural drought. Total and per reaction centre energy dissipation were significantly increased ($P < 0.01$), corroborating the reduced photochemical efficiency under natural drought. Leaf vapour pressure deficit and leaf temperature were significantly increased ($P < 0.01$) under natural drought with reduced transpiration from stomatal closure. Partial least squares regression analysis predicted grain yield with $R^2 = 60.4\%$ ($Q^2 = 0.54$) under natural drought, emphasizing the possibility of integrating instantaneous fluorescence and gas exchange as physiological markers for drought tolerance screening of wheat.

P60 - From climate data to durum wheat cultivar selection: an ai-based interpretable decision-support framework

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Abstract

The Mediterranean region is experiencing increasing temperatures, heat waves, and water availability, representing major challenges to durum wheat (*Triticum durum* Desf.), a strategic crop for regional food security. Identifying cultivars that optimize yield and grain protein content under specific stressors is crucial for climate-adaptive agriculture. This study integrates long-term phenotypic and climatic data to develop an interpretable machine learning framework to support climate-informed cultivar selection at the cultivar environment level across heterogeneous environments. For this study, phenotypic records from 219 durum wheat varieties cultivated across 119 locations in Italy over the last 24 years sourced from the CREA (Council for Agricultural Research and Economics) database were used, resulting in a robust dataset of 31,000 observations. These records were integrated with high-resolution, weekly ERA5-derived climatic variables specifically aggregated for the period from tillering to harvest. This weekly temporal scale allowed for a precise characterization of environmental stressors, including precipitation, growing degree days (base 5 °C), solar radiation, relative air humidity, wind speed, soil moisture at multiple depths, number of heat-wave days, and temperature metrics. Several machine learning algorithms were used to predict grain yield and grain protein content with their accuracies evaluated on an independent test set using RMSE, MAE, and R² metrics. While all evaluated algorithms demonstrated comparable predictive performance, random forest was selected due to its strong predictive performance and robustness. Model interpretability was subsequently achieved through SHapley Additive exPlanations (SHAP) analysis. After selecting the best-performing model, a Recursive Feature Elimination (RFE) procedure constrained by an R² tolerance threshold was implemented to obtain parsimonious models while preserving predictive performance. This approach enabled the identification of the primary climatic drivers influencing both yield and grain protein content, quantifying the direction and magnitude of their effects. Beyond identifying the most influential variables, the SHAP analysis highlighted the critical weekly windows most determinant for trait prediction, clarifying the specific stages where environmental stressors are most impactful. Furthermore, the model captured complex non-linear interactions and synergistic climatic effects on crop performance, contributing to the development of AI-based decision support tools for wheat farmers breeders, and agronomists.

P61 - Disentangling genetic and environmental control of photosynthetic nitrogen dynamics in wheat canopies

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Abstract

Photosynthesis and nitrogen availability jointly underpin crop productivity and resilience, yet dissecting the underlying mechanisms governing nitrogen allocation within the photosynthetic apparatus remains challenging. In particular, dynamic investment in light harvesting, electron transport, and carboxylation cannot be directly observed or selected for, limiting progress in breeding strategies targeting photosynthetic efficiency. We expanded a published photosynthetic nitrogen turnover model to explicitly account for environmental effects, describing the dynamics of nitrogen allocated to these functional pools as the balance between synthesis and degradation, with both processes modulated by light and temperature. To parameterize this framework, we combined repeated non-destructive measurements of chlorophyll content (SPAD) and hyperspectral reflectance with predictive models of photosynthetic capacity across six winter wheat genotypes. Measurements were conducted at four leaf ranks per plant throughout the leaf lifespan. Leaf-level light interception was simulated using a wheat functional-structural plant model driven by greenhouse climate data and incorporated as an environmental input to the turnover model. This integration of a mechanistic turnover framework, high-throughput spectral phenotyping, and canopy light simulation enabled estimation of genetic turnover parameters independent of leaf rank-specific microclimate.

The expanded model revealed systematic coordination among photosynthetic nitrogen pools in their environmental responses. Temperature sensitivity of synthesis and degradation differed among pools, with carboxylation and electron transport nitrogen showing higher thermal sensitivity and faster turnover than chlorophyll-associated pools. Light responses saturated at lower irradiance for chlorophyll and light-harvesting nitrogen compared with biochemical pools, indicating intrinsic constraints in the coordination of the photosynthetic machinery. Despite these shared patterns, fitted parameters varied across genotypes, illustrating alternative nitrogen investment strategies rather than uniform scaling among pools. The resulting turnover parameters—describing maximum synthesis capacity, degradation rates, developmental attenuation, and environmental sensitivities—constitute biologically interpretable traits capturing dynamic nitrogen use in photosynthesis. By quantifying how genotypes differ in the timing, magnitude, and environmental sensitivity of nitrogen allocation among photosynthetic pools, this framework provides breeders with mechanistically grounded targets to shape canopy nitrogen distribution and sustain carbon assimilation under variable and warming climates.

P62 - Rapid detection of wheat frost at seedling stage using UAV based phenotyping

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Abstract

Climate change has increased the frequency of extreme temperature events, posing major challenges to wheat growth. Frost damage in winter wheat during early growth stages can cause tissue damage, reduced tillering, and impaired grain formation, resulting in significant yield losses. Rapid and accurate monitoring of frost damage helps breeders select cold-resistant, widely adaptable, and high-yielding wheat varieties. This study examined 1,792 advanced wheat breeding lines. Ground-based normalized difference vegetation index (NDVI-G) measurements were collected during the seedling stage, including the overwintering and regreening periods. Additionally, red-green-blue (RGB) and multispectral (MS) imagery data were acquired using a multi-sensor unmanned aerial vehicle (UAV). By integrating remote sensing data with machine learning algorithms, frost damage in wheat was assessed. Results showed: (1) As frost damage increased, the NDVI-G values of wheat seedlings showed a significant decrease ($p < 0.001$). (2) In evaluating frost damage levels during the wheat seedling stage, MS data models generally outperformed RGB data models. Specifically, the RF model using MS data performed best during both overwintering and greening stages, achieving high accuracy and balanced precision, recall, and F1 scores (0.87/0.85, 0.69/0.75, 0.68/0.80, 0.68/0.77). (3) Integrating UAV remote sensing data with four machine learning algorithms (KNN, RF, NB, and Stacking) enabled accurate classification of frost damage in wheat seedlings. Among these, the RF model using MS data achieved the best predictive performance. This study presents an efficient and scalable approach for field-based frost assessment in wheat. It supports cold-tolerant breeding and timely frost mitigation to reduce yield loss.

P63 - High-throughput phenotyping and QTL analysis of wheat stomatal density enabled by portable microscopy and deep learning

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Abstract

Stomatal density (SD) critically regulates wheat photosynthesis and water-use efficiency, yet traditional phenotyping methods are destructive and labor-intensive, limiting large-scale genetic studies. In this study, an integrated pipeline combining portable microscopy, deep learning, and QTL mapping was established for high-throughput, non-destructive SD phenotyping and genetic dissection in wheat. A portable microscope (ProScope HR2) was employed to capture 19,148 stomatal images from live leaves of a ZM578/JM22 recombinant inbred line (RIL) population (n=270) across four environments (greenhouse, Xinxiang, Gaoyi, and Dezhou), with two irrigation treatments in Xinxiang. A Faster R-CNN model with ResNet-50 backbone was developed for automated stomatal detection, trained on 11 diverse datasets encompassing greenhouse-grown wheat, 1,500 germplasm accessions, and RIL populations. The model achieved precision of 0.87, recall of 0.99, and average precision of 0.99. Validation against manual annotations from 1,200 RIL images across three field locations showed high accuracy ($R^2=0.91-0.96$, RMSE=1.15-1.31 stomata/image), enabling rapid processing at 6-8 seconds per leaf. Phenotypic analysis revealed significant genotypic and environmental effects on SD ($P<0.01$), with broad-sense heritability of 0.58. Using a high-density genetic map (1,501 bin markers, 2,384.95 cM) from the Wheat 50K SNP array, QTL mapping identified a stable QTL, QSd-caas.7A, on chromosome 7A (267.60-494.78 Mb) explaining 4.59-5.40% of phenotypic variation across two environments. The favorable allele was contributed by parent Jimai 22. The flanking marker AX-179557282 was converted into a KASP marker (K_AX-179557282) and validated in 224 wheat cultivars. Lines carrying the favorable allele exhibited a significant 10.1% increase in SD ($P<0.05$), confirming its breeding potential. This study presents the first integration of portable microscopy with deep learning for field-scale, non-destructive SD phenotyping. The established pipeline overcomes major bottlenecks in stomatal trait acquisition by eliminating destructive sampling and enabling population-scale data collection. The identified novel QTL and validated KASP marker provide practical tools for marker-assisted selection to optimize stomatal density, potentially enhancing wheat yield and drought tolerance. This approach demonstrates the powerful synergy between advanced phenotyping, deep learning, and genetic analysis for dissecting complex physiological traits and accelerating crop improvement.

P64 - Future climate threatens Australian wheat yield and quality

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Abstract

the coming decades, climate change will bring higher atmospheric CO₂ concentrations as well as warmer air temperatures. Despite their joint presence under future climate conditions, the combined effects of elevated CO₂ (eCO₂) and elevated temperature (eT) on wheat performance remain understudied¹. When tested separately, eCO₂ increases wheat yield while diminishing grain nutritional values^{2,3}, whereas eT decreases yield⁴ with undetermined effects on grain nutrition.

Whether there are wheat varieties that can take advantage of the extra CO₂ and/or temperature to achieve better performance in yield and/or quality is unclear.

To address the currently limited understanding of the combined effects of eCO₂ and eT in wheat, we conducted a 2-year experiment and subjected 86 diverse Australian wheat lines under future climate conditions (800 ppm CO₂ and 5°C warming; projected climate conditions by 2100) and gained early mechanistic insights using several high-throughput phenotyping technologies. In both years, we observed a consistent yield reduction of 17±2% under future climate conditions. In the first year, high-throughput phenotyping of photosynthetic capacity showed V_{max}; 25 could predict lower yield loss across wheat lines. This suggest higher ecophysiological plasticity contribute to yield resilience under future climate conditions. Additionally, we also observed that the 5°C warming completely offset the seed quality dilution effect of eCO₂ for both seed nitrogen and iron concentrations. However, seed zinc concentrations remain negatively affected by the combined treatment of eCO₂ and eT by similar magnitudes to (8.2%) eCO₂ alone. This suggests that zinc-specific uptake and/or allocation may be particularly vulnerable under future climate conditions, thus requiring future investigations to ensure human food security

P65 - Utilizing high-throughput phenotyping to identify metribuzin tolerance in winter wheat

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Abstract

Plant breeders and weed scientists address weed management collaboratively by selecting for herbicide tolerance in breeding programs. Metribuzin, a Group 5 PSII-inhibiting herbicide, is labeled for use in wheat. However, application to currently available varieties results in frequent, variable, and unpredictable crop injury. Incorporating a new herbicide mode of action in winter wheat production would enhance rotational flexibility and weed resistance management. Selection for improved herbicide tolerance in crops has traditionally relied on visual estimation, yet assessments can be variable. The objective of this study was to improve the accuracy and efficiency of selecting for herbicide tolerance in a breeding program by utilizing a drone-mounted multispectral sensor. Multispectral data were collected on paired rows and advanced generation lines grown in paired plot yield trials. Vegetation indices calculated include NDVI, NDRE, TCARI, NWI, and MTVI. Visual assessments of injury, plant height, and grain yield were also recorded. Correlations between reflectance indices and grain yield were stronger than those between visual injury assessments and yield. The top ten varieties overlapped 45 to 53% when selected by highest yield and highest NDVI or NDRE, respectively, in sprayed plots. The relationship between yield and index differences in treated and non-treated plots showed that the difference in indices (multiple $R^2 = 0.0802$ to 0.5434) explained more yield variation than visual assessments (multiple $R^2 = 0.0003$ to 0.1915). These results suggest that multispectral analysis at the plot level is a more accurate and efficient indicator of herbicide injury in winter wheat than traditional visual assessments.

P66 - Developing nitrogen-efficient wheat using biological nitrification inhibition (BNI) technology for sustainable production in the indo-gangetic plains

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Abstract

Modern agriculture relies heavily on nitrogen fertilizers; however, nearly 70% of applied nitrogen is not utilized by crops, leading to environmental problems such as water pollution and increased greenhouse gas emissions. Improving Nitrogen Use Efficiency (NUE) is therefore essential for sustainable wheat production. To address this challenge, a JICA-CIMMYT-BISA-ICAR collaborative project titled "Establishment of Nitrogen-Efficient Wheat Production Systems in the Indo-Gangetic Plains through the Development of BNI Technology" was initiated in 2022. The project aims to enhance nitrogen retention in soils and reduce nitrous oxide emissions in major wheat-growing regions of India.

The breeding strategy focuses on introgression the Biological Nitrification Inhibition (BNI) trait into elite Indian wheat backgrounds. Seven widely cultivated Indian wheat varieties (DBW187, DBW303, DBW222, DBW327, DBW110, DBW296, and HI1612) and seven CIMMYT advanced lines were used as recurrent parents, while three BNI donor lines served as donor parents. A total of 40 crosses were made during the 2021-22 crop season at BISA Ludhiana, followed by two backcrosses to recover the recurrent parent genome.

Molecular markers were used to identify BNI-positive plants, and marker-assisted selection was applied in each generation. Shuttle breeding accelerated generation advancement at the IIWBR Regional Station, Dalang (Himachal Pradesh). By the BC₂F₅ generation, several BNI-derived lines with promising agronomic performance and resistance to yellow rust were identified.

Multi-location trials of selected BC₂F₅ lines were conducted through collaboration between BISA and IIWBR at BISA research stations (Ludhiana, Jabalpur, and Pusa) and IIWBR Karnal under 100% and 70% nitrogen regimes. Several BNI-derived lines showed superior phenotypic performance compared with their parental lines, indicating the potential of BNI technology to improve nitrogen efficiency without compromising yield. Given the substantial urea subsidy investment by the Government of India, BNI-enabled wheat varieties represent a promising strategy to reduce nitrogen losses, improve NUE, and enhance environmental sustainability. The BNI breeding pipeline is now at an advanced stage, and promising lines under multi-location evaluation are expected to enter national wheat trials in India next year.

P67 - Increasing the protein use efficiency of the magic-wheat-population WM-800

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Abstract

Winter wheat holds a crucial position in German agriculture, constituting the primary cereal both in terms of cultivation area and harvest quantity. However, the attainment of high quality standards demanded by the industry involves significant nitrogen (N) fertilizer inputs, leading to environmental challenges. This project aims to explore the genetic regulation of winter wheat for enhanced baking quality and protein use efficiency (ProtUE = loaf volume divided by the amount of grain protein content).

The winter wheat MAGIC-Population WM-800, developed from an eight-way cross of German elite cultivars, serves as the genetic resource for this investigation. A selected subset of recombinant inbred lines (RILs) with contrasting baking quality traits will be evaluated across multiple environments under different N management conditions. The study aims to identify potential genotypes with improved baking quality and ProtUE under reduced N fertilization to mitigate the crop's carbon footprint. Furthermore, Proteomic and metabolomic analyses will provide insights into the genetic regulation of baking quality, ProtUE, and metabolite profiles influenced by N fertilization.

P68 - Controlling wheat - rye interspecific crossability for wheat and tritcale improvement

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Abstract

Increasing genetic diversity remains one of the central pillars of breeding, especially with regards to new agronomical challenges. One way to face these challenges is to introduce original genes/alleles from related species. Interspecific hybridization therefore represents a key strategy to enlarge the genetic bases available for crop improvement. Among such crosses, wheat-rye hybridizations are of special interest, not only because rye has historically contributed valuable resistance loci to wheat (e.g. 1RS/1BL introgression), but also because these crosses lead to the biological foundation of × Triticosecale. However, Triticale improvement relies on the development of new primary triticales resulting from the cross between hexaploid cultivars and rye accessions (Laugerotte et al., 2022).

Interspecific crossability in wheat is genetically regulated, and modern European cultivars exhibit a strong prezygotic barrier preventing rye pollen tubes from progressing through the wheat style (Jalani and Moss, 1981).

We identified *Skr* 30 years ago as the major locus controlling incompatibility (Tixier et al., 1998), where the dominant allele confers rejection of rye pollen.

Here, we present recent advances that have enabled us to refine the genomic regions involved in wheat-rye incompatibility, as well as to implement VIGS-BSMV as a candidate gene validation strategy.

Using a combined approach consisting of (i) low-pass whole-genome sequencing of crossable and non-crossable Asian lines and (ii) targeted sequencing of the *Skr* region using TWIST capture probes, we achieved a substantial narrowing of the critical interval. This strategy provided new insights into the candidate genes underlying the *Skr* effect and generated valuable comparative data to better understand the genomic architecture of potential additional crossability loci. Finally, we validated one candidate gene as *Skr* through virus-induced gene silencing (VIGS), a technique that could potentially be used to directly enhance the production of primary triticale.

Building on these results and on international collaborations, we initiated the functional characterization of the *Skr* protein and began exploring rapid and applicable strategies to improve primary triticale production for breeding purposes. These advances bring us closer to overcoming the long-standing barrier of wheat-rye incompatibility and to enabling a more efficient exploitation of interspecific diversity in cereal improvement.

P69 - An automated untargeted metabolomics analysis platform for large-scale samples and its application in wheat polyploidization research

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Abstract

An automated untargeted metabolomics analysis platform for large-scale samples and its application in wheat polyploidization research

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Abstract

Untargeted metabolomics is an analytical strategy aimed at comprehensively detecting all measurable metabolites in biological samples without predefined targets. However, existing data-processing tools still exhibit limitations in peak detection stability, large-scale batch processing capacity, and usability for non-programming users. In this study, we developed a fully automated data-processing platform for high-resolution mass spectrometry data acquired under the data-dependent acquisition (DDA) mode. The platform was implemented in Java, providing high computational efficiency and effective memory management, and is suitable for automated batch processing of large-scale untargeted metabolomics datasets.

A combined strategy integrating region of interest (ROI) detection and continuous wavelet transform (CWT), together with peak ridge extraction, was employed to improve the stability and robustness of chromatographic peak recognition. Dynamic time warping (DTW) was applied to achieve cross-sample peak alignment and association, enabling joint multi-sample processing and intergroup comparative analysis. The platform integrates both graphical user interface (GUI) and command-line interface (CLI) modes, allowing flexible operation for users with different technical backgrounds.

The platform was applied to high-resolution grain metabolomics data from 149 synthetic wheat accessions with different ploidy levels, resulting in the detection of 9,142 metabolite features. Quantitative comparative analysis among tetraploid wheat, diploid *Aegilops*, and their derived hexaploid synthetic wheat populations revealed significant differences in amino acids and their derivatives as well as phenolic acid metabolites across ploidy levels. These findings suggest that polyploidization may be accompanied by the reprogramming of nitrogen metabolism and phenylpropanoid pathways. This study provides a new analytical tool and valuable data resources for elucidating the metabolic and genetic basis underlying wheat polyploidization.

Keywords: *Untargeted metabolomics; Automated data-processing platform; Synthetic hexaploid wheat; Polyploidization*

P70 - Assessment of in situ wild emmer wheat genome evolution over long-term periods

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Abstract

Wild emmer wheat (WEW - *T. turgidum* ssp. *dicoccoides* - AABB) is an important genetic resource that can be harnessed for the improvement of modern wheat. It contains largely untapped genetic diversity for traits that affect yield, such as grain quality, resilience to biotic and abiotic stress. Its conservation, in situ and ex situ, is thus critical for food security. One population, in Kibbutz Ammiad in Israel, is located at the center of WEW diversity and has been studied for the past 42 years. Analysis of this population, using GBS, shows stable genotypes associated with ecological microhabitats during a 36-year period, suggesting local adaptation (Dahan-Meir et al., 2024). Here, we expand this research in Ammiad by analyzing a longer period, and to capture both gene-space variation and repeat-driven genome dynamics at scale, we combine exome sequencing with transposable element (TE) profiling. In addition, we describe the long-term genetic changes in the makeup of several other populations in Israel. These samples represent a broad spectrum of environmental conditions. This time-series population genomics approach will help identify drivers of biodiversity and define strategies for in situ and ex situ conservation.

P71 - Seed germination and seedling establishment in durum wheat: the role of heterosis and its influence in stress tolerance

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Abstract

Seed germination is a crucial stage of a plant life cycle. The well establishment and growth of the plant and its ability to tolerate/resist stresses depend on this initial phase. This process is really complex because composed by very different phases: from seed recovering after maturation drying to synthesis of new DNA/ RNA transcripts, metabolism reprogramming, and cellular preparation/division for the seedling formation and growth. Frequent abiotic stresses (i.e., high/low temperatures and drought) cause collapsed seed germination, eventually resulting in grain yield loss worldwide. Hence, to ensure higher emergence rate and strong seedling vigour to avoid significant damages, a fast and more uniform germination is preferred. Several seed germination traits are now known to be affected by heterosis. Therefore, this study aims to investigate how seed structure, and hormone and gene expression levels change in durum wheat hybrids during germination. To reach this goal, two approaches have been adopted. The first one is based on the analysis of 7 different durum wheat varieties collected among Italy, Algeria, and Spain. The Algerian variety Fritissi resulted one of the fastest to germinate and one of the most tolerant to drought and salt stress applied during this initial phase, while the Italian variety Cappelli was the slowest and the least tolerant. Therefore, we selected these two varieties as inbred lines to cross reciprocally to obtain F1 hybrids that will be analysed for germination traits since the effects of heterosis should be stronger and more visible in the first generation. The second strategy is the study of a RIL population F7 generation by performing QTL mapping analysis to identify genes involved in germination traits. Moreover, we selected the two best and the two worst performing lines among the RIL population to observe more in details the differences between each other and the parents. We will determine the expression level of genes well known to be involved in germination through qPCR and the levels of ABA and GAs hormones through LC-MS, while the germinating seed structure will be observed at different timepoints through immunofluorescence analysis against cell wall components and histological staining with toluidine blue.

P72 - Wheat polyploidization - genome shock or business as usual?

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Abstract

Polyplloidizations are major events in the evolutionary history of cultivated wheats. It has been long suspected - and partially documented - that genomic incompatibilities between *Aegilops tauschii* L. and *Triticum turgidum* ssp. cause widespread reorganization of the genome after allohexaploidization. Changes reported from analyses of nascent allohexaploids ('synthetics') include sequence loss, activation of transposable elements (TEs), widespread gene expression changes, and restructuring of the epigenome. However, transcriptomes of some nascent allohexaploids are not strongly disrupted by the genome merger, and TE landscapes of bread wheat bear no traces of transpositional bursts related to polyploidization. So what exactly happens to the parental genomes in nascent wheat polyploids?

Analyses of different parental combinations, including various genotypes and a reciprocal cross, detected very modest changes in transcription after polyploidization. Barely any changes are found on the A and B subgenomes, while hundreds of genes are up- and downregulated on the D subgenome. Genes transcriptionally altered by polyploidization in seeds do not match those in leaves, and the vast majority of downregulations do not seem to be accompanied by sequence loss. The differential expression is not statistically associated with the distance or orientation of proximal TEs, and up- or down-regulation of genes cannot be generally explained by changes in DNA methylation around transcription start sites (TSS). Nucleolar dominance (silencing of 5S rDNA) is observed in leaves of the synthetics, but is not explained by changes in DNA methylation. Homeolog expression bias is generally a perpetuation of pre-determined parental expression differences, with polyploidization having a mild balancing effect. Differences in homeolog expression are not statistically related to differences in TSS methylation.

The genome of wheat synthetics is generally undisturbed by polyploidization. While some parental genotype combinations may be less compatible than others, some previous reports of rampant transcriptomic changes are flawed by technical artefacts associated with inter-ploidy comparisons. Methylome patterns are generally stable across polyploidization events, and subgenome differences in DNA methylation are retained even on evolutionary timescales. Transcriptomic changes in wheat synthetics are probably due to regulome conflicts, and may not be qualitatively or quantitatively different from epistatic interactions in intra-specific hybrids.

P73 - Integrated analyses of the *vrn-b1* locus reveal structural variations and novel allelic diversity in triticum spp.

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Abstract

The MADS-box VRN-1 gene, a key regulator of vernalization, controls the induction of the floral transition in wheat (*Triticum* spp.) in response to prolonged exposure to low temperatures (4-6 °C for 4-6 weeks). Mutations in the promoter and/or intron 1 regions of the homoeologous *Vrn-A1*, *Vrn-B1*, and *Vrn-D1* genes, located respectively on chromosomes 5A, 5B, and 5D, are responsible for the major differences between dominant and recessive alleles, thereby determining the wheat growth habit (spring/winter).

In this study, we aimed to elucidate the structural genetic variation of the *Vrn-B1* gene between hexaploid and tetraploid wheat using integrated in-silico and molecular approaches, and to assess how these variants influence the floral transition and heading time. The bioinformatic analyses were performed on 35 genomes from different *Triticum* spp., focusing on intron 1 and the promoter region. Notably, the in-silico analyses revealed that the *Vrn-B1* locus was identified on chromosome 7B instead of 5B in two bread wheat genotypes (SY Mattis and ArinalrFor), as a result of chromosomal translocation and inversion events involving portions of the 5B genomic region.

Although considerable variability was observed within intron 1, the promoter region of the VRN-box and CARG-box regulatory elements was highly conserved across the analyzed genomes. Furthermore, molecular marker screening of 355 *Triticum* genotypes revealed a predominance of the recessive allele and, for the first time, the presence of the dominant *Vrn-B1f* allele in tetraploid wheat species (*T. durum*, *T. dicoccum*, *T. dicoccoides*, and *T. turgidum*), suggesting a common evolutionary origin of this allele.

Future studies will focus on clarifying how *Vrn-B1f* regulates the floral transition and its effect on heading date among different tetraploid wheat subspecies, including functional validation and gene expression analysis. Overall, these findings provide new insights into the genetic regulation of vernalization and highlight the relevance of *Vrn-B1* allelic diversity for wheat breeding and genetic improvement programs targeting adaptation to contrasting environments.

P74 - Investigation of phenotypic and gene expression response to different vernalization regimes.

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Abstract

Flowering time in wheat is primarily regulated by the interaction between the vernalization and photoperiod pathways. Vernalization, the requirement for prolonged exposure to low temperatures, is controlled by key genes such as VRN1, VRN2, and VRN3, while photoperiod sensitivity is mainly mediated by PPD1. The integration of these signals allows plants to transition from the vegetative to the reproductive stage under favourable seasonal conditions. However, the stability of the vernalization response may vary among genotypes and can be influenced by interruptions of cold exposure.

In this study, the phenotypic response of different wheat genotypes to distinct vernalization regimes was evaluated. The analysed material included five cultivars of durum wheat (*Triticum turgidum* ssp. durum: Svevo, Iride, Polesine, Anco Marzio and Liberdur), one cultivar of bread wheat (*Triticum aestivum* ssp. aestivum, Bologna), two accessions of *Triticum turgidum* ssp. turanicum (PI624429 and CI11390), and one accession of wild emmer (*Triticum turgidum* ssp. dicoccoides, MG4330). Plants were subjected to four vernalization treatments including one regime with continuous cold exposure and three regimes with interrupted vernalization, in which periods of cold were separated by short intervals under greenhouse conditions. These treatments differed in the duration of cold exposure and in the timing of the interruption. Flowering time was recorded as the number of days from the final transfer to the greenhouse to heading. Preliminary phenotypic observations revealed a particularly strong response to interrupted vernalization in the cultivars Polesine and Bologna, which showed the most pronounced differences in flowering time among treatments. Observations on the other genotypes suggest a more stable flowering response across the different vernalization regimes.

To investigate the molecular basis of these differences, gene expression analyses were conducted using real-time PCR on Polesine and Bologna. RNA samples were collected at multiple time points during the interrupted vernalization treatments to monitor the expression of genes involved in the regulation of flowering time and the vernalization response. These analyses aimed to determine whether interruptions of cold exposure affect the stability of the vernalization response through changes in the regulation of flowering-related genes.

P75 - Beyond green revolution rht genes: candidate loci influencing growth in durum wheat

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Abstract

Over the last century, wheat ideotype development has been driven by the need to enhance yield through more efficient use of agricultural inputs. The Green Revolution marked a breakthrough with the introduction of gibberellin-insensitive dwarfing alleles (GA₃-insensitive Rht), including Rht-B1b and Rht-D1b, which enabled the development of shorter cultivars with improved lodging resistance and resource-use efficiency, resulting in substantial yield gains. However, climate change now demands cultivars that combine high productivity with resilience to environmental stresses and optimized natural resource use. In this context, GA-sensitive Rht genes are gaining renewed interest, as they allow reduction of plant height without compromising early vigour, coleoptile elongation, or root development—traits essential for crop establishment and stress adaptation. We investigated the genetic basis of plant height, coleoptile length, and GA₃ responsiveness in a segregating population derived from the cross between Castelporziano (semi-dwarf, long coleoptile, GA₃-sensitive) and Atoudur (dwarf, short coleoptile, GA₃-insensitive). Two phenotypically contrasting bulks were analyzed using integrated QTL-seq and RNA-seq approaches. Two major QTLs were identified on chromosomes 4B and 6A. The former co-localized with the GA-insensitive Rht-B1, confirming its contribution to plant height variations, whereas the latter pointed toward a GA-sensitive region associated with GA2-oxidase genes involved in gibberellin catabolism, highlighting TdGA2oxA9 as a strong functional candidate. Although TdGA2oxA9 was highly expressed in Castelporziano compared to Atoudur, no polymorphisms were detected in its promoter or coding region, suggesting that regulatory mechanisms upstream of TdGA2oxA9 may account for the observed phenotypic divergence. To further refine the candidate interval, fine-scale exploration of TdGA2oxA9 flanking regions led to the identification of a missense mutation in a Histone H2A deubiquitinase, a chromatin-associated factor potentially involved in epigenetic regulation of GA-related genes. Supporting this hypothesis, a Cadenza TILLING line carrying a splice donor mutation in this gene displayed increased plant height in homozygous mutants, indicating a functional role in growth regulation. KASP markers at Rht-B1b and the H2A deubiquitinase loci confirmed expected segregation in the F₆ population, strengthening the hypothesis that plant height and GA₃ responsiveness in this cross might be governed by both loci.

P76 - Screening and genetic dissection of common bunt resistance in a diverse wheat panel

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Abstract

Common bunt (*Tilletia caries*) is a wheat disease transmitted via seeds and soil. While chemically synthesized seed treatments are generally effective resistance breeding represents a sustainable strategy to prevent bunt infections. Known resistance genes are Bt1-13, BtZ, BtQ and Btp (Borgen et al. 2023). This study aims to: i) screen a gene bank collection for new genetic variation against common bunt, ii) identify wheat genotypes carrying resistance to common bunt, and iii) analyse the genetic architecture underlying these resistances.

Field trials with up to 810 accessions of the ex-situ gene bank (IPK, Gatersleben), a differential set proposed by Goates (2012) and breeding lines provided by the project partners were conducted at three locations in Germany (Bad Vilbel, Quedlinburg and Kassel) during the 2023/2024 and 2024/2025 growing seasons. In Bad Vilbel, artificial inoculation was carried out using local spores. In Quedlinburg and Kassel, artificial inoculation using a spore mixture was performed. At ear emergence, the number of infested ears per genotype was recorded. In Quedlinburg and Bad Vilbel, 132 from 431 and 41 from 354 genotypes, respectively, showed no infection in the field.

No correlation was detected between the two trials in Quedlinburg and a different distribution of infection levels of the individual genotypes was observed. The correlation between the infection level from the two field trials in Bad Vilbel was $r = 0.38$. Across all environments, only one genotype consistently exhibited less than 10% infection.

Afterwards, a preliminary genome-wide association study (GWAS) based on 4051 to 4432 markers published earlier (Schulthess et al, 2022) and the infection level from individual locations was conducted.

The GWAS based on 225 genotypes of the experiment in Quedlinburg in 2024/2025 revealed two marker trait association (MAS) at the chromosomes 4B and 7D. The GWAS based on 264 genotypes of the infection levels from the experiment conducted in Bad Vilbel (2024/2025) revealed one MAS on chromosome 2A, and three on 4B and one on 7D. The GWAS (with 505 genotypes) of the infection levels from Kassel (2024/2025) showed seven MAS on chromosomes 2A, 2B and 6A.

P77 - Genetic dissection of root architectural and biomass traits in durum wheat landraces using rhizotron experiments

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Abstract

Durum wheat (*Triticum turgidum* ssp. durum), a tetraploid cereal crop, is widely cultivated in rainfed and semiarid regions where water availability is often limited and unpredictable. Root system architecture (RSA) involves root spatial distribution and morphology, impacting a plant's ability to access soil resources. Key RSA components include total root length, average diameter, branching frequency, root growth angle, and root volume, all of which significantly influence resource acquisition and yield performance. The present study investigates the genetic basis of root traits in durum wheat using rhizotron experiments under controlled conditions (22°C, 16-hour light photoperiod). A total of 114 durum wheat landraces were evaluated to characterize root system architecture across a genetically diverse panel sourced from five distinct populations. For phenotypic comparison, 15 durum wheat cultivars and 19 bread wheat cultivars were included. The phenotypic comparison recorded the highest values for number of root tips, branching points, and total root length, indicating a more extensively developed root system in durum landraces. Additionally, they displayed a narrower root growth angle (77.4°), which is typically associated with deeper rooting potential. These findings suggest that durum landraces sustain larger, more intricate root systems that may enhance resource uptake. Heritability estimates in durum wheat landraces ranged from 60% to 77%, indicating that genetic factors play a substantial role. Genome-wide association studies identified 141 significant SNP-trait associations across multiple statistical models, reflecting both major-effect loci and polygenic influences underlying root traits. The consistency of signals across models enhanced the robustness of the 82 detected QTLs. Among these, 55 QTLs had been previously reported, whereas the remaining 27 represent potentially novel loci. Importantly, haplotype-based analyses refined QTL regions and demonstrated that specific haplotypes within stable LD blocks confer superior phenotypic performance. For instance, haplotypes at Qrt.ubo_5A.2 and Qrt.ubo_1A.2.3 were strongly associated with enhanced root volume and branching capacity, respectively, highlighting their potential value in marker-assisted breeding. Overall, the results underscore the complexity of root system regulation and establish a foundation for deploying favorable alleles to enhance drought resilience in durum wheat.

Keywords: RSA, durum wheat landraces, potentially novel loci

P78 - Investigating the relationship between grain morphology and polysaccharide content in ancient and modern wheats

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Abstract

Technological and nutritional quality are two very important aspects of wheat research. Public authorities seek to promote grain compositions aligned with current nutritional recommendations - moderate levels of easily hydrolyzable polysaccharides (starch) and higher dietary fiber - while maintaining suitability for grain processing. Among dietary fibers, mixed β -glucans should be considered for their benefits to human health, and because their content appears to be inversely proportional to that of starch. Furthermore, grain morphology, likely linked to polysaccharide composition, is an important factor in processing, particularly during milling where grain shape can influence flour yield.

Wheat domestication and the mechanization of processing have led to the genetic and morphological homogenization of species, which now limit the improvement and adaptation of this cereal to new economic and nutritional requirements. Ancient wheat varieties could provide new sources of genetic, compositional, and morphological variability for modern wheats. In this context, we aim to explore this variability and identify potential correlations between starch and mixed β -glucan content, as well as a possible relationship between polysaccharide composition and cereal grain morphology.

A continuum of wheat species, from wild to domesticated, has been selected to capture broad diversity in traits of interest, including grain morphology and polysaccharide composition. Morphometric parameters (grain dimensions and shape, hull thickness, cell and starch granule size) are being measured using imaging techniques such as X-ray microtomography, scanning electron microscopy and image analysis. At the same time, polysaccharide structure and composition are being investigated using biochemical methods, IR and NMR spectroscopy. Finally, multivariate analysis will be applied to explore potential correlations among these datasets across the different ancient and modern wheat species.

P79 - Mutation burden in wheat germplasm: it is time to address this genetic cost

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Abstract

Deleterious mutations are accumulating in plant genomes over time and they can reduce plant fitness, survival, fecundity, and resilience to variable environments. In this presentation, I will highlight the major findings generated from three mutation burden analyses of wheat germplasm. In a characterization of the genetic responses of 10 wild emmer wheat populations in Israel, sampling them in 1980 and again in 2008, through an exome capture analysis, it was found that these wild emmer populations were under elevated selection, displayed reduced diversity and temporal divergence, and carried elevated mutational burdens forward. This finding not only allows for better understanding of evolutionary changes in threatened populations, but also provides valuable empirical data for realistic modeling of plant population adaptability and vulnerability to global warming. An RNA-Seq based mutation burden analysis of 70 wheat accessions conserved up to 50 years under cold storage in Plant Gene Resources of Canada identified 5646 deleterious variants harbored across 21 wheat chromosomes, and revealed significant mutation accumulations over the 50 years of wheat germplasm conservation. This finding calls for the search for new conservation strategies to minimize the accumulative genetic risk in conserved germplasm. Another RNA-Seq based analysis of genome-wide deleterious genetic variants in 142 wheat cultivars released through Canadian breeding programs over the past century identified 3022 deleterious variants across all 21 chromosomes. These harmful variants were largely retained in a few cultivars and were involved with diverse biological processes, cellular components, and molecular functions. These mutation burdens were found to increase from early to recent wheat cultivars and were associated with higher cultivar yields, suggesting that purging deleterious mutations by breeding practice of selfing was not so effective, allowing for mutation accumulation in the wheat breeding gene pool. Together, these findings not only indicate that an assessment of mutation burden in wheat germplasm is technically possible and practically feasible, but also are informative to understand wheat adaptation, develop germplasm conservation strategy, and enhance wheat breeding.

P80 - Recent winter wheat cultivars from N.A.R.D.I. Fundulea possess a rare combination of high grain yield and good grain protein concentration

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Abstract

Combining high grain yield (GY) and grain protein concentration (GPC) is difficult because these traits are usually negatively correlated. We tested 10 winter wheat cultivars bred at NARDI Fundulea, along with 11 other cultivars for three years (2023-2025), at two levels of Nitrogen availability at Fundulea, South Romania (Lat 44°30'N, Long 26°51'E). Weather conditions during the three years were hot and dry, typical for recent climate changes. We analyzed the GY, GPC, and the deviations from the regression of GPC on GY. Years, availability of N and cultivars caused large variation of all three parameters.

Main source of variation was Years for GY (56.2%) and Nitrogen for GPC (60.3%). Cultivars explained 10.4% of GY variation and 4.7% of the GPC variation. Interactions of Cultivars with Nitrogen or Years had smaller contribution especially to the variation of GPC (0.5% and 2.2% respectively). This suggests that environment does not affect much the differences of GPC between cultivars.

Average grain yield of Fundulea cultivars was similar with that of the other cultivars (5692 vs. 5694 kg/ha), but average GPC was 14.9% (14.0 - 15.3) for the Fundulea cultivars and 14.2% (13.2 - 14.6) for the other cultivars. This superiority of Fundulea cultivars regarding GPC increased from the old to the newest cultivars.

Deviations from the regression of GPC on GY varied from -0.38 to 0.84% (average 0.345%) in Fundulea cultivars and from -1.26 to 0.18% (average -0.29%) in the other cultivars. Deviations from the regression of GPC on GY were significantly correlated with the release years of Fundulea cultivars, suggesting significant genetic progress in this respect. Recent cultivars FDL ABUND, FDL COLUMNNA, FDL CONSECVENT and PITAR, as well as the breeding line FDL AMURG, had highest positive deviations (more than 0.5% GPC). This might be related with the presence of introgressions from rye, *Aegilops ventricosa* and *Ae. Tauschii*. All these genotypes carry favorable alleles of the genes controlling HMW glutenin, conferring good bread-making quality.

In conclusion our results suggest that the recent wheat cultivars released by NARDI Fundulea could contribute to increasing diversity in breeding high yielding wheat with suitable bread-making quality.

P81 - Dissecting the root growth angle QTLome in tetraploid wheat (*triticum turgidum* ssp.) as a key component of drought stress resilience

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Abstract

Root system architecture (RSA) critically shapes water and nutrient uptake. We investigated the genetic control of root growth angle (RGA) in tetraploid wheat (*Triticum turgidum* subsp.) to identify breeding targets for drought tolerance.

RGA was measured on 1,084 accessions from the Global Durum Genomic Resources—521 cultivars (CVS) and 563 landraces (TWL)—using a high-throughput filter-paper assay on seminal roots at early stages. Phenotypes were analyzed by GWAS with the Illumina iSelect 90K SNP array, including subpopulation-specific models.

Both panels showed wide RGA variation, with 7 high-confidence QTLs in CVS and 13 in TWL, indicating greater diversity in landraces. Three major QTLs—QRGA.ubo-2A.2, QRGA.ubo-6A.2, QRGA.ubo-7A.2—were validated via KASP markers and meta-analysis, revealing haplotype-specific alleles for narrow (steep) vs wide (shallow) RGA. For each major QTL, 2-3 Hap-tag KASPs were developed to enable haplotype tracing and pyramiding.

A bibliographic survey showed a broader RGA range in tetraploid germplasm than in modern bread wheat; notably, QRGA.ubo-6A.2 was not detected by QTL projection in hexaploid wheat, suggesting tetraploid-specific alleles. Narrow RGA (favorable for deep water capture under terminal drought) predominated in ICARDA genotypes, whereas shallow RGA was more frequent in CIMMYT lines selected for high yield under irrigated, bed-planting systems.

Transcriptomics implicated conserved phosphorus-response pathways (PHR1, CLE14) and ROS-hormone crosstalk (auxin, ALMT1) in RGA modulation, consistent with low-phosphorus cues reshaping root angle for improved foraging.

Overall, we identify major RGA loci, provide diagnostic KASP markers for marker-assisted selection and haplotype stacking, and demonstrate that tetraploid landraces are a reservoir of adaptive alleles for breeding drought-resilient durum wheat.

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P82 - Characterization of α -Gliadin amplicons and identification of celiac disease epitopes in Spanish wheat landraces.

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Abstract

Wheat grain proteins, particularly gluten proteins, play a key role in determining baking quality in bread wheat (*Triticum aestivum*). Among them, α -gliadins are of special relevance because of their high immunogenic potential in individuals with celiac disease (CD). These proteins harbor several well-characterized toxic epitopes such as DQ2.5_glia_a1a, DQ2.5_glia_a1b, DQ2.5_glia_a2, DQ2.5_glia_a3, and the p31-43 region. In the context of renewed interest in ancient wheat germplasm for safer and more diverse food systems, the identification and characterization of toxic epitopes in traditional landraces is essential.

In this study, we sequenced an α -gliadin amplicon across 22 Spanish landraces and two commercial lines representing hexaploid bread wheat, tetraploid durum wheat and spelt. Using an optimized Illumina-based workflow, we identified 80 unique amplicons, including 52 putative genes and 28 pseudogenes, ranging from 240 to 320 bp in length. Epitope screening showed that 60 amplicons carried at least one known CD epitope, whereas 20 were epitope-free. Comparative analyses revealed that spelt exhibited the highest proportion of immunogenic amplicons (up to 82%), whereas durum wheats showed lower epitope abundance.

Overall, this work provides a detailed overview of α -gliadin diversity in Spanish wheat landraces and highlights genetic variation that could support the identification and breeding of wheat germplasm with reduced immunogenic potential for celiac patients.

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P83 - Semi-dwarf Italian durum wheats: thirty-five years of breeding progress under a changing Mediterranean climate

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Abstract

Durum wheat is a key cereal in Mediterranean agriculture, yet its productivity faces challenges from climate change and limited genetic improvement data. This study analyzed 35 years (1990-2024) of Italian National Variety Trials across four Mediterranean sites to quantify genetic gains in semi-dwarf durum wheat cultivars amid changing climatic conditions. Using long-term check cultivars to control environmental variation, we found consistent genetic gains in grain yield (~0.79% per year), mainly driven by increased kernel number per unit area, with stable or slightly improved grain protein content. Climatic trends showed warming and altered rainfall patterns, yet breeding progress accounted for approximately 63% of yield improvements. These results demonstrate that sustained breeding efforts have enhanced durum wheat adaptation and productivity under Mediterranean conditions, providing valuable insights for future cultivar development to mitigate climate impacts and support food security.

P84 - Induced mutant lines as a source of phenotypic variability for bread wheat (*Triticum aestivum* L.) improvement

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Abstract

Genetic variability is essential for sustained progress in plant breeding, especially in the context of climate change, global population growth, and the increasing pressure to ensure food security. Induced mutagenesis is a powerful strategy to generate novel genetic variations in bread wheat (*Triticum aestivum* L.), offering opportunities for the development of improved cultivars. Accordingly, seeds of winter wheat variety NS 40S were exposed to gamma irradiation at the International Atomic Energy Agency (IAEA), within the project RER/5/024 "Enhancing productivity and resilience to climate change of major food crops in Europe and Central Asia" in 2021. Over the following years, the population was advanced from M0 to M4, reaching the M4 generation in the 2024/2025 growing season, and included 200 lines. This study aimed to assess the extent of phenotypic variability in morphological and yield-related traits among 50 M4 mutant lines and their divergence from the original variety, and to identify promising lines for further evaluation. Plant height, spike length and peduncle length were measured at the experimental field at Rimski Šančevi, Serbia. Additionally, the presence or absence of awns was recorded. Grain length, grain width, and thousand grain weight were analyzed using MARViN device (MARViTECH). A wide range of trait variations was observed among lines, with some lines exhibiting noticeable deviations from the original variety, indicating mutation-induced divergence and generation of novel variability. Segregation for awn presence was also detected, indicating mutation-induced alterations in spike architecture. The observed variations highlighted the potential of certain lines, especially those with increased thousand grain weight compared to NS 40S. They are promising candidates for further evaluations, including agronomic performance, grain quality, and stress tolerance, with the aim of developing improved wheat varieties.

Keywords: *Triticum aestivum* L., phenotypic variability, induced mutation, morphological traits, yield-related traits

P85 - The complete chloroplast genome of triticum araraticum reveals a mismatch in the origin of georgian zanduri wheat (t. timopheevii)

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Abstract

The Zanduri wheat population of Georgia famously includes the cultivated tetraploid *Triticum timopheevii*, but its wild progenitor, *T. araraticum*, is notably absent from the region. This “Zanduri puzzle” obscures the domestication and migration history of this important wheat lineage. To trace the maternal origin of cultivated *T. timopheevii*, this study sequenced and analyzed the complete chloroplast (cp) DNA genomes from 14 wild *T. araraticum* accessions from Turkey, Iraq, and Armenia. These were assembled using CLC software from Illumina MiSeq data and compared to the *T. timopheevii* chloroplast genome. Our analysis identified 24 single nucleotide polymorphisms (SNPs), 30 indels, and 3 inversions across the wild *T. araraticum* samples relative to *T. timopheevii*. The cultivated *T. timopheevii* is distinguished from all 14 wild forms by only two unique SNPs (in the *matK* gene and *ndhA* intron). Based on the complete cpDNA sequence, the wild *T. araraticum* form from the Turkey-Syria border (Gaziantep) is the closest maternal relative, differing by only 3 SNPs, 2 indels, and 1 inversion. This finding is reinforced by two unique indels shared exclusively between *T. timopheevii* and this Turkish-Syrian group, and it aligns with previous cpDNA microsatellite studies. Significantly, this matrilineal evidence (cpDNA) conflicts with data from the nuclear genome. Nuclear markers, such as the Brittle Rachis 1 gene and a 24bp duplication, suggest the closest wild relative is an *T. araraticum* form from Iraq. This genomic mismatch suggests a complex origin, possibly involving hybridization, and supports the hypothesis that *T. timopheevii* may have been introduced to Georgia either before or after domestication by proto-Kartelian tribes migrating from Mesopotamia to Georgia, where they participated in the early stages of wheat domestication.

P86 - Dynamics of repetitive DNA sequences over the course of evolution and intraspecific divergence of tetraploid goat-grass species *Aegilops biuncialis* Vis.

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Abstract

Aegilops biuncialis is tetraploid grass species (UbUbMbMb genome) common in Mediterranean and the Middle East. It is of interest for wheat breeding due to disease and drought resistance, high micronutrient and protein content. However, introgression of beneficial traits from *Ae. biuncialis* to wheat is difficult due to significant modifications of Ub and Mb genomes and insufficient number of cytogenetic markers. Availability of cytogenetic markers permitting for easy and reliable chromosome identification are necessary for successful manipulations with alien genetic material and tracing introgressions in wheat genetic background.

Development of new markers will also be helpful for the establishing genetic nomenclature of *Ae. biuncialis* chromosomes and for detailed analysis of its intraspecific karyotype divergence.

We used fluorescence in situ hybridization (FISH) to study intraspecific karyotype diversity of *Ae. biuncialis*. Among others, the probes pTa-566, pTa713, and pSc119.2 proved to be most effective for chromosome identification and analysis of karyotype evolution. We discriminated three chromosomal groups in *Ae. biuncialis* designated as A, B, and C, which might have independent origins. The Mb genome in groups A and C was probably originated from *Ae. comosa* subsp. *comosa*, while in group B, from subspecies *heldreichii*. Divergence of *Ae. biuncialis* chromosomal groups was accompanied by structural chromosome rearrangements, and the Ub genome proved to be less modified compared to the parental than the Mb genome.

Using an appropriate set of DNA probes, we identified a reciprocal translocation between 1MbL and 7MbL chromosomes, followed by pericentric inversion of the modified 1Mb in group A accessions. Intraspecific divergence of *Ae. biuncialis* was also associated with amplification/elimination/redistribution of repetitive DNA families.

Based on ngs-sequencing of *Ae. biuncialis*, *Ae. umbellulata*, *Ae. geniculata*, *Ae. comosa*, subsp. *comosa* and subsp. *heldreichii* genomes we identified over 60 clusters of tandem repeats and analyzed their distribution on chromosomes of the studied species. Currently we determined physical localization of ten randomly selected repeats using sequential FISH. The location of some of clusters overlapped with position of known probes, while other clusters showed the unique distribution.

This work was funded by the Russian Science Foundation, project No. 24-16-00145.

P87 - Influence of the root system in the performance of wheat under sustainable systems - TRigoSost

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Abstract

Traditional varieties are characterized by their adaptation to the local environments in which they have been cultivated, often under low-input conditions. This adaptation makes them a valuable source of diversity capable of enriching the genetic pool of breeding programs, with particular interest in the search for adaptive traits in the context of ongoing climate change. Moreover, the European Regulation 2018/848, which recognizes the need to develop varieties adapted to organic farming, opens the door to the use of traditional varieties per se under these sustainable systems. In the context of previous works, a selection of sixteen varieties of bread wheat (*Triticum aestivum*) derived from the Spanish national collection (CRF-INIA) by the SSD technique have been extensively characterized in terms of agromorphology characters and quality traits. However, the root system (RSA) of these varieties has not been fully studied. Given the genetic variability present among the sixteen selected varieties and their diversity in terms of origin and growth cycle, the project TRigoSost hypothesizes that these materials may exhibit differentiated root system traits, considering both the seminal and the adult plant stages. The existence of specific RSA traits may provide an opportunity to select materials with enhanced adaptation to organic systems in strategic regions for wheat cultivation, mainly rainfed. Furthermore, the varieties are studied against the reference variety Chinese Spring, which is of great relevance for future genetic studies using populations derived from the cross between these materials.

Work supported by the Madrid Government (Comunidad de Madrid-Spain) under the Multiannual Agreement 2023-2026 with Universidad Politécnica de Madrid in the Line A, Emerging PhD researchers.

P88 - Digitalize wheat haplotype block diversity towards cost-efficient genotyping and knowledge integration

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Abstract

The food demands grow rapidly under the trend of rapid population growth; advanced computational algorithms are needed to enhance breeding efficiency and precision. However, for species exhibiting extensive genome size, intricate evolutionary history, frequent intra- and interspecific introgression, and lagged gene cloning, such as wheat, a more efficient and informative approach to digitizing germplasm remains essential. Based on our previous efforts in genealogy dissection, lcQTH, a computational tool for tracing parental haplotypes of mapping populations via ultra-low-depth resequencing (uld-WGS) data, has been proposed to greatly reduce the cost for gene mapping. The tool integrated multiple variation types, including SNPs and Mb-scale CNVs, with a machine learning method and can help locate the QTL resolution into gene level by iteratively segmenting the parental recombination map at different resolutions. At natural population scale, we present the gHapMap framework, which employs a hierarchical, block-wise, and annotatable haplotype data structure to archive and index haplotype blocks in wheat. Based on our previous works in genealogy dissection, the framework systematically profiles haplotype blocks at both ancestral and contemporary levels and records the genotype, phylogenetic location, and manual annotations of each haplotype block. To achieve cost-effective haplotyping and help scan the genetic potential of large-scale germplasm collections, the digital haplotype archive can support haplotype block recognition via uld-WGS. Leveraging a global diversity panel consisting of more than 2000 wheat accessions, we constructed a haplotype digital archive, namely wheat-gHapMap, and demonstrated that the archive can anchor genetic knowledge such as functional alleles and SVs, further clarify the utilization trajectories of specific alleles, and reveal the genomic spreading backbones of founder genotypes. We believe that the gHapMap framework and the haplotype block-based digital genetic description of genetic resources would effectively facilitate future genomic analysis and smart breeding design.

P89 - Accumulation of ph1 (zip4-5B) and ph2 (msh7-3D) mutations fails to boost homoeologous recombination in hexaploid wheat

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Abstract

Diversification of the hexaploid (bread) wheat genetic pool using wild genetic resources relies on effective meiotic recombination (crossover) between wheat chromosomes and their counterparts from related species (homoeologues). However, crossover between homoeologues is normally suppressed by two major genes, ZIP4-5B (Ph1) and MSH7-3D (Ph2). We investigated the effect of introducing zip4-5B and/or msh7-3D mutations into interspecific hybrids derived from crosses between wheat and *Aegilops variabilis*. Single and double mutants were exploited in Chinese Spring (CS) and Cadenza (Cad) genetic backgrounds, as well as in a CS/Cad recombinant background. Meiotic cells at metaphase I were scored for univalents, bivalents, and multivalents, from which chiasma numbers were deduced. We demonstrated a non-cumulative effect of simultaneous zip4-5B and msh7-3D mutations on homoeologous recombination, as homoeologous crossovers reached a maximum when ZIP4-5B alone was mutated. We also showed that hybrids carrying both the zip4-5B and msh7-3D mutations in the same genetic background exhibited a higher recombination rate compared to a double mutant in the CS/Cad recombinant background. The progression of meiosis was also monitored in the various interspecific hybrids mutants, revealing clear disruptions. Thus, our study provides key insights for optimizing the introgression of beneficial alleles from wild relatives into elite wheat germplasm; first by demonstrating the efficiency of ZIP4-5B and MSH7-3D mutations independently and in combination and second by elucidating the influence of the genetic background in which these mutations are present in an interspecific hybrid context.

P90 - Exploring seasonality in wheat through alternative growth habits

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Abstract

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

P91 - Molecular characterization of introgressions from *thinopyrum ponticum* conferring stem solidness in Canadian wheat

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Abstract

Breeders routinely incorporate novel alleles for desirable traits like pest and disease resistance, and improved agronomics from related species within the Triticaceae tribe into the bread wheat (*Triticum aestivum*), yet interspecific hybridization and subsequent characterization of introgressed DNA remain challenging and slow. This study aims to characterize *Thinopyrum ponticum* introgressions associated with stem solidness, the primary form of genetic resistance to the wheat stem sawfly and develop genetic molecular markers to facilitate their selection in breeding programs. Two wheat-*Thinopyrum* intergeneric lines developed at the University of Saskatchewan, Canada, from a cross between hexaploid spring wheat cultivar Crocus and *T. ponticum*; (cv. Orbit), will be characterised using fluorescence and genomic in situ hybridization combined with whole genome PacBio HiFi sequencing to determine the size and genomic location of introgressed segments. Genomic regions that are specific to *Thinopyrum* species and consistently present across solid-stem introgression lines will be prioritized for marker development. Kompetitive Allele-Specific PCR (KASP) markers will be designed and validated in backcrossed populations derived from intergeneric lines which are segregating for stem solidness. The results of this study will provide breeder ready tools to expedite integration of solid stem germplasm into wheat improvement programs and further our understanding of how chromatin derived from *Thinopyrum* contributes to stem solidness.

P92 - Multiple modes of chromosome elimination during hybrid embryogenesis in the subfamily wide hybridization of wheat, oat, and Pennisetum species

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Abstract

Wide hybridization is a practical approach for expanding genetic diversity in wheat breeding. However, hybridization among distantly related species often results in multiple levels of incompatibility. Wheat can hybridize with species within the same subfamily that are distantly related, such as maize (*Zea mays*), sorghum (*Sorghum bicolor*), and pearl millet (*Pennisetum glaucum* / *Cenchrus americanus*). In these crosses, sperm cells from non-wheat species can fertilize wheat egg cells under normal pollination conditions. However, non-wheat chromosomes are subsequently eliminated during early embryogenesis, resulting in wheat haploids.

In contrast, in oat (*Avena sativa*) × pearl millet crosses, all pearl millet chromosomes are retained within the haploid oat genomic background throughout embryogenesis and early seedling development. These findings indicate that maternal factors play a key role in chromosome elimination during wide hybridization among wheat, oat, and pearl millet. A deeper understanding of the mechanisms underlying chromosome elimination in hybrid cells, along with the ability to manipulate the factors involved, could facilitate the expansion of genetic diversity in wheat.

In this study, paternal factors involved in chromosome elimination were investigated. Wheat and oat were hybridized with several *Pennisetum* species, and distinct patterns of chromosome elimination during early embryogenesis were observed: (1) rapid elimination leading to maternal haploid cells, (2) gradual elimination also resulting in maternal haploid cells, (3) partial retention of chromosomes producing partial hybrids of oat and *Pennisetum* cells, and (4) no chromosome elimination, resulting in true hybrids. These results suggest that diverse chromosome elimination factors were present among different *Pennisetum* species.

P93 - Genome-wide association study of male reproductive traits reveals a novel locus in *aegilops tauschii*

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Abstract

Hybrid crop production is a powerful approach to increasing wheat yield; however, several barriers hinder the widespread adoption of this technology. Male parent lines that produce large number of pollen and long anthers are important traits for improving pollination efficiency. Nevertheless, pollen number and anther length have been shown to decrease during the process of domestication. Bread wheat originated from hybridization between domesticated tetraploid wheat and the wild species *Aegilops tauschii*, which is considered to contain greater genetic diversity than cultivated wheat.

In this study, we investigated pollen-related traits (pollen number, pollen size and anther length) in *Ae. tauschii* to evaluate their phenotypic diversity and to identify genetic loci controlling these traits using genome-wide association studies (GWAS). During the 2021-2022 season, pollen number and anther length were measured in approximately 200 accessions from an *Ae. tauschii* core collection, and GWAS was conducted; however, no significant peaks were detected. Therefore, in the 2024-2025 season, the number of accessions was increased to approximately 570 for further analysis. In addition, seed size was measured and time-series imaging of plants was performed using an unmanned aerial vehicle (UAV) during the 2024-2025 season.

Analysis of pollen-related traits in the 2024-2025 season identified a significant peak associated with anther length. Interestingly, although not significant, a peak at the same genomic position was also detected from the pollen number. This locus was distinct from peaks previously identified in GWAS of tetraploid and hexaploid wheat, indicating that it represents a novel genetic region derived from *Ae. tauschii*.

These findings highlight the importance of wild genetic resources for discovering new loci controlling pollen-related traits and provide valuable insights for improving male parent lines in hybrid wheat breeding.

P94 - A trait-customized Wheat (*Triticum aestivum* L.) core-collection provides sources of resistance against powdery mildew (*Blumeria graminis*) for its use in pre-breeding

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Abstract

We investigated the genetic architecture of powdery mildew (PM) resistance in a winter wheat collection (CC) comprising 200 modern European elite cultivars and 600 diverse IPK genebank accessions. All 800 genotypes were evaluated for resistance to natural PM infections in four multi-environment field trials and in detached leaf assays (DLAs) using isolates FAL92315 and Bgt 96224. Heritability was moderate to high in field trials and increased across environments, while DLA-based seedling resistance showed high heritabilities (0.73 and 0.77), reflecting the precision of controlled conditions. Seedling responses to both isolates were moderately correlated ($r = 0.65$), indicating partially overlapping virulence spectra. Preselection of 150 resistant (PMR) and 50 susceptible (PMS) genebank accessions based on preliminary genotyping-by-sequencing (GBS) data and seedling assays with FAL92315 effectively enriched phenotypically contrasting material. PMR accessions consistently exhibited higher resistance than PMS across isolates and field environments, demonstrating that selection with a single isolate enabled partial indirect selection for broader resistance. Although elite cultivars were on average more resistant—highlighting successful gene stacking in breeding—the PMR subset included individual accessions matching the best elite cultivars across testing systems. In some subpopulations, resistance distributions deviated from normality and followed bimodal patterns, suggesting the presence of major-effect loci alongside quantitative components.

To dissect the genetic basis of PM resistance, we conducted both reference-based SNP GWAS and reference-free k-mer-based association analyses. The k-mer GWAS identified two major loci on chromosomes 2A and 5B. The 2A locus co-localized with the known resistance gene *Pm4*, whereas the 5B locus on the long arm represents a novel resistance region. Synteny analyses indicated that this locus is unique to the elite cultivar 'Attraktion'. Identification of the underlying candidate gene(s) provides a promising new source of PM resistance, broadening the genetic basis of wheat improvement.

P95 - Activating the global potential of the Australian grains genebank with open data, digital tools and AI

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Abstract

The Australian Grains Genebank (AGG) houses one of the world's largest globally diverse wheat plant genetic resource collections. Through the AGG Strategic Partnership - a 5 year, \$30 million transformation program - the genebank is being reimaged from a traditional seed repository into an integrated bio digital resource centre powered by genomic innovation, open data and next generation digital tools.

This presentation highlights major achievements of the Partnership including the complete genomic characterisation of the AGG wheat collection of 50,000+ accessions - one of the largest wheat genotyping efforts to date. Building on this foundation, the Partnership has delivered an open source, connected ecosystem of digital tools designed to unlock the genetic potential of the collection for researchers, curators and breeders. These include platforms that link AGG genomics to global genebank and pan genome resources, integrate research and breeding knowledge directly with AGG accessions, and harmonise genotype datasets across technologies to enable high resolution cross genebank comparisons. For the first time, the full genetic landscape of the AGG collection can be explored alongside major global collections from CIMMYT, ICARDA and IPK, revealing both unique Australian holdings and shared diversity with international partners.

Completing this ecosystem is Bakery, an AI driven system currently in development that uses knowledge graphs and Large Language Models to connect a user's question - scientific, curatorial or breeding focused - to the most relevant genebank data, tools and resources. Bakery represents a step change in how users interact with genetic resources, lowering technical barriers and enabling rapid, evidence based decision making.

Together, these innovations are reshaping how Australian researchers and breeders access and apply plant genetic resources, accelerating the development of future wheat varieties and positioning the AGG as a globally connected, digitally enabled engine for crop improvement.

P96 - Discovery of stem rust resistance in a wheat wild relative using bulked segregant analysis sequencing

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Abstract

Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, remains a significant threat to global wheat production. The emergence of new races, such as the Ug99 lineage, highlights the need to identify and incorporate novel resistance into wheat breeding programs. This is particularly critical for Canadian durum wheat, where resistance is predominantly conferred by Sr13, to which virulence has already been detected. Wild wheat relatives harbour novel genes for disease resistance that can be utilized for wheat improvement. In this study, a tetraploid wheat diversity panel was screened against stem rust race DCB (pathotype TRRTF) to identify novel sources of resistance. One promising accession, domesticated emmer wheat (*Triticum turgidum* ssp. *dicoccum*) PI 94635, demonstrated strong resistance. Molecular marker analysis targeting known Sr resistance genes was conducted on PI 94635 to determine whether its resistance is attributable to a novel locus. PI 94635 was crossed with the universally susceptible durum wheat (*T. turgidum* ssp. *durum*), cv. Rusty and phenotypic evaluation of F₂ seedlings was used to determine the inheritance of resistance. Bulk segregant analysis sequencing (BSA-seq) was conducted on DNA bulks derived from F₂ plants expressing extreme resistant and susceptible phenotypes and aligned to reference genome Svevo (Svevo Rel. 2.0).

Marker assays for known Sr genes, confirmed resistance to DCB in PI 94635 is likely due to a novel resistance locus. Segregation in the PI 94635 x Rusty F₂ population indicated that resistance is controlled by a single dominant major gene. BSA-seq analysis identified a candidate region (~24 Mb) on distal end of chromosome 6BL. Sequence variants within this region were used to develop KASP markers, which were evaluated in the F₂ population to refine the candidate interval to 4.3 Mb.

These results identified a presumptive novel stem rust resistance locus on chromosome 6BL. The development of diagnostic markers will facilitate fine mapping and support marker-assisted introgression of this resistance into Canadian wheat breeding programs.

P97 - Population structure and genetic diversity of Japanese wheat collection assessed by genome-wide genotyping and gene targeted sequencing

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Abstract

Exploration of genetic diversity is essential for improving yield and environmental adaptability in wheat. Due to their geographical location, Japanese wheat varieties have evolved unique adaptations to high temperatures and humid conditions, providing valuable alleles such as Rht1, Ppd1 and Fhb1 to the global wheat breeding program. Although the Japanese Wheat Core Collection (JWC) has been established and characterized, its genetic diversity has not been fully explored because of limitations in the number of accession and the marker density. Here, we aimed to comprehensively characterize the genetic diversity of Japanese wheat by analyzing an expanded panel of 196 accessions, consisting of landraces and modern cultivars. To achieve this, genome-wide SNPs were obtained using a combination of SNP array, MIG-seq, and GRAS-Di technologies. In addition, we selected 548 genes associated with agronomically important traits based on previous studies in wheat and rice, and performed target capture sequencing of these genes. As a result, 42,731 high-confidence SNPs across the genome and within major functional genes were obtained. Population structure analysis using PCA and ADMIXTURE revealed that Japanese wheat accessions were classified into three major groups: cultivars from the northern region, traditional cultivars from the southern region, and modern cultivars from the southern region. In contrast, PCA analyses based on target capture SNPs showed that northern cultivars exhibited higher genetic diversity than southern traditional and modern cultivars in the agronomic traits-associated genes. Considering the breeding history of Japanese wheat, this elevated diversity in northern cultivars is likely derived from multiple introgressions through crosses with exotic germplasms. Furthermore, genome-wide association studies identified several QTLs associated with agronomic traits including culm length, days to heading, grain weight per spike, and protein content across multiple environments. These results provide a comprehensive view of genetic diversity within Japanese wheat and highlight Japanese germplasm as a valuable genetic resource for future wheat breeding.

P98 - Genomic analysis of *Thinopyrum* spp. introgressions on durum wheat 7AL arm via flow-sorted chromosome sequencing

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Abstract

The exploitation of beneficial yet largely unexplored gene content present in wild germplasm for wheat breeding is often hindered by interspecific cross-barriers, differences in ploidy level, and phylogenetic divergence among genomes. However, through the cytogenetic strategy of chromosome engineering (CE), it is possible to incorporate small chromosome segments from wild relatives into cultivated wheat and enable effective use of alien genes. Several durum wheat (DW) recombinants were developed via CE, carrying homoeologous segments from the wild *Thinopyrum* genus on their 7AL arm. These segments confer resistance to multiple diseases and improve yield- and quality-related traits under both optimal and stress conditions, including drought, heat and salinity. To investigate their genomic composition, three individual 7AL-*Thinopyrum* recombinant chromosomes (RC) were isolated by flow-sorting following FISHIS labelling and sequenced. The recombinants R23, R74 and R69 carry 40%, 28% and 23%, respectively, of the distal DW 7AL arm replaced by either *Th. ponticum* 7el1 chromatin alone (R23), or composite segments of *Th. ponticum* 7el1 + *Th. elongatum* 7E (R74, R69). Reads were aligned to the DW 'Svevo' and *Th. elongatum* reference genomes to identify introgression breakpoints (BPs), which were validated through the development of novel CAPS markers flanking the BPs. A total of 2,786 putative *Thinopyrum* orthologues were identified across the three segments. Gene ontology analysis highlighted that a total 61.3% of enriched Biological Process terms were shared among RC pairs and all three together, while others were RC-specific: "L-tryptophan metabolic process", "microtubule-based movement" and "photosynthesis, light reaction" were found only in R23 (30.7%), "fructose metabolic process" resulted unique to R74 (5.3%), while "biosynthetic process", "iron-sulphur cluster assembly" and "phosphatidylinositol metabolic process" were exclusively enriched in R69 (2.7%). Transcription factor analysis revealed 83 genes belonging to NAC (22), bHLH (9), MYB (5), MYB-related (5), WRKY (5), ERF (3), and other families. Using conserved synteny within Triticeae species, several putative *Th. ponticum* orthologues involved in plant development and molecular stress adaptation were mapped within defined *Thinopyrum* physical regions, providing a framework for future functional characterisation of alien genes and marker-trait association studies to support the development of more resilient and productive wheat cultivars.

P99 - Winter survival in Iceland explained by population structure in Nordic winter wheat germplasm

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Abstract

Changing climate is expanding the cultivation of winter wheat northwards while causing unstable winters threatening winter survival (WS). The aim of this study was to analyze WS and population structure in the germplasm of the Nordic Genetic Resource Center.

We characterized the population structure of 714 winter wheat accessions from 33 countries and comprised 60 landraces, 279 breeding lines, 274 improved cultivars, and 101 accessions of unknown origin. WS of these accessions was assessed, in Iceland. They were genotyped with a 25K Illumina SNP array. We used principal component analysis (PCA) and clustering methods to analyze population structure. We performed genome-wide association studies (GWAS) to identify markers associated with WS and frequency of significant markers across the admixture groups.

Results showed variation in winter wheat survival was associated with PC2. Results of the admixture analysis at K=3 showed group 1 (n=150) of Western European ancestry with the lowest WS (4.4%), group 2 (n=350) with Swedish ancestry the highest (57.3%), and group 3 (n=217) with Northern European ancestry showed intermediate WS (38.3%). Hierarchical clustering into three clusters using Ward D2 method based on Nei's genetic distance showed cluster I (North-Western European, n=136) had 4.6% WS, cluster II (Swedish-dominated, n=367) 56.5% WS, and cluster III (diverse origins including Finland, Italy, and USA, n=211) 38.7%. Population structure was consistent between the two methods ~86% of genotypes overlapping. GWAS showed 20 significant markers on 10 chromosomes associated with WS. For the most significant marker on Chr5a the frequency of the T/T genotype was 32.9% in cluster I, 1.4% in cluster II and 18.1% in cluster III. The frequency of the T allele in surviving and non-surviving accessions was 15% and 25%, respectively. Notably, 18% of surviving lines were heterozygous compared to only 4% of non-surviving lines. The frequency of heterozygosity was 1%, 6%, and 26% in clusters I-III, respectively.

We found a relationship between ancestry and winter survival and identified 20 regions associated with winter survival. The concordance between hierarchical clustering and admixture analysis demonstrates a strong relationship between genetic ancestry and winter survival.

P100 - Stability of grain yield and protein content in winter wheat under varying production conditions

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Abstract

The stability of grain yield (GY) and grain protein content (GPC) was evaluated in 25 winter wheat genotypes across 16 environments, defined as combinations of two locations, two growing seasons, and four nitrogen fertilization levels. The results of the AMMI analysis revealed statistically significant effects of genotype (G), environment (E), and their interaction (GE) for both traits studied. The environment accounted for the largest proportion of total variability, explaining 74% of the treatment sum of squares for grain yield and 76% for grain protein content. In comparison, genotype contributed 11% to the variation in grain yield and 20% to the variation in protein content, while the $G \times E$ interaction accounted for 15% and 4%, respectively. The AMMI analysis enabled differentiation of genotypes based on their stability and performance under varying production conditions. The Finlay and Wilkinson regression coefficient (b) showed a moderate positive correlation ($r = 0.40^*$) with mean grain yield, indicating that higher-yielding genotypes responded more favorably under improved production conditions. Conversely, the absence of a significant correlation between coefficient b and mean grain protein content suggests that simultaneous selection for high mean performance and stability of protein content is feasible.

P101 - Wheat genetic background selection: a core prerequisite for wide hybridization and efficient utilization of agropyron cristatum 6P elite genes

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Abstract

Wide hybridization is a critical technique for broadening the genetic basis of common wheat and breaking through the bottleneck of wheat genetic improvement. The selection of recipient wheat genetic background is a key determinant for the success of wide hybridization and the stable breeding value of elite alien genes. *Agropyron cristatum* ($2n = 4x = 28$, PPPP), an important wild relative of wheat, has been confirmed to carry multiple elite alleles conferring disease resistance, stress tolerance and yield improvement on its chromosome 6P, while its breeding adaptability in different elite wheat cultivar backgrounds remains unclear. In this study, the A. *cristatum* chromosome 6P was introgressed into two genetic backgrounds, Fukuho and the leading wheat cultivar Jimai 22 in China. We systematically confirmed the decisive effect of the recipient genetic background on the phenotypic effect of alien chromosomes. Introgression of chromosome 6P resulted in normal green leaves with significant positive agronomic effects in the Fukuho background, but stably induced a yellow green leaf phenotype with significant negative impacts on key agronomic traits in the Jimai 22 background, such as a 18.07 g reduction in thousand grain weight and a 24.14 decrease in grain number per spike. Genetic analysis confirmed that this phenotypic differentiation was caused by genetic interactions between a specific locus on chromosome 6P and genes in the Jimai 22 genome. Using hybrid populations derived from wheat A. *cristatum* 6P deletion lines, translocation lines, and Jimai 22, we mapped the locus controlling this background dependent phenotype to the 0.81-1.00 bin of the short arm of chromosome 6P (6PS), and annotated 50 A. *cristatum* derived candidate genes related to chlorophyll metabolism and chloroplast development in this interval. This study confirms the core regulatory role of recipient wheat genetic background selection on the phenotypic effect and breeding utilization value of alien chromosomes in wheat wide hybridization. It not only provides direct theoretical guidance for the efficient utilization of elite genes on A. *cristatum* chromosome 6P, but also establishes a research paradigm for the ubiquitous background dependence of alien genes in wheat wide hybridization.

P102 - Breeding for better durum: enhancing defense against fusarium headblight disease

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Abstract

Durum wheat is susceptible to Fusarium Head Blight (FHB), one of the most destructive fungal diseases in cereals, severely affecting grain yield and end-use quality. The most sustainable strategy for controlling FHB is resistance breeding. However, resistance breeding in durum wheat is constrained by its narrow genetic base. In its hexaploid wheat relative, anther extrusion has been associated with increased FHB resistance and is a useful criterion for indirect selection. This study aimed to investigate whether a similar association exists in durum wheat. Therefore, a diverse population of 687 lines was evaluated, comprising Central European cultivars and breeding lines (n=138), BOKU experimental lines (n=89), and 460 progeny lines derived from crosses between the old French cultivar Capdur, characterized by high anther extrusion, and BOKU experimental lines. All materials were artificially inoculated with *Fusarium culmorum* and phenotyped for FHB resistance, anther extrusion, and plant height over four consecutive years. The results showed large genetic variation and high heritability for all traits investigated. BOKU experimental lines exhibited the lowest disease severity, with a mean AUPDC value of 201, compared with the Capdur progeny population (AUDPC = 277) and the collection of cultivars and breeding lines (AUDPC = 390). Anther extrusion showed a strong and significant negative association with FHB severity ($r^2 = 0.48$, $p < 0.001$), which remained significant after correction for plant height, indicating that this floral trait is also associated with FHB resistance in durum wheat independent of plant stature. In addition, several short and moderately resistant genotypes were identified, combining favorable agronomic performance with reduced disease susceptibility. Thus, these results highlight the potential of anther extrusion as a robust and effective indirect selection for improving FHB resistance in durum wheat.

P103 - Variability of grain yield and quality in winter wheat accessions from the Croatian gene bank released over 60-year period

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Abstract

The aim of the study was to determine the variability of grain yield and yield components, as well as test weight and grain protein content, in a panel of 170 winter wheat varieties from the Croatian Gene Bank released between 1959 and 2018. A field experiment including these 170 varieties and five standards, arranged in an "augmented" design, was conducted at three Croatian locations over two consecutive growing seasons. Standard agricultural practice for wheat production in the region was used in the experiment, without fungicidal protection against diseases and with a sowing density of 500 grains per m². Changes in trait means and trait stabilities (expressed as Shukla's stability variance) over years were estimated by regressing the corresponding variety values on the year of its release. Grain yield significantly increased over time at a rate of 0.4% per year, while grain yield stability was not affected by the year of release. The increase in grain yield over time was accompanied by a significant increase in the number of spikes per m² and the number of grains per spike, at rates of 0.20% and 0.15% per year, respectively, while thousand grain weight was not affected. For test weight, both mean and stability significantly increased over time at rates of 0.1% and 1.2% per year, respectively. On the other hand, although mean grain protein content did not change over time, its stability increased at a rate of 0.9% per year. Across the entire panel, the correlation between grain yield and grain protein content was -0.32** and between test weight and grain protein content was 0.24**, while grain yield showed no significant correlation with test weight.

P104 - Yield and yield components evaluation in a subset of genotypes from the global durum panel (GDPv1) under drought and normal rainfall conditions

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Abstract

In durum wheat breeding, a key decision is which traits should be selected to increase yield potential. For this purpose, a field experiment was conducted using an alpha lattice experimental design with three replicates including 60 selected genotypes from the Global Durum Wheat Panel (GDPv1) and three local checks over two growing seasons: 2022/23, with an annual rainfall of 363 mm (drought); and 2023/24, with a normal rainfall regime of 660 mm. The ANOVA of yield and yield component using both growing seasons established a significant genotypic and environmental effects. The average grain yield in the season 2022/23 was 2211 kg/ha, while in 2023/24 reached 4270 kg/ha. Pearson correlation analyses showed that the number of grains/m² (GNSM) had the highest correlation with grain yield in both seasons ($r=0.74$ and $r=0.84$ for the first and the second year, respectively). The harvest index was the second trait highly correlated with grain yield and its importance was not affected by environmental conditions ($r=0.65$ and $r=0.64$). The number of spikes per square meter had a greater influence on grain yield under drought conditions ($r=0.49$ vs $r=0.38$). However, in the second year, the grain-filling period was a more influential factor ($r=0.66$ vs. $r=0.48$), with aerial biomass, grain number and spikelet number per spike showing secondary importance. On the other hand, the thousand-grain weight (TGW) remained relatively stable in both seasons ($r=0.31$ for the first season and $r=0.29$ for the second). Simple linear regression models confirmed that GNSM explained 61.5% and 69.93% of the yield variability in the respective years. TGW, meanwhile, explained 8% and 9.21% of the variability. A Mantel test was performed on the correlation matrices between the variables for both seasons resulting highly significant ($r=0.868$, $p=0.001$). Although all yield-determining components are important, GNSM was the primary determinant of yield. Variation in the grain-filling period also emerged as a key trait under normal rainfall conditions; therefore, both should be prioritized in high-yield breeding programs.

Keywords: *Durum wheat, GDPv1, yield components.*

P105 - Genome-wide association study of root morphology traits in a collection of durum wheat cultivars and landraces

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Abstract

Root architecture can be targeted in breeding programs to develop crops with more efficient capture of water and nutrients, and therefore more resistant to drought. A collection of 138 T. durum cultivars and 150 landraces, selected from the Global Durum Panel, were grown in ryzotrons in controlled conditions, in order to study morphological traits of the shoot and root apparatus. The root images were taken at five-leaves stage and the root measurements were performed using the Win-RHIZO system. Several morphological traits of the roots were recorded using the root analysis software, as length, surface area, mean diameter, volume, number of tips, crossing and root biomass. For shoot traits, maximum shoot length, number of shoots, and shoot biomass were evaluated. A wide phenotypic variation has been found in the two panels, particularly in the panel of the landraces. Genotyping data were available for 13,475 single nucleotide polymorphism (SNP) markers, used for genome-wide association study. For the cultivars, mixed linear model revealed a total of 50 QTLs for shoot traits, from 6 for plant height to 24 for total biomass, while 72 QTLs were identified for root traits, from 7 for diameter and surface area to 14 for root biomass. Some regions were found to be associated specifically to root traits, as the QTLs on chromosome 6A, position 16-20 Mb, for root biomass and average diameter. In other cases, we found the co-localization of QTLs involved in the control of both root and shoot traits, as the QTL on chromosome 6A at 598 Mb, for root biomass, root surface area, shoot biomass and total biomass. The work is in progress to identify genetic determinants of the traits under study in the panel of the durum landraces, in order to investigate the evolution and fixation of loci for root morphology with durum wheat breeding. Besides novel QTLs, some of the QTLs identified in the present study found correspondence with regions previously mapped, providing a validation of the mapping approach herein used.

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P106 - Epigenomic dynamics and changes in chromosomal architecture during synthetic wheat formation

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Abstract

Polyploidy has occurred frequently in most plant lineages and is common in crop species. In many polyploids such as wheat, their genomes are maintained independently. How these separate genomes occupying a common nucleus interact and modulate a common gene expression pattern is poorly understood, despite the importance of polyploidy in generating important crop phenotypes. We have explored the epigenomic states of newly formed wheat hexaploid synthetic lines generated by crossing a common elite *Triticum durum* (AABB) and two genetically divergent *Aegilops tauschii* (DD) lines. New patterns of gene expression are rapidly established and mirror in part those seen in elite wheat lines. Gene and repeat methylation patterns are essentially unchanged, while changes in histone modification are frequent and conform to changes in gene expression patterns, with the DD genome most affected. The major, and perhaps primary, epigenomic changes involve chromosome compaction such that the more extended diploid DD chromosomes compact to similar extents as the AABB chromosomes in the AABBDD nucleus. This compaction has profound effects on chromatin boundaries and leads to compaction of accessible chromatin domains with a concomitant reduction in transcriptome levels in the DD genome.

P107 - Morphological and genetic diversity in serbian wheat germplasm

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Abstract

Traditional wheat landraces represent valuable genetic reservoirs shaped by long-term farmer selection and local adaptation. To assess the diversity preserved within Serbian germplasm, we compared 18 Serbian landraces with 17 Serbian cultivars, including both pre- and post-Green Revolution varieties developed through formal breeding. Field evaluations conducted over two growing seasons revealed consistent phenotypic differentiation. Across seasons, plant height in landraces frequently exceeded 130 cm, whereas most cultivars ranged between 95 and 130 cm, reflecting breeding-driven reduction in stature. Flowering time also tended to be delayed in landraces, reflecting historical adaptation patterns, while modern cultivars have been selected for earlier flowering to escape heat and drought stress. Genetic diversity was assessed using SSR markers. A total of 400 alleles were detected. Landraces exhibited higher allelic richness (7.04 alleles per locus) than cultivars (6.02), and slightly higher gene diversity. Importantly, landraces harbored 189 private alleles and 162 rare alleles (<5%), substantially exceeding the numbers observed in cultivars (115 private and 62 rare alleles). These findings demonstrate that traditional germplasm retains unique variation that remains only partially incorporated into modern breeding pools. Principal Coordinate Analysis explained 18.3% and 14.6% of the total variation along the first two axes and revealed clear separation between post-Green Revolution cultivars and most landraces. Pre-Green Revolution cultivars largely overlapped with landraces, reflecting a transitional genetic profile. Together, phenotypic and molecular evidence highlights Serbian landraces as important genetic reservoirs for future wheat improvement. The analyzed genotypes are currently being utilized in a follow-up project focused on drought tolerance assessment, aiming to explore adaptive potential embedded within this traditional germplasm.

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P108 - The indigenous, traditional Georgian wheat species, disease-resistant and healthy food

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Abstract

Bread is a staple food in Georgia. Wheat consumption in Georgia is one of the highest in the world - about 130 kg per capita. Wheat grain has always been linked to Georgian food traditions and culture since its domestication. The importance of the breeding and nutritional value of the old (ancient) and relict wheats is appreciated, and their reintroduction to production is being discussed at present in Georgia.

All seven domesticated ancient hulled wheat species (*sensu stricto*) occur in Georgia (*Triticum palaeocolchicum*, *T. macha*, *T. timopheevii*, *T. zhukovskyi*, *T. monococcum*, *T. dicoccum*, *T. spelta*), while only three of them (*T. monococcum*, *T. dicoccum*, *T. spelta*) are found in other countries; the remaining four (*T. palaeocolchicum*, *T. macha*, *T. timopheevii*, *T. zhukovskyi*) are indigenous to Georgia.

Colchic emmer - *T. palaeocolchicum* (= *T. turgidum* subsp. *georgicum*) has important agronomic characteristics that may be utilized in wheat breeding: resistance to fungal diseases, fertile spikelets (34-39 spikelets per spike)

'Makha wheat' - *T. macha* (= *T. aestivum* subsp. *macha*), is a hulled wheat, which was highly priced for bread-baking among the local population. Its bread is white, tasty, and flavorful, not to mention its ability to stay soft for several days.

'Zanduri' is known as the most special local wheat landrace in Georgia. Three hulled domesticated species are identified in the 'zanduri' population: 1. *T. monococcum*, 2. *T. timopheevii*, and 3. *T. zhukovskyi*. Due to its outstanding resistance to fungal diseases, *T. timopheevii* deserves special attention from breeders. Bread baked from *T. timopheevii* flour is very tasty and flavorful; it remains soft for the whole week. Hexaploid wheat - *T. zhukovskyi* is known as a drought and frost-resistant plant. It has the potential to grow in all types of soil.

The fifth indigenous wheat species is free-threshing Karthlian wheat - *T. carthlicum* (*T. turgidum* subsp. *carthlicum*), mistakenly called 'Persian' wheat, characterized by early maturity and easy threshing. It is characterized by strong immunity to diseases, frost resistance, and a short vegetation period.

The indigenous, traditional Georgian wheat species, disease-resistant and healthy food

The indigenous, traditional Georgian wheat species are disease-resistant and healthy food.

P109 - Integration of molecular cytogenetic techniques and SNP genotyping to identify the genomic loci associated with Aegilops speltoides derived leaf rust resistance gene

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Abstract

Crop wild relatives like *Aegilops speltoides* (SS) are a great source of unique alleles/genes to improve the available variability in the wheat gene pool. Out of 83 designated Lr genes, six genes Lr28, Lr35, Lr36, Lr47, Lr51 and Lr66 have been introduced from *Ae. speltoides* into common wheat along with reports of some undesignated genes. Stem rust resistance genes Sr32, Sr39, Sr47 and powdery mildew resistance gene Pm12 have also been transferred from *Ae. speltoides*. The genetic stock Sel.2427 (*Triticum aestivum* cv Sonalika // *Ae. speltoides* acc. EC331772) possess dominant broad-spectrum resistance against leaf rust pathogen. Genomic in situ hybridisation studies in Sel.2427 revealed presence of three *Ae. speltoides* genome segments on two chromosomes. Karyotyping by FISH using repetitive probe (AAG)n revealed that the two chromosomes involved are possibly 2D and 2B. In the 2D chromosome, *Ae. speltoides* translocations have occurred in both the telomeric regions whereas in 2B chromosome, S genome translocation is limited to one sub telomeric end. Molecular characterisation using 35K Wheat breeder's SNP array revealed that 6.28% of genome is transferred from S genome with maximum introgression in homoeologous group 2. Bulk segregant analysis in the F5(Agra Local/Sel. 2427) population revealed that out of 35143 markers, 6172 showed parental polymorphism and 290 showed polymorphism among homozygous resistant and susceptible bulks. Out of these it was observed that 19 markers on the short arm of 2D chromosome co-localised in a 14 Mb (3.06-17.82Mb) region suggesting that the leaf rust resistance gene is present in this region.

P110 - Exploring the regulatory mechanisms of hybrid incompatibilities in synthetic hexaploid wheat by transcriptome analysis

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Abstract

Triticum turgidum is a valuable genetic resource, because this group includes diverse genetic variation not found in *T. aestivum*. To facilitate the genetic dissection of agronomic traits in *T. turgidum*, we developed synthetic hexaploid wheat populations by crossing intraspecific F1 hybrids of *T. turgidum* with *Aegilops tauschii*, resulting in populations segregating for *T. turgidum* alleles. During the development of these populations, we observed plants exhibiting hybrid incompatibilities caused by a gene located on chromosome 2BL (Nakanishi et al., 3rd IWC). However, the molecular genetic mechanisms of hybrid incompatibilities is still unclear. In this study, we performed phenotyping and transcriptome analysis to reveal the mechanisms using two synthetic hexaploid lines: one exhibits hybrid incompatibilities (SH18-40) and the other grows normally (SH2098).

First, we cultivated the two lines under normal temperature (20°C/18°C, 16h) and low temperature (4°C, 16h) conditions to examine the number of tillers and growth phenotypes. As a result, SH18-40 exhibited the Grass-clump dwarf (Gcd) phenotype under both temperature conditions. However, the Gcd phenotype was more pronounced at normal temperature than at low temperature.

Next, we conducted RNA-seq analysis using crown tissues of the two lines grown under field and controlled (20°C/18°C, 16h) conditions, just before week 6 when significant differences in tiller number became evident. GO enrichment analysis revealed that GO terms related to “defense responses” were significantly enriched under both conditions. Furthermore, as in previous studies (Matsuda et al., 2017; Okada et al., 2017), PR1 expression was upregulated, and SPL expression was downregulated under both conditions. Based on the above, a causal gene induces an excessive defense response, leading to increased miR156 expression. Elevated miR156 levels then promote excessive degradation of SPL, preventing the transition to the reproductive growth phase and resulting in Gcd phenotype.

Finally, to determine the timing of exhibiting Gcd phenotype based on transcriptome patterns, we sampled crown tissues weekly after germination and performed time-lapse RNA-seq using Lasy-Seq (Kamitani et al., 2019). The transcriptome profiles differed in week 3. GO enrichment analysis revealed that GO terms related to “photosynthesis” were specifically enriched in week 3, suggesting that light stress-like response results in Gcd phenotype.

P111 - Linking aneuploidy, meiotic irregularities and fertility to phenology in synthetic octoploid wheat derived from *Triticum turgidum* and *Aegilops columnaris*

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Abstract

We generated synthetic octoploid wheat (AABB UcUcXcXc) by hybridizing *Triticum turgidum* cv. Langdon and *Aegilops columnaris* and tracked generations F2 until F5 using mitotic chromosome counts, meiosis observations, FISH karyotyping, flow cytometry and plant phenotyping. Root-tip meristems and DNA-content data showed wide and chromosome number distributions that are often below the octoploid euploid number, $n = 56$. This demonstrates constant whole-chromosome aneuploidy, which is in contrast with euploid tetraploid and hexaploid control data. Meiosis observations show frequent univalents, laggards, chromosome bridges, micronuclei and polyads compared to Langdon. PCA positions higher seed set with earlier heading and plant growth while having negative correlation to days to heading. Flow cytometry shows synthetic octoploids having relative densities above the hexaploid marker and some results having wide DNA content distributions. FISH karyotyping then revealed systemic chromosome loss and structural changes which includes loss or trisomy of chromosome 5B. This suggests that synthetic octoploid wheat has persistent chromosomal instabilities that may contribute to the absence of octoploid and higher-order polyploid wheat in nature.

P112 - Unlocking global wheat diversity through the panphenome

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Abstract

The global wheat genebank network holds over half a million accessions, yet breeders still lack practical means to exploit this vast diversity. The central obstacle is not material availability but the absence of integrated, high-resolution characterization that makes this diversity discoverable, comparable, and usable. Despite advances in genebank genomics, current efforts remain fragmented, leaving adaptive haplotypes and promising alleles largely untapped. To address this gap, we assembled the largest coordinated wheat genebank dataset to date. By integrating genomic resources from 14 national and international institutes, we generated a molecular diversity atlas for 115,581 accessions, enabling global population genomic analyses and systematic detection of redundancy. Identity-by-state analysis revealed that only about half of the genotyped accessions represent unique entries, providing the first global quantification of wheat genetic uniqueness across genebanks and highlighting the need for coordinated curation. We further demonstrate how genetically identical entries can be leveraged as a strategic asset. By linking identical accessions across collections, we integrated historical seed-regeneration data from 11 genebanks to establish a robust blueprint for across genebank integration. To address environmental heterogeneity arising from divergent management and climates, replicated field trials across Europe defined data-driven mega-environments based on genotype-by-environment interactions for key agronomic traits in spring and winter wheat. Integrating historical data at the mega-environment level could provide more accurate trait estimates and rankings for specific target conditions. To further extend accession characterization, we drew on precision collections from 11 genebanks, evaluated for key agronomic traits and major biotic and abiotic stresses, together with additional public data. These more than 400 decentralized, environment-specific training sets enabled genome-wide prediction of trait performance for thousands of genotyped accessions lacking phenotypic data, allowing systematic characterization across contrasting environments. Together, this work delivers a scalable framework to transform fragmented genebank resources into a unified, queryable global diversity platform. It provides both the conceptual roadmap and practical tools required to accelerate the use of genebank accessions, optimize collection management, and embed genebank diversity into modern wheat breeding pipelines.

P113 - Potential of traditional Spanish wheat varieties for organic farming and end-use quality analysis

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Abstract

Traditional landraces adapted to a wide range of climatic conditions represent highly valuable genetic resources for breeding wheat varieties suited to organic farming. Previous studies have shown that Spanish bread wheat landraces harbor extensive genetic diversity and are structured into four distinct genetic subpopulations [1]. Phenotypic characterization of these materials identified a set of sixteen cultivars with competitive values for grain protein content (GPC), gluten strength (measured by SDSS-test), and thousand-kernel weight (TKW), in addition to a high degree of variability for adaptability-related traits [2].

We present the first agromorphological characterization of these cultivars, and four commercial checks, cultivated under organic management. Cultivars were evaluated for yield, phenology and end-use quality related traits, such as, growth habit, days to heading, days to maturity, plant height, lodging, spikelets per spike, grains per spike, spikes per meter. The plots were mechanically harvested and yield (kg/ha), grain moisture content (%), test weight and TKW were obtained. Small scale end-use quality tests included GPC and SDSS-test. The analyses confirmed the substantial phenotypic diversity maintained within the Spanish landraces, as well as, the strong performance of several landraces relative to currently cultivated varieties under organic farming conditions in Spain. As example, yield (kg/ha) ranged from 4305 to 1600 for landraces and from 4287 to 2179 for the checks; spikes per meter ranged from 25 to 116 for landraces and from 42 to 82 for the checks; GPC ranged from 13.1% to 7.5% for landraces and from 11.6 to 7.1% for the checks.

Those promising results support further multi-environment evaluations to establish their suitability as high-quality and resilient varieties for organic systems. Moreover, the high variability observed in these materials makes them extremely valuable for the development of the first Spanish Wheat Nested Association Mapping (NAM) population. We expect that this population, currently in F7, will provide new insights into the genetic basis of traits related to quality, adaptability, and yield.

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1. Pascual L et al. (2020) BMC Genomics 21: 122.

2. Lopez-Fernandez M et al. (2021) Plants 10(4): 620.

P114 - Potential of traditional Spanish wheat varieties for organic farming and end-use quality analysis

José Jorge Palma Pérez⁽¹⁾ - Laura Pascual⁽¹⁾ - Patricia Giraldo⁽¹⁾ - Elena Benavente⁽¹⁾

⁽¹⁾ Universidad Politécnica de Madrid, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas/Biotecnología-Biología Vegetal, Madrid, Spain

Abstract

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P115 - QTL mapping for seminal root traits in Meridiano × Kyperunda durum wheat RIL population

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Abstract

Root phenomics, a crucial aspect of plant research, plays a pivotal role in understanding the genetic determinants of plant development and adaptation to diverse environmental conditions. This project aims to phenotypically characterize a recombinant inbred line population of durum wheat for root system architecture (RSA) traits using soil-filled rhizotrons and map corresponding QTLs. To capture the RSA we have employed an automated phenotyping platform (GrowScreen-Rhizo III) in which plants are grown in soil-filled rhizotrons, coupled with a specialized imaging software. We collected and quantified six root traits: total root length, primary and lateral root length, root system depth and width, and convex hull area. The RIL population was developed at the University of Bologna from a cross between cv. Meridiano and cv. Kyperunda. Former results based on investigation on diverse durum wheat cvs. had revealed clear morphological differences between the two parental lines, with Kyperunda showing greater total and lateral root length. Principal component analysis (PCA) identified convex hull area as the main driver of variation among genotypes, while correlation analysis highlighted strong associations between root length-related traits and spatial expansion. This work provides a solid phenotypic basis for the genetic dissection of durum wheat root system architecture. Ongoing genetic map construction and QTL analysis will enable the identification of genomic regions associated with key root traits, providing useful targets for future breeding efforts aimed at improving adaptation and resource-use efficiency.

P116 - Uncovering alien defences: detecting rust resistance introgressions in wheat using high-density snp arrays and segmentation

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Abstract

Wheat rust diseases, caused by *Puccinia striiformis* (yellow rust), *Puccinia triticina* (leaf rust), and *Puccinia graminis* (stem rust), represent a major threat to global wheat production. The incorporation of resistance genes derived from wild relatives through chromosomal introgressions provides an efficient means of enhancing resilience in modern cultivars. However, the precise identification and characterisation of these alien genomic segments remain challenging due to the similarity of wheat and relatives genomes and limitations in genotyping resolution.

This study aimed to detect known and novel introgressions in bread wheat using high-density SNP array data. We tested our detection capacity on well-known rust resistance loci. A methodological framework integrating the intensity of Affymetrix chip hybridisation, segmentation algorithms, and the detection of Off-Target Variants (OTVs) was developed. Genomic signals indicative of structural variation were refined to maximise detection accuracy.

As a proof of concept, this integrative approach enabled the identification of canonical rust resistance introgressions, including Sr24, Sr31, and Sr38, thereby confirming the reliability and resolution of the detection pipeline. Importantly, several putative novel introgressed regions were also revealed. Using rust postulation data, we were able to find diagnostic markers that can be used to screen progenies.

P117 - Identification and mapping of Hessian fly resistance genes in elite spring bread wheat genotypes

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Abstract

The Hessian fly (*Mayetiola destructor*) is an important insect pest of wheat, causing significant yield losses worldwide. In Morocco, infestations can reduce wheat yields by 32-36% during drought years, highlighting the need to identify new sources of genetic resistance. In this study, a set of ICARDA elite spring bread wheat lines was screened under greenhouse conditions using a Hessian fly population collected from the Settat region of Morocco. Phenotypic data were used to conduct a genome-wide association study (GWAS) based on a mixed linear model (MLM). The results revealed substantial genetic diversity among the tested lines and identified several genotypes showing potential resistance to the Hessian fly. These lines represent valuable genetic resources that could be exploited in future wheat breeding programs.

P118 - Differential phosphorus acquisition strategies in triticum turgidum ssp. durum: plant nutritional insights for future breeding

Tobias Reineke ⁽¹⁾ - ***Steffen Parl*** ⁽¹⁾ - ***Mahdi Jalali*** ⁽¹⁾ - ***Mirriam Chishala Chibesa*** ⁽²⁾ - ***Raphael Tiziani*** ⁽²⁾ - ***Salvatore Esposito*** ⁽³⁾ - ***Tanja Mimmo*** ⁽²⁾ - ***Pasquale De Vita*** ⁽³⁾ - ***Jakob Santner*** ⁽¹⁾

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Abstract

While phosphorus (P) use efficiencies remain low across cereals, the decline of mineral phosphate reserves threatens to increase P shortages in agriculture. To successfully select and/or engineer P-efficient cereals, deeper understanding of factors driving P acquisition in these crops is needed. To map P acquisition parameters in durum wheat (*Triticum turgidum* ssp. *durum*), a set of 19 genotypes, encompassing modern and old cultivars, landraces and mutants of old cultivars, were cultivated under differing fertilizer regimes (12.5 and 100 mg P kg⁻¹ soil) on a silty clay loam with 1.32 mg P kg⁻¹. Once 60% of individuals reached inflorescence, plants were harvested and analysed for dry matter yield and P concentrations. While dry matter production and shoot nutrient concentrations showed no marked differences between genotypes, comparisons of P acquisition efficiencies per root dry mass yielded differences of up to 450% between fertilization regimes and 1100% between genotypes, closely tied to differences in root biomass of up to 1200%. Discrepancies between P fertilizer regimes occurred only rarely. This indicates substantial variation in P acquisition strategies, e.g., differences in length and abundance of root hairs, root system architecture, and exudation of protons, phosphatase and carboxylate anions. Overall, modern genotypes differed significantly from old genotypes and landraces in all parameters associated with P efficiency. For example, the average root/shoot ratio was 0.14 in modern genotypes compared with 0.28 across older genotypes, while P acquisition efficiency (PAE) averaged 19.3 mg g⁻¹ versus 8.98 mg g⁻¹ in older genotypes. These results highlight the success of modern breeding programs and suggest that a further improvement of P acquisition efficiencies might be possible with improved understanding of underlying physiological and genetic drivers. These results will be used to select varieties for low and high PAE. Upcoming experiments will use low invasive DGT sampling to study carboxylate exudation in selected durum wheat varieties and their link to root morphology and phosphorus acquisition.

We acknowledge financial support by the Autonomous Province of Bolzano/Bozen - South Tyrol (Joint Projects Südtirol-DFG 2023, D-SÜD, contract number 6/34, CUP153C22003410003, DGT Exudates AG2222) and by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation, project number 525026426).

P119 - Australian donors based wheat nested association mapping population enhanced genetic diversity for stripe rust adult plant resistance in high yielding cultivars from eastern africa and south asia

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Abstract

Wheat stripe/yellow rust (WYR) is threatening wheat production worldwide, whereas demand for wheat is rising due to high population. WYR is best managed by deploying durable adult plant resistance (APR) genes. A Nested Association Mapping (NAM) population was generated to provide improved germplasm and to enable the development of markers linked to high value APR genes to facilitate their use in pre-emptive breeding. NAM population was developed through backcrossing of Australian donors to susceptible but preferred cultivars selected from east Africa and south Asia. Recurrent parents included Enkoy, Digelu, Danphe and Picaflor (Ethiopia); DBW 17, HD 2733 and PBW 343 (India); Gautam and NL 971 (Nepal); Inqilab 91 and Sehar 2006 (Pakistan). Resistant donors including Baxter, Diamondbird, Kingbird, Sunlin, Synthetic AUS30515 and 7SRRSN Line ISR1043.15 were selected based on APR to WYR in field tests in Australia.

The F1s derived from different crosses were each backcrossed with the recurrent parents. Each BC1F2 family was space planted at the PBI research station and plants with good agronomic traits were selected by culling tall/lodged and bushy genotypes. BC1F3 genotypes were raised by accelerated generation in controlled environment rooms at PBI. More than 2,200 BC1F4 families were sown in the field and BC1F5 seed of each recombinant inbred line (RIL) was harvested. Further, population size was reduced and selected 1,452 BC1F5 RILs were distributed among the partner countries. The NAM population was screened for rust resistance in all five countries for two years, enabling selection of the most promising genotypes for use in local wheat breeding programs. Our studies identified 127 RILs that carried very high levels of APR, and 84 carrying all stage resistance.

Sequencing of the NAM population including 1452 genotypes and parents using Illumina Platform with PE150 bp read lengths with minimum coverage of 200K reads/sample was completed and filtration of data and physical alignment with Chinese Spring genome is in progress. GWAS of the NAM population will allow the identification of markers linked to the high value stripe rust APR genes that provide adequate levels of resistance across different environments to facilitate their use in resistance breeding.

P120 - Defining the juvenile-to-adult phase transition in wheat revealed its diversification among spring wheat varieties

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Abstract

Plants undergo a juvenile-to-adult (JA) phase transition, which is characterized by drastic changes in shoot morphology and physiology during the vegetative growth stage. Although the JA phase transition has been well studied in rice and maize, it remains unexplored in wheat. This study aimed to elucidate when and how the JA phase transition occurs in wheat and to investigate its association with the winter-spring growth habit. We first compared leaf morphology, including leaf blade length and width, trichome density, and leaf tip shape, among the 1st to 6th leaves on the main stem of a Japanese common wheat cultivar Norin 61 (N61). Major changes in leaf morphology were observed between the 1st and 2nd leaves. The expression levels of *miR156* and *miR172*, which regulate the JA phase transition in other plant species, also changed between the 1st and 2nd leaf stages. Observation of shoot apex morphology confirmed that the plants remained in the vegetative growth stage until the 4th leaf stage. These results indicate that N61 initiated the JA phase transition after the 1st leaf stage and completed it before the 4th leaf stage. We then compared the JA phase transition timing among three winter and three spring varieties. The two spring varieties showed an earlier change in the ratio of leaf blade length to width, a potential indicator of the phase transition identified in N61. In addition, the spring varieties showed lower expression levels of *miR156*. These results suggested that the two spring varieties undergo an earlier JA phase transition than the other spring variety and all the winter varieties. *VRN1* expression would not explain these differences, as it was not associated with JA phase transition timing in either the six varieties or the *VRN1* near-isogenic lines. Our findings suggest that the diversification of JA phase transition timing occurred among spring varieties after the establishment of the spring growth habit.

P121 - Evaluation, validation and mapping of unknown leaf and stripe rust resistances from wheat genetic resources

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⁽¹⁾ Julius Kühn-Institut (JKI-RS), Institute for Resistance Research, Quedlinburg, Germany - ⁽²⁾ Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Department of Breeding Research, Seeland, Germany

Abstract

Several wheat rust-resistance genes have been identified and cloned in recent decades. However, many of these resistances have been overcome by virulent races, as demonstrated by the 'Warrior' stripe rust races in recent years. Annual infections of leaf and stripe rust, caused by *Puccinia triticina* and *Puccinia striiformis* respectively, result in significant yield losses of up to 50%, as well as quality losses. Integrating unused germplasm shows potential for breeding new cultivars with improved resistance genes. Therefore, it is important to identify genotypes with new, previously unknown resistances in order to avoid epidemics caused by cereal rusts.

The main objective of evaluation programmes is therefore to convert wheat collections in various European gene banks, particularly at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, into usable breeding resources. Over the past few years, more than 18,000 winter wheat and around 8,000 spring wheat accessions have been evaluated at the Julius Kühn-Institut (JKI) in Quedlinburg using high-throughput techniques. Together with genotyping-by-sequencing and genome-wide SNP array data, genome-wide association studies (GWAS) have identified QTL associations for both diseases on nearly all wheat chromosomes. Many of these QTL associations are linked to unknown resistance loci. Furthermore, a core collection of 800 accessions analysed at the seedling stage was evaluated in field trials, enabling the identification of adult plant resistance alongside seedling resistance in various trials with high broad-sense heritability ($h^2 > 0.5$).

The most promising accessions ('superdonors') were crossed with elite cultivars to generate segregating biparental mapping populations, which were subsequently genotyped to construct genetic maps and verify resistance QTLs. Genetic maps of four backcross populations were generated, and in one of these populations, a QTL conferring resistance to both rusts on chromosome 7B was detected, explaining 72% (stripe rust) to 75% (leaf rust) of the phenotypic variance.

The aim of these evaluation programmes is to create a publicly available library of donors carrying rare resistance loci that are effective against different races of stripe rust and leaf rust in order to accelerate the breeding of resistant elite cultivars.

P122 - Genome assemblies and comparative genomics of 18 aegilops species reveal evolutionary dynamics in diploid and polyploid wild wheat relatives

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Abstract

The genus *Aegilops*, the closest wild relative of wheat, represents a critical reservoir of genetic diversity for wheat improvement. Following the completion of genome assemblies for 18 *Aegilops* species, we conducted comprehensive gene annotation, phylogenomic, structural variation (SV), and repeat analyses to investigate genome organization and evolution across diploid and polyploid lineages. Assembly sizes ranged from 5.24 Gb in diploids to 12.65 Gb in polyploids, with scaffold N50 values up to 749.2 Mb, providing a high-quality foundation for comparative analyses. Gene annotation of these 18 newly generated genomes identified gene repertoires consistent with ploidy level and produced high-confidence gene sets suitable for comparative analysis within the *Triticum/Aegilops* complex. Phylogenetic reconstruction based on near single-copy orthologs from 63 *Triticum* and *Aegilops* genomes and subgenomes resolved evolutionary relationships across the complex and confirmed the diploid progenitors of polyploid species. Genome-wide structural variation analyses, using diploid progenitors as references, revealed extensive genomic rearrangements in polyploids, including large insertions, deletions, duplications, inversions, and translocations. These findings highlight substantial genome restructuring following polyploidization and provide insights into subgenome divergence. Repeat annotation across all genomes showed that repetitive sequences constitute the majority of genome content, accounting for 85.44-88.10% of the assemblies, with broadly consistent proportions across species and ploidy levels. Together, these integrated analyses provide a comprehensive comparative genomic framework for understanding *Aegilops* diversity and evolutionary history, while supporting future functional studies and wheat improvement efforts.

P123 - Integrating high-throughput genomics and advanced bioinformatics to rationalize and enhance utilization of wheat genetic resources from the National Genebank of India

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Abstract

Advances in genomic technologies and bioinformatics are revolutionizing the way genebanks characterize and harness their extensive germplasm collections. These approaches enable accurate identification of duplicate accessions and support the development of representative core sets that capture maximum genetic diversity. Such strategically curated subsets provide valuable resources for identifying novel genes and genomic regions associated with traits essential for climate-resilient agriculture. India's National Genebank conserves one of the world's largest wheat germplasm collections, yet only a fraction has been explored for crop improvement. To unlock its potential, we genotyped ~6,100 accessions using the 35K Axiom SNP array. Population structure analysis revealed six genetically distinct groups, guiding the development of a refined core set of 650 accessions. The analyses of both the full collection and the core set have enabled the uncovering of genomic regions associated with major biotic stresses abiotic stresses, and important quality traits such as grain protein and amylose content. In addition, we developed a bioinformatic tool for the identification of duplicate accessions within germplasm collections, which was applied to detect redundancies in the genotyped set. The unique donor lines and genomic regions identified through this work provide valuable genetic resources to strengthen global wheat improvement efforts, accelerating the development of climate-resilient, high-yielding, and nutritionally superior wheat varieties.

P124 - Watkins wheat landraces: a treasure of stripe rust resistance alleles identified using multi-model association analyses

Jasneet Singh ⁽¹⁾ - ***Jawad Awan*** ⁽¹⁾ - ***Naveen Kumar*** ⁽¹⁾ - ***Samuel Holden*** ⁽¹⁾ - ***Rajdeep Khangura*** ⁽²⁾ - ***Gurcharn Brar*** ⁽¹⁾

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Abstract

Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), remains a major global constraint to wheat production. Rapid pathogen evolution, exemplified by the recent breakdown of Yr15 in Europe, underscores the need to identify diverse and durable resistance loci. The A.E. Watkins landrace collection represents a globally diverse pre-breeding resource with substantial untapped variation for stripe rust resistance. In this study, 297 Watkins landraces were evaluated against six diverse Pst isolates (representing six races and three North American lineages) and subjected to genome-wide association analysis using high-density whole-genome resequencing data. Continuous phenotypic variation was observed across isolates, with several accessions displaying stable resistance across all lineages. A total of 87 QTLs were identified across all 21 wheat chromosomes. Ten loci co-localized with designated or cloned Yr genes, including Yr84, Yr85, Yrql, Yr71, Yr60, Yr62, Yr50, Yr68, Yr34, and Lr34/Yr18/Sr57. An additional 34 loci overlapped previously reported stripe rust QTL, whereas the majority did not coincide with known loci, suggesting potential novel resistance regions. Eighteen QTLs were supported by multiple isolates, and fourteen showed supports across statistical models, indicating robust genomic signals. Several Watkins accessions carried favorable alleles at multiple Yr-aligned loci, identifying promising donor candidates for validation and pre-breeding.

P125 - Unlocking adaptive genetic diversity in Mediterranean durum wheat using genome-wide association analysis

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Abstract

Durum wheat (*Triticum turgidum* subsp. *durum*) originated in the Fertile Crescent around 10,000 years ago and subsequently spread across the Mediterranean Basin, where farmer-driven selection led to the development of highly adapted traditional varieties. Although many of these landraces were replaced during the Green Revolution by semi-dwarf, high-yielding cultivars, they retain substantial genetic diversity and represent a valuable reservoir of adaptive alleles, particularly under abiotic stress conditions. In the context of climate change and increasing food demand, identifying genomic regions associated with environmental adaptation is essential for sustainable wheat improvement.

This study aims to identify quantitative trait loci (QTLs) linked to climatic adaptation in a diverse collection of Mediterranean durum wheat landraces using a genome-wide association study (GWAS) approach. Environmental variables corresponding to the regions of origin of each accession were retrieved using CLIMWAT 2.0, while genotypic data based on single nucleotide polymorphism (SNP) markers were obtained from the GrainGenes database. An environmental GWAS (envGWAS) was conducted using TASSEL v5.0 under a mixed linear model (MLM) framework, accounting for population structure and kinship relationships to minimize false-positive associations.

Significant marker-trait associations were used to define QTL intervals based on flanking molecular markers. Candidate genes within these regions were subsequently identified through genomic database searches, enabling the exploration of potential functional roles in stress response, temperature tolerance, and water-use efficiency.

The results are expected to provide insights into the genetic architecture underlying environmental adaptation in Mediterranean durum wheat and to identify novel alleles of interest for breeding programs. By leveraging the natural diversity preserved in traditional varieties, this work contributes to the development of climate-resilient cultivars capable of maintaining productivity under increasing temperature and water scarcity conditions.

P126 - Identification of novel genes for early heading from wild emmer wheat collected in Israel

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Abstract

One of the ancestral species of bread wheat (*Triticum aestivum* L.), wild emmer wheat (WEW, *T. turgidum* ssp. *dicoccoides*) is useful genetic resources for improving agronomic traits. In particular, developing early-flowering cultivars is a primary objective in Japanese wheat breeding to ensure adaptation to the local climate. To explore novel genetic resources for this trait, we evaluated the heading dates of 30 WEW accessions from various regions. This screening led to the identification of an Israeli-derived line, KU-195, which consistently exhibits an early-heading phenotype. Next, to identify novel genes or alleles associated with the early-heading of KU-195, we established an F2 population derived from a cross between KU-195 and a durum wheat cultivar, 'Langdon'. The genotypes were obtained by MIG-seq (Nishimura et al. 2022) to construct linkage maps. QTL analysis was performed using heading date obtained from the F2 population cultivated at the experimental farm at Kyoto University in 2022 and 2023 autumn-sown seasons (2022KU, 2023KU), and at Okayama University in 2023 and 2024 autumn-sown seasons (2023OU, 2024OU). We detected two QTLs on chromosomes 2A and 2B and found that individuals harboring recessive alleles at both loci showed late heading and dwarf traits. After excluding these late-heading individuals to detect early heading gene of KU-195, we performed QTL analysis again. At that time, we integrated data from all environments for QTL analysis, using each environment as a covariate. As a result, no significant QTLs were detected, but peaks exceeding a LOD score of 3 were observed on chromosomes 4B and 7B. The peak marker on chromosome 7B significantly accelerated heading dates in individuals carrying the KU-195 homozygous allele in 2022KU and 2024OU. Notably, the known flowering-related gene FT-B1 is located within this region. Using de novo assembly data of KU-195 and Langdon, we discovered partial segmental duplication of FT-B1 and a TE insertion in its promoter region. These results suggest that the early-heading trait in KU-195 may be attributable to multiple genes, including a novel FT-B1 allele, and indicate that WEW could be a promising genetic resource for providing novel early-heading alleles.

P127 - Global diversity of arabinoxylans, alkylresorcinols and phenolic acids in 180 rye (*Secale cereale* L.) accessions: implications for functional food innovation

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Abstract

Unlike wheat and rice, which are predominantly consumed as refined grains, rye (*Secale cereale* L.) is mostly consumed as whole grain, making it an ideal vehicle of dietary fiber and phytochemicals. This study profiled arabinoxylans (AX), alkylresorcinols (AR) and phenolic acids in 180 genetically diverse rye accessions from 32 countries. Total AX ranged 70.1-133.0 mg/g, water-extractable AX 6.2-12.7 mg/g, total AR 718.7-2322.2 µg/g and ferulic acid 476.5-1778.1 µg/g on a dry matter basis. Developed cultivars matched or exceeded landraces for total AX (+8%) and ferulic acid (+19%), indicating that modern breeding has not compromised nutritional quality. Correlations were positive among bioactive classes but negative with thousand kernel weight. Elite accessions such as Caribou combined high levels of all three components, offering immediate options for high-fiber, antioxidant-rich product formulation. Overall, these findings broaden the biochemical landscape of rye and identify specific germplasm for functional food innovation.

P128 - Phenotypic characterization of serbian bread wheat landraces for breeding-relevant traits

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Abstract

The characterization of wheat genetic resources constitutes a fundamental prerequisite for their effective use in breeding programs aimed at preventing future food shortages. Continued technological developments in plant phenotyping for remote and proximal sensing have enabled multidimensional data acquisition and analysis, making the screening of large numbers of genotypes more accessible and cost-effective. Within this framework, 36 bread wheat landraces collected from different localities across Serbia were grown under rainfed conditions during the 2024/25 growing season at Rimski Šančevi, near Novi Sad (45.20° N, 19.51° E) and analyzed using several proximal non-destructive phenotyping devices. In the field trials, genotypes were evaluated at two growth stages for seven traits associated with plant productivity: green cover, leaf area index, maximum plant height, normalized difference vegetation index (Literal sensor, Hiphen), chlorophyll content, and nitrogen balance index (DUALEX optical leaf clip meter, Metos). After harvest, the landraces were assessed for thousand grain weight and grain size fractions (length, width, area) using the MARViN system (MARViTECH), and basic technological parameters (protein, moisture, carbohydrates, oil contents) using the GrainSense Analyzer (Oulu). Principal Component Analysis revealed a clear separation among the analyzed genotypes, reflecting their substantial genetic diversity with respect to the evaluated traits, and highlighting their potential as a valuable source of novel alleles for enhancing breeding value and developing high-yielding varieties with improved technological quality.

Keywords: *Triticum aestivum* L., genetic resources, yield-related traits, protein content

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P129 - A spike length QTL co-localizing with TaERF-A1 shows pleiotropic effects on plant height and agronomic traits

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Abstract

Spike architecture is an important trait in bread wheat. In this study, a quantitative trait locus (QTL) for spike length (SL) located on 5AL chromosome arm was identified and characterized using two independent mapping populations: a recombinant inbred line (RIL) population derived from the cross UC1110/PI610750 and a doubled haploid (DH) population derived from Baguette 19/BIOINTA 2002. The main objective was to assess the stability of this QTL across environments and to evaluate its pleiotropic effects on agronomically relevant traits.

QTL mapping revealed a consistent genomic region controlling SL on chromosome 5A in both mapping populations and across multiple environments, indicating strong environmental stability. In the RIL population, marker wPt-0707 explained 4.8% of the phenotypic variance, with an average allelic effect of 0.84 cm. In the DH population, marker BS00022818_51 explained 14.9% of the variance, with a mean allelic effect of 0.78 cm. In both cases, no significant marker × environment interaction was detected, confirming the robustness of this locus.

Beyond its primary effect on SL, the 5A QTL exhibited consistent pleiotropic effects on plant height (PH). In the RIL population, the UC1110 allele increased plant height by 8.72 cm, explaining 4.6% of the phenotypic variance. Similarly, in the DH population, the BIOINTA 2002 allele increased PH by 7.62 cm, accounting for 12.06% of the variance. These results support a strong genetic association between spike length and plant height.

In contrast, spikelet number per spike showed no significant allelic differences. However, spike density was significantly reduced in lines carrying the alleles associated with longer spikes. Grain number per spike showed small but significant effects, whereas grain weight was influenced only in one population, suggesting that the effects on yield components depend on the genetic background.

Comparative physical mapping showed that the QTLs detected in both populations co-localize within the same genomic interval on chromosome 5A, in close proximity (~5 kb) to TaERF-A1, an AP2/ERF transcription factor previously implicated in the regulation of plant height and spike architecture. This evidence supports TaERF-A1 as a strong candidate gene underlying the observed phenotypic effects.

P130 - A balkan durum wheat panel for resistance to mosaic and streak viruses under climate change

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Abstract

Durum wheat production faces increasing threats by persistent viral diseases and limited control options. Soil-borne cereal mosaic virus (SBCMV) and Soil-borne wheat mosaic virus (SBWMV), both transmitted by *Polymyxa graminis* challenge production due to their long persistence in soil, which can last for decades. In parallel, emerging and climate driven vector dynamics increase the relevance of Wheat streak mosaic virus (WSMV), a tritimovirus transmitted by the wheat curl mite. To broaden resistance sources beyond modern elite cultivars, we established a Balkan Durum Panel comprising 167 tetraploid wheat accessions (*Triticum turgidum* ssp. *durum*, *turgidum* and *dicoccon*) and 16 reference cultivars. Among them, the Montenegrin "Rogosija" represents a traditional, long-maintained landrace collection that has been recently characterized and represents unexploited source of genetic diversity and adaptive potential. The panel was analyzed using Genotyping-by-Sequencing (GBS), generating more than 20,000 SNPs markers to resolve population structure and enable Genome-Wide Association Studies (GWAS). Resistance phenotyping will integrate controlled inoculation assays and standardized symptom scoring, supported by confirmatory diagnostics using Double-Antibody Sandwich Enzyme-Linked Immunosorbent Assay (DAS-ELISA) and Reverse Transcription Polymerase Chain Reaction (RT-PCR) for virus detection. For all viruses, we will additionally implement non-destructive digital phenotyping via visible and near-infrared (VNIR) reflectance spectroscopy (380-1000 nm) at multiple post-inoculation time points, with spectral preprocessing and extraction of simple vegetation indices reflecting early physiological stress. Morphological, spectral, serological, and molecular datasets will be integrated with SNP profiles to identify resistance-associated loci using mixed-model GWAS. Selected resistance loci will be converted into deployable Kompetitive Allele-Specific PCR (KASP) markers for routine selection and introduction in elite breeding programs. This integrated, multi-virus framework positions Balkan genetic resources as a strategic reservoir for durable resistance and supports resilient, sustainable pasta wheat production under changing agroecological conditions.

P131 - Yield performance of synthetic-derived winter wheat lines in the U.S. southern great plains

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Abstract

Hard red winter wheat is a major crop in the U.S. Great Plains. Texas A&M AgriLife Research has a productive winter wheat breeding program. Our cultivars (TAM prefix) are widely grown in dryland and irrigated systems and have been used as parental germplasm by wheat breeding programs worldwide. Two of our most popular cultivars, TAM 111 and TAM 112, have been cultivated over one million hectares annually. Over the years, our breeding program has been utilizing primary synthetic hexaploid wheat (SHW) developed by CIMMYT in spring wheat. An elite set of the SHW from which to introgress traits for high biomass and grain yields, abiotic stress tolerance, and biotic stress resistance has been introgressed into our elite wheat cultivars TAM 111 and TAM 112. As a result, we developed thousands of synthetic hexaploidy-derived winter wheat (SDW) lines. The objective of this study was to evaluate yield performance and related physiological traits in a panel of 298 diverse SDW lines. The panel of lines was grown in 15 environments with combinations of years (2014-2017), locations, and water regimes (dryland, limited irrigation, and full irrigation) in the Southern Great Plains. Data collections included grain yield, plant height, biomass at maturity, harvest index (HI), three major yield components (spikes/m², seeds/spike and thousand-kernel weight, TKW), and some early-stage traits. Among the 15 environments, grain yield ranged 1,000-4,500 Mg/ha kg under dryland and 3,000-7,000 kg/ha under irrigation. Although grain yield varied largely among the water regimes, there were significant genotypic differences in yields among the SDW lines. Many SDW lines had higher grain yield than TAM 111 and TAM 112, particularly in high water regime. Although both biomass and HI contributed to higher grain yield in the SDW lines, HI is more related to yield than biomass across environments. Among the yield components, grain yield is more related to seeds per spike and TKW than spikes/m². In addition, some early-stage traits have improved in SDW lines as compared to conventional genotypes. The results of this study also provided opportunities for identifying major QTLs and candidate genes for higher yield and yield components.

P132 - Deleterious mutational load across wheat evolution: from wild diploid progenitors to hexaploid bread wheat

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Abstract

Deleterious mutational load in wheat may correlate with reduced crop productivity, and is expected to be elevated in modern cultivars due to accumulation during polyploidization and domestication bottlenecks. Here, we aimed to quantify and compare the deleterious load across wild and domesticated wheat species and subgenomes. We focused on current population-level deleterious load, analysing SNPs segregating within each taxon using population-scale genomic data (VMap 1.1)^[1] from 795 accessions representing six wheat species in genic regions, with the Chinese Spring genome as reference. Analyses were restricted to SNPs in genic regions. Variants were polarized into ancestral and derived allelic states using species from the genera *Secale*, *Thinopyrum*, and *Elymus* as outgroups. For each SNP, deleteriousness was scored using the Evo2 DNA language model^[2] (7-billion-parameter model, 512 bp context window) as the difference in sequence log-likelihood between the ancestral and derived allelic states. Deleterious load per species was estimated as a weighted sum of derived allele scores, normalized to the sum of neutral derived alleles, defined as the bottom 20% of variants by predicted effect size.

Deleterious load generally increased with ploidy level across all three subgenomes. For the A subgenome, load increased from wild diploid *T. urartu* through wild tetraploid *T. turgidum* ssp. *dicoccoides* (+3.8%), domesticated tetraploids *T. t. dicoccum* (+8.7%) and *T. t. durum* (+12.7%), to hexaploid *T. aestivum* (+20.9%). A similar trend was observed for the B and D subgenomes. Both domesticated tetraploid wheat and hexaploid bread wheat showed higher load than wild emmer, while diploid einkorn domestication showed a marginal decrease compared to wild einkorn. Deleterious variants were enriched in pericentromeric chromosomal regions.

The ploidy-associated increase in load is consistent with reduced efficacy of purifying selection due to subgenome buffering, while domestication showed a more variable pattern across ploidy levels. This map will serve as a foundation for prioritizing genome editing targets aimed at improving wheat yield.

^[1] Zhao et al. Nat. Plants (2023). doi:10.1038/s41477-023-01367-3

^[2] Brixi et al. BioRxiv (2025). doi:10.1101/2025.02.18.638918

P133 - An anarchist's guide to public/private collaborations

William Zorrilla ⁽¹⁾

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Abstract

This talk will not focus on the technical research, but is for those seeking to explore non-traditional mechanisms to launch or strengthen longterm multi-stakeholder collaborations and attract substantial research investments. Will Zorrilla, Managing Director of the Wheat Genetics Resource Center (WGRC), will describe the development of the public/private research consortia successfully in operation since 2013. Made up of 9 industry members across seed companies, millers, and grower associations, and 5 universities in collaboration with USDA ARS, the mission of the WGRC is to bring novel traits from wild wheats into improved bread wheat germplasm. He will walk the audience through the incentive structures, operations, philosophy, intellectual property agreements, and appropriation activities that have led to approximately \$31 million in large scale research and infrastructure investments.

P134 - Annotation is the new bottleneck in plant genomics: frame-sensitive detection of CDS discrepancies with CDScompare, applied to hexaploid wheat

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Abstract

High-quality wheat reference genomes are now available across ploidy levels, from diploid relatives to hexaploid bread wheat. As genome assemblies become routine, the key challenge is ensuring accurate and biologically meaningful gene annotation.

For a given wheat genome, multiple annotation sources frequently coexist. The reference annotation is often produced by the sequencing consortium itself — for example, the International Wheat Genome Sequencing Consortium (IWGSC) for *Triticum aestivum* cv. Chinese Spring — and made accessible through platforms such as URGI. In addition, automated structural predictions (sometimes separated into high- and low-confidence sets), manually curated annotations focused on specific gene families, and independent annotations from public repositories such as NCBI may also be available. Researchers may further generate refined annotations for particular loci of interest. Pseudogenes add another layer of complexity, as they are often inconsistently predicted, partially annotated, or difficult to distinguish from functional copies in large and polyploid genomes. As a result, discrepancies between annotations are common and can substantially affect gene counts, gene family analyses, pseudogene catalogues, and functional interpretation.

In this context, systematic and functionally informed comparison of alternative annotations becomes essential to support expert curation and robust biological conclusions. We developed CDScompare, a tool dedicated to the comparison of structural annotations with a specific focus on coding sequences (CDS). A key feature is the integration of reading-frame information, enabling the detection of conflicts that directly impact predicted protein sequences—conflicts that may remain undetected when relying solely on coordinate overlap or exon-intron structure comparisons.

Applied to multiple wheat annotation sets, CDScompare revealed numerous CDS-level inconsistencies between alternative gene models, including about 1000 frame-related discrepancies missed by other comparison tools, and highlighted loci requiring expert review.

As wheat genomics moves beyond the assembly phase, improving annotation quality and coherence across diploid, tetraploid and hexaploid genomes represents a major source of added value. Tools that facilitate rigorous comparison of gene models are therefore critical to fully exploit the growing wealth of wheat genomic resources.

P135 - Towards developing a pangenome and haplotype catalogue for yield and yield related traits in wheat

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Abstract

Understanding the genetic basis of yield and adaptive traits is critical for developing resilient wheat cultivars suited to increasingly variable rainfed production environments. In this study, we evaluated a diverse wheat panel of 300 wheat genotypes under rainfed conditions across three drought prone Australian locations: Lake Grace (Western Australia), Pinery (South Australia), and Pinnaroo (South Australia). Comprehensive phenotyping was conducted for key agronomic and physiological traits, including days to flowering, NDVI, thousand grain weight (TGW), screenings, hectolitre weight, grain yield, and grain protein content. Preliminary analyses revealed substantial phenotypic variation across all traits, highlighting the broad diversity within the panel and its potential for identifying favourable alleles associated with yield and stress adaptation.

To complement field phenotyping, all 300 genotypes were subjected to whole genome resequencing (WGRS) at ~15× coverage. Population structure and genetic diversity were assessed using principal component analysis (PCA), multidimensional scaling (MDS), and phylogenetic analyses, which collectively demonstrated clear genetic stratification. Based on these analyses, a subset of 11 representative genotypes, capturing approximately 90% of the total genetic variation, was selected for high resolution sequencing. PacBio HiFi and Omni C sequencing (~20× coverage) has been completed for all 11 lines, and genome assemblies are in progress to support the construction of a wheat pangenome.

In the next phase, two year, multi location phenotypic datasets will be integrated with WGRS-derived SNPs/ pangenome-SVs to conduct genome wide association studies (GWAS) for major yield and yield related traits. Candidate genes identified through GWAS will be prioritised based on functional annotation and supporting evidence, followed by haplotype mining to define superior haplotypes associated with target traits. The resulting genomic resources including the wheat pangenome and haplotype catalogue will accelerate breeding strategies aimed at improving wheat productivity and resilience under Australian rainfed conditions.

P136 - Studing fusarium head blight resistance in durum wheat through snp-based linkage analysis

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Abstract

Fusarium head blight (FHB), primarily caused by *Fusarium graminearum* and *Fusarium culmorum*, is a complex quantitative disease severely affecting durum wheat productivity and grain quality. Dissecting the genetic architecture underlying resistance is fundamental for marker-assisted breeding.

A recombinant inbred line (RIL) population derived from the cross cv Aureo × R1 (a breeding resistant line) was phenotyped for FHB incidence and severity following artificial inoculation with *F. graminearum* under controlled conditions for three years. A subset of resistant and susceptible lines was further evaluated for response to *F. culmorum* to investigate the genetic relationship between resistance to the two pathogens. The population was genotyped using the 25K Illumina iSelect SNP array, and a high-density genetic linkage map was developed including SNP markers distributed across 14 linkage groups, covering both A and B genomes.

The genetic map provides adequate genome coverage for QTL detection. Phenotypic data for grain quality traits (protein content, wet and dry gluten, yellow index, moisture content) and productivity (grain yield per spike) were also collected to evaluate possible co-localization between resistance and quality-related loci. QTL mapping analyses are currently underway. Multi-environment trials are ongoing to evaluate QTL stability across environments and to characterize genotype × environment interactions. In parallel, RNA-seq analyses will be conducted on the parental lines to investigate differential gene expression patterns associated with FHB resistance and to support candidate gene identification within QTL regions.

The integration of linkage mapping and transcriptomic approaches will provide deeper insight into the molecular basis of FHB resistance and accelerate the development of diagnostic markers for marker-assisted selection and resistance pyramiding strategies in durum wheat breeding programs.

P137 - Genetic variation and association mapping studies in elite spring bread wheat genotypes for yield and other agronomic traits under irrigated and rainfed environments

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Abstract

Bread wheat (*Triticum aestivum* L.) is crucial for food security in North Africa, where climate change and water scarcity threaten its productivity. Optimizing agronomic practices and understanding genetic traits can enhance yield. This study evaluated 159 spring bread wheat genotypes from ICARDA under raised bed, flat, and rainfed conditions in Egypt and Morocco. Five traits, including grain yield (GY), were assessed, and a genome-wide association study (GWAS) was performed using 17,968 SNPs. A total of 181 significant marker-trait associations (MTAs) were identified, with the highest under raised beds (148), followed by rainfed (75) and flat (53) conditions. The B genome had the most associations (91). Raised bed conditions yielded an average of 8.7 t/ha, surpassing flats (7.8 t/ha) and rainfed conditions (4.0 t/ha), demonstrating a +1 t/ha advantage. The topperforming genotype, G147, achieved yields of 11.4 t/ha, 10.7 t/ha, and 4.1 t/ha under raised beds, flats, and rainfed conditions, respectively. Genotypes G91 and G87 also showed stable performance. Notably, the marker "AX-94704405" on chromosome 6B (raised beds) and "AX- 109853614" on chromosome 6D (rainfed) were significantly associated with GY, making them promising for marker-assisted selection after validation. The identified high-yielding genotypes will be considered for direct release following adaptation trials and for use as parents in breeding programs to enhance wheat productivity under diverse environments.

P138 - QTL mapping of Fusarium head blight resistance in durum wheat using near-isogenic lines

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Abstract

Fusarium head blight (FHB), mainly caused by *Fusarium graminearum*, is one of the most destructive diseases affecting small-grain cereals, including durum wheat. Besides causing significant yield losses, FHB leads to grain contamination with harmful mycotoxins, posing serious risks to food safety and marketability. Genetic resistance represents the most sustainable and economically viable strategy for disease control; however, the molecular mechanisms underlying resistance and susceptibility remain only partially understood.

FHB resistance is a complex quantitative trait controlled by multiple loci and strongly influenced by plant architecture and genotype-environment interactions. Increasing evidence highlights the pivotal role of cell wall components as the first barrier against fungal invasion, with structural and signaling elements contributing to defense responses.

In this study, a set of near-isogenic lines (NILs) was developed from crosses between the elite durum wheat cultivar Maciste and a resistant breeding line developed at the University of Bari. The NILs were evaluated through replicated pathogenicity assays under controlled conditions. Combined genetic and phenotypic analyses identified eight quantitative trait loci (QTLs) associated with FHB resistance, located on chromosomes 2A, 3BS, 3BL, 4B, 5BS, 5BL, and 6BS.

To further investigate the molecular basis of resistance, selected resistant and susceptible NILs were subjected to RNA sequencing (RNA-Seq) analysis. Differential expression profiling focused on genes belonging to the pectin methylesterase (PME) and wall-associated kinase (WAK) families, which are known to play key roles in cell wall remodeling and defense signaling pathways.

These findings contribute to a better understanding of the genetic architecture of FHB resistance in durum wheat and provide valuable targets for marker-assisted selection and breeding programs.

P139 - Identification and analysis of the TCP gene family in wheat

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Abstract

Identification and Analysis of the TCP Gene Family in Wheat

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The TCP family, a group of plant-specific transcription factors, plays a central role in coordinating key processes of plant growth and development. This study investigates the wheat TCP gene family to elucidate its structural features and functional mechanisms. In this study, the TCP genes from *Arabidopsis thaliana* and rice were compared with the protein sequences of wheat. Domain analysis via NCBI and Pfam confirmed 30 TCP family genes in wheat. Their encoded proteins range from 88 to 419 amino acids, with molecular weights of 9-43 kD, isoelectric points of 4.56-9.95, and aliphatic indices of 44.60-83.30. All identified proteins are hydrophilic, unstable, and localized in the nucleus. Chromosomal mapping revealed that the wheat TCP genes are distributed across 17 chromosomes, predominantly near the proximal or distal ends. Gene structure analysis revealed that all wheat TCP genes, except for TaTCP2, TaTCP4, and TaTCP23, contain UTR regions. TaTCP17 possesses the longest sequence, while TaTCP4 is the shortest. Conserved motif analysis identified eight motifs across the wheat TCP family. Except for TaTCP4, TaTCP22, TaTCP25, and TaTCP28, which did not contain motif 2, the other genes all contained motifs 1 and 2. The evolutionary tree of the species could be divided into 4 subgroups. Wheat and rice, both monocotyledonous plants, had a closer genetic relationship, while *Arabidopsis* and potato, both dicotyledonous plants, had a closer genetic relationship. The expression analysis of the 30 wheat TCP genes showed that TaTCP7 and TaTCP8 had better expression in leaves. Under adverse cold stress, TaTCP9, TaTCP11, and TaTCP12 had higher expression levels, and under adverse salt stress, TaTCP14, TaTCP16 had higher expression levels. This study offers a theoretical foundation for further functional exploration of the wheat TCP gene family.

P140 - Genome assembly and annotation of bread wheat and synthetic hexaploid wheat lines as a resource for structural variation analysis and leaf rust resistance gene discovery

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Abstract

Synthetic hexaploid wheats (SHWs) are effective genetic resources for transferring useful traits from *Aegilops tauschii* to common wheat (*Triticum aestivum* L.). Mapping and isolation of these traits' causal features remain challenging, but the burgeoning number of reference genomes and sequencing data are facilitating these tasks. To date, several high-quality genome assemblies of common wheat genotypes have been produced, but there is an inherent lack of SHW genome assemblies. Here we generated chromosome-scale assemblies of five SHWs and the Canadian cultivars Carberry and Emerson using a combination of long reads (Oxford Nanopore Technologies (ONT) and PacBio HiFi), short reads (Illumina) and scaffolding with either Hi-C or Omni-C data. The assembly sizes ranged from 13.6-14.2 Gb with scaffolds N50s of 69.1-70.2 Mb. BUSCO scores of 97.6-98.3% indicated the degree of completeness. The assemblies comprised 79.64-81.36% repetitive elements of the genomes. Protein-coding gene annotation identified 98,254 -111,387 gene models. SHW lines C44 and C66 were nullisomic, lacking chromosomes 2D and 6A, respectively, and C52 was missing the short arm of chromosome 6B. These assemblies therefore revealed key structural variations in SHWs. They also constitute a foundational resource for the discovery, fine-mapping, and deployment of agronomically important genes such as leaf rust resistance genes.

Carberry possesses many leaf rust resistance genes, including Lr16. The comparative analysis of the assemblies revealed an introgression at the Lr16 locus on 2BS (6-8 Mb).

To further characterize this locus, five SHW-derived BC₁F₅ populations from crosses between five SHW lines and the elite cultivars Carberry were developed, and Genotyping-by-sequencing-based QTL mapping confirmed the overlap between the introgression and the Lr16 locus. We also performed bulked segregant RNA sequencing (BSR-seq). For Lr16, five independent R-S bulk pairs consistently revealed two significant peaks on 2BS, including a major peak at 7.5-7.9 Mb that coincides with the Carberry-specific introgression. Within 100-kb windows flanking these peaks, we annotated 24 genes, of which ten carried Carberry-specific variants when compared to that of genes from 18 Lr16- wheat genomes, defining a focused candidate set for this gene. Analyses of Lr16 mutants are underway to pinpoint the causal features and the latest progress will be reported.

P141 - De-novo annotation of the wheat pangenome reveals complexity and diversity of the hexaploid wheat pan-transcriptome

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Abstract

Wheat is the most extensively cultivated crop worldwide, occupying more than 215 million hectares each year. Nevertheless, breeders face the significant challenge of increasing wheat production by approximately 60% over the next forty years to satisfy growing global demand. As part of the 10+ Wheat Genomes Project, genomes from 15 wheat cultivars were sequenced and assembled, enhancing our understanding of genetic diversity and selection within the wheat pan-genome. Precise structural gene annotation is essential for robust pan-genome research, particularly given the size and repetitive nature of the wheat genome, since inaccuracies may result in misleading conclusions.

In this study, we implemented an enhanced gene annotation protocol that standardizes gene predictions across all sequenced accessions. Building on the annotation framework established in the IWGSC 2018 wheat reference genome, we further refined methodologies to minimize annotation errors. For each accession, RNA-seq data from five different tissues or developmental stages, as well as ISO-seq data from root and shoot, were produced. These datasets, combined with protein homology and ab initio predictions, facilitated the accurate characterization of gene models for each accession. Despite producing high-quality annotations, additional consolidation was necessary to achieve consistency across genomes.

With these improved annotations, we identified genes absent from the Chinese Spring reference, detected cultivar-specific genes and tandemly duplicated genes in high-resolution, and delineated the core and dispensable components of the wheat genome. Our work also introduces a wheat pan-transcriptome. Differential expression analyses revealed that numerous key homeologous genes display conserved expression patterns; however, subgenome homeolog expression biases vary among cultivars. This research provides a valuable resource for the wheat research community and emphasizes gene content and expression differences across global cultivars.

P142 - Transposable element exaptation as a source of gene innovation in bread wheat

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Abstract

Transposable elements (TEs) are major drivers of genome plasticity and structural variation in plant genomes. Furthermore, thanks to their unique ability to move from one locus to another, TEs can induce a broad spectrum of changes in gene expression and function, contributing to the reshaping of regulatory networks but also creating new functional genes. In some cases, when a TE confers a positive phenotypic advantage to the host, it may lose its ability to self-replicate and acquire features typical of conventional genes. This evolutionary process is known as exaptation, and the resulting novel gene-like sequences are referred to as exapted TEs (ETEs). Despite growing interest, the genomic scale, evolutionary trajectories, and functional relevance of ETEs remain poorly characterised.

Here, we present a genome-wide survey of TE-derived genes in bread wheat (*Triticum aestivum*) and its key relatives, providing a framework to link exaptation to wheat evolution and domestication. We identify 8,873 high-confidence ETEs in *T. aestivum*, corresponding to ~8% of annotated protein-coding genes. Functional enrichment highlights plant hormone signal transduction as the main significant KEGG category, alongside GO terms related to quinone/ubiquinone processes, ketone metabolism, and pollen development, suggesting that TE exaptation contributed to specific functional modules involved in signalling, metabolism, and reproduction. Notably, 1,314 ETEs are present on only one of the three homoeologous chromosomes, consistent with loci inherited from a single progenitor or arising more recently during polyploid evolution and domestication. Extending the identification to bread wheat tetraploid and diploid relatives (i.e., *Triticum turgidum*, *Aegilops tauschii*, *Ae. speltoides* and *T. urartu*), we detect comparable ETE fractions, accounting for approximately ~10% of protein-coding genes.

Overall, most wheat ETEs are traceable to progenitor genomes, and several are associated with genes implicated in agronomically relevant processes such as vernalisation, signalling, and circadian regulation. These results support a non-random contribution of TE exaptation to wheat genome evolution and suggest that TE-derived gene innovation has helped to shape adaptive traits during domestication and polyploidization.

P143 - Use of AI in wheat databases: overview and prospects

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Abstract

In the frame of the Wheat Information System expert group of the Wheat Initiative, we share our experiences and practices in using AI, including LLMs, in our wheat databases.

This presentation provides an overview of different uses in some of the most internationally renowned wheat databases: EnsemblPlants (EMBL-EBI), GrainGenes (USD-ARS), GnpIS (INRAE-URGI), KnetMiner (Rothamsted Research) and at the Centre for Applied Bioinformatics (University of Western Australia).

It will introduce the main prospects for the coming years, which promise to be a game changer for wheat research.

P144 - High-resolution mapping of the 5B-7B reciprocal translocation in wild emmer wheat via de novo assembly

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Abstract

Wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) serves as a vital genetic resource for wheat improvement due to its environmental adaptability. In this study, we identified and focused on KU-195, an early-flowering accession collected in Israel. While this accession is of particular cytogenetic interest as it harbors a 5BS/7BS reciprocal chromosomal translocation, the precise genomic structure and the prevalence of this translocation among related accessions have remained unclear due to the complexity of the wheat genome. Recent advancements in sequencing technologies, particularly the introduction of Nanopore V14 chemistry, have dramatically improved read accuracy (Q20+), making de novo assembly of large, repetitive polyploid genomes increasingly feasible. In this study, we reconstructed the chromosome structure of KU-195 by combining this high-precision long-read technology with Hi-C proximity ligation technology. High molecular weight genomic DNA was extracted from leaf blades and size-selected using BluePippin. Libraries were prepared using Ligation Sequencing Kit (V14) and Ultra-Long DNA Sequencing Kits (V14) and sequenced on a PromethION 2 Solo. The draft genome was assembled using Hifiasm and ntLink, with Hi-C scaffolding utilized to determine contig order and orientation.

The sequencing yielded 376 Gbp of data (read N50 = 29 kbp), resulting in a 10.5 Gbp assembly (contig N50 = 104 Mbp). The final scaffolds corresponded to the 14 expected chromosomes, achieving a BUSCO completeness score of 99.4%, which is comparable to the WEW_v2.1 reference. Notably, telomeric sequences were identified at both ends of 13 out of 14 chromosomes, indicating a near-complete assembly. Synteny analysis against WEW_v2.1 successfully visualized the 5BS/7BS translocation breakpoints. Although PCR amplification using primers flanking the predicted translocation junctions yielded a 3 kbp product, this was significantly shorter than the expected 16 kbp. This study illustrates that the combination of Nanopore sequencing, Hifiasm, and Hi-C facilitates a remarkably efficient de novo assembly of complex wild emmer wheat genomes. Although further investigation is required to resolve the fine-scale sequence of the translocation breakpoints, this high-quality genome serves as a foundational tool for genomic screening. Our approach paves the way for high-throughput pangenome studies to elucidate the evolutionary significance of chromosomal translocations in *Triticum* species.

P145 - K-mer based approaches to exploit haplotypes and introgressions from genebank collections

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Abstract

Genebanks maintain a reservoir of untapped diversity left behind in modern breeding. Exploiting these resources represent a challenge since these collections are often large to be phenotypically evaluated in breeding programs across multiple environments. Reduced or whole genome sequencing has been a strategy to characterize these large collections and provide a population structure or evolutionary perspectives relying on SNP based analysis. Most recent k-mer based methods provide a complementary road map on genomic analysis.

In this research we are employing publicly available and own sequencing data from wheat genebank collections using k-mer based algorithms to capture diversity and further characterize agronomically important genome regions from landraces and crop wild relatives (CWR) absent in modern cultivars. First, we detect cultivars and landraces with above-average genomic regions from multiple wheat CWR in genebank collections naturally introgressed. Prioritizing these genotypes, we then apply WGS to further characterize long-range haplotype blocks to determine their precise genome location at 50 kb resolution. We have used this strategy in a pre-breeding program to track haplotype blocks selected by breeders and found previously unreported introgressions. We provide examples where these novel CWR-origin blocks deliver agronomically important traits from modern cultivars and untapped novel haplotypes for further investigation.

Our methodology applies k-mer based methods and multi-genome reference, using partially (cheap) or WGS to extract agronomically important haplotype blocks available in germplasm banks from CWR and landraces absent in modern cultivars. Extracted haplotypes are first incorporated into a pre-breeding program before being deployed globally. Our approach envisions a digital genebank haplotype database based on k-mers, where new WGS generated can be quickly integrated and compared in the context of already available long-range haplotypes from multiple wheat and CWR collections. This strategy avoids the need of re-calling SNPs every time in current alignment methods. Although this method has been tested in hexaploid wheat, this knowledge is applicable for haplotype-guided decision making in other crop breeding programs.

P146 - Genomic gain and loss estimation in the D genome of asian wheat landraces and modern cultivars inferred from pangenome graph

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Abstract

The D genome of hexaploid wheat (*Triticum aestivum* L.) provides critical adaptability and grain quality. However, it suffers from a significant genetic bottleneck, retaining only about 16% of the nucleotide diversity present in the A and B genomes. While structural variants (SVs) are primary drivers of phenotypic evolution, a systematic quantification of genomic gains and losses at the genome level between landraces and modern cultivars from structural variation remains largely unexplored. In this study, we constructed a pangenome graph to quantify genomic gains and losses in the D genome of 13 Asian wheat accessions. The D genome pangenome graph revealed 1.8 Gb of sequence missing from the D genome of Chinese Spring reference genome, highlighting substantial hidden diversity. The core pangenome accounts for ~48% (2.78 Gb) of the total length, while variable regions (dispensable and private) comprise over 50%. Evolutionary inference based on maximum parsimony revealed a lack of balance between genomic gain and loss events. For INDELs, deletion events generally outnumbered insertions, except in modern Chinese bread wheat cultivars (XY6 and XN6028), which exhibited more gain events. In contrast, SVs showed a predominant trend of genomic gain across all examined taxa. These gains were primarily driven by repetitive elements, particularly DNA transposons and LTR-retrotransposons such as Gypsy and Copia. Functional analysis demonstrated that while most variants reside in intergenic regions, thousands intersect with coding sequences (CDS) and regulatory regions (UTRs and 1kb flanking regions). Notably, variants within the CDS exhibited higher average lengths compared to other gene structures. These findings demonstrate the potential of pangenome graphs for inferring wheat genome evolution and providing a framework for dissecting the genomic consequences of domestication and a resource for recovering agronomically valuable alleles in wheat breeding.

P147 - From k-mers to candidates: dissecting structural diversity and novel resistance haplotypes at the wheat Yr47/Lr52 locus

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Abstract

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

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

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

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

P148 - Bioinformatics analysis of the ADK gene family in wheat

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Abstract

1 Experimental Design

Adenosine kinase (ADK) gene, mapped to 10q22.2 on human chromosome 10, mediates cellular adenosine metabolism by catalyzing adenosine conversion to AMP. Cloned from diverse organisms, ADK is critical for plant growth but unreported in wheat. Arabidopsis ADK sequences were aligned with wheat proteins genome-wide, validated via NCBI/SMART (redundancy removed). ExPASy, Cell-PLoc/SignalP/TMHMM, TBtools and MEGA11 analyzed physicochemical properties, localization, gene visualization and NJ phylogenetic tree (five species), respectively.

2 Main Results

Thirty-three wheat ADK members were unevenly distributed on 17 chromosomes: 177-637 aa, 19418.09-69919.11 Da, pI 5.09-10.86, aliphatic index 61.73-97.11, all negative GRAVY (hydrophilic). Most had UTRs; TraesCS7A02G163500.1/TraesCS4B02G324400.1 were longest/shortest with most/fewest exons/introns. Ten motifs showed differential inter-group but conserved intra-group distribution. Phylogenetic analysis clustered five species' ADKs into 3 subgroups (all wheat ADKs included), indicating high conservation.

3 Conclusions

Thirty-three wheat ADK members were identified, mostly chloroplast-localized, hydrophilic, without signal peptides/transmembrane structures. Bioinformatics analyses inferred their characteristics, consistent with other plants, providing a theoretical basis for subsequent wheat ADK research.

P149 - Harnessing skim-sequencing for high-throughput genomic analysis in wheat and wild relatives

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Abstract

While the cost of next-generation sequencing continues to decrease, high-coverage whole-genome sequencing remains expensive for large wheat populations due to the large genome size and the relatively expensive fixed costs of library construction. Ultra-low coverage skim-sequencing using and optimized low-volume library construction provides a scalable and cost-efficient alternative. We successfully applied skim-sequencing for genome-wide analysis in wheat and its wild relatives, demonstrating its broad utility across multiple genomic applications at coverage levels as low as 0.03-0.2x, while multiplexing thousands of samples simultaneously. We developed a comprehensive bioinformatics pipeline to support various downstream analyses. Read-depth-based analyses enabled the detection of chromosomal introgressions, aneuploid, and telosomic lines. Despite substantial missing data, genome-wide SNP discovery combined with bin-based mapping enabled the construction of high-resolution genetic maps, validation and correction of genome assemblies, and precise trait localization in *Triticum monococcum*. As an example, low-coverage sequencing followed by imputation in an F₂ population of *Aegilops tauschii* enabled accurate mapping of leaf rust resistance. Similarly, in a wheat genomic selection panel low-coverage sequencing at ~0.14x with imputation facilitated high-density SNPs discovery at minimal cost. We further demonstrate the effectiveness of skim-sequencing for deletion mapping using extremely low-coverage datasets. Overall, skim-sequencing represents a flexible, multi-purpose genomic platform that integrates discovery, validation, and breeding applications. By dramatically reducing genotyping costs while maintaining analytical power, this approach accelerates trait mapping, genomic selection, and the development of improved wheat germplasm.

P150 - Wheat genotype impacts plant responses to biosolutions

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Abstract

With growing ecological and economic pressures, there is increasing interest in finding alternative ways to boost plant production. One promising approach is the use of biostimulant products, which help plants better cope with abiotic stresses and improve nutrient assimilation. These biostimulants come from a wide range of sources natural, synthetic, or mixed including amino acids, enzymes, algal extracts, plant hormones, beneficial microbes, plant extracts, minerals, and nutrients. While their potential is clear, the exact mechanisms behind their effects are still not fully understood. This requires better characterization of the molecular responses they trigger in order to promote their safe use by farmers, with respect for both human and environmental health.

In our work, we aim to bridge this knowledge gap by characterizing the responses triggered by different biostimulants in durum wheat. These biostimulants activate various pathways that can enhance nutrient assimilation, improve drought tolerance, and boost seed quality. To achieve this, we combine molecular, metabolomic, and physiological approaches across four durum wheat varieties.

Our analyses highlight that molecular, metabolomic, and physiological responses are strongly shaped first by the genotype, and then by the applied biosolutions. We were able to show that specific molecular pathways are activated depending on both the biostimulant used and the plant's genetic background. We also identified correlations between transcriptomic, metabolomic, and physiological traits.

To really push the "lab-to-field" transition forward, we are testing how biosolutions perform under a wide range of stresses from drought and nutrient shortages to temperature fluctuations and biotic challenges. By taking this broader view, we are uncovering key mechanisms underlying biostimulant activity and demonstrating their real potential to enhance plant resilience and productivity in the field.

P151 - TaPIF3 integrates light and gibberellin responses to control chloroplast development and growth in wheat

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Abstract

The semi-dwarfing mutant alleles of Reduced height-1 (Rht-1) introduced during the Green Revolution that were key to wheat yield improvement are now prevalent in wheat cultivated worldwide. The mutant Rht-1 alleles encode RHT-1 DELLA proteins that have reduced sensitivity to gibberellin, resulting in a reduced plant stature that is more resistant to lodging. However, negative pleiotropic effects associated with Rht-1 dwarfing alleles are impacting agronomic performance. We are therefore investigating the targets of RHT-1, with the aim of tailoring wheat growth and development more specifically. Potential downstream targets of RHT-1 include Phytochrome Interacting Factors (PIFs), which are a family of transcription factors whose function is modified by DELLAs in Arabidopsis. We have identified TaPIF3 as an orthologue to AtPIF3, and a split-luciferase assay demonstrated that TaPIF3 interacts with RHT-1 in planta. In addition, TaPIF3 interacted with the wheat photoreceptors, phytochromes A and B. Using the TILLING population of hexaploid wheat, we generated a triple loss-of-function *tapif3* mutant (*tapif3-1*). Characterisation of *tapif3-1* demonstrated that TaPIF3 has a role in repressing chloroplast development and promoting coleoptile growth, with *tapif3-1* displaying reduced sensitivity to both light and gibberellin. RNA sequencing analysis of dark-grown seedlings showed that *tapif3-1* had elevated expression of photosynthetic genes relative to wild-type. Consistent with this, *tapif3-1* seedlings exhibited accumulation of the chlorophyll precursor protochlorophyllide in the dark and altered etioplast structure, demonstrating impaired chloroplast development. A second *tapif3* mutant allele (*tapif3-2*) generated by CRISPR-Cas9 also showed reduced coleoptile elongation in the dark, while overexpression of TaPIF3 increased coleoptile length. Taken together, these findings are consistent with TaPIF3 acting together with RHT-1 to integrate gibberellin and light signalling pathways in wheat. The resulting regulation of chloroplast development and growth establishes TaPIF3 as a promising target for enhancing wheat physiology to improve crop performance.

P152 - Breaking the silence: understanding recombination suppression in wheat wild gene introgressions

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Abstract

Introgression of beneficial genes from wild species such as *Aegilops ventricosa* represents an important strategy for enhancing disease resistance in bread wheat (*Triticum aestivum*). However, recombination is strongly suppressed within these introgressed segments once they are incorporated into the wheat genome. This suppression limits the reduction of introgression size and often results in linkage drag. Understanding the mechanisms responsible for this recombination suppression is therefore critical for fully exploiting the genetic resources in breeding programs.

Meiosis is a cornerstone of genetic diversity, driven by homologous recombination, where homologous chromosomes exchange genetic material to create new allele combinations. This process is tightly associated with the formation of the synaptonemal complex, a meiosis-specific structure that stabilizes homolog pairing and promotes recombination. In the cultivar Renan, the absence of recombination within *Ae. ventricosa* introgressed regions raises the question of whether structural or molecular defects in double strand break (DSB) formation, recombination or synapsis occur during meiosis.

To address this question, we evaluated three hypotheses focusing on two already fixed introgressions coming from *Ae. ventricosa* in the cultivar Renan.

First, we tested whether the frequency of meiotic DSBs, a prerequisite for crossover formation, is reduced within introgressed regions. To this end, we developed a ChIP-seq approach targeting DMC1, a recombinase that marks recombination intermediates, enabling the identification and quantification of DSB sites within the introgressions.

Second, we established an oligo-FISH approach to observe chromosome pairing and synaptonemal complex formation in hybrids generated between Renan (carrying *Ae. ventricosa* segments) and Chinese Spring (lacking these segments). This experiment will allow us to detect potential synaptic defaults.

Finally, we explored whether epigenetic mechanisms or chromatin structure contribute to the suppression of recombination by rendering these regions inaccessible during meiosis.

By integrating these complementary approaches, this study aims to identify the molecular and structural mechanisms underlying recombination failure within introgressed segments, supporting more effective and precise wheat breeding strategies. Deciphering these barriers will provide essential knowledge to develop innovative tools for inducing recombination in recombination-cold genomic regions.

P153 - Transcriptome analysis of durum wheat under heat stress

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Abstract

Durum wheat is a major crop cultivated in the world. High temperature stress after heading can reduce grain yield and quality. This study aimed to investigate the molecular responses of durum wheat to heat stress. Two durum wheat varieties (Anvergur, Relief) and two breeding lines (TE1401, TE1203) were tested. Relief and TE1401 are presumably more sensitive to heat stress than Anvergur and TE1203. This material was tested under two conditions ("heat stress", HS versus "no stress", NS) in a greenhouse experiment. Plants were sown in pots and cultivated under standard conditions (day / night temperatures of 21°C and 15°C). Seven days after anthesis, plants of the HS condition were moved to a compartment of the greenhouse with elevated temperatures (day / night temperatures of 31°C and 23°C) during seven days and then moved back to the standard conditions. Samples of leaves and grains were collected seven days after anthesis (5 hours after moving the plants to the HS condition) on three biological replicates and immediately frozen in liquid nitrogen. Total RNA was extracted using the RNeasy Plant Mini kit (Qiagen). Libraries were produced with the TruSeq Stranded RNA Library Prep Kit and sequenced on the Illumina NOVASEQ6000. Clean reads were mapped to the Svevo reference genome v1 and read count tables were generated. Differential gene expression analysis (DEGs; false discovery rate (FDR) < 0.01; fold change > 2) allowed identifying 50,745 genes expressed across all the samples. 3,543 DEGs (1,816 upregulated and 1,727 downregulated) were identified. From 164 (TE1203) to 1,296 (TE1401) DEGs between the HS and NS conditions were identified in the leaves and from 3 (TE1203) to 1,100 (Anvergur) were identified in the grains. Gene ontology (GO) enrichment analysis revealed that genes related to "protein folding", "protein-folding chaperone binding" and "response to heat" were significantly upregulated in the leaves in the tolerant varieties while "transmembrane transport", "ABC-type transporter activity" and "ATP hydrolysis activity" genes were significantly downregulated in the sensitive varieties. The differentially expressed genes identified in this study could be interesting targets in breeding heat-tolerant durum wheat cultivars.

P154 - Assessing aquaporin phospho-regulation and drought response relationships in wheat

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Abstract

Aquaporins (AQPs) are integral membrane proteins that facilitate the movement of water and, for some isoforms, small solutes relevant to nutrient transport and signalling across cellular membranes. In crops, a key knowledge gap is how AQP substrate selectivity and transport capacity are dynamically regulated, particularly under environmental stress. Post-translational modifications, including phosphorylation at cytosolic regulatory regions, are known mechanisms for rapidly tuning AQP permeability and/or gating. In this study, we characterised substrate permeability profiles for two wheat (*Triticum aestivum* L.) aquaporins (TaAQPs) using heterologous expression in yeast and growth-based functional assays. Both TaAQPs are candidates for enabling permeability to water and additional substrates relevant to osmotic and oxidative stress responses, including H₂O₂, NH₄⁺ and Na⁺. Regulatory control by phosphorylation was assessed by modifying serine residues located in distinct cytosolic loop regions, specifically substituting these residues to mimic phosphorylated and dephosphorylated states. Yeast expressing each wild-type TaAQPs exhibited permeability phenotypes that differed from empty vector controls. The phospho-mimic variants displayed altered permeability phenotypes relative to their corresponding wild-type proteins, indicating that the phosphorylation state at the tested sites is likely to influence TaAQP function. Leaf RNA-seq data is being generated from four wheat genotypes that were subjected to a water stress experiment involving checking for drought-responsive AQP transcript changes. These genotypes have varying physiological responses to water deficit. Differential expression analysis is expected to reveal which TaAQP genes were responsive to the water deficit treatment and resolve whether there were genotype-specific expression signatures. By integrating phosphorylation-sensitive functional phenotypes with stress-responsive transcriptional patterns, we aim to identify which TaAQP candidates are of interest for further functional testing. We expect the knowledge gained will inform strategies for improving wheat performance under osmotic and oxidative stress.

P155 - OPRIII-B1 copy number variation association with root system architecture (RSA) and growth dynamics in tetraploid wheat

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Abstract

Root system architecture (RSA) is a major determinant of wheat adaptation to contrasting environments. The 12-OXOPHYTODIENOATE REDUCTASE SUBFAMILY III (OPRIII) genes function in genes have a critical point in the jasmonic acid (JA) biosynthesis pathway, a key regulator of root development. In hexaploid wheat, OPRIII-B1 copy number variation (CNV) was negatively associated with root length in hexaploid wheat (Gabay et al., 2023). Here, we examined whether this relationship extends to tetraploid wheat, focusing on wild emmer wheat (*Triticum dicoccoides*, WEW), the progenitor of domesticated wheat. OPRIII-B1 CNV was estimated from whole-genome 10x Illumina sequencing of 152 accessions, including WEW (n=64), *T. dicoccum* (DEW; n = 44), and *T. durum* (DW; n= 44). CNV showed clear taxonomic differentiation: DEW and DW carried uniformly low copy numbers (0.5-1.7), whereas WEW exhibited broad variation (0.5-4.64 copies). Hydroponic phenotyping of 15 WEW accessions with contrasting CNV revealed distinct root growth trajectories, with higher OPRIII-B1 copy number (CN) associated with reduced root length (RL) ($r = -0.651$, $p = 0.0117$, $R^2 = 0.423$). Two of these WEW accessions, IDH107 (CN 1.3; RL 33.5 ± 3.01) and IDH110 (CN 4.7; RL 18.6 ± 0.9), were further characterized using 3D root scanning of plants grown in 10L quartz sand. Among 26 RSA traits analyzed, 18 differed significantly between genotypes. Compared with IDH110, IDH107 displayed a more robust root system, with greater depth, network area, and total root length, increased branching intensity (root tips), and larger overall root volume and surface area. IDH110 was distinguished primarily by a higher proportion of fine roots. OPRIII-B1 expression analysis using RT-qPCR comparing IDH110 and Zavitan (CN 0.7, RL 29.2 ± 2.3) revealed stronger expression in IDH110 at 10 days after germination (DAG), consistent with an early developmental stage in which increased OPRIII-B1 copy number may contribute to JA-mediated restriction of root elongation. Together, these findings identify WEW as a reservoir of functionally relevant OPRIII-B1 CNV influencing RSA and highlight its potential for improving wheat adaptation to heterogeneous environments. Future work will involve developing a mapping population to validate the genetic relationship between OPRIII-B1 CNV and root length.

P156 - Environment-dependent epigenetic modulation of stem solidness in wheat

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Abstract

Solid stem in wheat is a unique trait, known to provide lodging tolerance and pest resistance. Wheat Stem sawfly is an important pest in the Northern US plains and Canada that can cause up to 80% yield loss and grain quality deterioration through stem cutting. Sawfly larvae feed on the stem pith, boring the stem basipetally, which leads to lodging due to stem weakening and damage to vascular tissues. Stem solidness serves as a mechanical barrier to larval feeding, providing resistance to plants. However, despite being controlled by a major locus on chromosome 3B, solidness expression is highly plastic, suggesting additional epigenetic regulation. This study investigates the underlying epigenetic mechanism of environment-dependent expression of stem solidness using genome-wide DNA methylation and transcriptome profiling. Three winter wheat genotypes with contrasting stem solidness (solid, semi-solid and hollow) were grown in greenhouse and field conditions promoting and suppressing pith formation in known solid stem lines, respectively. Stem tissues were used for whole-genome bisulfite and RNA sequencing. Both profiles suggested environment-dependent genome-wide epigenetic modulation. Global differences were observed between the treatments for C methylated across the contexts (CpG, CHG and CHH). These results suggested a higher gene body and transposon methylation derived from environment-dependent epigenetic modulation. A similar pattern was observed for the transcriptome profiles for the total number of upregulated and downregulated genes. In co-analysis, across the profiles, approximately 130 unique differentially methylated and differentially expressed genomic regions were identified across Genotype-Treatment combinations. A weighted Gene Co-expression Network Analysis followed by GO enrichment analysis revealed that differential regions were rich with the genes involved in cell wall remodeling and lignin biosynthesis. Additionally, a subset of methylation events was observed in cis regulatory elements mainly associated with photoperiod and circadian rhythm. Further advancement of this study is underway; however, the existing results provide valuable information to advance the understanding of the epigenomic basis of Genotype×Environment interaction for stem solidness and inform breeding strategies to stabilize this trait under variable production environments.

P157 - Deciphering the transgressive yield in commercial cultivar ND5181 through the lens of transcriptional modules

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Abstract

Breeding achieves phenotypic innovation by selecting rare recombinants with superior traits exceeding parental niche primarily through genome reshuffling rather than introducing de novo mutations. However, the mechanism underlying transgressive phenotypes remains elusive and polyploidy adds complexity to this enigma via its unique homoeologous buffering and dosage effects.

Leveraging a practical wheat breeding population with transgressive tiller number as the focal trait, we constructed precise recombination map and high-resolution time-series transcriptomic map of tiller nodes for the commercial high-yield variety ND5181 and both parental lines. We then stepwise decoded a polyploid-specific mechanism for creating such transgressive phenotypes by reconstructing a causal trajectory from recombination through nested transcriptional re-establishment to phenotypic plasticity. Our study successfully addressed the question of why breeder selected ND5181 for its transgressive yield trait.

Field phenotyping confirms ND5181's yield gain over both parental lines is driven by transgressive pre-winter tillering, and the major locus mapped in the breeding population is insufficient to explain ND5181's transgressive tiller number. We then dissected the potential non-Mendelian mechanisms by constructing the transcriptional landscape and tillering gene regulatory networks, uncovering extensive transcriptional re-establishment driven by genomic recombination. We found individual homoeologs largely preserved parent-of-origin expression, while widespread homoeologous reassortment reshaped total triad expression dosage by combining higher- or lower-expressing parental homoeologs. Notably, the dosage remodeling of regulators propagated through rewired regulatory networks and affected downstream genes.

To identify key drivers, we designed a network-based quantitative framework to prioritize drivers for phenotypic plasticity, identifying recombination-driven aggregation of subtle advantageous homoeologous alleles within TaNLP4-triad significantly boosts total dosage and therefore activates tillering modules and promotes transgressive tiller number in ND5181. Further functional assays validated TaNLP4-triad as a positive regulator of tiller number. Importantly, selecting optimal homoeolog combinations raises transgressive recovery to 238% of the full breeding population while boosting mean yield by 5.4%. These results reveal homoeolog dosage convergence as a polyploid-specific route to transgressive phenotypes, and establish a homoeolog-combination-guided strategy for efficiently designing desirable transgressive phenotypes.

P158 - Integrating GWAS, haplotype mapping and genomic selection to unlock the diversity of ancient indian dwarf wheat (*Triticum sphaerococcum*) for biotic, abiotic stresses, nutrition and nitrogen use efficiency

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Abstract

Triticum sphaerococcum, ancient Indian hexaploid dwarf wheat, is a forgotten crop with unique genetic diversity and inherent resistance to biotic/abiotic stresses. Its reintroduction offers potential to enrich the genetic base of modern wheat cultivars. *T. sphaerococcum* landraces are unique to India and crop differs even from the fertile crescent, European and Chinese landraces of wheat. Its genetic diversity can serve as valuable reservoir for unique resistance alleles/genes for broadening the genetic base of contemporary wheat cultivars. In this study, a global panel of 143 *T. sphaerococcum* accessions were procured from Indian Gene Bank. Over the past three years, this panel has been extensively phenotyped under field conditions for a wide spectrum of traits, including cold tolerance, foliar blight, stripe rust, pre-harvest sprouting tolerance (PHST), yield- and quality-related traits, nutritional attributes and nitrogen use efficiency (NUE). For genomic characterization, the panel was genotyped using a high-density 35K SNP array, and whole-genome resequencing (WGRS) is being done in collaboration with the Centre for Crop and Food Innovation (CCFI), Murdoch University, Perth, Australia. Integrating high-resolution phenotypic and genomic datasets, we performed multi-locus genome-wide association studies (GWAS) to identify robust marker-trait associations (MTAs), candidate genes and QTLs linked to key agronomic and stress-related traits. Additionally, haplotype analyses were undertaken to detect favourable haplotypes/alleles associated with superior performance across traits. Correspondence between GWAS results and haplotype-based regions were evaluated to pinpoint stable and biologically relevant loci. In addition, genomic selection will be implemented to predict genomic estimated breeding values (GEBVs), enabling the identification of superior genotypes with the highest breeding potential. This work provides a comprehensive genomic and phenotypic framework for exploiting the unique diversity of *T. sphaerococcum*. The identified superior genotypes, allelic variants and favourable haplotypes will serve as promising donors for introducing resilience and productivity traits into elite wheat cultivars. Leveraging these insights through speed breeding will accelerate the development of biotic/abiotic stress resilient, high-performing wheat varieties.

P159 - Refining the candidate region of a major gene *Ymhk* responsible for resistance to wheat yellow mosaic virus

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Abstract

Wheat yellow mosaic disease adversely affects winter wheat production, especially in Japan and China. Infected plants typically show yellow mosaic symptoms and growth suppression, leading to yield reduction under disease-favorable conditions. The etiological agent, wheat yellow mosaic virus (WYMV), is transmitted by the soil-inhabiting plasmodiophorid protist *Polymyxa graminis* via wheat roots. Breeding resistant wheat cultivars is an effective strategy for stable wheat production in affected regions. The resistance gene *Ymhk*, derived from a Japanese winter wheat 'Hokkai 240', has been reported to confer broad resistance to multiple pathogenic WYMV strains. This gene was originally identified on chromosome 2A through quantitative trait locus analysis based on field evaluation, with its physical position previously estimated at approximately 5.9 Mb in the Chinese Spring RefSeq v2.1 genome assembly (Kawaguchi et al., 2024). In the present study, we further characterized *Ymhk* using controlled virus inoculation assays and molecular analyses. A segregating recombinant inbred lines (RILs) population derived from the resistant parent 'Hokkai 240' and the susceptible parent 'Nanbukomugi' was evaluated using mechanical inoculation, and resistance responses were assessed using an enzyme-linked immunosorbent assay. Resistance responses observed in inoculation assays strongly agreed with those obtained from conventional field evaluations, validating the effectiveness of inoculation-based resistance assessment for analyzing *Ymhk*. To genetically refine the *Ymhk* region, multiple DNA markers were developed based on the reference genome and used for high-resolution mapping in the RILs population. This approach substantially reduced the candidate region to less than 1 Mb in the Chinese Spring RefSeq v2.1 genome assembly. Gene annotation within the refined region identified several genes with predicted functions that may be relevant to disease resistance. Further efforts are currently underway to identify the candidate gene of *Ymhk*. Simultaneously, DNA markers linked to *Ymhk* are being used to examine the relationship between genotype and phenotype in wheat cultivars with diverse genetic backgrounds.

P160 - Dynamic atlas of histone modifications and gene regulatory networks in endosperm of bread wheat

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Abstract

Dissecting the genetic basis of wheat seed traits has long been hampered by limited genetic polymorphism resources and substantial phenotypic plasticity driven by environmental fluctuations and seed positional effects within spikelets. Endosperm development, the core determinant of seed growth and function, is tightly governed by spatiotemporally specific gene transcription, with chromatin state decisive in shaping this regulatory landscape.

We focused on wheat endosperm development, systematically characterizing genome-wide dynamic distributions of three pivotal histone modifications (H3K27me3, H3K4me3, H3K9ac) and a comprehensive transcriptomic atlas. Our results showed that combinatorial interplay between active (H3K4me3, H3K9ac) and repressive (H3K27me3) histone marks establishes a precise regulatory network for spatiotemporal gene expression, particularly prominent in starch biosynthesis-related genes.

Scanning transcription factor binding motifs in ATAC-seq-identified accessible chromatin regions allowed identification of hub regulators of seed traits. Association analysis in a natural germplasm panel confirmed significant correlations between hub regulator sequence polymorphisms and seed trait phenotypic variation.

Collectively, this study establishes an integrated strategy combining genomic regulatory profiling and genetic variation analysis, providing a robust approach to overcome technical bottlenecks in dissecting wheat seed trait genetic basis.

P161 - Investigating the regulatory mechanism of VRN2 and VRN3 in mediating adaptation to photoperiod and vernalization in wheat (*Triticum aestivum* L)

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Abstract

Investigating the Regulatory Mechanism of VRN2 and VRN3 in Mediating Adaptation to Photoperiod and Vernalization in Wheat (*Triticum aestivum* L)

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Abstract: The coordinated response of wheat to photoperiod and vernalization confers robust environmental adaptability and developmental plasticity, which is essential for achieving high and stable yields. Therefore, deciphering the molecular mechanisms underlying wheat's adaptation to photoperiod and temperature is crucial for enhancing its yield potential.

To systematically characterize the functions of VRN2 and VRN3, we generated VRN2 knockouts in both the spring cultivar Fielder and winter cultivar KN199, and VRN3 knockouts in the KN199 background. Results showed that *vrn2*-null mutants in both backgrounds exhibited significantly earlier heading dates. Notably, the *vrn2*-null winter wheat lost its vernalization requirement and completed floral transition without cold treatment. Furthermore, in VRN2 overexpression and complementation lines, we observed delayed and restored heading dates, respectively, confirming the central role of VRN2 in regulating spring-winter growth habit and flowering inhibition. In *vrn3*-null mutants, wheat failed to flower, whereas the presence of any single functional VRN3 copy was sufficient to initiate flowering, indicating that VRN3 acts as an indispensable switch for floral transition in wheat.

As a central hub integrating environmental signals, VRN2 expression is negatively regulated by short-day conditions and vernalization, and it strongly suppresses VRN3 transcription. This study aims to identify the genome-wide downstream targets of VRN2 and VRN3, thereby constructing a regulatory network for wheat's photothermal adaptation. Elucidating the mechanism by which VRN2 perceives photoperiod and vernalization signals to precisely regulate VRN3 will enhance our understanding of wheat's environmental adaptability and provide a theoretical basis for molecular breeding.

Keywords: *Wheat; Photoperiod; Vernalization; Adaptation; Regulatory Network; Yield*

P162 - The investigation of genetic control of leaf senescence in wheat

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Abstract

The circadian clock is a biological time-keeping mechanism that coordinates key physiological processes in plants. While extensively studied in *Arabidopsis thaliana*, its roles in agriculturally important crop bread wheat (*Triticum aestivum*) remain underexplored. Wheat yield and grain quality are heavily influenced by environmental and genetic factors. Understanding the genetic basis of circadian control over the timing of senescence is crucial for enhancing agricultural productivity. This project investigates how circadian variation influences senescence timing in wheat, with a particular focus on the clock gene *EARLY FLOWERING 3* (*ELF3*). Our lab's previous study using near-isogenic lines (NILs) differing at the *ELF3* locus, showed that *ELF3* deletion affects senescence timing (1). Transcriptome analyses identified two alternative *ELF3* isoforms across all wheat homeologs. Expression profiling of these two isoforms reveals that *ELF3* deletion specifically affects β -transcript expression. These findings implicate alternative splicing as a potential mechanism underlying *ELF3*-mediated regulation of senescence. Beyond *ELF3*, this project examines whether broader circadian genetic variation contributes to natural diversity in senescence timing across wheat cultivars. Previous analyses revealed correlations between circadian period and senescence traits, as well as extensive variation among circadian multilocus genotypes, indicating that additional clock genes are involved (1). To investigate the genetic basis of these relationships, we conducted genome wide association studies (GWAS) using a subset of 244 cultivars from the OzWheat panel grown under controlled glasshouse conditions. Multiple phenology-, nitrogen-, and senescence-related traits—including heading and flowering date, nitrogen uptake, timing of senescence, thousand-grain weight and GPC—were measured. Combined with SNP genotyping data, these phenotypic traits will enable GWAS to identify novel genomic loci associated with senescence and grain quality in Australian wheat, both of which are crucial targets for wheat breeding. This research aims to uncover genetic variation underlying circadian-regulated traits, providing new insights into the molecular basis of senescence and potential strategies for crop improvement.

References:

1) Buckley CR et al. (2025) A circadian transcriptional subnetwork and *EARLY FLOWERING 3* control timing of senescence and grain nutrition in bread wheat. *New Phytologist*.

P163 - QTL mapping for sulfur utilization efficiency traits in wheat seedlings

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Abstract

Sulfur (S) is an essential nutrient for plants and plays critical roles in photosynthesis, protein synthesis, and overall metabolic function, thereby influencing crop yield and quality. To elucidate the genetic basis of sulfur utilization efficiency in wheat, we developed a recombinant inbred line (RIL) population and evaluated 13 SUE-related traits at the seedling stage under three hydroponic sulfur supply levels: low (0.1S, T1), medium (0.5S, T2), and high (1.5S, T3), and quantitative trait loci (QTL) were identified through genetic mapping. A total of 170 QTLs were detected across different environments, including 89, 103, and 101 QTLs under T1, T2, and T3, respectively. Among these, 63 QTLs were consistently detected across multiple treatment environments, while 107 were environment specific. We further identified 13 relatively high-frequency QTLs (RHF-QTLs) and 11 QTL clusters. 5 RHF-QTLs (QSh-1D, QRn-1D, QSdw-1D, QTdw-1D, and QTsc-1D) were located in cluster C3, while 6 RHF-QTLs (QRdw-6A, QSdw-6A, QTdw-6A, QRsc-6A, QSsc-6A, and QTsc-6A) were located in cluster C10. These 13 RHF-QTLs and 11 QTL clusters represent valuable genetic targets for marker-assisted selection (MAS) in wheat, providing a foundation for accelerating the development of wheat varieties with enhanced sulfur utilization efficiency.

P164 - Breeding implications of Wheat Tiller-1 (WT-1) in Optimizing tiller architecture and yield potential

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Abstract

Tiller number and spikelet number per spike are key architectural traits directly influencing grain yield in bread wheat. However, the genetic determinants governing coordinated regulation of these traits remain insufficiently characterized. In this study, we investigated the functional role of Wheat Tiller-1 (WT-1), a GRAS domain-encoding gene, in modulating tiller architecture and reproductive development, with particular emphasis on its breeding relevance under changing climatic conditions. Histological cross-section analysis of the crown region during early seedling stages revealed that tiller bud differentiation and apical meristem transition toward spikelet formation are initiated early in development, suggesting coordinated genetic regulation. WT-1 was initially identified through Virus-Induced Gene Silencing (VIGS) using a conserved sequence surrounding the VHID motif homologous to the Lateral Suppressor (LS) gene of tomato. Subsequent silencing using the wheat-specific sequence resulted in a pronounced unicum phenotype with significantly reduced tiller number. Although WT-1 shares only 37.6% predicted protein similarity with the tomato LS gene, the conserved VHID motif confirms its placement within the GRAS transcription factor family. The gene is present as three homoeologous copies located on wheat group 7 chromosomes, exhibiting >98% sequence similarity but distinct spatial and temporal expression patterns across tissues and developmental stages. Stable RNAi-mediated suppression of WT-1 led to significant reductions in both tiller and spikelet number. Scanning electron microscopy further demonstrated impaired tiller bud initiation in silenced lines. Importantly, phenotypic variation among independent RNAi progenies correlated with the degree of WT-1 transcript reduction, confirming a dosage-dependent regulatory role. Considering climate change and diminishing natural resources, wheat crops frequently experience environmental stresses that drastically reduce effective tiller number, often resulting in sterile or unproductive tillers. Therefore, optimizing tiller architecture toward fewer but fully fertile tillers is becoming increasingly important for yield stability. Screening germplasm based on WT-1 allelic variation and expression potential could facilitate the identification of genotypes producing an optimal number of productive tillers, thereby improving resource-use efficiency and ensuring stable yield under stress-prone environments. Collectively, these findings establish WT-1 as a key regulator of wheat architectural development and highlight its strong potential as a molecular target for breeding climate-resilient, high-yielding wheat cultivars.

P165 - TaRCR1-A enhances wheat regeneration by modulating cytokinin levels via CKX activation

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Abstract

Wheat is one of the major staple crops essential for global food security, and increasing its yield remains a primary goal in agricultural research. Molecular design breeding has become an integrated strategy for enhancing both yield and quality, relying heavily on efficient plant genetic transformation. As regeneration capacity of explants is a critical determinant of transformation success, identifying regulators of regeneration is of significant practical value.

In this study, we identified a transcription factor, TaRCR1-A, through early-stage ATAC-seq profiling of wheat regeneration. TaRCR1-A exhibits high chromatin accessibility during early regeneration, which decreases at later stages. Overexpression of TaRCR1-A significantly increased the regeneration frequency of immature embryos, a phenotype consistently reproduced in stable transgenic lines. Transcriptome analysis of downstream targets revealed that TaRCR1-A enhances regeneration by modulating cytokine homeostasis, specifically through repression of cytokinin oxidase (CKX) genes. Regeneration assays further demonstrated that Ubi::TaRCR1-A transgenic plants developed normal shoots on hormone-free medium, indicating that elevated endogenous cytokinin levels in immature embryos sustain the observed regeneration enhancement. Collectively, our findings identify TaRCR1-A as a novel transcription factor that improves wheat regeneration by regulating cytokinin metabolism, and TaRCR1-A represents a valuable genetic resource for improving wheat transformation efficiency and accelerating molecular design breeding.

P166 - Investigating the influence of genomic location: gene expression and fusarium head blight response in wheat-rye introgression lines.

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Abstract

Triticum aestivum (bread wheat) is a critical staple crop, contributing ~20% of global caloric intake. Modern bread wheat emerged ~10,000 years ago from hybridization between Aegilops tauschii and Triticum turgidum, followed by inbreeding that limited genetic diversity and reduced the capacity of breeders to produce cultivars able to meet present and future environmental challenges. Introgression, the transfer of genetic material from related species, offers a promising avenue to expand bread wheat's genetic diversity and introduce valuable traits, yet the biological activity of introgressed elements and their impact on host genome structure and function remain largely unknown.

Here, using RNA-sequencing, we studied transcriptome changes in wheat-rye introgression lines compared to Gabo, an Australian commercial wheat variety. These introgression lines harbour the short arm of rye chromosome 1 (1RS) in different wheat genomes (1A, 1B, 1D) and at distinct positions within chromosome 1D. Analysis of 1RS chromatin introgressed into these locations allowed us to identify shared and unique differential gene expression patterns among wheat-rye introgression lines. The results enhance understanding of interactions between introgressed genes and the host genome and highlight positional effects of introgressed segments on gene expression.

Using the TaNGv1.1 genotyping microarray, we corroborated the genotypes of all introgression lines, confirming that the improved TaNGv1.1 supports genome-wide variation studies. Fusarium head blight (FHB), primarily caused by Fusarium graminearum, poses a major global threat to wheat yield. Wheat-rye introgression lines have demonstrated improved resistance to fungal diseases. Characterising host-pathogen interactions in these lines improves understanding of changes in transcription factor expression and chromatin structure.

Our results show that FHB disease progression, deoxynivalenol toxin accumulation and the amount of fungal DNA present in the wheat head post infection differ significantly between recombinant lines within the 1RS.1DL translocation and the reference cultivar Gabo, known to be highly susceptible to FHB. This study reveals the critical role of the integration site within the wheat genome. Understanding how the location of introduced material influences the entire genome is crucial for developing future wheat varieties adapted to a changing climate.

Keywords: *Wheat-rye introgression, gene transcription, genome interactions, Fusarium head blight, deoxynivalenol mycotoxin accumulation.*

P167 - Identification of novel resistance loci to septoria tritici blotch (stb) in winter wheat using genome-wide association mapping

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Abstract

Septoria tritici blotch (STB), caused by the necrotrophic fungus *Zymoseptoria tritici*, is one of the most important foliar diseases of wheat. To date, 23 major STB resistance genes have been identified. This number remains relatively small, which limits the possibilities of introducing effective resistance genes into breeding materials. Therefore, there is a need to search for new sources of resistance to the disease, especially among local or historical varieties that represent a much broader genetic variability than modern cultivars, and often originate from regions of common host-pathogen co-evolution, which increases the chances of identifying new resistance genes.

A panel of 200 winter wheat accessions, including landraces, historical cultivars and breeding lines originating from 62 countries, was evaluated under field conditions in 2022-2024. Plants at the fully expanded flag leaf stage were inoculated with a mixture of four *Z. tritici* isolates. Disease severity was assessed approximately three weeks after inoculation using computer-assisted image analysis. Two disease parameters were measured: percentage of leaf necrosis (%NEC) and percentage of leaf area covered by pycnidia (%PYC).

A total of 3746 SNP markers were used to construct 2479 haploblocks. The resulting haplotypes (unique SNP allele arrangements located within the identified haploblocks) were used in GWAS analysis performed with the rrBLUP package in R.

GWAS analysis identified 17 haploblocks significantly associated with STB response parameters (%NEC and %PYC) at the suggestive significance threshold ($-\log(p) > 3.15$). These haplotypes were located on 11 wheat chromosomes and explained between 0.4% and 20.1% of the phenotypic variation (R^2). Eight haplotypes showed effects greater than 5% and, among them, three were associated with reduced disease symptoms: Chr3A_HB3_CHGH ($R^2 = 9.39\%$), Chr2B_HB43_TG ($R^2 = 8.53\%$), and Chr1D_HB24_AG ($R^2 = 12.94\%$). These haplotypes co-localize with previously reported major resistance genes (Stb6/StbSm3 and Stb19) as well as quantitative trait loci. The remaining haplotypes with $R^2 > 5\%$ were associated with increased susceptibility and were located near known STB resistance loci such as Stb1, Stb8, Stb13, and Stb18.

P168 - Spatial transcriptomic dissection of floral meristem fate in multi-ovary and single-ovary wheat

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Abstract

Increasing grain number per spikelet is a promising strategy to boost wheat yield potential. The multi-ovary (MO) wheat line, which forms up to three functional ovaries per floret, contrasts with its near-isogenic single-ovary (SO) counterpart, where only one ovary forms per floret. This trait is associated with increased expression of a D-genome copy of a key meristem maintenance gene, *WUSCHEL-1*, leading to enlarged floral meristems and altered determinacy. To investigate how gene expression patterns underlie this developmental shift, we applied spatial transcriptomics (Stereo-seq) to transverse sections of MO and SO spikes at the lemma primordium stage, when floral organ identity is first established. Our dataset captures spatially resolved gene expression patterns across inflorescence meristem, rachis and spikelet domains in both genotypes. These spatial profiles are being analyzed in conjunction with bulk RNA-seq data from the same developmental stage, which revealed transcriptional differences in genes associated with meristem function, hormone signaling, and floral organ identity. Spatial expression analysis has identified key regulatory shifts that may underlie ovary number variation, particularly in regions governing floral meristem maintenance and determinacy.

This work represents one of the first applications of spatial transcriptomics to a floral meristem mutant in wheat. By comparing gene activity in MO and SO lines within their native tissue context, we aim to uncover regulatory mechanisms that control floral organ number and determinacy. These insights provide a foundation for future strategies to modulate grain number through developmental gene networks in wheat.

P169 - From triticeae to avenae: translational dissection of the miR156/SPL and VRN Modules to fine-tune flowering in hexaploid oat

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Abstract

The molecular architecture of flowering time in wheat—anchored by the interaction between the vernalization (VRN1, VRN2, VRN3/FT), photoperiod and age-dependent (miR156/SPL module) pathways—serves as the primary paradigm for understanding flowering in cereals. While these pathways are well-defined in the Triticeae, their translational potential to the closely related hexaploid oat (*Avena sativa* L.; $2n = 6x = 42$, AACCCDD) remains largely unexplored. This gap is critical, as the lack of winter-hardy, early-maturing oat cultivars in northern latitudes necessitates a genetic solution to avoid frost injury and reduce reliance on chemical desiccants. This study adopts a wheat-comparative genomics framework to understand the complexity of flowering regulation in oat. Leveraging the recently assembled 12.5 Gb hexaploid oat genome, we mapped the orthologs of wheat SPL transcription factors and VRN3/FT in oat. Structural analysis revealed a striking syntenic relationship between oat and wheat, despite a massive inversion on oat chromosome 7D. This region harbours VRN3D within a major QTL for heading date, and exhibits promoter motif conservation, suggesting that regulatory logic is shared between the two hexaploids. To functionally validate these wheat-inferred targets, we developed CRISPR-Cas9 genome-editing constructs targeting specific SPL and VRN3 homologues. This represents the first-ever use of precise gene editing in oat. By modulating these conserved pathways, we aim to decouple the linkage between maturity and yield, replicating the success of allele mining in wheat breeding. By successfully translating wheat genetic models to the complex oat genome, we establish a cross-cereal platform that not only addresses agronomic challenges in oat but also reinforces the utility of wheat research as a foundational blueprint for polyploid crop improvement.

P170 - Genome-wide association analysis of wheat core collection based on grain protein content

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Abstract

Grain protein content (GPC) is a key determinant of wheat flour quality and an important target in breeding programs aimed at improving end-use performance. However, GPC in Korean wheat cultivars has become increasingly unstable due to climate change, particularly high temperatures and concentrated rainfall during the heading and grain-filling stages. Therefore, identifying genetic factors associated with GPC is essential for developing cultivars with stable protein content across diverse environments. In this study, a genome-wide association study (GWAS) was conducted to identify genomic regions associated with GPC using a core collection of 614 accessions. The grains harvested in 2019, 2021 and 2022 year were measured using near-infrared spectroscopy (NIR). The average GPC was 14.2% in 2019, 10.9% in 2021, and 11.3% in 2022, indicating substantial environmental variation. GWAS identified 11 significant single nucleotide polymorphisms (SNPs) located on chromosomes 1D, 2B, 2D, 4A, 4B, 4D, 5B, 6A, and 7D. Among these, SNP AX-94894883 (C/T alleles) on chromosome 1D showed a strong association with GPC and linked to the omega-gliadin gene (MG560142.1; GenBank). This genomic region contains multiple storage protein genes, including omega-gliadin D1, gamma-gliadin D1-3, delta-gliadin, and low-molecular-weight glutenin genes. Genotypic analysis revealed distinct differences in GPC among allelic groups. Among the core collection lines, 273 carried the TT genotype, 238 carried CC, 2 carried CT, and 103 lines were not detected. Evaluation of AX-94894883 will be performed to analyze its correlation with grain protein content and to validate its utility as a molecular marker. The validated marker will be applied in wheat breeding programs to improve GPC stability and enhance flour quality.

P171 - SQUAMOSA Promoter Binding-Like (SPL) proteins interact with pullulanase to regulate starch metabolism in wheat

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Abstract

Common wheat (*Triticum aestivum* L.; $2n = 6x = 42$, AABBDD) is a globally important cereal crop, and optimizing its starch composition has significant implications for food production, biofuel, and industrial applications. Pullulanase (PUL) is a key starch-debranching enzyme that hydrolyze both α -1,6 and α -1,4 glycosidic bonds, and its activity is tightly regulated by its endogenous inhibitor, PULI. While SQUAMOSA promoter binding-like proteins (SPLs) are well known for controlling the vegetative-to-reproductive phase transition, yet their roles in seed development and germination, both critical developmental transitions, remain poorly understood. We focused on SPL3, a relatively understudied SPL in cereals, in regulating the PUL/PULI module during seed development. RNA-sequencing analysis revealed that SPL3 and PUL homeologs are co-expressed during early grain-filling, whereas PULI transcript levels were barely detectable, supporting the antagonistic relationship between PUL and PULI. Gene expression analysis in imbibed seeds further showed transcript abundance of SPL3A, homoeolog, highlighting its primary role in wheat. Using electrophoretic mobility shift assay (EMSA), we confirmed that SPL3 directly binds to the PULI promoter, providing molecular evidence that SPL3 regulates the PUL/PULI system. To further dissect this regulatory network, we are currently targeting PUL, PULI, and SPL3 individually using CRISPR-Cas9. These findings uncover a previously unrecognized role for SPL3 in starch debranching regulation and offer new avenues to enhance wheat grain quality and improve the performance of industrial starch-modifying enzymes.

P172 - TaERE gene improves shoot regeneration and transformation efficiency in wheat

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Abstract

Genetic transformation is of vital importance for both gene functional analysis and genetic improvement of crop species. For many major crops, including wheat, rice and maize, the production of transgenic plants requires extended tissue culture, which typically results in low transformation efficiency. The incorporation of regeneration-promoting genes into in vitro culture systems offers a promising approach to address this limitation. Here, we show that overexpression of the wheat gene TaERE (a regeneration efficiency-enhancing gene) significantly increases regeneration efficiency. This enhancement appears to be mediated through the activation of cytokinin biosynthesis genes and modification of cell wall components in immature embryos. Furthermore, TaERE homologs similarly improves shoot regeneration in maize and soybean, demonstrating that this strategy is effective across both monocotyledonous and dicotyledonous crops.

P173 - Telomere-to-telomere genome assembly reveals the genomic architecture of disease resistance and yield coordination in elite wheat YM33

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Abstract

Wheat production is threatened by Fusarium head blight and powdery mildew and other disease, breeding cultivars that harmonize disease resistance with high yield remains challenging. Here, we present the first telomere-to-telomere genome of elite wheat Yangmai 33, which combines dual disease resistance and exceptional yield. Using hybrid sequencing (ONT, HiFi, Hi-C), we generated a gap-free assembly, resolving centromeres and structural variations. Exogenous chromosome introgression on chromosome 6A harbors Pm21 explained powdery mildew immunity of YM33. The Fhb1-contained chromosomal segment in YM33 exhibits sequence variations in comparison with SM3 and WSB, indicating that the Fhb1 containing segment in YM33 derives from a genomic background distinct from SM3 and WSB. Interestingly, Yangmai 33 integrates 66%-73% favorable alleles for spike traits and semi-dwarfing genes (Rht8, Rht-B1b), thus bypasses the yield-resistance trade-off. The T2T genome unveils genomic mechanism enabling trait coordination and provides a roadmap for designing wheat through pyramiding of disease resistance and yield QTLs

P174 - Consideration on the design of inflorescence for high yield potential of wheat

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Abstract

Meeting the increasing global demand for food in the face of limited arable land and diverse environmental constraints remains a fundamental challenge in modern agriculture. Since the Green Revolution in the 1950s to 1970s, improvements in developmental traits, such as plant nutrition, morphology and inflorescence architecture, have led to a threefold or even higher increase in the yields of our major staple cereals, including rice (*Oryza sativa* L.), maize (*Zea mays* L.) and wheat (*Triticum aestivum* L.). Throughout their evolutionary history, Poaceae species have developed distinctive inflorescence architectures that significantly influence grain number per spike/panicle, thereby impacting overall yield. In the context of emerging industrial models, wheat varieties with greater yield potential are required to synergize with improvements in plant architecture, nutrient absorption, photosynthesis, and resource allocation. To address this, comparative analysis of inflorescence development mechanisms in major cereal crops has been conducted to explore their differentiated contributions to yield performance. By employing systematic multidimensional comparison methods, our study comprehensively evaluates both conserved and divergent regulatory pathways governing inflorescence structure. Through precision design, these findings will provide critical breakthroughs for significantly enhancing yields in wheat and other cereal crops.

P175 - Genetic dissection of end-use quality in wheat to facilitate breeding

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Wheat (*Triticum aestivum* L.) is one of the most significant staple crops, providing 20% of the calories and protein consumed worldwide (FAO, <http://faostat.fao.org>). Enhancing the end-use quality traits of wheat is a primary goal in breeding programs. Gluten proteins, which are crucial for determining end-use quality, consist of two types: polymeric glutenins and monomeric gliadins. Together, these proteins impart unique viscoelastic properties to wheat dough. However, aside from high molecular weight glutenins, the role of other seed storage proteins (SSPs) in processing quality and their application in breeding remain poorly understood. This is due to the high sequence repetitiveness, numerous gene copies, and complex structural variations associated with these proteins. In this study, we aimed to identify key genes that influence quality traits and constructed a multi-layered regulatory network underlying end-use quality. We specifically identified the γ -gliadin genes γ -1 and γ -2, along with elite alleles crucial for processing quality. We also characterized transcriptional regulators, including TaGAMyb, TaNAC019, TaCAMTA2, the histone acetyltransferase GCN5, and the transcriptional adaptor ADA2, which interact to regulate the expression of SSP genes. Additionally, we discovered LGP1 (a gliadin) and LGP2 (a purindoline) through map-based cloning, whose aberrant signal peptide cleavage causes abnormal gluten protein accumulation. We identified 23 SSP genes associated with end-use quality by employing k-mer-based genome-wide association studies and developed a tool called "PanSK" (Pan-SSP k-mer) for high-accuracy prediction of flour quality phenotypes based solely on SSP genotypes. Furthermore, we propose a comprehensive approach termed "WiseCookie," which integrates digital phenotyping, machine learning, and a thorough understanding of the grain-to-cookie transformation, thereby facilitating early-generation selection for breeders. These findings provide strong support for improving wheat end-use quality through the identification of key genes to enhance breeding efforts.

P176 - Genetic and molecular dissection of brassinosteroid-regulated plant architecture in barley

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Abstract

Brassinosteroids (BRs) are essential steroid hormones that regulate multiple aspects of plant growth, development, and stress adaptation. In cereals, BRs play pivotal roles in determining plant architecture traits such as leaf angle and root system structure, both of which are crucial for optimizing light interception and nutrient uptake. However, the cellular and genomic mechanisms through which BRs regulate these traits in barley remain poorly understood.

In this study, we integrated genetic mapping, transcriptomics, cytology, and pangenome analyses to investigate BR-mediated regulation of leaf angle and root development in barley. Through mapping, two novel alleles of BR-related genes—*brd* in the biosynthesis pathway and *uzu* in the signalling pathway—were identified, each displaying a compact, erect-leaf phenotype. RNA-seq and weighted gene co-expression network analysis (WGCNA) of lamina joint tissues revealed that differentially expressed and hub genes were significantly enriched in pathways related to cell wall biosynthesis, xylan modification, and lignin metabolism. Cytological and immunolabeling studies showed that, compared with the wild type, mutant cells on the adaxial side were markedly smaller and insufficiently elongated, exhibiting a pronounced reduction in unsubstituted xylan backbone epitopes, along with a complete absence of lignin deposition on the abaxial side. These cellular features pinpoint the adaxial region as the key site where BR signalling modulates cell-wall composition to drive asymmetric cell expansion, ultimately determining the leaf angle.

Furthermore, pangenome-wide copy number variation (CNV) analysis of BR biosynthesis and signalling genes revealed distinct evolutionary patterns. BR signalling genes were highly conserved, while several biosynthetic genes exhibited copy number diversification. Notably, a cytochrome P450 gene (*HvCYP*) showed increased copy number in domesticated barley relative to wild barley. Its copy number was positively correlated with expression level, which was particularly high in roots. RNA in situ hybridization and RT-qPCR confirmed that this gene is highly expressed at lateral root initiation sites and in mature root zones, suggesting its involvement in BR-mediated root development.

Together, these findings reveal both the cellular mechanisms and genomic variations underlying BR-regulated morphogenesis in barley, providing new insights into the evolutionary and functional diversification of BR pathways in shaping cereal plant architecture.

P177 - A spatial transcriptomic atlas of early wheat spike development

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Abstract

Deciphering the molecular regulatory mechanisms underlying wheat (*Triticum aestivum* L.) spike development is essential for yield improvement, yet many aspects of these processes remain incompletely understood. Here we focused on a critical developmental window spanning from the early double-ridge stage (W2.0) to the initiation of floret primordia (W3.5) and generated a comprehensive spatial transcriptomic atlas covering five key stages of early wheat spike development. This atlas enabled the identification and annotation of nine major cell types, and the characterization of spatiotemporal expression patterns for genes involved in major biological processes, including hormone signaling and energy metabolism. Notably, genes associated with energy metabolism were highly enriched in the rachis region, indicating that rachis cell populations may serve as central hubs for nutrient and energy distribution during spike morphogenesis. By integrating pseudotime trajectories with RNA velocity, we constructed the dynamic progression of cell fate transitions within the spike meristem. In addition, detailed analysis of cells at the base of spikelet primordia, combined with genome-wide association study (GWAS) results, allowed us to identify potential regulatory modules associated with lateral organ development and grain number determination. Collectively, this study provides a high-resolution spatiotemporal resource and conceptual framework for dissecting the molecular mechanisms that govern early wheat spike development.

P178 - Multi-omics analyses uncover regulatory networks governing flavonoid biosynthesis in *Triticum aestivum*

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Abstract

The metabolites of wheat are not only indispensable for its own growth, development, and environmental adaptation, but also play an important role in human health. However, studies based on integrated analyses of metabolomic, transcriptomic, and genomic data in wheat natural populations remain limited. Here, we performed a widely targeted metabolomic analysis of 300 wheat natural accessions and quantified 1,495 metabolites in leaves at the jointing stage using liquid chromatography-mass spectrometry (LC-MS), followed by comprehensive profiling. Focusing on 315 flavonoids, we conducted metabolite genome-wide association studies (mGWAS) and metabolite-transcriptome association analyses, enabling the construction of a genome-scale metabolic regulatory network. By integrating expression genome-wide association studies (eGWAS), we further established a tripartite association network encompassing 12,690 nodes and 31,125 edges among metabolites, metabolite quantitative trait loci (mQTLs), genes, and expression quantitative trait loci (eQTLs). Data mining identified seven candidate enzyme-encoding genes and four transcriptional regulators potentially involved in flavonoid biosynthesis. As proof of concept, three candidate genes affecting metabolic traits were functionally characterized or annotated. Collectively, our study delineates a systems level framework of flavonoid metabolic regulation in wheat, provides mechanistic insights into flavonoid biosynthesis and regulation in leaves, and offers valuable genetic resources for improving wheat nutritional quality.

P179 - The establishment of the first speed breeding facility in central asia and fine-tuning of its protocol

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Abstract

One of the main drawbacks of conventional breeding is the long time required to develop pure lines with outstanding adaptive characteristics, which can take over a decade. Therefore, crop breeding should be accelerated to address the growing human population, global warming, and negative climate change, such as drought, floods, and extreme temperatures. In plant breeding, several methods are used to accelerate the breeding cycle, and one of the latest approaches that significantly reduces the plant growth cycle is Speed Breeding. Here, we report the initial establishment of the first Speed Breeding Facility (SBF) in Central Asia and optimization of its protocol for wheat. The protocol involved manipulation of optimal temperature, potting mixture, light distance and intensity, timing and dosage of nutrient application, and a single seed descent breeding strategy. To support optimal wheat development under Speed Breeding, a light-bench distance of 1,5 meters was found to be the most suitable in both indoor and outdoor SBF. In addition to light optimization, the potting mixture influenced plant performance, with the highest productivity achieved in a plant growing substrate containing 65% peat, 18% perlite, 12% sand, and 7% bio humus across 15 different treatments. Furthermore, the timing and dosage of nutrient application played a crucial role, as the best results were observed with the 21d_L fertilizer application time, which optimized plant productivity and improved the efficiency of Speed Breeding.

As a result, we reached the heading stage within 30 days after germination for spring wheat varieties, thereby significantly reducing the plant's growth cycle. The optimized protocol enabled us to obtain multiple generations per year, thereby accelerating wheat improvement programs in Kazakhstan, where wheat plays a vital role, because the country is one of the main contributors to regional and global food security. Adopting this technology for local and international wheat genotypes has become a technological achievement and a source of practical knowledge for other developing nations, thereby strengthening local pre-breeding and breeding processes.

P180 - Phenological adjustment: a tool for developing advanced durum wheat lines adapted to Chile Mediterranean rainfed areas

Christian Alfaro Jara ⁽¹⁾ - ***Marcela Opazo*** ⁽²⁾ - ***Felipe Rubilar*** ⁽³⁾ - ***Iván Matus*** ⁽⁴⁾ - ***Dalma Castillo*** ⁽⁴⁾

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P181 - Wheat: staple and strategic crop in Uzbekistan

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Abstract

Wheat is one of the most widely grown crops in the world. It is also a staple and strategic crop in Uzbekistan with more than 1.3 million ha of planting area and 6-million-ton production providing most of the daily calory of the people.

International Winter Wheat Improvement Program (IWWIP) is a tri-party program based in Turkey and carried out by Turkey-CIMMYT-ICARDA developing Winter Wheat (WW) germplasm and providing it to for more than 80 breeding programs in more than 35 countries in the world: International WW community. More than 100 cultivars originating from IWWIP germplasm were registered in 12 different countries; in addition, the germplasm have widely been used as parents in many breeding programs.

Uzbekistan is one of the countries IWWIP have closest cooperation for a long time, especially in the last 15 years. Uzbekistan wheat research experienced the most impact from collaboration with IWWIP among the CAC countries. IWWIP provides wide range of germplasm that may fit to the diverse environmental and growing conditions of Uzbekistan for both irrigated and rainfed areas. As a result, more than 10 cultivars originating from IWWIP germplasm were released in Uzbekistan where they cover large acreages in the Uzbekistan farmers' fields that provide higher yields contributing to have higher incomes of the farmers. Most of the IWWIP originated cultivars are yellow rust resistant; recently, yellow rust epidemics are frequent in Uzbekistan that cause yield reduction and quality deterioration if not controlled either by chemical application or planting yellow rust resistant cultivars. As most the IWWIP originated cultivars have good level of resistance to yellow rust, they save chemical cost of the farmers providing extra income to them. IWWIP Uzbekistan cooperation also served other CAC countries in developing high yielding, disease resistant cultivars with good bread making quality such as Azerbaijan, Georgia, Turkmenistan, and Tajikistan.

Uzbekistan has reached a strong National wheat research program with qualified scientists not only in breeding but also in pathology, quality, agronomy-physiology, etc. that would develop high yielding wheat cultivars, which serve country's need for increasing the wheat production in coming years.

P182 - Improving Lr34 adult plant rust resistance in wheat

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Abstract

The wheat Lr34/Yr18/Sr57/Pm38/Ltn1 (hereafter Lr34) gene encodes an ATP-binding cassette (ABC) transporter that confers durable, partial adult-plant resistance to multiple fungal pathogens, i.e., leaf rust, stripe rust, stem rust, and powdery mildew. Lr34, located on short arm of chromosome 7D, has been widely deployed in hexaploid bread wheat for many decades, with no evidence of pathogen adaption. Several lines of evidence indicate that elevated Lr34 expression enhances resistance, including its endogenous developmental expression pattern and results from multiple transgenic studies. Lr34 overexpression via transgenesis is feasible, however the products remain constrained by regulatory and public acceptance barriers. In this study, we evaluated two independent, non-transgenic strategies to enhance Lr34 expression. In the first approach, a chimeric 7D/7A chromosome carrying Lr34 on a small 7DS introgression was used to generate lines homozygous for two copies of Lr34 i.e., 7D/7A-Lr34 and the endogenous 7D-Lr34 locus. Adult plants containing both loci exhibited a two-fold increase in Lr34 transcript levels, correlating with a 30% reduction in stripe rust severity in field trials and a similar reduction in leaf rust severity under controlled conditions. No obvious pleiotropic effects on plant growth and development were observed. Whole genome sequencing identified the recombination breakpoint in the 7D/7A chromosome enabling development of a highly specific diagnostic marker for this haplotype. In the second approach, a high-throughput wheat protoplast-based mutagenesis strategy was undertaken on the Lr34 promoter to identify sequence variants with increased expression levels. A number of variants were identified, amongst 3,000 independent base mutations, that confer higher levels of Lr34 expression. These Lr34 promoter mutations represent ideal targets for future SDN1-based gene-editing to generate higher-expressing alleles without regulatory constraint. Collectively, these findings demonstrate that both chromosome engineering and promoter modification offer effective non-transgenic routes to increase Lr34 expression and thereby strengthen durable, multi-pathogen resistance in elite wheat cultivars.

P183 - Genomic prediction of stem structural biomass uncovers productivity trade-off under Mediterranean climate

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Abstract

Terminal drought is the primary environmental constraint on wheat productivity in the Mediterranean basin, and it intensifies due to climate change. Previously, we showed that investment in stem biomass promotes grain-filling under stress conditions. However, the genetic architecture of stem traits and optimal genomic selection strategies remains poorly understood. We evaluated a bread wheat panel of 295 genotypes (WheatMore) across three Mediterranean environments: well-watered (635mm), terminal drought (228mm), and rain-fed (468mm). Our goals were to assess phenotypic and genetic trade-offs between stem traits and yield components; identify genomic regions associated with stem traits; and implement multi-environment genomic selection models for stem traits. Increased investment in stem structural biomass (dry weight, diameter, and peduncle length) was positively associated with grain size and yield per spike, particularly under terminal drought. GWAS identified 80 significant SNP markers and 77 candidate genes; 14 were stable across environments, 61 were environment-specific (26 drought-specific, 20 well-watered, and 15 rain-fed), and 21 SNPs exhibited pleiotropic effects. Novel pleiotropic regulation at the Sst1 locus on chromosome 3B shows a genetic trade-off between stem diameter and solidness, mediated by antagonistic alleles. This limits the possibility to simultaneously select for investments in these stem traits. Multi-environment genomic prediction outperformed single-environment models; integrating genotype-by-environment interactions increased accuracy by 46.51%, with heritability traits showing highest improvement. Results demonstrate that crop investment in structural stem biomass, quantified as accumulated stem and peduncle dry matter, is associated with increased grain size and yield per spike under Mediterranean conditions, with a stronger effect under terminal drought, where grain-filling relies more on stem reserves remobilization. Our results indicate that these two traits can be increased by selecting for wider stem and peduncle diameter, and longer peduncle, thereby providing a pathway to improve grain size and grain yield.

This underlines stem traits as a viable breeding target for enhancing wheat resilience under terminal drought. The identified markers, candidate genes, and genomic selection models provide practical tools for breeders to optimize parental selections for developing a wheat stem ideotype suitable for changing environmental conditions.

P184 - CRISPR/Cas9-mediated mutagenesis of the RING-type E3 ubiquitin ligase, TaGW2, in the elite Canadian cultivar AAC Brandon increases grain size and weight but reduces total grain number per plant

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Abstract

Grain size is a key determinant of yield in bread wheat and remains an important target for genetic improvement in elite cultivars. The gene Grain Weight 2 (TaGW2), encoding a RING-type E3 ubiquitin ligase, is a negative regulator of grain development in cereals and represents a promising target for precision breeding. In this study, we used CRISPR/Cas9 to disrupt TaGW2 in the widely grown Canadian hard red spring wheat cultivar AAC Brandon. A single guide RNA targeting exon 1 was designed to edit the A, B, and D homeologs. Following Agrobacterium-mediated transformation, heat-shock-enhanced editing, and segregation of the transgene, we obtained transgene-free lines carrying homozygous mutations in either the A subgenome or both A and B subgenomes, whereas no D-genome mutants were recovered. Frameshift mutations in the A and B copies introduced premature stop codons and reduced transcript abundance in mature grains. Edited lines showed a 9% increase in grain area and ~14% higher 1000-grain weight compared with wild type. However, grain number per plant declined by approximately 30%, in the double mutant, resulting in no significant change in total grain weight per plant. These results confirm TaGW2 as a negative regulator of grain size in elite Canadian wheat line.

P185 - Introgression and in-field validation of stem solidness from *Thinopyrum ponticum* into adapted Canadian hexaploid wheat germplasm

Martha Liliana Bonilla Betancourt ⁽¹⁾ - ***Pierre Hucl*** ⁽¹⁾ - ***Carlos Erazo*** ⁽¹⁾ - ***Curtis Pozniak*** ⁽¹⁾ - ***Adam Carter*** ⁽¹⁾

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Abstract

Development of solid-stem cultivars remains the most effective strategy against wheat stem sawfly (WSS; *Cephus cinctus*), a major pest in the Canadian Prairies. However, the availability of solid-stem genetic resources is limited, and breeding progress has been hindered by crossing incompatibilities, inconsistent pith expression, and difficulties in maintaining competitive agronomic and end use quality performance. This research addressed these limitations through a two-phase breeding strategy aimed at introgressing stem solidness into adapted Canada Western Red Spring (CWRS) wheat germplasm.

In the first phase, stem solidness was introduced into the hexaploid spring wheat cultivar Crocus through hybridization with perennial decaploid tall wheatgrass (*Thinopyrum ponticum*; cv. Orbit). Twenty-one intergeneric lines were advanced to near homozygosity (F7-F8), and ten lines expressing high stem solidness were evaluated in replicated field trials over three growing seasons. Nine lines exhibited pith expression equal to or greater than the solid-stem check AAC Concord and were shorter and more lodging tolerant, although grain yield and end use quality were generally inferior to elite CWRS cultivars.

The second phase employed a backcross breeding approach using adapted CWRS cultivars as recurrent parents and two intergeneric lines with the highest pith expression as donors of solidness. More than 400 inbred lines from 15 populations were evaluated in multi-location replicated trials (2022-2024) for stem solidness, agronomic traits, end-use quality, and WSS damage. Among 77 selected lines, grain yield ranged from 4,600 to 5,133 kg ha⁻¹, with approximately 70% yielding comparably to elite CWRS checks. Across environments, 64% of these lines expressed stem solidness equal to or greater than AAC Concord, while 98% exceeded the partially solid cultivar CDC Landmark.

End-use quality evaluation showed that most solid-stem breeding lines met CWRS standards for protein content, test weight, thousand-kernel weight, and falling number, with all lines classified as hard grain types. Overall, this research demonstrates the successful introgression and stabilization of stem solidness in adapted CWRS germplasm and provides valuable genetic resources for breeding programs targeting durable resistance to wheat stem sawfly.

P186 - Advancing fusarium head blight resistance in wheat: genetic gains and genomic selection strategies

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Abstract

Public wheat breeding programs (BPs) play a key role in developing cultivars that combine high yield, desirable quality, and resistance to major diseases. In the Northern Great Plains of the United States, Fusarium Head Blight (FHB) remains the most damaging wheat disease, causing significant yield losses and mycotoxin contamination. Breeders have actively sought FHB resistance by using collaborative inoculated nurseries and incorporating quantitative trait loci (QTLs) associated with resistance.

In this work, we evaluated three decades of breeding progress for FHB resistance and evaluated strategies to improve the use of genomic selection (GS) in four public BPs. Using data from a cooperative historical nursery, we measured genetic gains for FHB resistance over the past 30 years and tracked changes in allele frequencies at three major FHB resistance QTLs. We observed substantial progress, including an average reduction of 0.4% per year in visually scabby kernels (VSK) and a significant increase in resistance allele frequencies, with up to a 300% increase in *Fhb1* frequency. All QTLs had significant and positive effects on FHB-related traits without harming other agronomic traits. However, genetic gains have plateaued in the last five years, highlighting the need to identify and utilize additional minor-effect loci.

To support continued improvement, we investigated key factors influencing predictive ability in GS. Genomic prediction within the four individual BPs yielded, most of the time, the highest predictive ability (e.g., $r=0.70$ for North Dakota BP for VSK). Using nursery data to predict BP performance was beneficial only when the BP training set was small (100-200 genotypes). For example, Montana State BP's deoxynivalenol predictive ability increased from 0.18 to 0.33 when trained with BP or nursery data, respectively. Cross-prediction between BPs or pooling all available data rarely increased predictive ability relative to nursery data alone when predicting BPs. These findings demonstrate a critical trade-off between training population size and genetic relatedness and show the usefulness of having such a cooperative nursery. Together, these results provide a roadmap for accelerating FHB resistance improvement and lowering the barrier to deploying GS in public breeding settings.

P187 - Genomic strategies to accelerate genetic gain in wheat (Wheatboost)

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Abstract

The WheatBoost project addresses the growing vulnerability of Norwegian spring wheat quality to pre-harvest sprouting (PHS), a major challenge under wet harvest conditions that causes significant losses across the cereal value chain. With more unstable weather linked to climate change, conventional breeding is too slow and uncertain to efficiently improve this complex trait. There is therefore a need to integrate modern genomic tools and faster breeding approaches adapted to Norwegian germplasm and production conditions. The main objective is to implement genomics-based speed breeding at Graminor to accelerate the development of high-performing Norwegian spring wheat with improved resistance to PHS. Combining accelerated generation turnover with marker-assisted and genomic selection will shorten breeding cycles, improve selection accuracy, and support domestic wheat production and food self-sufficiency.

P188 - John Innes Centre - wheat transformation and gene editing

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Abstract

Recent breakthroughs in gene editing technologies, together with major improvements in transformation efficiency and increased genotype flexibility, have transformed wheat research and breeding. In parallel, recent amendments to UK legislation have reduced the regulatory burden associated with gene-edited field trials, creating a more supportive framework for innovation in crop improvement.

The John Innes Centre Wheat Transformation and Gene Editing Facility is at the forefront of these developments, providing world-class transformation and gene editing services to academic researchers.

Our platform is based on *Agrobacterium*-mediated transformation of immature embryos, delivering high-efficiency transformation across a wide range of wheat genotypes. We continue to develop bespoke protocols tailored to diverse germplasm, including elite varieties and landraces. Notably, we have established a highly efficient durum wheat transformation pipeline with strong editing efficiencies, expanding gene editing applications into this important wheat class.

Our expertise enables precise genome modifications in elite wheat backgrounds, accelerating the integration of gene editing into pre-breeding and cultivar development pipelines. We have extensive experience with advanced gene editing technologies, including multiplex CRISPR/Cas systems, base editing, and prime editing, enabling targeted and versatile genome modifications.

In addition, we are developing transgene-free gene editing platforms to advance precision genome engineering approaches that generate field-ready wheat lines. By eliminating the need for crossing to segregate transgenes, this strategy significantly reduces development time, cost, and regulatory complexity, enabling more rapid evaluation of edited plants under agronomic conditions.

P189 - Advances in wheat genetics in Brazil - 1991 to 2025

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Abstract

Wheat breeding in Brazil has played a key role in increasing grain yield, improving end-use technological quality for breadmaking, and incorporating resistance to major biotic and abiotic stresses in both subtropical and tropical production environments.

The objective of this study was to estimate the genetic gain achieved by Brazilian wheat breeding programs from 1991 to 2025. Data from State Wheat Cultivar Trials, conducted in partnership with wheat breeding companies in Brazil, were used to assess grain yield progress. Advances in end-use technological quality for cultivars recommended for cultivation in Brazil were evaluated using analytical data from the Embrapa Wheat Quality Laboratory. Improvements in agronomic traits were assessed based on the agronomic profiles of recommended cultivars as reported in the Proceedings of the meetings of the Brazilian Wheat and Triticale Research Commission. For grain yield, the results showed an average genetic gain of 27.7 kg ha⁻¹ year⁻¹ over the study period. When analyzed by decade, genetic gain was 36.63 kg ha⁻¹ year⁻¹ (1991-2000), 28.11 kg ha⁻¹ year⁻¹ (2001-2010), 23.03 kg ha⁻¹ year⁻¹ (2011-2020), and 16.18 kg ha⁻¹ year⁻¹ (2021-2025). Significant improvements were also observed in end-use technological quality. In the subtropical region, mean gluten strength increased from 204.6 to 283.5 × 10⁻⁴ J; farinograph stability, from 4.1 to 13.8 minutes; and test weight, from 74.8 to 80.8 kg hL⁻¹. In the tropical region, the corresponding values increased from 253.9 to 325.3 × 10⁻⁴ J, from 9.6 to 24.9 minutes, and from 78.1 to 82.1 kg hL⁻¹. Regarding agronomic traits, the proportion of cultivars classified as moderately resistant or resistant to wheat blast increased from 0% (2005) to 51.6% (2025); resistance to leaf rust increased from 35.2% to 67.74%; and tolerance to pre-harvest sprouting increased from 47.05% to 80.64% over the same period. Wheat cultivars released in Brazil over the past 30 years have contributed to improve the profitability and market competitiveness of the crop. However, it is important to note that genetic progress in grain yield has been gradually decreasing with each passing decade.

P190 - Combining GRF-GIF-enhanced Cas9 editor plants and a virus-based gRNA delivery for functional gene validation in durum wheat

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Abstract

The development of efficient in vivo transformation strategies and genome editing systems is essential to overcome genotype-dependent constraints in wheat transformation and regeneration, enabling the rapid functional validation of genes of interest.

In this study, we developed and characterized a genome editing platform in durum wheat based on a virus-mediated guide RNA (gRNA) delivery system. Stable transgenic “editor” plants were generated in three durum wheat cultivars (Antalis, Monastir, and Svevo) through Agrobacterium-mediated transformation using a vector carrying the Cas9 nuclease and the GRF-GIF chimeric protein.

Transgenic lines were characterized to estimate T-DNA copy number and evaluate Cas9 expression levels in leaves and caryopses. In parallel, phenotypic characterization was conducted to assess major morpho-physiological traits. Our results confirmed the generation of stable lines and indicated that Cas9 and GRF-GIF expression had an overall neutral effect on most traits analyzed, supporting their suitability as a genetic resource for functional genome editing.

Barley stripe mosaic virus (BSMV) vectors were engineered to carry gRNA cassettes into the γ chain and were previously tested for editing efficiency in bread wheat. To assess editing efficiency in durum wheat, leaves of Cas9-expressing plants were directly co-inoculated with transcripts of the α , β , and γ BSMV vectors. Overall, this work establishes a versatile genome editing platform combining stable Cas9 editor plants and virus-mediated gRNA delivery for the rapid functional validation of candidate genes across three durum wheat genetic backgrounds.

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P191 - Synergistic application of speed breeding for genetic studies and cultivar release in wheat (*Triticum aestivum* L.)

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Abstract

While rapid genetic improvement is critical for global food security, conventional field-based wheat breeding programs remain a significant bottleneck due to their prolonged breeding cycles. This study demonstrates an integrated speed breeding (SB) framework that supports both fundamental genetic research and practical cultivar development. First, high-resolution QTL mapping was conducted using an SB-derived recombinant inbred line (RIL) population. A major, stable QTL for heading date, qDH-3A, was identified on chromosome 3A, explaining 72.6% of the phenotypic variance with an average LOD score of 59.4. Second, a novel QTL for protein content, qPC-3A, was mapped to a 0.76 Mbp interval on chromosome 3A, providing a 1.2 percentage point increase in protein content independent of yield-related kernel traits. Alongside these genetic studies, we used the SB framework to develop a new wheat cultivar, 'Irum', the first official cultivar released through this system in South Korea. By utilizing SB protocols and multi-year and multi-environment field trials, the total breeding cycle was reduced from 128 months to 80 months, achieving a significant 4-year reduction. 'Irum' exhibited a 14.6% yield increase over the check cultivar and superior bread-making quality. Overall, these results show that the SB framework is effective for a wide range of tasks, from genetic studies to rapid cultivar development.

P192 - Optimisation of genetic gain for two negatively correlated traits: the case study of winter bread wheat yield and grain protein content.

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Abstract

It is not uncommon for the joint selection of multiple agronomic traits to be constrained by a negative correlation (Chi et al., 1969; Bandillo et al., 2015; Simmonds, 1995). This is the case for grain yield and grain protein content in bread wheat. These two traits are nonetheless of major importance for cultivar registration and for the commercialization across different markets (Arvalis, 2024). Several hypotheses have been proposed regarding the physiological bases of this negative correlation (Triboi et al., 2006; Gregersen et al., 2008). From a genetic perspective, it may result from pleiotropic genes affecting both traits, as well as from close genes in linkage disequilibrium that have antagonistic effects on the two traits (repulsion linkage) (Chen & Lübberstedt, 2010). This negative correlation shows substantial variability across panels of old and modern varieties and across the offspring of crosses, with individuals deviating from statistical expectations (Oury & Godin, 2007), suggesting that it may be possible to optimize the genetic gain of both traits simultaneously by designing mating plans that minimize repulsion linkage.

In this context, the objective of the thesis is to assess if an improved management of the breeding scheme, particularly at the mating plan stage, can lead to reduced constraints on a secondary trait while maintaining genetic gain on the primary trait by (1) finely characterizing the genetic architecture of two negatively correlated traits (using grain yield and grain protein content in bread wheat as a model), (2) assessing our ability to predict cross value (Danguy des Déserts et al., 2023; Oget-Ebrad et al., 2024), and in particular the correlation between two traits, in order to optimize the mating plan using UC (Utility Criterion) strategies (Lehermeier et al., 2017). An in-silico proof of concept, thanks to stochastic simulations, demonstrating that it is possible to improve the primary trait while at least maintaining an acceptable level for the negatively correlated trait is necessary before considering an in vivo proof of concept, which would require a considerably demanding experimental design.

P193 - Adaptation and quality traits of winter durum wheat cultivars developed in martonvásár over the last decade

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Abstract

Durum wheat is the second most widely cultivated species of genus *Triticum*. Global annual production has fluctuated between 31.4 and 38.7 million tonnes during the last decade. Worldwide interest in durum wheat is increasing due to population growth and changing dietary habits. During the last growing season, the durum wheat area in Hungary reached its historic maximum, 70 thousand hectares. In response to the needs of farmers and the processing industry, the breeding objectives of the Martonvásár (Mv) winter durum wheat programme include stable high yield, earliness, good winter hardiness, and reduced plant height, alongside with continuous improvement of technological quality. The aim of this study was to summarise breeding results from the past decade. During the last ten years, eight Mv varieties had been officially registered in the National List of Varieties in Hungary. Their average grain yield (6.8 t/ha) exceeded that of the official standard varieties by 12%. The highest yield was recorded in 2025 for 'Mv Verdoro' (9.85 t/ha) in a fungicide-protected trial. The recently released cultivars show excellent winter hardiness and stress tolerance, and several are resistant to one or more major pathogens. Technological quality has also improved significantly. The average gluten index (GI) of tested varieties and advanced lines was 64.03 over ten years. Most cultivars fall into the "good-very good" category (GI 66-85) according to the Cubbada classification, while 'Mv Pilledur' and 'Mv Trilladur' repeatedly reached the "excellent" class (GI > 85). Yellow pigment content and gluten quality (i.e. GI) now meet industrial processing requirements. Exceptionally high yellow pigment content was recorded for 'Mv Masnidur' and 'Mv Trilladur' in the year of their registration. Targeted breeding has enabled the combination of stable high yield and excellent pasta-making quality within the same varieties, like 'Mv Magnadur'. Consequently, recently registered winter durum cultivars have become technologically competitive with spring types.

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P194 - Evaluating genetic variability and biometric indicators in bread wheat varieties: Implications for modern selection methods

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Abstract

Abstract. Major grain-producing countries such as Canada, the United States of America, Mexico, Brazil, Australia, China, India, Turkey, and Russia, in the direction of selection for the creation of new varieties of wheat resistant to abiotic factors, are paying great attention to creating new wheat varieties by developing new genotypes by identifying donors with high-quality and positive indicators of valuable economic traits and introducing them into modern selection methods. Progress has been made in this direction worldwide. Today, many varieties of wheat with valuable economic traits and high grain quality have been created and introduced to large areas. In this study, 23 genotypes were selected from 45 genotypes of bread wheat varieties and lines. The nursery's growth period lasted between 233-238 days, and the lines appeared more mature than the local check varieties. Compared to the local check varieties, among the plant's biometric indicators, 15 lines showed positive results in terms of plant height, 10 lines in peduncle length, 5 lines in spike length, 1 line in spike number, and 1 line in resistance to lodging. The statistical analysis of grain yield and grain quality using the Dospekhov method showed that the experimental error rates for various indices as follows: 0.888% for yield, 3.018% for weight of 1000 grains, 0.627% for Test weight, 2.028% for protein content, 1.519% for gluten content, 2.001% for IDK, and 4.01% for grain glassiness. It was noted that the experiment was conducted correctly in terms of repetitions and showed a positive result. 10 genotypes with yield of genotypes 72.6-96.7 c/ha, weight of 1000 grains 37.9-43.2 g, test weight 803-835 g/l, protein content 16.2-19.3%, gluten content 28.5-30.4% were selected. Accordingly, it was observed that the amount of iron was 1.0-1.8 mg. It was observed that the sample was 1.3 mg in the Gozgon variety and 1.4 mg in the Antonina variety. KR20-27-FAWIR-67, KR20-BWF5IR-2625, KR20-27-FAWIR-138 lines 1.6 mg relative to the local check variety. Lines KR20-BWF5IR-2460, KR20-27-FAWIR-39, KR20-BWF5IR-246 1.7 mg. It was observed that the KR20-27-FAWIR-154 line showed a high result of 1.8 mg.

P195 - Implementation of multi-trait rapid-cycle recurrent genomic selection in Canadian wheat breeding

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Abstract

Canada Western Red Spring (CWRS) wheat is valued for its superior end-use quality, yet progress in improving complex traits like grain yield remains slow due to negative relationships with other agronomic traits and lengthy breeding cycles. This project aims to accelerate genetic gain in CWRS wheat by implementing a multi-trait rapid-cycle recurrent genomic selection (RCRGS) system designed to shorten cycle time while simultaneously improving grain yield, protein content, and other key agronomic traits. To achieve this, we developed genomic prediction models using a training population of 960 recombinant inbred lines from 16 elite CWRS families, which were phenotyped across two locations near Saskatoon, SK, Canada in 2025 and genotyped using the TraitGenetics 25K Wheat Array. We benchmarked four Bayesian regression models and observed strong multi-trait prediction accuracies, with correlation coefficients (r) exceeding 0.7 for plant height and yield. Based on agronomic performance, the top 10% of lines (96 individuals; 6 per family) were selected and intermated to generate C_1F_1 seed. These individuals initiate a three-cycle RCRGS pipeline in which each six-month cycle involves genotyping, multi-trait genomic selection, recombination, and advancement of lines from each cycle via single-seed descent to produce field-testable F_4 lines. Comparisons among C_0 - C_3 derived lines will estimate realized genetic gain per cycle and evaluate the extent to which multi-trait selection improves yield while maintaining appropriate phenology and quality. This work establishes the first RCRGS framework for CWRS wheat and demonstrates a pathway for rapid improvement without compromising critical end-use quality.

P196 - Responding to Yr15 virulence to strengthen wheat resistance

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Abstract

In May 2025, *Puccinia striiformis* f. sp. *tritici* (Pst) isolates were identified that had overcome resistance to the widely deployed yellow rust resistance gene Yr15. First reported in the UK by the UK Cereal Pathogen Virulence Survey, these Yr15-breaking Pst isolates were rapidly detected across multiple countries in Europe. Because Yr15 had been extensively deployed in European varieties, nearly 50% of the UK national wheat area was potentially vulnerable, underscoring the risks associated with reliance on single resistance genes. In June 2025, we conducted rapid genetic analyses at the John Innes Centre and confirmed that the Yr15-virulent Pst isolates emerged from within the existing 'Warrior' Pst race group rather than through an exotic introduction. Prior screening of the Watkins heritage landrace collection had identified 33 lines resistant to the 'Warrior' group, and we confirmed that 32 of these lines retained resistance to the Yr15-breaking Pst isolates. We are now exploring corresponding mapping populations to accelerate identification of the underlying resistance loci, to provide novel resistance sources that can be used to diversify the resistance gene pool. In parallel, we are characterising the current resistance diversity in UK wheat varieties to identify those with single gene reliance that may be highly vulnerable to future breakdowns, whilst also generating more reliable markers to better track resistance genes in the breeding pipeline. Together with gene stewardship strategies, these efforts aim to promote more durable and diversified resistance. By integrating rapid pathogen analysis, resistance gene stacking and deployment of optimised molecular markers, we seek not only to address current vulnerabilities but also to strengthen our capacity to respond swiftly to future virulence shifts.

P197 - A pan proteome of wheat and its use for breeding

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Abstract

Wheat is a very important stable crop dealt along worldwide supply chains. Breeders address requests of the different stakeholders of the wheat supply chain to get advantages in selling their varieties. Consequently, many traits from agronomy but also techno-functional quality have to be worked and are successfully improved since decades in parallel by breeders. New developments in different -omics technologies aim to understand more the architecture behind traits. In this project, we have established a high throughput workflow for proteomic analyses of whole grain flour in wheat. Using that workflow, we were able to detect 6,567 proteins per sample in 282 wheat varieties grown under four different environments in Germany. For 3,461 proteins we determined a heritability > 0.5 and determined the correlation coefficients to 105 phenotypic traits from agronomy and baking quality. Surprisingly, they were quite low for most proteins.

In a second step we run a genome-wide association mapping study on the highly heritable proteins using genotyping-by sequencing data. 237 QTL were identified, which explained >60% of the phenotypic variance of the respective proteins. Differential expression analyses elaborated major QTL for proteins influencing different traits in parallel. This unique data set represents an important resource for future wheat research.

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P198 - SNP genotyping with large, intermediate and small marker panels in hexaploid wheat

Martin Ganal⁽¹⁾ - Joerg Plieske⁽¹⁾ - Eva Grafahrend-Belau⁽¹⁾ - Karolina Greziak⁽¹⁾ - Dagmar Kulosa⁽¹⁾ - Naser Poursarebani⁽¹⁾ - Thomas Gross⁽¹⁾ - Heike Molenaar⁽¹⁾ - Heike Gnad⁽¹⁾

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Abstract

Nowadays, the genotyping of hexaploid wheat (*Triticum aestivum*) for genetic analysis and within plant breeding is mainly performed using single nucleotide polymorphisms (SNPs). Based on large scale genome sequencing, SNP markers are available in essentially unlimited numbers. For genotyping with large marker numbers, many different SNP genotyping panels are now available that range from lower densities with several thousands of markers to high density markers sets with more than 100,000 markers. Most of these panels are screened on arrays and are used for germplasm and variety analysis in marker-trait association studies, complex genetic structure studies and relationship analyses. Optimized second generation genotyping arrays contain marker sets that have been carefully selected for marker quality, genome distribution based on genetic data, and haplotype structure. The main use of such optimized arrays is for genomic selection in plant breeding. In recent years, genotyping-by-sequencing (GBS) especially with defined marker sets (targeted GBS) has become a technology of interest for the analysis of wheat material with several hundred to 1,000 markers. Such tGBS panels based on optimized marker sets are a very cost-efficient tool for genetic relationship analysis and genomic selection in combination with imputation based on parental sequencing data. tGBS produces reliable data in highly inbred material such as SSD and DH derived material if one can accept a certain amount of missing data. In highly heterozygous materials such as F2 or backcross populations, tGBS delivers robust and reliable results when focusing only on genotype calls derived from markers that meet the highest quality standards. Single marker analysis is currently mostly performed using KASP or other technologies mainly for markers diagnostic for specific traits and seed quality analyses. We present a summary of criteria (including costs) for the optimal SNP analysis of wheat material for research and breeding applications.

P199 - Stem elongation phase as a key trait to improve grain number and yield: Preliminary results from BC4 lines with similar anthesis dates but advancing beginning of stem elongation

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Abstract

The stem elongation phase (SEP; from first node to anthesis) has been proposed as a key developmental trait to increase grain number and yield in wheat. Previous evidence, mainly from environmental manipulations (e.g., photoperiod), suggested that extending SEP may enhance yield potential. In this study, we developed wheat lines to directly test the hypothesis that increasing SEP duration without modifying anthesis date would increase grain number and yield. Two cultivars adapted to the Pampas region of Argentina, ACA-303 and Baguette -11, were selected as parents because they differ in the onset of SEP (earlier and later, respectively). The F1 was backcrossed four times to Baguette -11. Lines for backcrossing were selected for reaching to first node at a similar date to ACA-303 while maintaining anthesis date comparable to Baguette -11, aiming to obtain Baguette-11-like genotypes with longer SEP. In 2023, BC4S1 lines were field-grown alongside the parents and seven lines combining early SEP onset (similar to ACA-303) and anthesis timing close to Baguette-11 were selected. In 2025, BC4S3 lines and parents were evaluated in field plots (five rows, 0.20 m apart, and five m long) under potential growing conditions, using a randomized block design with three replications. Sowing was within the optimal window (June 2). SEP duration ranged from 47.3 ± 0.6 to 49.0 ± 0 days in the selected lines, compared with 42.3 ± 1.2 days in Baguette-11. Shortening of the sowing-first node phase did not negatively affect yield. Baguette-11 yielded 757 g m^{-2} . One line matched this yield (-0.3%), whereas the remaining lines showed a trend to increase yield ranging from 7.7 to 13.4% ($p > 0.05$). Baguette-11 reached $20,102 \text{ grains m}^{-2}$; while the lines increased grain number by 3-13%, with two lines approaching significance (line 7.3 p -value = 0.0698 and line 3.1 p -value = 0.0982, pairwise t-test). Overall, these preliminary results are encouraging and justify additional field testing to determine the impact on yield of increasing SEP duration without changing anthesis date.

P200 - Seven decades of global impact: CIMMYT's end-to-end framework for accelerating bread wheat breeding

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Abstract

Wheat provides nearly one-fifth of the world's caloric and protein intake and remains central to global food and nutrition security. For more than seven decades, the wheat breeding program of the International Maize and Wheat Improvement Center (CIMMYT) has supplied improved germplasm that underpins a large share of wheat varieties grown across the developing world. CIMMYT's breeding pipelines have consistently delivered strong rates of genetic gain across diverse wheat production environments. Recent restructuring and modernization of breeding pipelines have further accelerated progress. CIMMYT employs an accelerated genomics-assisted rapid-cycle recurrent selection (RCRS) strategy to enhance population improvement while maintaining broad adaptation. The Rapid Bulk Generation Advancement (RBGA) scheme has reduced the effective breeding cycle from approximately five years to three years, representing a ~40% reduction in cycle time. Early-generation advancement in screenhouses combined with targeted field evaluations enables faster fixation of elite lines, allowing early testing of stage 2 lines in the Target Environments (TEs).

Analysis of yield data from 20 TEs across South Asia shows sustained yield gains of approximately 1-2% per year, including lines developed under the first phase of the accelerated breeding program launched in 2020. By integrating breeding cycle acceleration, genomic selection, speed breeding, target-environment phenotyping, and innovative partnership models with NARES, the initiative aims to sustain genetic gains of 1.5-2.0% per year along with gains in Zn enhancement of 1-2% per annum. As a result, the average age of parents in the crossing block has declined from approximately 6.25 years to about 3.5 years, with further reductions expected. The first set of trait augmentation pipeline lines derived from MAS showed promising lines with traits of interest. These advances have already delivered annual yield gains of 1.2-1.9% in key wheat breeding pipelines while simultaneously mainstreaming climate resilience, durable disease resistance, and grain zinc biofortification. Together, they demonstrate how modern breeding systems can accelerate the development and global dissemination of climate-resilient, nutritious wheat varieties to support future food security.

P201 - Major-effect QTLs and validated markers for improving stripe rust resistance in wheat breeding

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Abstract

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), remains a major constraint on global wheat production and requires durable, genetically defined resistance sources. In this study, four recombinant inbred line (RIL) populations sharing a common recurrent parent (PBW621) were evaluated for both seedling and adult-plant responses to three predominant Pst pathotypes (238S119, 46S119, and 110S119). Seedling assays revealed a clear segregation pattern, confirming the presence of a single dominant resistance gene in each cross. Field evaluation of 395 RILs further revealed clear phenotypic differentiation: 203 lines expressed high to moderate resistance, while the remaining lines were susceptible; donor parents consistently displayed resistance, and the recurrent parent, PBW621, remained susceptible. High-density genotyping using the 90K SNP array enabled the development of 66 KASP markers, of which 35 were polymorphic, and 19 were validated across the relevant RIL populations. Inclusive composite interval mapping five major QTLs (qYr-pau-1A_P5, qYr-pau-5B_P5, qYr-pau-5A_P11, qYr-pau-6A_P11, and qYr-pau-2B_P7) and one minor QTL (qYr-pau-3B_P9). These QTLs were mapped on chromosomes 1A, 5B, 5A, 6A, 2B, and 3B, respectively, with phenotypic variance explained (PVE) ranging from 28% to 65% for major loci and 7.5% for the minor locus. Candidate gene mining highlighted defence-related genes, including NB-ARC proteins, peroxidases, helicases, and glycoside hydrolases, consistent with known rust-resistance pathways. These validated KASP markers and major-effect APR QTLs provide breeder-ready tools for targeted introgression and strategic pyramiding of stripe rust resistance in wheat improvement programs.

P202 - Improving genomic prediction accuracy for wheat stem sawfly resistance in winter wheat

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Abstract

Wheat stem sawfly (WSS; *Cephus cinctus* Norton) is a native grass-feeding insect that oviposits their eggs inside the stem of wheat (*Triticum aestivum*). The larva will then eat the pith of the stem before making a hibernaculum in the base, predisposing the plant to lodging. Damage due to WSS is responsible for an estimated USD \$350 million loss in the United States and Canada annually. The only currently known genetic resistance is the solid stem trait on chromosomes 3B and 3D, but this trait is highly environmentally variable. Genomic prediction can be used by plant breeders to more effectively make predictions and advancements. Since no work has currently been published for genomic prediction in WSS resistance, research understanding how to improve this methodology will aid breeders in meeting the needs of growers in WSS prevalent areas. In this study, a panel of 2,503 individuals with WSS resistance phenotypes collected from 2014 through 2025. A variety of genomic prediction models were used including Genomic Best Linear Unbiased Prediction models, Bayesian models, and machine learning models to assess which model structures were the best at estimating stem solidness and damage due to WSS (cutting score). Additionally, to assess methods for further improving prediction accuracy, the same models were used with training data from environments that had a heritability greater than 0.4. Better understanding which genomic prediction models perform best will aid plant breeders in making effective predictions for WSS within their programs, including years where variation for WSS resistance is low. This project is ongoing and results are not yet finalized.

P203 - Haplotype-based autoencoders for dimensionality reduction and haplotype block effect estimation

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Abstract

Machine learning (ML) methods are increasingly explored in plant breeding as alternatives for genomic prediction. However, ML algorithms typically require substantially more computational resources than established approaches such as Genomic Best Linear Unbiased Prediction (GBLUP). To address this limitation, we developed a novel autoencoder architecture inspired by haplotype block construction, with the goal of reducing the dimensionality of genetic data, thus decreasing computational demands and training time, while maintaining or increasing prediction accuracy.

We first evaluated a standard fully connected autoencoder, a type of unsupervised neural network, on a dataset of German winter wheat genotypes to reduce the dimensionality of SNP marker data. While this approach significantly decreased computation time, it also caused a notable reduction in prediction accuracy. To overcome this issue, we designed a linkage-based locally connected autoencoder that groups markers into genetically linked haplotype blocks, producing one encoded feature per block. The resulting block-level features were used as inputs for GBLUP and Random Forest models to predict grain yield. Additionally, we implemented a semi-supervised variant of the autoencoder by incorporating yield information directly into the training objective which presents a new way of estimating haplotype block effects.

In two reduction steps, the linkage-based autoencoder reduced dimensionality by 77% and 98%, respectively, while maintaining prediction accuracies equal to those obtained using the full marker dataset and outperforming predictions based on principal components. Across all analyses, the reduced feature sets substantially decreased computation time for ML models. Although the semi-supervised component did not improve predictive performance, it generated interpretable block-level effect estimates that differed from block-wise sums of marker effects calculated using conventional methods, potentially capturing local epistatic effects.

Our approach introduces a new perspective on processing haplotype blocks for genomic prediction, potentially providing more flexible modelling opportunities without the use of multiple binary dummy variables for each block variant. In a breeding context, the resulting block-level features and effect estimates can be used for selection decisions, for example to prioritize parents carrying favourable haplotypes in key regions and to support cross planning by assessing the expected contribution of rare or even previously unseen block variants in progeny.

P204 - Plant-plant interactions and canopy complexity in winter wheat

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Abstract

Crop mixtures offer considerable potential for sustainable intensification, but how increasing canopy heterogeneity (the number of distinct neighboring genotypes) induces genotype-specific plasticity (GSP) and affects canopy productivity through plant-plant interactions remains poorly understood.

Here we investigated GSP under homogeneous and heterogeneous canopies and addressed the role of breeding history by mixing eight old winter wheat genotypes released between 1966-1975 (OLD) or eight modern genotypes from 2008-2018 (NEW). Canopy complexity was arranged as 1) homogeneous pure stands and 2) fully randomized heterogeneous mixtures at constant planting density. 20 traits were measured destructively at booting and at anthesis to capture stage-specific responses. Linear mixed models estimated marginal means and quantified trait plasticity.

Increasing canopy heterogeneity strongly induced GSP, but responses differed clearly between age groups. At anthesis, OLD showed a 12% increase under full mixture compared to pure stands, while NEW showed no response. Tiller number increased under full mixture (OLD: +10%, NEW: +15%), but OLD were able to translate this into greater ear number (+23%) and ear biomass (+7%), whereas NEW showed limited responses in both ear traits (+4% and -2%). Interestingly, more leaves stayed green with increasing canopy heterogeneity for both age groups at anthesis (OLD: -7%, NEW: -11% in full mixture compared to pure stands), suggesting a delayed response to shading from genotypically distinct neighbors. Leaf-level GSP differed between age groups: NEW exhibited a competitive response to canopy heterogeneity by increasing leaf area (+34%) driven by higher leaf length (+30%) and reduced leaf thickness (-9% in LMA) with no change in leaf width, indicating active neighbor sensing rather than a response to reduced light.

Although modern genotypes are known to be higher yielding and less competitive, reduced competitiveness did not translate into greater cooperativeness or higher productivity in mixtures. Instead, older genotypes displayed greater plasticity and achieved higher canopy productivity under heterogeneous canopies. These findings emphasize that targeted plasticity for inter-genotypic interactions, rather than reduced competitiveness per se, is key to designing productive crop mixtures and informing future breeding strategies.

P205 - The ARCs spring wheat breeding program for the dryland winter rainfall region of the Western Cape.

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Abstract

The ARCs Spring wheat breeding program for the dryland winter rainfall region of the Western Cape
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It is estimated that a yield increase of up to 40% will be required to produce enough wheat for human consumption by the year 2050. Taking on the challenge of increasing wheat production in South Africa, the Agricultural Research Council (ARC) has established a spring wheat breeding program for the winter rainfall region of the Western Cape. The primary objective of the breeding program is to develop new cultivars with better yield performance by assembling trait variants in ways that increase overall genetic yield potential. Breeding lines are screened across a range of environments that range from semi-arid to dry arid regions to ensure rust resistance, a degree of climate resilience as well as high yield potential. A secondary objective of the breeding program is to develop high yielding lines that are tolerant to broad spectrum herbicides. Ryegrass and other broadleaf weeds have become serious problems in farmers' fields in recent years, having a deleterious effect on yield. Therefore, herbicide tolerant lines will be evaluated under various conditions to simplify broad spectrum weed control for grassy and broadleaf weeds, leading to a reduction in production costs, cleaner fields and potentially higher yields. Finally, wheat production in South Africa, especially the Western Cape, is under severe pressure primarily due to the lack of profitability as a result of low international wheat prices and a surge in production costs. Various ways to reduce production costs are being explored, including the development of lines that require less Nitrogen and are less sensitive to saline and poor soil quality. These efforts will contribute to a more profitable and sustainable wheat industry in South Africa.

P206 - Molecular overview of Eastern Canadian winter wheat germplasm for agronomic, quality and disease resistance traits using KASP and STS markers

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Abstract

Wheat production in Eastern Canada is under constant pressure from climate-driven environmental stressors and increasing disease intensity. To aid breeding programs that seek to improve genetic gain, we conducted a targeted molecular characterization of the Eastern Winter Wheat Genomic Selection (EWGS) panel, which consists of 352 cultivars and breeding lines from the four major Eastern Canadian public breeding programs. Using 21 Kompetitive Allele Specific PCR (KASP) assays and one sequence-tagged site (STS) marker, alleles related to winter survival, agronomic performance, disease resistance, and end-use quality were determined. Results revealed a strong genetic foundation for winter environment adaptation, with high frequencies of favorable alleles for frost tolerance (Fr-A2) and vernalization (Vrn-A1), as well as soft wheat quality determinant alleles such as Pinb-B2a, and Pina-D1a. However, relatively low frequencies of resistance alleles were observed across programs for Fusarium head blight (e.g., Fhb1, Fhb2) and adult plant resistance loci (Sr2, Lr34), indicating differences in both historical selection pressures and opportunities for improving disease resilience. Notable variation in allele frequencies for plant height (Rht-B1, Rht-D1, Rht8) and gluten strength (Glu-A1, Glu-D1) further highlighted program-specific breeding priorities. While Eastern Canadian breeding programs have succeeded in integrating key adaptive and quality traits, significant opportunities for improvement may be realized through targeted germplasm exchange and the expanded use of marker-assisted selection. These results provide a molecular benchmark that will shape future introgression efforts, support genomic selection model development, and facilitate collaborative improvement of winter wheat for the evolving growing environments of Eastern Canada.

P207 - Identifying the genetic drivers of wheat's endogenous Biological Nitrification Inhibition (BNI) capacity

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Abstract

Over 2.5 billion people depend on wheat as a primary food source. Sustaining current yields, however, demands intensive synthetic nitrogen (N) fertilization, which are economically costly and environmentally damaging. A major component of this inefficiency is nitrification. Soil nitrifying communities rapidly convert applied ammonium (NH_4^+) into highly mobile nitrate (NO_3^-). Consequently, agricultural systems experience pronounced N losses via groundwater leaching and the emission of nitrous oxide (N_2O), a greenhouse gas with profound climate impacts.

Crop species generally lack the physiological capacity to outcompete native microbes for available NH_4^+ . Yet, specific wheat genotypes exhibit an adaptive advantage through Biological Nitrification Inhibition (BNI). By exuding targeted secondary metabolites from their root systems, these plants actively repress nitrifier populations (Subbarao et al., 2021). Exploiting BNI could fundamentally restructure agricultural N management. Translating this trait into applied breeding, however, remains difficult: the logistical challenge of phenotyping belowground root exudation dynamics at scale has limited its genetic characterization. My research addresses these hurdles by establishing a comprehensive strategy to identify the genetic fingerprint of BNI capacity occurring into the wheat germoplasm. By using a state-of-the-art, high-throughput phenotyping platform (Jáuregui et al., 2023) and utilizing the vast genetic diversity represented in the Watkins Collection (Cheng et al., 2024), this study maps the complex traits governing BNI. We report the identification of key candidate genetic regions associated with this trait using GWAS, alongside a validation approach using QTL.

The primary objective is to translate these findings into actionable breeding tools, accelerating the integration of BNI traits into elite germplasm. By fostering the development of eco-efficient wheat varieties, my approach offers a scalable, sustainable path to reducing dependency on synthetic inputs, enhancing soil health, and mitigating the environmental footprint of global wheat production.

P208 - MosaicFarmAI: An innovative deep learning model for accurate genomic predictions in ultra-sparse field trials

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Abstract

The evaluation of different cultivars should be conducted in multiple environments to assess the effect of genotype by environment (GxE) on the performance of population to select stable high-yielding plants across various environmental conditions. However, multi-environmental trials (MET) on large populations are very costly and requires massive laborious efforts. One effective way to reduce the experimental efforts when evaluating MET by using 'sparse testing', in which a subset of the reference population is evaluated in each field trial. Sparse testing can increase the evaluation capacity at reduced cost leading to improved representation of the studied population across wider environmental conditions. However, such designs require precise planning allied with advanced statistical and artificial intelligence models to maximise their benefits.

Here, we are proposing MosaicFarmAI, a deep learning model that has the potential to significantly enhance in highly sparse field trials. The model was tested on MET of spring wheat population planted across 20 field trials. Compared to the standard prediction models whether they modelled GxE or not, MosaicFarmAI showed an enhanced prediction accuracy (up to 3 times higher Pearson correlation coefficient) for different traits when the evaluated environments had generally a positive average correlation among them (>0.35). When the environments had very or negative correlations among each other's, MosaicFarmAI showed comparable or slightly reduced prediction accuracy compared to the standard models.

Interestingly, and under all scenarios of environmental correlations, highly sparse scenarios, e.g. when only 20% or less of the whole population size was included in the reference, MosaicFarmAI showed remarkable superiority over all evaluated standard models and this superiority increased when increasing the sparsity of the trials. When only around 10% of the population size per trial was used in the reference, the prediction of the standard models became inaccurate with large standard errors, unlike the prediction of MosaicFarmAI, which was still robust even when using as low as 5 individuals per trial.

MosaicFarmAI demonstrates substantial improvements in prediction accuracy for various traits in highly sparse field trials, particularly in environments with generally positive correlations. This superiority has the potential to optimise field trial designs and reduce farm operation costs.

P209 - Diallel analysis of local bread wheat (*Triticum aestivum* L.) cultivated in Uzbekistan

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Abstract

Diallel analysis assumes that the genetic interactions contributing to trait variation can be adequately captured by GCA and SCA effects. However, in reality, genetic interactions can be more complex, involving higher-order epistatic interactions, pleiotropy, and other factors that are not accounted for in the traditional diallel analysis, for this purpose, studies were conducted to study the combinatorial ability of wheat varieties widely planted in Uzbekistan. The mode of inheritance for the 1000- kernel weight, vegetation period, plant height, vitreousity, grain yield, mass of grain in the ear and productive accumulation of 4x4 full diallel crosses of wheat varieties was estimated in F1 generation. The results indicated significant differences between the parents for General Combining Ability and cross for Specific Combining Ability, reciprocal effect for 1000- kernel weight, vegetation period, plant height, vitreousity, grain yield, mass of grain in the ear and productive accumulation. However, analysis of variance of combining capable for grain yield indicated that General Combining Ability and Reciprocal effects were highly importance while Specific Combining Ability. Highly significant General Combining Ability and Specific Combining Ability variances showed the predominance of additive, epistatic and dominant genes in controlling this character. Combining ability is a concept in genetics and plant breeding that refers to the ability of a particular genotype to combine with other genotypes to produce offspring with desirable traits. It's especially relevant in the context of hybridization and is used to evaluate the potential of parental lines for producing superior hybrids, in this regard, the Combining ability of varieties planted in large areas in Uzbekistan was analyzed. The use of diallel analysis in the development of new transgressive varieties and lines with a high 1000 grain weight of bread wheat is one of the advantages. It was found that the combined ability of 1000 grain weight of bread wheat F1 hybrids was positive 1.404 (GCA) in the Zarrin variety, and 0.594 (GCA) was observed in the F1 crossbred of the Gozgon variety. Positive combination ability of Zarrin x Gozgon combination was positive 5.214 and Bunyodkor x Jaykhun combination's F1 hybrid was positive 2.169.

P210 - Inheritance patterns in F_1 hybrid generations of durum wheat

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Abstract

Abstract. Hybridization plays a crucial role in the development of new varieties of durum wheat (*Triticum durum*). This study investigated the inheritance of economically important traits such as plant height, number of grains per spike, and grain weight per spike in F_1 hybrid generations. Field experiments were conducted from 2019 to 2021 on irrigated plots at the Central Experimental Farm of the Scientific Research Institute of Rainfed Agriculture. According to the results, most of the 20 hybrid combinations studied exhibited high levels of dominance, indicating heterosis. Notably, heterotic effects were observed in combinations such as "Mingchinor $\times$ Istiqbolli," "Istiqbolli $\times$ ICAMOR TA04," "ICAMOR TA04 $\times$ Istiqbolli," "Makuz-3 $\times$ Krupinka," "Makuz-3 $\times$ Omrabi 5," "Makuz-3 $\times$ Kristella," "Mingchinor $\times$ Krupinka," "Makuz-3 $\times$ IcaKader," "Omrabi 5 $\times$ Makuz-3," "Makuz-3 $\times$ Omrabi 5," and "Makuz-3 $\times$ ICAMOR TA0462." The use of local varieties as maternal parents often resulted in pronounced heterosis in the hybrid progeny. This research provides a valuable genetic resource for the development of high-yielding and quality durum wheat varieties adapted to Uzbek agro-ecological conditions.

P211 - Effect of *Vrn1* and *Rht8* genes on wheat performance in South Eastern Europe

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Abstract

Wheat cultivation across diverse climates and under various biotic and abiotic stresses requires cultivars that are well adapted to specific growing environments. Variation in phenology and related traits plays a key role in enabling this adaptation. The main objective of this study was to understand how different combinations of alleles for reduced height (*Rht8*) and vernalisation (*Vrn1*) genes can support the breeding of wheat varieties with optimal performance in the South Eastern growing region. Field experiments were conducted over two growing seasons (2022 and 2023) at Rimski Šančevi, near Novi Sad, Serbia (45.20° N, 19.51° E). Near-isogenic lines (NILs) carrying different combinations of *Rht8*, *Vrn1A*, and *Vrn1B* alleles, along with the recurrent parent Paragon, were evaluated in a randomized complete block design with five replicates. The well-adapted Serbian cultivar NS 40S was included as a control. Phenological traits (booting, heading, flowering time), plant architecture traits (plant height, peduncle and spike length), and physiological parameters (NDVI and chlorophyll content) were assessed. Year, genotype, and their interaction significantly affected most traits. Compared with Paragon, *Rht8* alleles, alone or combined with *Vrn1A* and *Vrn1B*, reduced plant architecture traits but increased physiological parameters in both seasons. Phenological responses showed strong genotype × year interactions, with variable allelic effects. The influence of *Vrn1* alleles differed between seasons: in 2022, their effects were minor, whereas in 2023 they promoted later phenology and reduced plant architecture traits and chlorophyll content. These findings indicate that *Rht* and *Vrn* allele combinations can be effectively exploited to fine-tune phenology, physiology, and productivity in regionally adapted wheat breeding programs.

Keywords: wheat, reduced height, vernalisation, genes, alleles, regionally adapted breeding

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P212 - Pyramiding of alien genes for high grain Fe and Zn in bread wheat using marker assisted selection

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Abstract

Wheat serves as the primary source of staple food for the global human population, thus also making it a significant portion of the calories intake in our daily vegetarian diet. However, in most of the improved wheat cultivars used for food, the grain is deficient in iron (Fe) and zinc (Zn). Among different alien species, *Ae. kotschy* exhibits an efficient genetic system for uptake and translocation of these essential micronutrients. Therefore, biofortification involving improvement of grain Fe and Zn has become an important area in the current wheat breeding programmes. For this purpose, efforts have been made to develop alien substitution lines and utilize them for transfer of desirable alien genes to improved wheat cultivars. In the present study, two such genotypes in the background of improved cultivar PBW343LrYr were utilized for pyramiding of the following six desirable genes for enrichment of grain Fe and Zn: IRT2, MTP3, IREG, FRO7, YSL15 and NAS2. A forward breeding strategy, involving crossing of the two genotypes followed by inbreeding was used. Marker-assisted selection (MAS) of the genes of interest associated with grain Fe/Zn and plant type was used following selfing of F1 hybrids. The grains of F6 lines that were derived in this programmes were rich in both Fe and Zn contents in the grain. Among the six best derived lines, the values of improved contents of grain Fe ranged from 47.3 to 60.4 ppm and that of Zn ranged from 39.35 to 47.85 ppm. There was no yield penalty in these improved lines, such that the yield was either equal or better than the checks used in field trials.

P213 - Western Canadian wheat breeding: the path ahead

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Abstract

Global wheat (*Triticum* spp.) production in 2024-2025 is estimated at approximately 790 million tonnes, remaining near historically high levels despite regional variability in yields. Canada continues to be one of the world's leading wheat producers and exporters. National wheat production was 32.0 million tonnes in 2023, increased to nearly 35 million tonnes in 2024, and reached a record ~40 million tonnes in 2025, driven largely by improved Prairie yields following late-season precipitation. Wheat contributes approximately \$8-9 billion annually to the Canadian economy. Excluding durum, approximately 60-65% of Canadian wheat production belongs to the premium-quality Canada Western Red Spring (CWRS) class. Canada exported approximately 23-26 million tonnes of wheat annually during the 2023-2025 crop years to over 80 countries, accounting for roughly 15-16% of global wheat export value and generating \$7-8 billion in export revenues. In recent years, spring hexaploid wheat has accounted for approximately 65-70% of total wheat production, followed by durum wheat (17-20%) and winter wheat (8-10%). Approximately 98% of Canadian wheat is produced in the Prairie provinces, with Saskatchewan (about 40-45%), Alberta (30-35%), and Manitoba (15-20%) contributing the majority of national output. The Eastern, Western, and Northern Prairies differ substantially in climate, soils, and disease pressure; consequently, regional wheat breeding programs focus on region-specific challenges, including biotic stress, abiotic stress, and early maturity, respectively. Key challenges for Canadian wheat breeding programs include pyramiding resistance to major diseases such as *Fusarium* head blight (FHB) and rusts, as well as managing insect pests such as orange wheat blossom midge and wheat stem sawfly. To achieve sustained genetic gains under increasing climate variability and evolving pathogen pressure, wheat breeding efforts must continue to integrate conventional breeding with advances in genomics, phenomics, big data analytics, and artificial intelligence. The expanding availability of multi-omics resources, gene discovery and manipulation tools, and advanced computational platforms is enabling breeders to make more informed decisions, from parent selection to the development of field-ready cultivars. This poster will highlight recent advances in plant science and their application to wheat breeding for the Canadian Prairies.

P214 - Root traits as breeding targets for improved nitrogen use efficiency in durum wheat

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Abstract

Enhancing nitrogen use efficiency (NUE) is essential for durum wheat. Nitrogen is a major nutrient used as fertilizer to increase crop yield and improve the protein content and production quality. In addition, root system architecture (RSA) plays a major role in nitrogen capture. Still, not much is understood; one question is how it affects NUE variance in field conditions. This study included 140 durum wheat genotypes composed of landraces and lines derived from wide crosses, investigated under fertigation using three nitrogen treatments (0, 30, and 60 kg N/ha) for phenotypic diversity of RSA traits and their relationship with yield and grain quality.

We anticipate that genotypes with deeper, steeper, and more branched root systems will maintain higher yield stability under low-N conditions. We are also expecting important correlations between RSA traits, soil N depletion patterns, and grain protein content.

The anticipated results will aid in the development of appropriate genotypes for sustainable, low-input farming systems and improve knowledge of the RSA-NUE relationship in durum wheat.

P215 - DPFlow: a flexible and reproducible pipeline for the processing and visualization of multi-sensor drone data for wheat breeding

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Abstract

Wheat (*Triticum aestivum* L.) is a vital crop worldwide. Increasing number of breeding programs are applying drone-based sensors to achieve high-throughput phenotyping and enhance genetic gain. However, processing image data, especially data from multi-sensor and multiple time points, requires specific expertise in remote sensing and image analysis, which still remains a bottleneck. This work presents a flexible and reproducible pipeline designed to extract and visualize image-based features from diverse and multi-temporal drone data. The pipeline's input data such as reflectance ortho-images and Digital Elevation Models (DEMs) were generated by commercial software, and shapefiles were used to identify plots. It automatically masks non-vegetation areas by DEM and calculates numerical features, including reflectance, vegetation indices (VIs), Grey-Level Co-occurrence Matrix (GLCM) texture features, and plant height. The architecture is flexible to add new features via custom R functions. The developed integrated dashboard visualizes: 1) geographical and statistical plot properties, 2) time-series growth trends, 3) correlation among features, and 4) unsupervised clustering. We implemented the pipeline using data from a wheat breeding trial in Halle, Germany (2025), utilizing nine RGB/multispectral flights from April to July, and one Visible Near-infrared (VNIR) hyperspectral/LiDAR scan in July. The workflow successfully processed all image data, extracting reflectance from both multispectral and hyperspectral images, calculated 37 multispectral VIs (34 default and 3 custom), 8 multispectral GLCM features, and plant height from DEM of RGB images. Visualizations revealed the field heterogeneity, and time-series plots showed the ability to distinguish genotypic responses that correlated with field observations. The Correlation heatmap identified multicollinearity among indices, which needs consideration during modeling. In addition, the clustering results based on Uniform Manifold Approximation and Projection (UMAP) algorithm identified the association between VIs and the disease severity at certain growth stages. Overall, this automated, flexible pipeline enables breeding teams to efficiently convert complex image data into analyzable numerical features, and the visualization dashboard provides important preliminary insights into the statistical properties and temporal trends. When combining image features with ground truth phenotypic data, it can facilitate subsequent detailed analysis and modeling, which assist breeders in selecting for superior genotypes under a changing climate.

P216 - Powerful one-dimensional scan to detect heterotic quantitative trait loci

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Abstract

Meeting the growing global demand for food requires substantial yield improvement, and harnessing heterosis remains one of the most effective strategies in modern agriculture. A deeper understanding of the genetic basis of heterosis has led to quantitative genetic frameworks incorporating both dominance and epistatic effects. However, explicitly modeling all pairwise epistatic interactions is computationally prohibitive, particularly in populations with high-density whole-genome sequencing data and large sample sizes needed to dissect complex traits.

Here, we develop hQTL-ODS, a one-dimensional scanning approach that directly evaluates the net contribution of each quantitative trait locus (QTL) to heterosis without exhaustively testing all pairwise interactions. Through extensive simulations, we demonstrate that hQTL-ODS substantially reduces computational burden while achieving higher statistical power and a lower false-positive rate compared to conventional approaches.

We applied hQTL-ODS to a population of 5,243 wheat hybrids with whole-genome sequencing profiles and identified key epistatic hubs that play central roles in shaping heterosis. Notably, we detected a prominent hub on chromosome 4A that emerges as a compelling candidate region. However, this locus colocalizes with an introgression from emmer wheat, posing challenges for fine-mapping due to suppressed recombination. Additional promising regions, including one on chromosome 7B, may provide valuable entry points for dissecting the genetic architecture of heterosis and informing future hybrid breeding strategies.

P217 - Loss of Dicer-like 5 induces temperature-sensitive male sterility in wheat

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Abstract

The advent of hybrid varieties revolutionized crop production by significantly enhancing yield and stability. Although hybrid corn dominates global cultivated areas and hybrid rice now accounts for more than 50% of rice cultivation, hybrid wheat remains far behind, covering less than 1% of the global acreage. A major contributing factor to this limited adoption is the absence of an efficient male-sterility system.

In this study, we propose a hybrid wheat production system based on the sensitivity of male reproduction to temperature. The system relies on the elimination of DCL5, a “dicer” responsible for processing a group of small RNAs produced exclusively during male meiosis, 24-nt phasiRNAs (phased secondary small interfering RNAs).

Durum wheat (*Triticum turgidum* ssp. durum; 2n = 4x = 28; AABB) has two DCL5 copies: TtDCL5-A1 and TtDCL5-B1. We generated single (AAbb, Aabb, aabB, aaBB) and double (aabb) dcl5 mutant lines to investigate the molecular and developmental response to environmental conditions. We found that homozygous double mutants (aabb) exhibited complete male sterility under normal temperatures, which could be restored by raising the growth temperature, demonstrating their potential for a hybrid seed production system. Further investigation revealed that loss of DCL5 eliminated the accumulation of both premeiotic and meiotic 24-nt phasiRNAs, while 21-nt phasiRNAs remained unaffected. Surprisingly, cytological analysis revealed that developmental defects occurred during pollen maturation, not during meiosis when 24-nt phasiRNAs typically accumulate. Detailed microscopy and single-cell RNA sequencing revealed disruptions in tapetal cells, pollen development and problems with pollen release.

Overall, this work establishes DCL5 as a key regulator of a temperature-sensitive sterility system and uncovers a novel sRNA-based pathway with potential applications in hybrid wheat breeding. This approach offers a promising alternative to chemical or cytoplasmic male-sterility systems and could enable more cost-effective and scalable hybrid seed production in wheat and other grasses.

P218 - QTL for winter hardiness in western Canadian winter wheat (*Triticum aestivum* L.)

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Abstract

Winter hardiness is critically important for winter wheat grown in cold climates. In field trials, winter hardiness results from the crown's tolerance of cold temperatures and freeze-thaw cycles. The former is generally considered more important in western Canada, but damage from freeze-thaw cycles is becoming more common. A genome-wide association study (GWAS) was used to study winter survival, plant height, and days to heading in locations in Manitoba, Canada. The GWAS population was composed of 279 western Canadian hard red winter wheat varieties and breeding lines, 24 winter wheats from eastern Canada, 51 winter wheats from USA, 49 winter wheats from Europe, and 12 winter wheats from Asia. GWAS was conducted with single-locus and multi-locus models. Numerous QTL were detected for all three traits. No winter hardiness QTL was detected at the Fr-A1 locus, presumably most lines carry a winter hardy allele. The most consistent QTL for winter hardiness were located on chromosomes 5A (near Fr-A2) and 6B. For plant height, major QTL were detected on chromosomes 2A, 2D (Rht8), 4B (Rht-B1), and 4D (Rht-D1). Segregation at the Rht-B1 and Rht-D1 loci was expected since many lines predate the deployment of these loci in this breeding germplasm, while modern breeding lines carry either allele. A minor plant height QTL was detected near Rht24 suggesting its deployment to some degree in this breeding germplasm. No major QTL were detected for heading date, however, QTL were detected on chromosomes 1A, 2A, 5A (two loci), and 7B. One of chromosome 5A QTL mapped near the Vrn-A1 locus. The detected QTL should be considered for marker-assisted selection to improve winter hardiness in winter wheat for cold climates.

P219 - Stigma longevity is not a major limiting factor in hybrid wheat seed production

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Abstract

Hybrids offer a promising approach to improve crop performance because the progeny are often superior to their parent lines and they outyield inbred varieties. A major challenge in producing hybrid progeny in wheat, however, lies in the inefficient fertilization of maternal parent ovaries by airborne pollen from male donor lines. This is often attributed to suboptimal synchronization of male and female flowering, as delayed pollination can result in reproductive failure due to female stigma deterioration. To test this accepted dogma, we examined the seed set capacity of six male-sterile (MS) cultivars, each varying in the onset of stigma deterioration. To mimic a hybrid seed production scenario, MS cultivars were grown during two consecutive field seasons, and open pollination was allowed up to 15 d after flowering of the female parent using a blend of seven male fertile cultivars with varying flowering times. Detailed analysis of the temporal and spatial distribution of hybrid seed set along the spike across the six MS cultivars showed that seed production remained remarkably stable during the pollination window tested. These findings suggest sustained receptivity of stigma to pollen across all tested MS cultivars throughout the entire time course. We therefore conclude that stigma longevity does not represent a limiting factor in hybrid wheat seed production, and that breeding efforts should prioritize the study of other female traits, such as enhanced access to airborne pollen.

P220 - Tracking transgenes with color: evaluating ruby as a visual marker in CRISPR-edited mutant plants in triticum species

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Abstract

CRISPR-Cas9 is a powerful tool for precise genome editing in plants, but the presence of foreign DNA, such as T-DNA, raises regulatory concerns and complicates mutant screening. Detecting and removing T-DNA from edited plants is both time-consuming and costly. To address this, we developed a system that uses the non-destructive RUBY reporter, linked to the CRISPR-Cas9 cassette via a P2A linker, and expressed under the ZmUbi1 promoter. To assess the applicability of the system, it was tested on two triticum species, targeting three genes in either tetraploid or hexaploid wheat. Strong correlations were observed in T0 and T1 plants between betalain content and Cas9 expression. Allowing for the quick identification of plants likely to be edited. The same RUBY reporter used to identify plants likely to be edited could also be used to select against them in subsequent generations at both the seed and seedling stages, thereby reducing the number of plants that needed to be screened to identify edited lines without T-DNA. This approach, using a nondestructive reporter, enabled rapid distinction between transgene expression in primary transgenics and served as a negative selection in the T1 generation, streamlining selection towards T-DNA-free edited progeny.

P221 - Changes in Pannonian wheat spike architecture during the past 90 years

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Abstract

Breeding progress in winter wheat yield in the Pannonian Plain has mostly been associated with increased grain number and improved spike productivity. However, breeding-induced changes in spike architecture and the distribution of grain number and grain weight within spikelets have been insufficiently quantified. Therefore, we analysed long-term changes in grain number and single-grain weight at different positions within spikelets to determine their contribution to yield improvement over the past 90 years. The present study is part of a broader series of investigations conducted on a historical set of winter wheat cultivars grown in the southern Pannonian Plain. A historical set of winter wheat cultivars, released and widely grown in the southern Pannonian Plain (in Serbia and neighboring countries), was evaluated over two growing seasons. At maturity, spike samples were analyzed to determine individual grain number and dry weight at proximal (G1), central (G2), and distal (G3) grain positions across spikes and spikelets.

Grain number per spike increased linearly with year of release, followed by a parallel rise in spike grain weight at a rate of 0.25 g yr⁻¹. Results indicated that breeding activities under conditions of the Pannonian Plain increased the number of grains at the G1, G2, and G3 positions, with the number of G3 grains showing the highest improvement rate. Changes in individual grain weight at different spikelet positions were less pronounced compared to grain number, indicating that spike grain weight improvement was mainly due to the increase in grain number per spike.

Overall, modern cultivars achieved higher yield mainly through increased grain set and improved performance of distal grains, suggesting that modification of spike architecture—particularly enhancement of G3 grain contribution—has been a key mechanism of historical genetic gain and represents an important target for future wheat breeding in the Pannonian Plain.

Keywords: wheat, breeding progress, grain position, and weight

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P222 - Association mapping to identify loci associated with stripe rust adult plant resistance in hard winter wheat

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Abstract

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is a major threat to wheat production with an upsurge seen in recent decades. Identification and deployment of stripe rust resistance (Yr) genes have become pivotal due to the emergence of virulent Pst races adapted to warmer climates. To identify sources of stripe rust resistance in contemporary hard winter wheat, we evaluated a panel of 619 wheat breeding lines and cultivars from the Oklahoma State University and Kansas State University wheat breeding programs at the seedling stage against the U.S. Pst race, PSTv-37 and at the adult plant stage in field experiments in Oklahoma (Stillwater and Chickasha), Kansas (Rossville and Hutchinson) and Washington state (Central Ferry and Pullman). The panel was genotyped using genotyping-by-sequencing (GBS) and kompetitive allele-specific PCR (KASP) markers linked to the known Yr genes Yr5, Yr15, Yr17, Yr18, Yr29, Yr36, Yr40, Yr46, and QYr.tamu-2B. Genome-wide association studies (GWAS) were conducted using phenotypic data, GBS-single nucleotide polymorphism (SNP) markers and KASP markers linked to Yr genes. Seedling evaluation showed that only 2% and 10% of the genotypes were highly resistant and moderately resistant to race PSTv-37, whereas 51-76% showed resistance at the adult plant stage across field environments. KASP markers showed that Yr17, Yr18, Yr29, and QYr.tamu-2B were present at 48%, 17%, 61%, and 13%, respectively, while the other five genes were absent. GWAS identified 129 significant adult plant resistance loci. Genomic regions on chromosome arms 3BS and 4BL showed the most consistent associations with stripe rust response across field environments. KASP markers, KASP_S3B_6196129 and KASP_S4B_524362674, were developed for these two loci located on chromosome arm 3BS at 6,196,129 bp and on chromosome arm 4BL at 524,362,653 bp, respectively. Both KASP markers showed allele differentiation identical to their respective SNP markers. These identified loci and developed KASP markers will enable marker-assisted selection to enhance stripe rust resistance in wheat.

P223 - Introgression and development of tetraploid durum wheat material integrating the common wheat QTL2D_wssmv and Sbm1 resistance loci against WSSMV and SBCMV mosaics

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Abstract

Wheat spindle streak mosaic virus (WSSMV) and Soil-born cereal mosaic virus (SBCMV) are two diseases that affect common wheat and durum wheat and are extremely damaging to the durum wheat cultivation in France. No currently registered durum wheat variety is resistant to both mosaics, leading to a dead end in regions affected by these viruses, which simply leads to the abandonment of this crop. Searching for natural genetic diversity and its deployment in breeding is one solution to improve sustainably durum wheat varieties resistance to mosaics.

A major WSSMV resistance QTL (QTL2D_wssmv) and the Sbm1 gene conferring resistance to SBCMV, were described in common wheat. Combined, these two loci provide very good resistance to the WSSMV/SBCMV mosaic complex. Through this study, we attempted to introduce the QTL2D_wssmv locus and the Sbm1 gene, located respectively on chromosomes 2D and 5D, into a genetic background of tetraploid durum wheat. Crosses were made between the bread wheat variety RGT Montecarlo, carrying the QTL2D_wssmv and Sbm1 loci, and the durum wheat cultivar Cappelli, carrying the deletion at the Ph1 locus - thus promoting chromosomal rearrangements. Several recombinant plants with 28 chromosomes integrating the QTL2D_wssmv locus and/or Sbm1 gene into their genome by chromosomal substitution or translocation, were obtained after three rounds of recombination. This innovative material could be used in breeding programs to introduce these two resistance loci into new durum wheat varieties. Some molecular and cytogenomic tools have also been developed to specifically track these loci in breeding lines or registered cultivars resistant to WSSMV and SBCMV.

P224 - Genetic basis of breeding gains in yield component traits in Nordic spring wheat

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Abstract

Nordic spring wheat breeding has achieved substantial yield improvements since the 1970s. Previous studies suggest that increased grain number per spike has contributed to recent yield gains in spring wheat. However, the phenotypic characteristics of spike-related traits and their underlying genetic factors are still not well understood in the local germplasm. This study aimed to investigate the genetic basis of yield-related spike and grain traits improvements in Nordic spring wheat.

A recombinant inbred line (RIL) population derived from a cross between two contrasting spring wheat cultivars, Runar (released in the 1970s) and Felgen (a modern high-yielding cultivar), was evaluated in field trials at Vollebekk Research Farm in Ås, Norway during 2023-2025. Thirteen agronomic, spike, and grain traits were measured at relevant developmental stages. A genetic linkage map consisting of 4,378 single-nucleotide polymorphism (SNP) markers derived from a 25K SNP array was constructed to perform QTL mapping.

A total of 159 QTL regions were detected across the analyzed traits. Among these, 28 QTL regions were environmentally stable and detected across multiple environments and years. 38 QTL regions overlapped across multiple traits, indicating genomic regions that may influence several yield related traits simultaneously. Some of these regions showed opposite effects for traits related to grain number and, spikelet number versus grain size, suggesting potential trade-offs between grain number and grain size. Other regions showed overlap between plant height and grain number traits, highlighting the potential importance of plant biomass in supporting increased grain production. In addition, phenotypic analysis confirmed that the modern cultivar produced a higher number of grains per spike compared with the older cultivar.

These findings provide new insights into the genetic architecture of yield components in Nordic spring wheat and highlight genomic regions that may serve as potential targets for marker assisted breeding aimed at improving grain yield.

P225 - Identification of salt tolerant maize-wheat and pearl millet-wheat cybrid lines produced through in vitro fertilization system

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Abstract

Using in vitro fertilization system, we produced wheat cybrid possessing maize-wheat or pearl millet-wheat hybrid mitochondria. Cytoplasmic hybridization increases the nucleus-cytoplasm interactions, which are relevant from both agricultural and evolutionary perspectives, as the proper functioning of metabolism, cellular homeostasis and environmental sensing is largely dependent on plasmotypic activity. In this study, the performance of maize-wheat and pearl millet-wheat cybrids against salt stress conditions was evaluated to identify elite lines and to unravel the underlying genetic networks and tolerance mechanisms, transcriptome analysis was conducted on salt-resistant wheat cybrid.

Seed germination test was done in petridish containing 200 mM NaCl using F3 generation seed of maize-wheat and pearl millet-wheat cybrid lines, including control wheat (cv. Fielder) at both 25 and 30 degree celsius for seven days. To check early vegetative stage salt tolerance, 7-days old seedlings grown in soil pots were subjected to 600 mM NaCl for three weeks. Chlorophyll content was measured weekly, and shoot and root lengths, and plant biomass were recorded three weeks after salt-treatment. Salt-treated leaf, shoot and root tissues from maize-wheat cybrids with or without possible salt-resistance and fielder were subjected to transcriptome analysis.

Among the eighteen maize-wheat and ten pearl millet-wheat cybrid lines tested, two maize-wheat and three pearl millet-wheat cybrid lines showed higher germination rate (about 60%) compared to fielder (about 30%) under salt stress at 25 degree celsius. Additionally, at 30 degree celsius, higher germination rate (about 50%) was detected in three maize-wheat and two pearl millet-wheat cybrid lines in comparison to fielder (about 10%). In the vegetative-stage salinity experiment, two maize-wheat and one pearl millet-wheat cybrid lines showed tolerance with longer shoot/root and higher chlorophyll content, while the other wheat plants exhibited severe growth defects. rRNA-depleted transcriptome analyses for the elite lines suggested that nuclear gene products related to lipid membrane remodelling and secondary metabolite production may contribute to salt tolerance in maize-wheat cybrid, and that the expression of several mitochondrial ORFs were specifically induced or suppressed in salt-resistant maize-wheat cybrid upon salinity-stress. We will report the possibility that mitochondrial hybridization across subfamily leads to create salt tolerant elite wheat cybrids.

P226 - Effects of high temperature stress during grain filling on yield and grain quality of bread wheat genotypes

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Abstract

Global climate change is currently having a negative impact on the productivity and quality of agricultural crops cultivated in the Republic of Uzbekistan. In particular, consecutive drought conditions observed in recent years, characterized by annual precipitation significantly below the long-term average, as well as intense heat occurring at the end of the spring season, have caused serious damage to the growth and development, grain yield, and quality of winter bread wheat grown under irrigated conditions. Wheat is one of the most widely cultivated agricultural crops in the world. Its grain contains nearly all essential substances required for normal human development, including proteins, carbohydrates, and minerals. Wheat serves as a staple food for approximately 35% of the world's population and supplies about 20% of global dietary energy requirements. Considering the above factors, scientific research was conducted to select new winter bread wheat (*Triticum aestivum* L.) genotypes possessing a combination of valuable traits and suitability for irrigated areas under local soil and climatic conditions. In total, 20 genotypes were evaluated. The characteristics of the tested varieties and genotypes were analyzed in relation to the prevailing weather conditions of the research region. During the study, development stages, biometric parameters, yield components, grain quality indicators, chlorophyll content in leaves at different growth phases, and the Normalized Difference Vegetation Index (NDVI) were assessed. Based on these evaluations, genotypes with superior agronomic and physiological traits were selected. In the competitive cultivar testing nursery of winter bread wheat, four genotypes with high chlorophyll content and green biomass accumulation in early spring were identified, with grain yields ranging from 7.08 to 9.13 t/ha. Comprehensive analysis of the results indicated that the genotype KR20-BWF5IR-2463 (Orzu) matured 3 days earlier than the standard variety Shams and 11 days earlier than the Krasnodar-99 variety. This genotype is characterized by medium plant height and resistance to lodging. It achieved a grain yield of 91.3 t/ha, a thousand-kernel weight of 46.7 g, grain test weight of 776.8 g/L, protein content of 14.6%, and gluten content of 29.5%.

P227 - Comparative analysis of durum wheat varieties with different breeding origins across multiple cultivation systems: insights into nitrogen metabolism gene expression

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Abstract

The objective of this study was to comparatively evaluate durum wheat varieties with different breeding origins under organic, low-fertilizer, and conventional farming systems, focusing on their yield, protein content, and the expression levels of nitrogen transporter genes in these genotypes. The study was conducted over the 2019-2020 and 2020-2021 growing seasons under rainfed conditions in the organic and conventional fields of the Field Crops Department, Faculty of Agriculture, Dicle University, Diyarbakir. Under organic conditions, grain yield and protein content fluctuated between years due to low spring rainfall, uneven water distribution, and limited nutrient availability. Genotypes such as AYM-3 consistently achieved high yields, whereas DYM-13 produced lower yields. Local varieties showed superior adaptability and environmental resilience compared to control varieties. Eyyubi showed high nitrogen translocation, and NPF6.3 correlated with yield, confirming key roles of NRT2.1, TaNRT2.1, and GS1 in nitrogen uptake. In low-input conditions, genotypes displayed distinct strategies for yield, protein, and nitrogen use efficiency. DYM-6 achieved the highest yield, YM-5 the highest protein content, and Sena the highest nitrogen use efficiency, with clustering analyses confirming these differences. Key nitrogen transporter genes, including NRT2.1, NPF6.3, and AMT2.1, were strongly associated with yield and protein traits under limited nitrogen. Under conventional systems, UYM-2 had the highest yield and Selçuklu-97 excelled in protein content, while DYM-27 showed strong association with TANRT2.1. Overall, this study demonstrates that genotype-environment interactions significantly influence yield, quality, and nitrogen metabolism, highlighting the importance of considering both environmental adaptability and nitrogen use efficiency in variety selection.

P228 - Transferring rye chromosome in to wheat using triticales as bridge species for leaf rust resistance

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Abstract

Leaf rust being an important disease of wheat, affecting its productivity in many regions of the world. Rye (*Secale cereale*), is considered as tertiary gene pool relative of wheat. It has contributed to broaden the genetic base, biotic and abiotic stress resistance, grain yield and high-protein content in wheat breeding. In the present studies, Triticale (AABBRR; $2n=6x=42$) is used as bridge species to transfer rye chromosomes into wheat for leaf rust resistance. SW288 (T/W17-5) was developed through hybridization using TL2942 (Triticale) and HS562 (Wheat) as parents. In seedling resistance tests (SRT), SW288 has been recorded resistant to leaf rust races; 10, 11, 12 (12-1, 12-2, 12-3, 12-5, 12-A, 12-7, 12-18), 16-1, 17, 20-1, 20-2, 57, 77 (77-1, 77-2, 77-5, 77-7, 77-8, 77-9, 77-10, 77-A-1, 77-9+, 104-1, 104-2, 104-2+, 106, 107-1, 108-1, 143, 162-1, 162-2, 162-3, 162-4, 162-A. SW288 has also shown resistance to leaf rust under field conditions. Leaf rust resistance shown by SW288 (T/W17-5) under artificial and natural conditions, might be due to the presence of rye chromosomes transferred from TL2942 into wheat variety HS562. Genomic in-situ hybridization (GISH) was utilized to confirm the presence of rye genome in SW288 (T/W17-5) using whole rye genome probe tagged with Alexa Fluor 488 dye. SW288 carry 42 chromosomes, probably two wheat chromosomes have been replaced with a pair of rye chromosomes.

P229 - Improving glutenin subunit genotypes to develop “K-ExtraStrong” wheat for strategic blending

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Abstract

The bread market in South Korea is expanding rapidly, with per capita daily consumption rising from 18.2g (2012) to 21.5g (2023) and the market size projected to reach 4.5 trillion KRW by 2026. This growth necessitates a stable supply of high-quality hard wheat with over 12% protein and superior gluten strength. However, domestic wheat faces challenges in quality consistency and yield. To address these, a blending strategy utilizing “extra-strong” wheat is essential to compensate for the quality variations of domestic varieties.

While previous breeding programs focused on High-Molecular-Weight Glutenin Subunits (HMW-GS), this study emphasizes Low-Molecular-Weight Glutenin Subunits (LMW-GS) to further enhance dough stability. Molecular marker selection identified 23 varieties with Glu-A3d and 11 with Glu-B3g. Quality analysis confirmed that Glu-A1a and Glu-D1d genotypes significantly improve protein and gluten content. Notably, Glu-B3g was identified as a key genotype for extra-strong wheat, providing the extreme dough strength required for industrial blending, despite the risk of reduced baking performance if used alone.

Current domestic lines with these alleles often possess unfavorable HMW-GS scores or poor agronomic traits (e.g., late heading). To overcome this, we are pyramiding Glu-D1d and Glu-B3g genotypes. Utilizing speed breeding and Single Seed Descent (SSD), populations such as YW3263-2B-33/Keas are currently undergoing field selection in 2026. This research will provide the genetic foundation for “K-Extrastrong wheat,” enhancing the competitiveness of the domestic wheat industry through strategic blending.

P230 - Marker-assisted introgression of effective yellow rust (Pst) resistance loci into triticale

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Abstract

Yellow rust caused by *Puccinia striiformis* f. sp. *tritici* (Pst) remains a major constraint for triticale production, and deployment of genetic resistance supports the goals of Integrated Pest Management. The objective is to introgress effective Pst resistance loci into triticale breeding materials using marker-assisted backcrossing. In 2025 F1BC4 seed of the triticale cross Kasyno × Mondeo was grown under controlled phytotron conditions to collect tissue for DNA isolation (CTAB). Target loci were tracked by PCR-based marker linked to resistance genes *csLV46G22* (Yr29/Lr46), including BspEI digestion. Amplicons were separated in agarose gels. To quantify recovery of the recurrent parent genome, selected plants were genotyped using the high-density DArTseq platform; only informative markers (missing data <20% and polymorphic between parental genotypes) were used for background analysis.

Marker screening identified 66 plants from Kasyno × Mondeo carrying Yr29. DArTseq data comprised codominant DArTsnps and dominant silicoDArT markers. The recurrent parent genomic background among F1BC4 individuals ranged from 75% to 97%. Based on the joint criterion of target-locus presence and high recurrent background, 30 triticale plants were selected. After vernalization and self-pollination, F2BC4 seed was obtained and used for marker-assisted selection in 2026. This year 200 F2BC4 seeds were sown, DNA was isolated and the target loci was tracked with *csLV46G22* (Yr29/Lr46) as in year 2025. A total of 90 plants carrying the gene were selected to obtain F3BC4.

These results demonstrate that combining locus-specific markers with genome-wide background selection enables efficient and accelerated introgression of valuable yellow rust resistance into elite triticale breeding pools.

P231 - Integrating genomic selection and biofortification to improve grain nutritional quality and productivity in wheat

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Abstract

Micronutrient malnutrition and rising temperatures pose major challenges to global wheat production, limiting both yield and grain nutritional quality. While biofortified wheat genotypes carry the genetic potential for high zinc (Zn) and iron (Fe), innovative nutrient management strategies are needed to unlock this potential under field conditions. In this study, eleven CIMMYT-derived biofortified wheat genotypes were evaluated using a novel integrated Zn-Fe strategy combining soil application at sowing with foliar sprays during early grain filling. Morphological traits, physiological indicators (chlorophyll content, stress tolerance), yield components, and grain Zn and Fe concentrations were measured, and multivariate analyses identified key traits and responsive genotypes. The integrated soil + foliar approach produced a synergistic increase in grain Zn and Fe, surpassing single treatments. Genotype G-445 exhibited superior agronomic performance, including larger flag leaf area, more spikelets, higher 1000-grain weight, and maximum grain yield per plant, while G-439 achieved the highest grain micronutrient density. Flag leaf area, spike length, and tiller number were identified as critical traits influencing both yield stability and nutrient accumulation. These findings demonstrate that strategically timed soil + foliar Zn-Fe application is an innovative, scalable approach to enhance wheat yield and nutrition. Genotypes G-445 and G-439 represent promising candidates for climate-smart, nutrient-rich wheat production, aligning with IWC2026's goal of promoting sustainable and healthy wheat systems.

P232 - Innovations paving (half)-way towards hybrid wheat breeding

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Abstract

Two areas of innovation are crucial to the success of hybrid wheat breeding: increasing the efficiency of seed production and selecting complementary parental lines to create high-performing hybrids. In my presentation, I will discuss innovations in these areas.

P233 - Physiological diversity and trait composition in elite CIMMYT bread wheat: implications for yield potential, stress adaptation, and pre-breeding

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Abstract

Within the CIMMYT bread wheat breeding program, sustained genetic gain for yield has been achieved across optimal and stress environments. Previous analyses of selected representative lines have demonstrated associations between grain yield and physiological traits such as radiation use efficiency and grain filling rate, highlighting the relevance of physiological evaluation in breeding. However, comprehensive assessments of physiological trait distributions and diversity across entire elite nurseries and release years remain limited. We compiled 10 years of physiological and agronomic data from elite CIMMYT bread wheat nurseries evaluated under optimal (ESWYT), late heat (HTWYT), and drought (SAWYT) conditions. The dataset includes grain yield, yield components, phenology, biomass, dry matter partitioning, and proxies for radiation use efficiency (RUE). Coupled with release year information, this framework enables quantification of temporal trends in yield and physiological traits, evaluation of changes in trait variability within elite germplasm, and assessment of how multi-trait physiological composition relates to yield performance under optimal, heat, and drought conditions.

By examining full nursery distributions, the analysis captures the breadth of physiological diversity present within CIMMYT's breeding pipeline and allows identification of traits consistently associated with performance across environments. The results provide a quantitative basis to identify potential constraints in physiological diversity and to prioritize traits for targeted introgression from exotic and pre-breeding materials. In particular, the analysis supports evidence-based trait prioritization for physiology-driven improvement efforts, enabling more strategic incorporation of physiological attributes into crossing and selection schemes aimed at enhancing yield potential and adaptation across diverse environments. In parallel, ongoing pre-breeding activities are leveraging these insights to introduce novel physiological variation into the CIMMYT bread wheat breeding pipeline.

P234 - Integrating grain imaging for deoxynivalenol (DON) prediction using fusarium-damaged kernel assessment in Canadian wheat

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Abstract

Fusarium head blight (FHB), a fungal disease of wheat caused by multiple *Fusarium* species, causes Fusarium Damaged Kernels (FDK), leading to significant yield losses. These infected kernels also contain a harmful mycotoxin, deoxynivalenol (DON), which poses significant food safety risks, a critical grading factor at Canadian grain terminals. Recent studies have demonstrated a strong positive correlation between FDK severity and DON concentration. Therefore, FDK can be a reliable predictor of DON concentration, reducing the need of costly laboratory-based DON analysis. However, visual FDK assessment is labor dependent and error prone. To overcome these limitations, we evaluated the use of the Vibe QM3i grain analyzer as a rapid, non-destructive tool to estimate FDK and evaluate its potential as a predictor of DON concentration. We used a Vibe QM3i, with a custom developed calibration model, to differentiate FDK from healthy kernels by utilizing 3000 color pixels. We analyzed both durum and hexaploid wheat samples encompassing a broad range of FDK severity and DON concentrations. The dataset included a durum doubled haploid (DH) population (A0132& N=128) grown over three years (2022-2024) across two locations; Indian Head, Saskatchewan, Canada, and Morden, Manitoba, Canada. In addition, a spring wheat DH population (B0767& N=196) was grown over two years (2023-2024) at the same locations, and only Indian Head being evaluated in 2025. To enhance robustness, a durum genomic selection (GS) panel and a hexaploid GS panel were included as calibration sets. These samples were first imaged for FDK and then quantified for DON content using ELISA. Using both these data (FDK and DON) we developed a linear regression model for DON prediction. Preliminary results on the B0767& population (2023, Indian Head) showed a strong correlation ($r = 0.90$) between Vibe-predicted and ELISA measured DON. Additional environments and years are currently being analyzed, along with the integration of machine learning models to further improve prediction accuracy. These findings demonstrate the potential of image analysis technology to support rapid image-based DON estimates.

P235 - Biological nitrification inhibition in wheat: from genetic integration to mechanistic understanding, field validation, and deployment pathways

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Abstract

As wheat production accounts for a large share of global nitrogen (N) use, genetic solutions that improve N retention offer significant potential to reduce agricultural N pollution and greenhouse gas emissions. Biological nitrification inhibition (BNI) provides a breeding-based, seed-deliverable strategy to reduce N losses from cereal systems through plant-derived nitrification inhibitors released by roots. By slowing down the nitrification process, BNI has the potential to decrease nitrate leaching and nitrous oxide emissions while maintaining crop productivity. Here, we synthesize recent advances that move BNI wheat from proof-of-concept toward a deployable breeding trait for N-loss mitigation. Elite bread wheat lines carrying a BNI translocation introgressed from wild relatives have been developed, validated with molecular and cytogenetic tools, and evaluated through multi-location trials across contrasting agro-ecological environments. Preliminary results indicate that BNI expression can be compatible with competitive yield performance in several target geographies, although responses remain environment- and background-dependent, consistent with significant genotype x environment effects and the potential influence of linkage drag in some backgrounds. Critically, field evidence demonstrates that BNI wheat can significantly suppress soil nitrification and reduce N loss under alkaline conditions, extending BNI relevance beyond acidic soils and broadening its global applicability. To support trait optimization, high-throughput phenotyping approaches have been implemented to quantify BNI activity earlier in development and at greater scale, including rhizosphere-based assays using nitrifier bioreporters. In parallel, multiple biologically active BNI compounds have been detected in wheat root systems, and their known biosynthetic pathways provide direct entry points for reverse genetics, candidate gene discovery, and prospective genome-editing strategies aimed at increasing BNI expression, stability, and transferability across elite germplasm. Genomic tools to trace, refine, and shorten the introgressed segments are enabling next-generation lines with improved adaptation, while marker-assisted selection and accelerated generation advance are facilitating introgression into winter wheat backgrounds. Adoption research based on multi-country stakeholder consultations and diagnostic assessments suggests that widespread adoption of BNI will require seed-system readiness, supportive policy incentives, effective extension systems, and alignment with fertilizer and climate policies. Overall, BNI wheat represents a promising genetic innovation to reduce the N footprint while supporting climate-smart agricultural intensification.

P236 - Assessment of tall and short plant height controlling alleles on wheat adaptation and yield using near-isogenic lines

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Abstract

Wheat is a key cereal crop ensuring global food security, providing approximately 20% of the world's protein and caloric intake. For Kazakhstan, wheat has strategic importance due to its role in national food security and export capacity.

Under climate change and population growth, improving wheat productivity is increasingly important. Plant height is a key trait affecting biomass allocation and lodging resistance, which strongly influences yield and grain quality in Kazakh wheat growing environments. Therefore, the development of semi-dwarf genotypes remains a major breeding objective to improve lodging resistance while maintaining high productivity.

In this study, near-isogenic lines (NILs) were developed through reciprocal backcrossing to assess the effects of tall and semi-dwarf loci on wheat adaptation in Kazakhstan. The UK spring wheat cultivar Paragon (short stature, stable traits) served as the donor parent, while the Kazakh cultivar Pamyati Azieva (taller architecture ~20 cm, locally adapted) served as the recurrent parent. The research was conducted using glasshouse and speed breeding facilities, which significantly accelerated the development time of NILs, and KASP markers co-segregating with loci controlling plant height on wheat 5A and 6A chromosomes initially identified in a mapping population developed from the cross of Pamyati Azieva x Paragon.

For both, development of tall and short NILs the initial crosses (tall x short and reciprocal) produced heterozygous F₁ plants. Successive backcrossing to the recurrent parent progressively restored its genome (BC₁ - 75%, BC₂ - 87.5%, BC₃ - 93.75%) while maintaining 1:1 segregation at the target loci and gradually recovering the genetic background of the recurrent cultivar. Self-pollination BC₂ heterozygotes generated the expected 1:2:1 Mendelian ratio, confirming single-locus inheritance of height alleles. NILs on the Paragon background showed clear height differences but no positive effect on yield components under tested environments. Statistical analysis of BC₂ NILs indicated borderline significance for chromosome 5A ($p = 0.06$) and weaker association for 6A ($p = 0.09$), suggesting their contribution to height variation. BC₃ crosses were done recently and currently hybrids are being genotyped for the NIL and recombinant development.

Thus, NIL-based analysis of height loci enabled evaluation of allelic effects in reciprocal backgrounds and supports wheat improvement strategies.

P237 - Power calculations for testing genetic correlation between pure- and mixture line effects in wheat breeding

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Abstract

Cultivar mixtures have been increasingly popular and more than a third part of the wheat cropping area in Denmark is cultivar mixtures. Cultivar mixtures have several benefits such as increased yield and stability, and reduced severity of diseases. This project aims to investigate genetic and non-genetic benefits of cultivar mixtures in wheat. In the coming three years we will run trials that include both pure lines plots and mixture line plots, and all lines will be genotyped candidates from a breeding program for new wheat cultivars at Nordic Seed. The aim of this power calculation study is to suggest optimal experimental design for estimation of the genetic correlation between the pure line genetic effects and the mixture line genetic effects. Mixtures of three wheat lines are considered, and for about 25 new candidate lines there are many possible combinations between three wheat lines in the mixture plots. To select the most informative mixture plots and to estimate the number of replicates needed for each line we use the predicted breeding values of traits from pure line trials of the new candidate lines and thereby increases the genetic variation between the selected lines for mixture plots. We assume a statistical model that simultaneously estimates genetic and non-genetic co-variances of pure- and mixture line effects. Our results suggest a selection strategy for mixtures that increases the genetic variances within mixtures and thereby increases the power for testing the significance of the additive genetic co-variances between pure line and mixture line effects for the current trait on interest. The strategy will contribute to the development of more robust models that predict more accurate breeding values for wheat lines used for cultivar mixtures crops.

P238 - Vision for hybrid wheat through key male trait integration: a path towards optimizing hybrid grain set

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Abstract

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 these traits, 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 VAEX, AL, AES and PSC collectively explained 78% of the variation for hybrid grain set in the 35-elite pollen-donor lines. Despite the challenges associated with phenotyping these microscopic traits, their high heritability emphasizes their importance for developing proxy traits that 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.

P239 - Towards accelerating nitrogen use efficiency in five Australian wheat varieties through molecular breeding

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Abstract

Nitrogen is a critical macronutrient for achieving optimal yield and grain quality in wheat. Yet, wheat exhibits significant nitrogen inefficiency, with less than 40% of the applied nitrogen being absorbed and approximately 33% of the partitioned into the end grain. This inefficiency constrains productivity and contributes to environmental losses, underscoring the need for improved nutrient utilization. Improving Nitrogen Use Efficiency (NUE) with higher grain protein content (GPC) without compromising grain yield is a critical objective in wheat breeding around the world. This study investigates the genetic and molecular pathways underlying NUE to support the development of high-performing, nitrogen-efficient wheat varieties. Based on our previous study, QTL Cluster 2_2D, which contains 2 QTLs with significant phenotypic variation for NUE and GY, was targeted for introgression into five elite Australian wheat germplasm varieties: Ironbark, Leverage, Sunmaster, Sundancer, and Shotgun, using a marker-assisted backcrossing strategy. Donor lines were selected based on superior nitrogen uptake, yield, and grain protein, with St3B_H029 and St3B_H341 identified as optimal carriers through SNP polymorphism analysis. Crosses between elite recipient varieties and donor parents carrying the target QTL cluster were used to generate F1 progeny, which were subsequently backcrossed to recover the recurrent parent genome while retaining the favourable QTL alleles. BC1F1 lines underwent KASP SNP genotyping for foreground selection to confirm the presence of target alleles, followed by background selection using a 5K AgriSeq panel to quantify the recovery of the recurrent parent genome. Selected heterozygotes were used to develop the BC2F1 generation, achieving a higher recovery of the elite parent genome while maintaining the target QTL Cluster 2_2D. In parallel, a QTL-Seq approach is being implemented using DH lines contrasting for the target QTL alleles. This will enable the validation of candidate genes underlying the QTL Cluster. The outcomes of this research are expected to provide a strong foundation for molecular breeding strategies that aim to overcome the long-standing trade-off between GY and GPC, while improving NUE in modern wheat production systems. Achieving this balance is essential for sustainable wheat production, ensuring food security, farmer profitability, and reduced ecological impacts.

P240 - Replaying the green revolution in wheat landraces through advanced gene editing

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Abstract

We applied advanced gene-editing technologies to unlock and utilise the extensive genetic diversity preserved within the Watkins Landrace wheat collection. This globally significant resource captures over 10,000 years of evolutionary adaptation across diverse agroecological environments, providing a valuable foundation for future crop improvement. By integrating precision breeding with this rich diversity, we aim to develop novel pedigrees that retain beneficial adaptive traits while enhancing key agronomic characteristics.

The primary objective of the Watkins Precision-Bred pedigree is to generate elite lines suitable for inbred breeding programs through the targeted fixation of four major alleles: RHT-1 (plant height regulation), PPD-1 (photoperiod sensitivity), R (grain colour/pre-harvest sprouting resistance), and PIN (grain texture and milling quality).

In this presentation, we demonstrate the use of next-generation gene-editing including Base Editing, Prime Editing, and CRISPR-Cas9 to precisely introduce and recreate these alleles within Watkins landraces, accelerating the development of improved germplasm while maintaining broad genetic diversity.

P241 - Toward resilient wheat production: stress physiology and disease resistance in hybrids

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Abstract

Climate change increasingly threatens wheat production worldwide, while genetic gains in grain yield have slowed. To meet future food demand, innovative breeding strategies are required. Hybrid wheat offers a promising solution, with reported grain yield advantages of 15-20%, improved yield stability, and enhanced tolerance to abiotic and biotic stresses. However, the physiological and molecular bases of hybrid superiority under stress conditions remain insufficiently understood. The objective of this project is to elucidate the mechanisms underlying drought tolerance and Fusarium head blight (FHB) resistance in wheat hybrids compared with their parental lines.

We hypothesize that hybrids exhibit improved drought resistance through enhanced antioxidant defense, altered regulation of abscisic acid (ABA) and salicylic acid (SA), and superior photosynthetic performance. Furthermore, we expect hybrids to display stronger early defense responses to Fusarium infection, reflected in elevated expression of pathogen-related (PR) genes, ultimately resulting in higher and more stable grain yield. Physiological assessments will include chlorophyll a fluorescence parameters and stomatal conductance in flag leaves during anthesis. Biochemical analyses will focus on oxidative stress markers (such as malondialdehyde content) and antioxidant defense components, including glutathione and enzymes of the ascorbate-glutathione cycle. Hormonal profiling will examine ABA and SA involvement in drought responses. Resistance to biotic stress will be assessed through controlled Fusarium infection. Disease severity will be visually evaluated, and molecular responses characterized by quantifying the expression of PR1, PR3, PR5, TGA2, and NPR1 genes at early stages of infection.

Hybrid seeds in the field experiment will be produced using a chemical hybridizing agent system, based on prior successful testing of male sterility and pollination efficiency. Additionally, hybrid performance will be evaluated through the estimation of heterosis (mid-parent and better-parent heterosis) for grain yield under field conditions. General and specific combining ability effects will be assessed to identify superior parental lines and best hybrid combinations. The relationship between combining ability, heterosis expression, and antioxidant, hormonal, photosynthetic, and molecular defense responses will be analyzed to elucidate the genetic and physiological basis of hybrid superiority. This research is the first comprehensive study of hybrid wheat production and stress-response mechanisms in Croatia.

P242 - Decoding wheat G×E dynamics: insights from elite germplasm and BNI (Biological Nitrification Inhibition) lines in Australia

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Abstract

Understanding genotype × environment (G×E) interactions is essential for accelerating genetic gains in wheat breeding programmes, particularly under the increasing variability of global production environments. This study applies a multi-environment trial (MET) framework to characterise G×E patterns in elite germplasm alongside lines carrying the Biological Nitrification Inhibition (BNI) trait—a novel attribute with potential to improve nitrogen-use efficiency and support sustainable production systems. The analysis spans diverse agro-ecological zones, integrating phenotypic performance with environmental covariates to identify trends in stability and adaptability. Insights from the analysis provide a foundation for combining elite backgrounds with BNI functionality to deliver yield resilience and ecological benefits. Australian wheat breeders have long leveraged MET analyses to understand G×E interactions, setting a global benchmark for precision in genotype deployment across variable environments. This work underscores the importance of G×E-informed decision-making in modern wheat improvement in Australia and establishes a pathway for evaluating BNI as a valuable trait in future breeding pipelines.

P243 - Genetic improvement of FHB and DON resistance by combining the *Fhb1* gene with additional resistance QTL, and favorable morphological traits, in winter wheat population

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Abstract

Winter wheat production is important for Eastern Canada. Fusarium head blight (FHB) of wheat, mainly caused by *Fusarium graminearum*, is a major wheat disease that causes significant yield and quality loss. Deoxynivalenol (DON) is the most detected mycotoxin in contaminated wheat grain in Canada. The use of resistant cultivars is an effective tool for managing FHB; however, FHB resistance is a complex trait. The objectives of this study were to identify QTL associated with FHB resistance in the Triumph/25R51 doubled haploid (DH) population, validate selected KASP markers, and relate favorable morphological traits to FHB resistance. The DH population was evaluated for FHB resistance across nine field environments and an additional greenhouse study. Genotyping of the population was conducted using SNP markers and the linkage map was developed with a total map length of 3018 cM consisting of 26 linkage groups. KASP markers for *Fhb1*, *Ppd-D1*, *Rht-B1* and *Rht8* were screened across the population. Morphological traits (spike length, number of spikelets per spike, number of kernels per spike and spike density), plant height and heading date were also recorded. QTL analysis identified multiple FHB resistance loci, including on chromosomes 2B, 2D, 3B, 5A, and 7D. The QTL on chromosome 3BS was the most important QTL for all FHB related traits and explained 27%, 25%, 14% and 13% of phenotypic variation for FHB severity, FHB index, Fusarium damaged kernels (FDK) level, and DON content, respectively. KASP marker validation and haplotype analysis confirmed this QTL was due to *Fhb1*, with the resistance allele from 25R51 parent. FHB resistance QTL on 2D was collocated with both plant height and days to anthesis QTL at the *Ppd-D1* locus. The population segregated for *Rht-B1* locus, coincided with plant height QTL on 4B, but was not linked with FHB traits. This study showed that combining *Fhb1* with additional resistance alleles enhances resistance to FHB, and the significant QTLs identified will be further useful for introgression in winter wheat breeding.

P244 - Decentralized wheat breeding pipeline: serving the region from the hotspot

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Abstract

By 2050, one in four people globally will be African, and Africa will be the only continent to keep growing after that. This trend highlights the urgent need for secure, resilient food systems to boost crop productivity, improve nutrition, and reduce losses from pests and diseases. Wheat plays a key role in Africa's food security; however, smallholder farmers are increasingly affected by climate change and rapidly evolving wheat disease pathogens. In response, the CIMMYT Global Wheat Program (GWP) established a regional breeding pipeline in 2022 that applies science-based strategies to accelerate genetic gains in the region. The pipeline uses targeted crossing, rapid generation advancement, and multi-stage phenotyping across diverse agroecologies in KALRO-Kenya, EIAR-Ethiopia, and other partner countries to increase selection accuracy. Intensive field screening under high natural inoculum enables early elimination of susceptible lines, particularly to stem rust (Ug99+), stripe rust (PstS16), and emerging virulent pathotypes. The first cohort of regional targeted crossings is currently under evaluation in Kenya and Ethiopia and will be distributed to partner countries as a yield trial over the coming years. In parallel, this collaborative breeding pipeline strengthens NARS's breeding capacity through training in networked breeding, use of genomic data, sparse phenotyping, breeding analytics community of practice, and bilateral initiatives to develop a hybrid wheat breeding pipeline for Africa. These integrated activities improve wheat yield, modernize breeding operations, and expand the use of digital and data-driven tools in the region's wheat breeding program. Close collaboration with national partners ensures that breeding targets align with farmers' needs and accelerates varietal release. Overall, this East African wheat breeding pipeline exemplifies how leveraging natural selection environments for breeding and strong partnerships can deliver resilient, demand-driven wheat varieties for vulnerable farming systems, ultimately strengthening food security in the region.

P245 - West and central africa wheat development network (WECAWheat): leveraging partnerships for wheat transformation in Africa

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Abstract

In spite of the sharp rise in wheat consumption in West and Central Africa, driven largely by urbanization, fast population growth and dietary shifts, the region remains heavily dependent on wheat imports making it highly vulnerable to price shocks and supply chain disruptions. West and Central Africa is endowed with suitable agro-ecologies for competitive, profitable wheat production and value chain development to significantly contribute towards enhanced regional food self-sufficiency and economic development. Yet, current domestic wheat production in West and Central Africa, is constrained by several factors including low adoption of innovative technologies, limited adoption of improved varieties, inadequate seeds and input systems, climate risk, limited mechanization, lack of integrated market systems and lack of enabling policy coherence across countries. WECAWheat serves as a regional network to catalyze wheat research, development, and policy; and geared towards unlocking wheat's potential as a strategic crop for agricultural transformation in West and Central Africa. WECAWheat was established in 2023 with the overarching goal of enhancing wheat productivity, production and income of farmers using appropriate technologies, and to boost wheat sector investments in the West and Central African region. WECAWheat leverages partnerships from National Agricultural Research Institutions (NARIs) in Nigeria, Cameroon, Senegal, Chad, Ghana, Gabon, Burkina Faso, Mali, Niger, Congo Brazzaville, Togo, Benin Republic, the Gambia, Cote D'Ivoire, Guinea; as well as international and regional organizations including AfDB-TAAT (Transformation for African Agricultural Development), CIMMYT, ICARDA, PRASAC, CORAF/National Wheat Center (NWC) of Specialization in Chad, Wheat Initiative (WI), AHEAD, among others. Private sector industry actors along the wheat value chain, farmers/farmer cooperatives, public servants, and development partners/donor institutions form a critical segment of WECAWheat membership. WECAWheat has fostered networking among wheat experts; engaged several stakeholders/partners and relevant Government Ministries of member countries on various initiatives and strategic plans for wheat sector transformation; undertook CIMMYT-enabled capacity building of WECAWheat breeders from member countries; fostered several regional wheat trials; and held two (2) regional wheat Summits, with the 3rd regional wheat summit 2025 expected to hold in N'Djamena, Chad. We envision wheat transformation in West and Central Africa for regional food security, economic growth, and food sovereignty.

P246 - Why people don't prefer to do gamma irradiation mutation breeding using wheat seed

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Abstract

The gamma irradiation of seed for mutation breeding has been used for many years now, but people recently don't prefer to use it because of specific reasons. Firstly, the prediction of the ideal gamma irradiation dosage for mutation breeding may be difficult to do. The IAEA's predictions by making use of 50% reduction of shoot length, mostly predicts a dosage that is twice as high as the ideal dosage. I have developed a method for the prediction of the ideal dosage for seed gamma irradiation of small grain species that can be modified for the prediction of other species. I made use of the efficiency of energy conversion into growth that predicts a dosage range that is in line with the recent "preferred" dosages for mutation breeding as issued by the IAEA. Polyploid species have a higher and wider optimal dosage range than diploid species. A second reason for not using gamma irradiation of seed is that segregation of the mutated genes occur and you may end up with no desired genes after four to five generations in polyploid species like bread wheat (*Triticum aestivum*). The created mutations must have major effects to be useful in mutation breeding, while small effect mutations disappear over generations. A third reason for not using gamma irradiation of seed is that the assumption that seeds can be transported and store for some time before germination takes place, doesn't hold. After a period of two to three weeks after the irradiation the usefulness of the seeds decline due to what is called "storage time". Storage time reduces the useful mutations observed, until there are no useful mutations left. Storage time has an additional negative effect complementing the effect of gamma irradiation on the efficiency of energy conversion into growth at a specific dosage. The higher the gamma irradiation, the larger the contribution made by storage time. A possible explanation for the effect of storage time may be that no DNA repair takes place due to it.

P247 - Haplotype-based identification and deployment of rust resistance loci in elite wheat

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Abstract

Wheat production is continually threatened by stripe and leaf rust because virulent races rapidly overcome single race-specific genes. Durable, broad-spectrum resistance is needed. Adult plant resistance (APR) provides partial, stable resistance from multiple minor-effect loci acting additively; pleiotropic loci like Lr34/Yr18 and Lr46/Yr29 add durability. We used an elite Australian panel (OzWheat=589) and a diverse landrace panel (Vavilov=295), genotyped with ~30K SNPs and phenotyped across environments. Linkage disequilibrium partitioning defined 7,659 genome-wide haploblocks. To prioritise robust signals, we ranked haploblocks by haplotype effect variance and examined the top 100 per trait. For stripe rust, 52/100 were significant, with 32 shared across panels; for leaf rust, 50 were significant, 29 also detected in Vavilov. Several intervals co-localised with APR regions (Lr46/Yr29), and one 7BL interval intersected seedling gene Lr14a. To translate mapping into breeding decisions, we developed an introgression fitness index to quantify the value of resistant haplotypes in elite backgrounds. Using elite cultivar Scepter, we applied a genetic algorithm to select 50 donor parents carrying desirable haplotypes. Simulations showed that pyramiding these haplotypes can enhance resistance while maintaining the elite genomic background.

P248 - Unlocking the genetic potential of Central Asian wheat through molecular breeding, genomic selection and speed breeding

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Abstract

Wheat is a strategic crop in Central Asia, especially in Kazakhstan. The country produces ~16 m/t of high-protein wheat annually, half of which is exported. However, the primary challenge of country's wheat sector is its declining profitability. Improving the wheat grain yield is one of the ways of making "wheat attractive and profitable again". This can be achieved with replacing the wheat gene pool with new high yielding varieties, because we - Kazakhstani wheat breeders - may have reached the maximum limits of productivity using the current breeding scheme that relays mainly on conventional methods. Therefore, our strategy is trying to improve grain yield through modern breeding tools. So far, we have identified several genomic regions associated with important yield components such as plant height, coleoptile length and seed architecture. Through MAS and development of NILs, the economic benefits of these loci have been and are being tested under multi-location field trials. Moreover, the Central Asian Wheat Panel (CAWP), consisted of ~450 spring and winter genotypes, was established. Currently, WGS of CAWP is being conducted to develop a reference genome and identify structural variations that could potentially add values to wheat. Importantly, we have established a first large-scale speed breeding (SB) facility in Central Asia and fine-tuned the global SB protocol (potting soil, light spectrum and intensity, growing conditions) to wheats adapted to wide range of environments. The facility currently is being used for the development of new genetic resources, generation advancement, NIL development and genetic standardization of germplasm panels.

P249 - International partnership and investment on capacity building enhanced ethiopian wheat productivity

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Abstract

Ethiopia is the first wheat producer in Sub-Saharan Africa and third in Africa next to South Africa and Egypt. However, Ethiopia still demands wheat to satisfy the ever-increasing population demand due to food habit change, urban expansion and food processing companies' engagement. Wheat is one the Ethiopian government top priority crop to be self-sufficiency and insure food security. Wheat productivity was below 1.5 tonnes per hectare (t/ha) in the 1990's and showed slow yield increment. Yield stagnation is a complex issue, which might be the result of a combination of factors, such as approaching a genetic ceiling in crop improvement, declining soil fertility in lowland dry land areas, emerging diseases and recurrent epidemics of aggressive wheat rust pathogens breakdown resistance genes deployed in widely grown cultivars which also associated with abiotic stresses (drought, heat) that caused catastrophic effect due to climate change. To change the local wheat yield scenario, the National Wheat Research Program (NWRP) in Ethiopia has been working closely with International Centre for Maize and Wheat (CIMMYT) and International Centre for Agricultural Research in Dry Areas (ICARDA) through collaborative research in Shuttle breeding through the use of dedicated disease screening nurseries to harness genetic resources and fast track variety release approaches where NWRP released high yielding, disease resistance, drought tolerant improved varieties which replaced low yielding traditional cultivars. Wheat varieties developed through joint efforts were adopted and disseminated for large scale production in dry land and irrigated agro-ecologies and preferable by wheat growers/farmers and widely covered most wheat growing areas. Joint international partnership and policy support from the government has increased Ethiopia's wheat productivity by 2-fold (1.5 t/ha to 3.2 t/ha) in the last two decades where the production become flourished and emerging agro-processors engaged in wheat sector across the value chain.

P250 - Genomic prediction with haplotype blocks in wheat

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Abstract

Haplotype blocks may contain more information than individual SNPs and have therefore been proposed as alternative independent variables for genomic prediction. Research across various species has shown that they can improve prediction accuracy for certain traits, whereas for others no advantage over single SNPs was observed. Moreover, the optimal strategy for constructing haplotype blocks to maximize prediction accuracy is still unclear.

The aim of our study was to evaluate genomic prediction based on different types of haplotype blocks in comparison with single SNPs for 11 traits in winter wheat. Using marker data from 361 winter wheat lines, we constructed haplotype blocks according to linkage disequilibrium (LD), fixed numbers of SNPs, fixed genetic distances in cM, and with the R package HaploBlocker. These blocks were combined with single-year field trial data in a cross-validation framework to generate predictions using RR-BLUP, an alternative approach (RMLA) that accounts for heterogeneous marker variances, and GBLUP implemented in the software GVCHAP.

The highest prediction accuracies for resistance to *B. graminis*, *P. triticina*, and *F. graminearum* were achieved with LD-based haplotype blocks. In contrast, blocks defined by a fixed number of markers or a fixed genetic length (cM) yielded the best accuracies for plant height. HaploBlocker-derived haplotype blocks outperformed the other approaches for predicting protein concentration and resistance to *S. tritici*, *B. graminis*, and *P. striiformis*.

We propose that the dependence on trait type arises from characteristics of haplotype blocks that exert both overlapping and opposing influences on prediction accuracy. Although they may better capture local epistatic interactions and reflect ancestral relationships more effectively than single SNPs, their multi-allelic structure can introduce unfavorable properties into the design matrices of the models, potentially reducing predictive performance.

P251 - Multiplex genome editing enables simultaneous improvement of multiple elite traits in wheat

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Abstract

As a staple crop worldwide, wheat plays a pivotal role in ensuring national and global food security through stable yield production. Although conventional breeding has generated numerous high-yielding, high-quality, and disease-resistant germplasms, it is increasingly challenged by rapid population growth, intensifying climate change, and the limited availability of elite parental resources. The emergence of genome editing technologies offers a transformative approach to breeding by enabling the creation of novel genetic variation and the simultaneous improvement of multiple traits.

Wheat is a hexaploid species characterized by a large and complex genome with extensive functional redundancy. Long-term evolution has retained a substantial number of unfavorable genes. Precise modification of these genes using genome editing technologies provides a promising avenue for enhancing wheat yield potential and environmental adaptability.

In this study, we focused on the development of an innovative multiplex genome editing system for wheat. Through systematic optimization of sgRNA expression architectures and multi-sgRNA assembly strategies, we successfully established a highly efficient multiplex editing platform capable of simultaneously targeting up to 42 (14×3) genes. Leveraging this system, we performed coordinated editing of multiple gene categories, including negative regulators of spike development, positive regulators of plant height, negative regulators of nitrogen uptake, and susceptibility genes. Our objective was to generate elite germplasm with comprehensive improvements in spike morphology, plant height, nitrogen use efficiency, and disease resistance. This work provides a novel technological framework and breeding strategy for wheat molecular breeding, offering a powerful solution to overcome the limitations of conventional breeding and accelerating the genetic improvement of wheat.

P252 - From farmers' fields to future harvests: yield and quality evaluation of new wheat varieties under dry season conditions in Morocco

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Abstract

Wheat production in Morocco faces increasing challenges due to recurrent drought, climate variability, and the need to meet growing demand for both quantity and quality of grain. Identifying wheat varieties that combine high yield potential with desirable grain quality under water-limited conditions is therefore a key priority. This study aimed to evaluate the agronomic performance, yield potential, and grain quality of newly developed wheat varieties through on-farm trials conducted during the dry season in collaboration with local farmers.

Field trials were established across several farmer-managed fields using a comparative design that included newly released varieties alongside commonly grown local varieties used as checks. Conducting the experiments directly in farmers' fields enabled the assessment of varietal performance under realistic production conditions and typical management practices. Data were collected on grain yield and key agronomic traits such as plant height, phenological stages, and adaptation to prevailing environmental stresses. In addition, grain quality parameters, including, test weight, grain size, and selected end-use quality indicators, such as grain protein content, yellow index (Durum wheat), starch and fat content and other traits; were evaluated to determine the suitability of the varieties for market and processing requirements.

The results revealed significant variability among the tested varieties. Several new wheat ones exhibited higher yield potential than the farmers' standard varieties while maintaining favorable grain quality characteristics. These varieties demonstrated promising adaptation to dry-season conditions, suggesting their potential to enhance both productivity and grain value in local production systems.

The study highlights the importance of participatory on-farm trials in bridging the gap between breeding programs and farmers' needs. The identification of high-performing and quality wheat varieties under dry-season conditions provides valuable information for variety release, dissemination, and adoption strategies aimed at strengthening wheat production systems in Morocco.

Keywords: wheat, on-farm trials, grain yield, grain quality, dry season, varietal evaluation, Morocco.

P253 - Genomic and spectral signatures of PSII heat tolerance in cereals

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Abstract

Increasing photosystem II heat tolerance (specifically the critical temperature for PSII disruption [Tcrit]) in cereals may contribute to minimising crop yield losses to climate change. However, mechanisms underpinning Tcrit remain unclear. Integrating high-throughput phenotyping of leaf Tcrit, leaf hyperspectral reflectance, and genome-wide association studies (GWAS) across 200 wheat and 213 barley genotypes enabled the development of spectra-based prediction of Tcrit with moderate accuracy ($R^2 = 0.43$ for wheat; 0.60 when barley was added) and identification of four loci in barley and one in wheat associated with Tcrit. Diurnal and heatwave experiments showed that Tcrit is dynamically regulated, with heat-tolerant genotypes acclimating earlier and sustaining higher Tcrit. Transcriptome analyses of wheat genotypes during heat stress revealed differential expression of genes linked to acclimation capacity. These results uncover physiological, spectral, and genomic signatures underpinning PSII heat tolerance in cereals and identify molecular targets for improving resilience to extreme temperatures.

Keywords: GWAS; heat acclimation; hyperspectral reflectance; PSII heat tolerance; Tcrit

P254 - Genetic dissection of root architectural and biomass traits in durum wheat landraces using rhizotron experiments

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Abstract

Durum wheat (*Triticum turgidum* ssp. *durum*) is widely cultivated in rainfed and semiarid regions, where water availability is often limited and unpredictable. Root system architecture (RSA), defined by the spatial distribution and morphology of roots, strongly influences a plant's capacity to acquire soil resources. Key RSA traits include total root length, average diameter, branching frequency, root growth angle, and root volume, all of which affect nutrient and water uptake efficiency. This study investigates the genetic basis of RSA traits in durum wheat using rhizotron experiments under controlled growth conditions (22°C, 16-hour photoperiod).

A total of 114 durum wheat landraces from five genetically distinct populations were characterized, alongside 15 durum cultivars and 19 bread wheat cultivars used for phenotypic comparison. Landraces showed the highest values for number of root tips, branching points, and total root length, indicating more extensive root systems. They also exhibited a narrower root growth angle (77.4°), consistent with deeper rooting potential and enhanced resource access. Heritability estimates for RSA traits ranged from 60% to 77%, confirming a substantial genetic contribution.

Genome-wide association studies identified 141 significant SNP-trait associations across multiple statistical models, capturing both major-effect loci and polygenic components. The consistency of associations across models reinforced the robustness of the 82 detected QTLs. Among these, 55 overlapped with previously reported loci, while 27 represent potentially novel genomic regions controlling RSA traits.

Haplotype-based analyses refined QTL intervals and demonstrated that specific haplotypes within stable LD blocks significantly improved trait performance. For example, haplotypes at *Qrt.ubo_5A.2* and *Qrt.ubo_1A.8* were associated with enhanced root volume and higher branching frequency, respectively, highlighting their potential for marker-assisted breeding.

Overall, these findings reveal substantial RSA diversity in durum landraces and provide a genetic foundation for exploiting favorable alleles to improve drought resilience in modern durum wheat breeding.

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P255 - Genomic loci for preharvest sprouting resistance in spring wheat (*Triticum aestivum* L.)

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Abstract

Preharvest sprouting (PHS) causes significant yield and quality losses in wheat. PHS is tightly associated with seed dormancy, an adaptive trait that inhibits germination under favourable conditions. Seeds with a low level of dormancy are, thus, PHS susceptible. Since seed dormancy and PHS are polygenic traits governed by multiple genes, identifying specific genomic regions related to these traits holds significant promise in addressing the problem of PHS in wheat. This study, therefore, performed a genome-wide association analysis of a diverse panel of spring wheat genotypes grown over five different environments to detect loci and candidate genes controlling seed dormancy/PHS resistance. Population genetic analysis revealed that the panel comprises two main subpopulations. Mature seeds of each genotype of the association mapping panel were characterized for their germination index (GI), which exhibited significant variation in seed dormancy levels among the genotypes. Marker trait and linkage disequilibrium (LD) decay analyses identified 14 significant markers and three QTLs associated with seed dormancy/PHS on chromosomes 4A, 5B and 5D. The 11 significant markers representing the QTL on 4A explained 10.7% to 20.8% of the variation in seed dormancy/PHS resistance while the markers forming the QTLs on 5B and 5D explained 10.2 to 11.4% of the variation. The three QTLs were found to harbour over 700 genes involved in different biological processes, and expression analysis of selected genes implicated their role in regulating the level of seed dormancy/PHS resistance. The genomic loci, markers and candidate genes identified by the study could be applied for enhancing resistance to PHS through marker-assisted selection.

P256 - Insights into the role of arbuscular mycorrhizal symbiosis in environmental stress tolerance of different durum wheat genotypes

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Abstract

In the Mediterranean and semi-arid regions, durum wheat (*Triticum turgidum* subsp. durum) is frequently exposed to climate-related stresses. Arbuscular mycorrhizal fungi (AMF) represent a promising strategy to enhance plant resilience; however, their effectiveness depends on host genotype, soil resource availability, and stress intensity. Dissecting genotype-specific responses to AMF is therefore essential for improving the sustainability of cereal-based agroecosystems. To address this aspect, a greenhouse experiment was conducted to evaluate seven durum wheat genotypes, including wild types and mutant lines, following inoculation with *Rhizophagus irregularis* and exposure to two different water conditions: water deficit (WD) and waterlogging (WL). Physiological parameters were monitored throughout the experiment, including pot relative water content (RWC_{pot}, %), whereas root colonization was assessed by staining with cotton blue and microscope observation. At the end of the stress, leaf and root tissues were collected for molecular and biochemical analyses.

The results revealed a clear stress- and genotype-dependent modulation associated with AMF symbiosis. Root phytohormone profiling showed distinct ABA, IAA, and SA accumulation patterns in mycorrhizal (MYC) compared to not-mycorrhizal (NMYC) plants under both WD and WL, suggesting AMF-mediated fine-tuning of root hormonal signaling during stress. At the leaf level, AMF-inoculated plants exhibited modulation of epicuticular wax components, along with specific changes in sugars, amino acids, and carbon-related metabolites under both conditions. Root RNA-seq analysis was performed on four selected genotypes (Svevo, Kronos, and two Kronos-derived mutants), revealing targeted transcriptional reprogramming in response to AMF under stress. Although the transcriptional variation was primarily driven by the stress condition, AMF inoculation specifically modulated distinct gene clusters in a genotype-dependent manner, including transport-related genes and core components of the symbiotic signaling pathway. Overall, transcriptomic data highlight genotype-dependent responses to AMF symbiosis, indicating a differential contribution to stress tolerance. Integration of these RNA-seq data with previously generated datasets for the same genotypes will enable a deeper characterization of the regulatory networks underlying symbiotic stress responses and support the identification of durum wheat lines with enhanced resilience.

P257 - Hormonal and thermopriming of seeds impart acquired terminal heat stress tolerance through modulation of proteostasis in wheat *Triticum aestivum* L.

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Abstract

The global increase in ambient temperature is a critical factor and is one of the most important abiotic constraints in wheat. Ubiquitination is intricately involved as a central regulatory pathway enabling plants to sense, respond and cope with heat-induced proteotoxicity. Ubiquitin proteasome system (UPS) is a post-translational modification process which target damaged proteins for degradation, modulates signaling components and coordinates multiple stress-responsive pathways. SKP1 (S-phase kinase protein1) is an essential regulatory component of SCF (Skp1-cullin-F-box) E3 ubiquitin ligases involved in maintenance of cellular protein homeostasis through ubiquitin mediated proteasome system. A transgenerational heat stress memory analysis was carried out after seed priming of wheat seeds with various hormones and high temperature. To assess the functional role of SKP1 under terminal heat stress (THS) in wheat, genetic variability analysis was carried out in a panel of 25 contrasting germplasm through extensive phenotyping and transcript profiling of TaSKP1-6B-4 during anthesis under ambient and THS in field experiments for two consecutive years. Whole genome wide search of SKP1 gene family identified 95 SKP1 genes which were structurally characterized. Grain yield, leaf senescence and other agronomic-morpho-physiological parameters combined with transcript profiling, cvHD2967, was found to be the best positively responsive to THS which by pedigree was not heat tolerant. Further analysis of role of UPS was also analyzed after seed priming with two plant hormones. The results document regulatory involvement of SKP1/UPS and proteostasis in wheat climate resilience.

P258 - Response to high temperature stress in bread wheat genotypes: a comparative evaluation of organic and conventional production systems

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Abstract

In this study, conducted in Diyarbakır, 13 bread wheat genotypes were evaluated under organic and conventional production systems with normal sowing (control) and late sowing (heat stress) treatments. Stress selection indices were used to comprehensively assess the genotypes' responses to heat stress. In both production systems, a marked reduction in mean grain yield under stress confirmed that high temperature stress is a key factor limiting wheat yield. Genotype performance was largely similar across production systems. DZ17-1, Empire, and Karacadağ-98 exhibited high Yp (mean yield under control conditions), Ys (mean yield under stress conditions), and strong stress tolerance indices, demonstrating broad adaptability in both environments. Aşure and 6-DZT-03-01, characterized by low TOL (stress tolerance) and high YSI (yield stability index), were identified as materials maintaining yield stability under stress, whereas YE-94, Murat-1, and Alada were notable for low performance and high stress sensitivity (RSI) in both systems.

Correlation analyses revealed that production systems differentially influenced genotype responses. In organic conditions, Yp showed positive relationships with both yield and tolerance indices, suggesting that high yield was accompanied by greater stability. Conversely, in conventional conditions, Yp exhibited strong positive relationships with TOL and SSPI (stress susceptibility percentage index), indicating that high-yielding genotypes experienced substantial yield loss under stress. In both systems, Ys consistently displayed positive correlations with stability-related indices such as STI (stress tolerance index), GMP (geometric mean productivity), HM (harmonic mean), and MRP (mean relative performance), confirming its reliability as an indicator of stress tolerance. The stronger associations observed in organic systems suggest that stress tolerance is more phenotypically expressed under organic conditions.

Overall, this study demonstrates that heat stress is a critical factor limiting wheat yield, and that genotypic responses to stress may vary depending on the production system. Organic conditions better reflect the balance between high-yielding potential and stress tolerance, whereas conventional conditions reveal the stress sensitivity of high-yielding genotypes more clearly. Genotypes with high Ys values in both systems emerge as reliable indicators of true stress tolerance, making them strong candidates for sustainable wheat production under heat stress conditions.

P259 - Introgression of rye chromosome arm 1RS enhances climate resilience in german winter wheat

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Abstract

Climate extremes increasingly threaten wheat production and yield stability globally. Rye (*Secale cereale* L.) chromosome arm 1RS has long been deployed in wheat breeding, yet its agronomic performance under drought, and its interaction with elite genetic backgrounds, remain insufficiently characterized. We evaluated 1RS translocations in elite German winter wheat using integrated molecular diversity analyses, multi-environment field phenotyping, and genomic modeling. Under near-optimal precipitation in 2021, matching the 1961-1990 reference period, wheat genotypes exhibited substantial genetic variation for yield and agronomic traits, indicating that high yield potential is still present in current German winter wheat breeding germplasm. In contrast, severe drought conditions in 2022 resulted in a 13.7% average yield decline, highlighting climate vulnerability. We show that 1RS translocations exhibit background-dependent effects on grain yield and stability. In particular, T1AL.1RS rye translocation originating from 'Insave' rye and stacked T1AL.1RS/T1BL.1RS translocations combining 'Insave' and 'Petkus' rye segments demonstrated favorable yield performance under drought conditions, although effects were context-dependent. Genomic modeling confirmed a significant translocation-by-background interaction, indicating that deployment of 1RS requires consideration of recipient genetic background. Our results highlight substantial response diversity within elite germplasm and demonstrate that targeted introgression of rye chromatin can contribute to improved stress resilience when systematically introgressed into adapted genetic backgrounds.

P260 - Identification and functional characterization of Iron-binding Proteins of bread wheat using hierarchical computational approaches

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Abstract

Iron-binding proteins (IBPs) are fundamentally important molecules for growth and development of bread wheat. Our study presents a comprehensive inventory of putative IBPs in wheat, established through a systematic, hierarchical computational biology pipeline. We analysed the complete wheat proteome at both sequence and structural levels, we found that approximately 0.97 % of wheat proteins possess the capacity to bind iron ions, preferably the Fe³⁺ state, contributing to diverse biological and molecular activities. Using multiple databases to classify these identified IBPs, we catalogue them into their- subcellular localisations, functional domains, and gene ontology. These proteins were broadly categorised based on to their orthologous groups, further followed by a comprehensive analysis of protein-protein interaction networks and identification of hub proteins within the network. Majority of these proteins were localised in plastid region and are involved in metabolic activity, encode for GT1-Gtf like protein family, and participate in numerous molecular functions within wheat, including oxidoreductase activity, ion binding, and reactive oxygen species (ROS) management. This report offers good insights into the putative iron-binding proteins and their possible functional importance, understanding the iron homeostasis in wheat which will pave the way for further experimental confirmation, and offering potential applications for the development of biomarkers in climate-resilient biofortification initiatives.

P261 - Development and characterization of salt tolerant wheat variety through integrated breeding approaches

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Abstract

Salinity stress poses a significant threat to global food security, affecting crop productivity and quality. Wheat is a staple food crop consumed worldwide, and understanding its tolerance mechanisms to salinity stress is crucial for developing resilient varieties. The current study aimed to investigate the genetic mechanism of sixty wheat genotypes under salinity stress. In a controlled laboratory experiment, three salt solutions with NaCl concentrations of 10, 15, and 20 dS/m were applied in passive hydroponic conditions. Concurrently, a field experiment was conducted using an alpha lattice design, wherein the wheat genotypes were cultivated in normal (NIAB) and saline soil (Pacca Anna). The results revealed that certain salt-tolerant wheat genotypes, such as SG3/12-21, KCT7/12-44, SCT6/9, SG1/12-41, LU-26-S, Anaj-17, Akbar and Sassui exhibited elevated levels of antioxidant enzymes, maintained higher relative water content, demonstrated a maximum total phenolic content, retained significant chlorophyll content, and exhibited a balanced Na/K ratio. Based on a reduction of less than 50% in various growth parameters, wheat genotypes such as KCT7/12-44, SG3/12-21, LU-26-S, Anaj-17, Akbar, and Sassui demonstrated salt tolerance. SG2/12-27, Sarsabz, NIA-Zarkaiz, Sehar-2006 and Galaxy-13 were identified as moderately salt-tolerant, while Dilkash, Khirman, and Bhittai exhibited medium sensitivity to salinity. These findings highlight promising avenues for enhancing salinity tolerance in wheat varieties and underscore the significance of identifying and promoting resilient genotypes to ensure food security in salt-affected regions.

P262 - Increased night temperature and seed rate effects on grain weight analysed by graphic-mathematical modelling the plastic and elastic growth during grain filling of wheat

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Abstract

Climate change imposes higher temperatures, especially at night. Its negative impact affects both yield components of wheat, grain number and average grain weight (TGW). Conversely, very low seeding rates may enhance TGW. However, the mechanistic basis of grain weight determination remains incompletely understood. Our study proposes a conceptual graphic-mathematical model based on the cell wall mechanical properties, distinguishing between plastic (irreversible) and elastic (reversible) growth to explain the contrasting effects of night warming and low seeding rate on individual grain weight (IGW). Two wheat cultivars (Bacanora and Kambara) were evaluated over two seasons in Valdivia, Chile. Treatments included night warming increase of 4°C applied at pre- or post-anthesis and contrasting seeding rates (370 vs. 44 seeds m⁻²). Grain volume, width, and height dynamics of the most contrasting grain positions within the spike were fitted using a tetra-linear broken-stick model to identify growth rates and durations of plastic and elastic phases.

Under control conditions, Kambara exhibited up to 30% greater IGW than Bacanora. Within spikelets, grain position strongly influenced IGW ($P > 0.05$), with G2 consistently larger than other positions, whereas night warming reduced IGW up to 15% ($P > 0.05$). On the other hand, low seed rate increased ($P > 0.05$) IGW (5-24%), particularly in distal grains. Similar effects were observed for grain volume and dimensions.

Plastic growth was identified as the primary determinant of final grain weight and size, showing a strong positive association with IGW ($R^2 = 0.88$). In contrast, elastic growth contributed minimally to final dimensions due to shrinkage near physiological maturity. Night warming shortened the grain-filling period, and low seed rate enhanced IGW ($P > 0.05$) by increasing the rate and duration of the plastic growth.

This study demonstrates the negative impact of night temperature on TGW and IGW, even at pre-anthesis, showing different sensitivity among grain positions within the spike, and the improvement of these traits by the very low seed rate. In addition, plastic growth, defined as a primary and irreversible structural expansion, is associated with dry matter deposition, whereas elastic growth represents reversible fluctuations primarily driven by water dynamics.

P263 - Is yield plasticity a conservative genotypic attribute? Responses of contrasting cultivars to a broad range of conditions

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Abstract

Phenotypic plasticity is considered a fundamental determinant of crop performance, enabling genotypes to adjust physiological, morphological, and developmental traits in response to heterogeneous environments. In wheat and other crops, plasticity is frequently regarded as an intrinsic property of the genotype, yet it remains unclear whether cultivars consistently express similar degrees of plasticity across different types of resource limitations. This uncertainty is particularly relevant because modern breeding programs implicitly assume that genotypes classified as “stable” will display reduced sensitivity to resource constraints. This study aims to (i) quantify genotypic plasticity across broad resource gradients, (ii) assess whether phenotypic plasticity or stability represents a conserved cultivar attribute or varies with the type and severity of resource limitation, (iii) relate the plasticity of key traits to yield sensitivity across contrasting environments, and (iv) evaluate potential trade-offs among major plastic traits linked to biomass partitioning and reproductive efficiency. We conducted three complementary experiments during the 2023–2025 seasons across contrasting environments in three locations of Spain (Lleida, Bell-lloc and Valladolid). Four commercial wheat genotypes representing two winter types (Filon and Fortunato) and two spring types (Rota and Artur Nick) were grown under variable levels of nitrogen supply, soil water availability, and plant density (i.e., thinning as an indirect increase in resources) making a total of 20 environments for Filon and Fortunato and 16 for Rota and Artur Nick, providing a broad gradient of resource availability. The outcomes are expected to improve our understanding of how modern wheat cultivars adjust to resource variability and to identify the trait-based mechanisms underlying yield responsiveness under limiting conditions.

P264 - Remodeling of lipid metabolism in wheat anthers under high temperature stress

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Abstract

Remodeling of lipid metabolism in wheat anthers under high temperature stress

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Abstract: Lipids play fundamental roles in plant adaptation to various environmental stresses, with comparative lipidomic analyses under heat, drought, and saline-alkaline conditions revealing consistent remodeling patterns such as elevated phosphatidic acid (PA) and decreased monogalactosyldiacylglycerol (MGDG). This study combined physiological and lipidomic approaches to investigate lipid-mediated mechanisms in wheat anthers under high-temperature stress using heat-tolerant (Hub) and heat-sensitive (Saada) cultivars. The thermotolerant cultivar maintained significantly higher pollen viability and more stable pollen morphology under stress, while lipidomic analysis demonstrated a consistent shift toward increased lipid saturation. This was evidenced by a reduced fatty acid unsaturation index and marked remodeling of membrane lipids, including increased saturated species such as PC (34:0) and PA (36:0) alongside decreased polyunsaturated galactolipids like MGDG (36:6) in the tolerant cultivar. Hub exhibited more pronounced and coordinated changes in acyl chain composition across phospholipid and galactolipid classes compared to Saada, while cuticular lipid analysis revealed reduced polyunsaturated cutin monomers and cultivar-specific accumulation of very-long-chain alkanes in Hub, suggesting a reinforced protective barrier. These findings demonstrate that coordinated lipidome remodeling toward reduced unsaturation constitutes a key biochemical mechanism underlying wheat thermotolerance, with the more effective lipid reprogramming in the tolerant cultivar correlating with preserved pollen function and yield stability under heat stress.

Keywords: wheat; heat stress; anther; lipidomics; pollen fertility

P265 - Developing a high-throughput platform for anatomical phenotyping in plants

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Abstract

Developing a high-throughput platform for anatomical phenotyping in plants

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Plant anatomical structure plays a pivotal role in determining physiological function and environmental adaptability. However, conventional anatomical methods are constrained by low throughput, limited efficiency, and inadequate automation. To address these challenges, we developed an integrated anatomics platform that combines high-throughput multi-tissue sectioning with a fully automated image processing tool, enabling efficient imaging and precise quantitative analysis of plant tissues at cellular level. Firstly, we designed a device, AnatomyArray, and optimized the high-throughput paraffin-based plant tissue sectioning. This system is compatible with various molecular techniques, including in situ hybridization and immunofluorescence, demonstrating its potential for plant tissue applications. Secondly, we developed AnatomyNet, a deep learning-based tool that automatically quantifies anatomical traits across different tissue types at the cellular level. The system demonstrates its application in various tissues and species and supports customized model training. Anatomics-based GWAS was performed in wheat and a total of 97 QTLs were identified. One of the candidate genes, TaSPL14, was associated with root tissue size. Further analysis revealed that TaSPL14 coordinates multi-tissue development through phytohormone homeostasis regulation in roots. In summary, this study successfully addresses the two major bottlenecks in plant anatomy—high-throughput sample preparation and anatomical phenotyping. We propose a pipeline for large-scale anatomics based genetic studies using the AnatomyArray system, enabling the dissection of genetic basis underlying plant anatomical structure and environmental adaptation.

Keywords: *wheat; anatomics; AnatomyArray; AnatomyNet; GWAS*

P266 - Developing a high-throughput platform for anatomical phenotyping in plants

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Abstract

Developing a high-throughput platform for anatomical phenotyping in plants

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Plant anatomical structure plays a pivotal role in determining physiological function and environmental adaptability. However, conventional anatomical methods are constrained by low throughput, limited efficiency, and inadequate automation. To address these challenges, we developed an integrated anatomics platform that combines high-throughput multi-tissue sectioning with a fully automated image processing tool, enabling efficient imaging and precise quantitative analysis of plant tissues at cellular level. Firstly, we designed a device, AnatomyArray, and optimized the high-throughput paraffin-based plant tissue sectioning. This system is compatible with various molecular techniques, including in situ hybridization and immunofluorescence, demonstrating its potential for plant tissue applications. Secondly, we developed AnatomyNet, a deep learning-based tool that automatically quantifies anatomical traits across different tissue types at the cellular level. The system demonstrates its application in various tissues and species and supports customized model training. Anatomics-based GWAS was performed in wheat and a total of 97 QTLs were identified. One of the candidate genes, TaSPL14, was associated with root tissue size. Further analysis revealed that TaSPL14 coordinates multi-tissue development through phytohormone homeostasis regulation in roots. In summary, this study successfully addresses the two major bottlenecks in plant anatomy—high-throughput sample preparation and anatomical phenotyping. We propose a pipeline for large-scale anatomics based genetic studies using the AnatomyArray system, enabling the dissection of genetic basis underlying plant anatomical structure and environmental adaptation.

Keywords: wheat; anatomics; AnatomyArray; AnatomyNet; GWAS

P267 - Cold acclimation induced freezing tolerance and recovery dynamics in winter and spring wheat cultivars

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Abstract

Freezing stress causes severe and often irreversible damage to many plant species worldwide. As sessile organisms, plants cannot escape environmental extremes and must adapt to survive. In regions prone to freezing, successful crop establishment relies heavily on adequate cold hardiness. Climate projections further warn of increasingly frequent early autumn and late spring freezes periods when plants are least prepared. Wheat, one of the world's most important cereals, is particularly vulnerable to such temperature fluctuations, yet possesses a unique cold acclimation (CA) mechanism that enhances freezing tolerance (FT). Identifying cultivars with strong CA capacity is therefore essential for sustaining productivity under prolonged freezing conditions.

This study evaluated the effects of CA on growth, freezing survival, and post-freezing recovery in two winter wheat cultivars (Yumechikara and Norin-61) and one spring cultivar (Haruyokoi). Growth assessments revealed a trade-off between vegetative growth and FT, where Yumechikara achieved the highest freezing survival but exhibited reduced growth, whereas Haruyokoi and Norin-61 showed vigorous growth but poorer recovery after freezing. Crown tissue viability, assessed using the 2,3,5-triphenyltetrazolium chloride (TTC) assay, indicated that under non-acclimated conditions Haruyokoi survived to -6°C , Yumechikara to -4°C , and Norin-61 to -3°C , with further temperature reductions resulting in weak or absent staining. After one week of CA, Haruyokoi and Norin-61 showed light staining at -14°C , while Yumechikara maintained strong staining at this temperature. Interestingly, after four weeks of CA, differences among cultivars became minimal.

Overall, these findings underscore the importance of selecting wheat cultivars with superior FT and recovery capacity to ensure stable production in regions increasingly affected by freezing stress.

P268 - Plant growth promoter rhizobacteria-mediation for improving drought tolerance in spring bread wheat (*Triticum aestivum*).

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Abstract

Bread wheat (*Triticum aestivum* L., $2n = 6x = 42$, AABBDD) is critical for food security, especially in Central and South Asia, North Africa, and Sub-Saharan Africa. However, its production is highly constrained by drought. To offset this challenge, researchers have investigated the use of plant growth-promoting rhizobacteria as an alternate technique for improving plant drought tolerance. Despite this understanding, the interaction of rhizobia with non-legumes was generally overlooked as a research topic until the last few decades.

Here we show that the application of *Rhizobium* as a plant growth promoter (PGP) under abiotic stress can have a positive effect on wheat yield components. Two elite spring bread wheat genotypes—Malika (drought-sensitive) and Qafidou (drought-tolerant)—were primed with three plant growth promoter rhizobacteria (PGPR) strains, and cultivated in plastic tunnels under moisture stress and well-watered conditions. The strains were evaluated recently for their ability of phosphate solubilization (PSA) and phytohormones production under moisture stress conditions.

The application of PGPR strains 1159N11 (S1) and 686N5 (S3) had a positive effect on both wheat genotypes. Particularly under drought conditions, the drought sensitive genotype (G1) primed with S1 at 50% field capacity (FC) increased tiller count by 34%, while Qafidou (G2) primed with S3 at 75% FC enhanced seed count by 75% compared to the uninoculated control genotype. Notably, each wheat genotype responded differently to the strains. The 1159N32 (S2), showed minimal impact on plant performance in most conditions, and multi-strain inoculations positively impacted root traits, yet for overall yield-related traits, single-strain applications generally led to better results. For seed weight, the same combination G1-S1 under the driest condition resulted in a 19% increase compared to non-inoculated pots.

The findings highlight the positive effects of the plant growth promoter Rhizobacteria strains used, with the combinations G1-S1 and G2-S3 being particularly effective in promoting growth under both well-watered and drought-stressed conditions. This study opens avenues for further exploration of the genetic factors that regulate plant growth promoter Rhizobacteria interactions with wheat.

Keywords: *Wheat _ plant growth promoter Rhizobacteria _ Drought Stress_ Coating*

P269 - Farmer-validated performance of climate-resilient bread wheat varieties under real production conditions: breaking the yield ceiling in Moroccan Dryland Systems

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Abstract

Background and Objectives

Bread wheat production in Morocco faces critical challenges from climate variability, generating unstable yields that undermine national food security. Despite sustained breeding efforts, improved varieties show limited impact due to persistent yield gaps between experimental stations and farms, coupled with slow farmer adoption. This disconnect suggests breeding programs inadequately account for real-world constraints and farmer priorities. To develop effective climate adaptation strategies, validating newly released varieties under authentic farmer management and documenting acceptance criteria are essential. This study validated on-farm performance of climate-resilient bread wheat varieties across Morocco's diverse agro-ecological zones while capturing farmer preferences to inform breeding priorities.

Methods

Participatory on-farm trials were conducted across diverse agro-ecological zones. Three INRA varieties (B1-Ibtissam, B2-Lina, B3-Snina) were evaluated against Arrehane, a traditional check variety. Trials used farmer practices—local irrigation, fertilization, and pest management—to reflect real constraints rather than optimal conditions. Participatory methods captured farmer evaluations of drought tolerance, disease resistance, lodging resistance, grain quality, and yield satisfaction. Adoption indicators including re-sowing intentions and seed requests were documented. Agronomic data quantified yield performance, stability, and genotype × environment interactions.

****Results****

Significant yield variation and strong genotype × environment interactions occurred. Ibtissam consistently outperformed others, yielding 22-31 quintals/ha with stable performance. Its maximum (31 quintals/ha) represented a 605% advantage over Arrehane's maximum (4.4 quintals/ha) under comparable conditions. Lina showed 5-23 quintals/ha but high management sensitivity, indicating adaptation to better-resourced farms. Snina produced 10-26 quintals/ha with reasonable stability. Arrehane consistently underperformed (4.4-10 quintals/ha). Farmers strongly favored Ibtissam for yield reliability, early maturity enabling drought escape, robust tillering, and bread-making quality. Many expressed intentions to replace Arrehane, generating substantial seed demand.

Conclusions and Impact

Participatory validation revealed insights obscured by station trials. Under water-limited conditions, farmers prioritized yield stability, early maturity, and grain quality over maximum potential. Integrating farmer-defined criteria into breeding objectives is essential for accelerating adoption and realizing genetic gains in climate-variable dryland systems, strengthening food security resilience.

P270 - Genome-wide association study for identifying drought-tolerance mtas associated with grain yield and related traits in spring bread wheat (*Triticum aestivum* L.)

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Abstract

Drought and heat stress significantly impacts bread wheat (*Triticum aestivum* L.) production, particularly in the West Asia, North and sub-Saharan Africa region. To develop wheat that can resist climate challenges, we need to better understand the underlying genetics. For this purpose, a genome-wide association study (GWAS) was conducted on a panel of elite wheat genotypes developed at the International Center for Agricultural Research in Dry Areas (ICARDA) to identify significant markers linked to drought and heat tolerance, explore candidate genes, and assess genomic prediction. Five agronomic traits: days to heading (DHE), days to maturity (DM), plant height (PLH), thousand-kernel weight (TKW), and grain yield (GY), were evaluated across multiple environments over two consecutive years followed by GWAS and genomic prediction high-quality SNP markers. Significant phenotypic variation was observed among genotypes, with heritability ranging from low for grain yield to high for developmental traits, depending on the environment. Multi-locus and mixed models analyses revealed numerous significant marker-trait associations (MTAs) across traits and environments. Strong and consistent associations were particularly noted for DHE, DM, and GY, with key genomic regions identified on several chromosomes. Chromosome 5A emerged as a major hotspot, harbouring loci repeatedly linked to phenology, grain weight, and yield under drought- and heat-stress conditions. Population structure analysis indicated clear clustering into distinct breeding-related subgroups. Functional annotation of prioritized loci highlighted variants located within or near genes involved in stress signalling, redox processes, hormonal regulation, cell-wall biosynthesis, and other pathways related to adaptation. The marker-trait associations and genomic regions identified in this study provide a useful foundation for future validation efforts and may ultimately support breeding strategies aimed at developing stress-resilient wheat varieties.

Keywords: *Wheat, drought stress, heat stress, GWAS, MTAs, ICARDA, agronomic traits*

P271 - Characterization of genes to induce early flowering in spring wheat for escaping terminal heat stress

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Abstract

Abstract

Bread wheat (*Triticum aestivum* L.) is a globally important cereal crop whose productivity is increasingly challenged by heat stress under changing climatic conditions. Phenology is a key target for adapting wheat varieties to ongoing climate changes. Optimization of flowering time is an adaptive strategy in wheat improvement programs, particularly in spring wheat growing regions. Spring wheat is widely cultivated in regions where the crop completes its life cycle within a single growing season without requiring prolonged cold exposure. Wheat in Pakistan is mainly cultivated as spring wheat and flowering time significantly important for ensuring adaptation to local agro climatic conditions and avoiding terminal heat stress during grain filling. The timing of flowering in wheat is largely controlled by the vernalization pathway, vernalization gene *Vrn-1* plays a central regulatory role in the transition from vegetative to reproductive growth by modulating the requirement for cold exposure and influencing heading and flowering time. Strategic manipulation of *Vrn-1* allelic variation offers great potential to hasten flowering without reducing yield. The research was done to determine early flowering genotypes of wheat which can retain high yields even under normal agronomic conditions. A randomized complete block design (RCBD) with standard replications was used to achieve a diverse set of genotypes included in a field experiment to reduce the effects of environmental variation and achieve the necessary accuracy in statistics. The early flowering of these genotypes because of dominant spring alleles at the *Vrn-1* loci (*Vrn-A1*, *Vrn-B1* and *Vrn-D1*) that promote constitutive expression of the flowering pathway genes. Favorable allele combinations at *Vrn-1* can reduce vegetative period enough to avoid terminal heat stress and maintain grain filling period and yield components. In conclusion, this research shows that when *Vrn-1* alleles are used appropriately, it is possible to have early flowering without reducing yield. The newly identified genotypes are good parental materials in breeding programs aimed at developing climate resilient high yielding spring wheat varieties. The findings are useful in the international community to improve wheat adaptability and productivity in heat-vulnerable agro-ecological regions.

Keywords: *Triticum aestivum*, vernalization, *VRN1*, *VRN3*, flowering time, terminal heat stress, marker-assisted selection, climate resilience

P2872 - Genome-wide identification and functional characterization of Ta4CL genes in wheat: key roles in salt tolerance, cold acclimation, and lignin biosynthesis

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Abstract

The 4-coumarate-CoA ligase (4CL) gene family is essential in the phenylpropanoid pathway, affecting plant development, lignin production, and responses to environmental stresses. Although critical, the 4CL genes in wheat (*Triticum aestivum* L.) remain understudied. This research identified 40 Ta4CL genes across 20 chromosomes, analyzing their gene structures, evolutionary relationships, and predicted subcellular locations. Cis-regulatory elements in their promoters were associated with stress responses, hormonal signals, and light responses. Expression profiling showed that certain Ta4CL genes, including Ta4CL8-5A and Ta4CL4-7D, were strongly induced by high salt levels, underscoring their contribution to salt tolerance. Light-mediated cold acclimation tests revealed varied expression patterns among Ta4CL genes, with Ta4CL2-6D and Ta4CL3-6B prominently upregulated under blue light and cold conditions. Protein network studies confirmed Ta4CL involvement in lignin and flavonoid pathways, especially via interactions with phenylalanine ammonia-lyase and other phenylpropanoid enzymes. Physiological data linked Na⁺ buildup and Na⁺/K⁺ ratios to Ta4CL expression, further supporting their role in stress resilience. These results illuminate the multifaceted functions of 4CL genes and suggest promising candidates for developing salt- and cold-tolerant wheat varieties.

Keywords: 4CL gene family, Gene expression, Light-regulated cold acclimation, Salt tolerance Wheat

P273 - Linking root traits to nitrogen use efficiency in winter wheat

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Abstract

Nitrogen is quantitatively the most important nutrient driving wheat yields and protein contents. However, use of synthetic nitrogen fertilizers come with high environmental costs such as eutrophication of surface waters due to runoff and leaching as well as CO₂ emissions and high energy consumption for the production of the fertilizers. One possible strategy for a sustainable reduction of nitrogen fertilizers while maintaining yield potential is the increase of nitrogen use efficiency (NUE) through breeding, specifically for improved root traits. To do so, a deep knowledge on field-based associations between root traits and nitrogen nutrition related yield performance is needed. Here we present morphological and anatomical root traits of a set of 54 contrasting winter wheat genotypes grown in two seasons at two different locations under normal and reduced nitrogen supply, representing four different nitrogen levels. The effect of nitrogen deficiency on several root traits, physiological and yield parameters is shown. We explore associations between root traits and aboveground parameters, including physiological traits, plant height, yield components, and grain nitrogen content as indicators of NUE.

Based on previous studies on NUE of the genotypes, eight crosses of contrasting parents were generated and are now in the F₄ stage. Initial screening under greenhouse conditions of selected populations of mentioned crosses already showed clear segregation of tolerance to low nitrogen nutrition based on SPAD-values. To further elucidate the genetic basis of low nitrogen tolerance, bulked segregant analysis based on these segregating populations is planned.

P274 - Roots vertical distribution and physiological characteristics in high-yielding and waterlogging-tolerant wheat

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Abstract

The comprehensive understanding of root development under waterlogging stress is essential for high-yielding and waterlogging-tolerant wheat cultivars in the scenario of sustainable production in high-precipitation regions. A pot experiment was conducted to investigate the vertical distribution and physiology of root systems in the four commercial wheat cultivars (Yangmai24, Ningmai13, Ningmai9, and Yangmai25) which exhibit diverse grain yield and waterlogging resistance. The results indicated that waterlogging stress caused a reduction of 21.5% in grain yield, 34.4% in root weight, and 34.5% in root length. Among the four cultivars, Yangmai25 is considered as the cultivar with both high yield and waterlogging tolerance, with only 11.8% of reduction in grain yield. Yangmai25 also exhibited the lowest shallow (0-20 cm) root weight percentage but the highest deep (60-100 cm) root weight percentage at maturity. These findings indicate that Yangmai25 maintained a numerous root system and balanced vertical growth pattern throughout the grain-filling stage. Waterlogging stress inhibited the vitality, the activity of nitrate reductase (NR) and glutamine synthetase (GS), as well as the expression of nitrate and Ammonium transporter genes (TaNRT1.1, TaNRT2.1, and TaAMT1.1) in shallow roots, but those in Yangmai25 and Ningmai9 exhibited significantly higher. The 3rd leaf area, 2nd, and 3rd leaf photosynthetic rate (Pn) at milk-ripe stage were greatly decreased by waterlogging, indicating that older leaves were primarily affected. Among the four cultivars, the flag leaf of Yangmai25 displayed the largest, potentially contributing to its strong photosynthetic capacity. Grain yield and shoot weight were significantly and positively correlated with root weight and length at maturity as well the Pn of the top three leaves at milk-ripe stage. The Pn levels in the top two leaves mainly depended on the weight, length, vitality, NR, and GS activity of shallow roots, and the 3rd leaf Pn was associated with an increased distribution of deep roots. This study indicated that improving the quantitative traits and nitrogen assimilation of shallow roots while maintaining an appropriate distribution of deep roots will be beneficial for photosynthesis capacity enhancement in leaves and the alleviation of waterlogging-induced yield losses, offering a novel perspective on achieving high and stable wheat production.

P275 - Flowering time governs responses to temperature stress: seasonal shifts and asymmetry in wheat yield

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Abstract

In wheat, grain yield is largely determined by grain number and set during a critical developmental window from stem elongation to flowering, whereby flowering time plays a central role in adaptation by determining exposure to frost, heat and drought. In Australian rainfed systems, growers manage flowering time through cultivar choice and sowing date to balance frost risk associated with rapid development against increasing heat and water stress and declining photothermal quotient with delayed flowering. Defining optimal flowering periods (OFPs) and quantifying yield penalties associated with deviations from these optima are essential for improving wheat yield stability under increasing climate variability. We aimed to quantify OFPs for wheat across diverse environments, characterise seasonal and spatial variation in flowering dates associated with peak yield, and assess the symmetry of yield penalties associated with flowering earlier or later than the optimum. Comparative analysis using barley provided a physiological benchmark to interpret wheat sensitivity to temperature stress during the critical period. Co-located wheat and barley field experiments were conducted across 31 sites in southern and western Australia from 2010 to 2022, spanning annual rainfall from 117 to 978 mm. Multiple sowing times generated wide ranges in phenology. Flowering date, grain yield, and exposure to frost and heat during the critical period were measured, and yield-flowering relationships were used to estimate OFPs and quantify yield penalties.

Wheat achieved maximum yield at later flowering dates than barley, with mean wheat optima occurring 15.8 days after barley. Wheat exhibited greater phenological diversity and asymmetric yield penalties, with larger yield losses associated with flowering earlier than the OFP, consistent with sensitivity of reproductive development to frost. Barley showed narrower flowering windows and more symmetric penalties. When flowering concurrently, both species responded similarly to cumulative heat load, but barley maintained higher yields under equivalent frost exposure. Flowering time is a primary physiological determinant of wheat yield stability, mediating temperature stress during the critical period for grain number determination. These results support OFP-based frameworks for sowing time and cultivar choice in wheat and highlight the need to better represent asymmetric temperature stress responses in crop models under a changing climate.

P276 - Integrated genome-wide association analysis of grain yield and adaptive traits in bread wheat across contrasting environments in the MENA region

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Abstract

Grain yield improvement under increasing heat and drought stress remains a major challenge for bread wheat (*Triticum aestivum* L.) breeding. To elucidate the genetic basis of yield performance and adaptation, we integrated results from two complementary genome-wide association studies (GWAS) conducted on diverse wheat panels evaluated across multiple contrasting environments. The combined analyses targeted key agronomic traits, including grain yield (GY), thousand kernel weight (TKW), days to heading (DHE), days to maturity (DM), and plant height (PLH), assessed under both irrigated and stress-prone conditions across North Africa and the Middle East. High-density SNP genotyping and multi-environment phenotyping were coupled with robust GWAS models (BLINK, FarmCPU, and TASSEL-based approaches), accounting for population structure and kinship.

Across environments, grain yield consistently exhibited low heritability and strong environmental dependence, confirming the limited effectiveness of direct yield selection under heat and drought stress. In contrast, early heading and maturity emerged as reproducible adaptive escape mechanisms under terminal stress, while the relative stability of thousand kernel weight contributed to buffering yield losses during shortened grain-filling periods. Genome-wide analyses revealed convergence on a restricted set of recurrent genomic regions, particularly on chromosomes 1A, 2A, 2D, 3A, 5A, 6D, and 7A. Candidate gene analysis indicated that these regions frequently harbor upstream regulatory genes involved in signal perception and integration, including flowering-time regulators, protein kinase-mediated signaling components, and central metabolic pathways.

Overall, this integrated GWAS approach highlights complementary escape and tolerance strategies shaping wheat adaptation to heat and drought and identifies robust genomic targets for indirect selection and marker-assisted breeding of climate-resilient wheat cultivars.

P277 - Non-histone deacetylation of TaAREB3 by TaHDA8 fine-tunes root elongation and drought resilience in wheat

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Abstract

Wheat root systems adapt dynamically to drought stress through intricate regulatory mechanisms that mitigate adverse effects. Understanding and harnessing these mechanisms is critical for breeding drought-resistant wheat varieties. Here, we identify TaHDA8, a histone deacetylase, as a key negative regulator of root elongation and drought tolerance in wheat. Under drought conditions, TaHDA8 expression is finely modulated to relieve its inhibition of root growth, thereby enhancing plant adaptation to water deficit. Notably, reduced TaHDA8 protein levels restore the DNA-binding activity of TaAREB3—a positive regulator of root elongation and drought tolerance—by preserving acetylation at its K248 and K281 residues. This enables TaAREB3 to bind the TaKOR1 promoter and activate its expression, promoting root elongation through enhanced cell proliferation in the root meristem. Further analysis reveals that natural variation in the TaKOR1 promoter influences TaAREB3 binding affinity, and wheat germplasm carrying the TaHDA8-TaAREB3-TaKOR1 regulatory module has been preferentially selected during breeding. Together, our findings uncover a mechanism by which lysine deacetylation of a non-histone protein regulates root development under drought stress, offering genetic targets for improving root architecture and developing drought-resilient wheat varieties.

P278 - Variation in weather conditions have significant effects on winter wheat flag leaf stomatal traits

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Abstract

Stomata, the gatekeepers on the leaf surface, regulate gas exchange between the leaf and the atmosphere. Weather extremes, like high temperatures, drought, and heavy rainfall, cause stress in plants and reduce grain yield. Studies examining the relationships between wheat stomatal traits and grain yield under field conditions remain limited. In wheat, the flag leaf is an essential organ that determines grain filling duration and yield. Yet, few studies have examined the effects of flag leaf removal on winter wheat yield components in northern regions. Therefore, our study aimed to investigate stomatal traits, their relationship with grain yield under field conditions, and the effect of flag leaf removal on grain yield components.

We conducted a three-year field trial (2023-2025) with 25 winter wheat varieties. From each plot, we randomly selected six plants to measure flag leaf stomatal conductance (Gs). After removing the flag leaves, we made leaf imprints to determine stomatal density (SD) and size. We also performed yield component analyses (spike length, grain number spike⁻¹, grain weight spike⁻¹). In 2025, we included ten spring wheat varieties as a comparison.

Results revealed higher SD in the warmer year of 2023 compared to the cooler, wetter year of 2025, when Gs was higher. Lower SD in 2025 was mainly due to a larger leaf area in 2025, leading to more widely spaced stomata. Both genotype and year significantly affected SD and Gs, whereas stomatal distribution between leaf surfaces was influenced only by genotype. Grain yield was lower in 2025 than in 2023 and 2024, likely due to extreme cold waves during the active spring growth period. Across the trial years, genotypes with smaller stomata exhibited higher grain yields. The removal of the flag leaf in winter wheat moderately lowered grain weight spike⁻¹ in the pooled data and in 2025. In contrast, flag leaf removal in spring wheat in 2025 resulted in both decreased grain weight spike⁻¹ and grain number spike⁻¹, with more pronounced declines than in winter wheat.

As unfavourable conditions due to climate change become more frequent, these findings provide valuable insights for breeding climate-resilient wheat varieties that maintain high yields.

P279 - Spatio-temporal dynamics of heat sensitivity: how reproductive developmental gradients govern wheat grain-set processes

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Abstract

Grain number is a major determinant of wheat yield, integrating the fate of individual florets and showing high sensitivity to short heat stress events during vulnerable stages such as meiosis and anthesis. Dissecting grain-setting determinism ecophysiologically under heat is crucial for yield modeling and breeding. However, developmental asynchrony among tillers, spikelets, and florets complicates separating true heat-stress tolerance from stress escape.

We aimed to derive a unit day response curve (grain loss per day per degree above threshold) through the full crop life cycle. We first quantified developmental gradients from spike to single-floret level, then evaluated how grain-setting processes interacted with these gradients to constitute overall grain-set response under heat, and finally modeled these processes under different heat scenarios. Using morphological and destructive measurements of spike and anther length from four controlled-environment experiments, we developed a framework to track floret developmental stages at the whole-plant level, with particular resolution around meiosis. This enabled construction of a developmental map for individual florets based on simple external traits.

This framework linked within-plant developmental asynchrony to reproductive success under heat stress of varying magnitude and duration applied from floret initiation to grain filling, allowing response comparisons at floret, spike, and plant levels. We identified sensitivity of precise reproductive processes including spikelet and floret formation, meiosis, and anthesis. Early stress between single-ridge and terminal-spikelet stages primarily reduced grain number through spikelet loss, whereas stress during meiosis caused the most severe reductions in floret fertility, followed by stress at anthesis.

Grain loss at the floret level was structurally heterogeneous and shaped by developmental gradients among florets. Plant-level responses masked and attenuated floret-level responses, with the true peak of sensitivity temporally shifted. This temporal distortion obscured both the physiological window of vulnerability and heat sensitivity magnitude. Heat intensity and duration effects were modeled by multiplicative additivity, yielding a unit heat response curve (%/day/°C) for prediction.

Our findings enable precise determination of critical developmental stages and response magnitudes across the crop cycle, providing a reliable breeding approach by integrating floret-scale dynamics for selecting genotypes with true physiological resilience.

P280 - Genomic breeding for heat tolerance at ICARDA

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Abstract

Durum wheat production and productivity are increasingly challenged by rising temperatures, particularly in vulnerable regions such as the Senegal River Valley, where daytime temperatures during the coolest season regularly exceed 30°C. Addressing this, breeding for heat tolerance has become a central focus for ICARDA in the region.

To accelerate genetic gain, we have implemented genomic tools to identify and deploy heat tolerance loci. Through genome-wide association studies (GWAS) across three diverse panels subjected to a range of heat-stressed environments, we identified 36 loci significantly associated with heat tolerance. The corresponding SNPs were converted into Kompetitive Allele Specific PCR (KASP) markers and validated in an independent panel. Each marker explained up to 9% of the phenotypic variation for grain yield under heat stress. These markers are now integrated into genomic selection pipelines targeting the West African savannahs.

In parallel, we initiated fine mapping of a major heat tolerance QTL located on chromosome 1A, spanning an initial interval of 179 Mbp. To refine this region, 16 full-sib crosses were developed (including six semi-near isogenic lines (NILs) and 10 true-near isogenic lines) derived from progenies segregating for the QTL but sharing 51-91% genetic similarity. These lines represent the foundational material for QTL refinement. The semi-NILs and the true-NILs were phenotyped over two growing seasons under field heat stress in Senegal. Additionally, controlled heat stress was applied during flowering using plastic tunnel facilities in Morocco. A GBS-based k-mer approach was employed for genotyping. Significant markers were identified through stepwise regression, enabling the detection of tightly linked or co-located genomic regions. These k-mers were aligned to a newly assembled durum wheat reference genome to further narrow the QTL interval and identify candidate genes

P281 - Physiological basis of spike fertility variation in wheat

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Abstract

In wheat, grain number per m² (GN) is a key determinant of yield and further gain in yield would likely require further increases GN that must come from improvements in spikes per m² (SN) and/or in grains per spike (GS). The main objective of this study was to elucidate the physiological basis of crop fertility variation by integrating yield components with tillering and floret developmental dynamics. Two field experiments were conducted in Bell-lloc (NE Spain) during the 2022-23 growing season under irrigation, one sown in an optimal date and the other in a late sowing. In both experiments we compared bread (*Triticum aestivum*) and durum (*Triticum durum*) wheat genotypes combined factorially with two source-strength conditions: a control and a thinning condition in which half of the plants were removed at the onset of stem elongation. Across experiments, variation in GN was mainly explained by differences in fertile florets per m² (FF), whereas grain abortion played a comparatively minor role. However, the pathways leading to high FF differed between experiments. In Experiment 1, higher GN was associated with greater SN, primarily explained by the capacity of cultivars to reduce tillers mortality. In contrast, in Experiment 2, variation in FF was mainly driven by spike fertility, reflecting differences in floret survival within the spike rather than changes in spike number. Thinning enhanced both tiller and floret survival.

Tillering dynamics indicated that variation in SN was more strongly associated with tiller survival to anthesis than with maximum tiller production. Similarly, differences in FF/spike were mainly driven by floret survival rather than by floret initiation. Together, these developmental processes revealed alternative physiological pathways to achieve fertile florets per unit area and final grain number.

Keywords: wheat, spike fertility, grain number, tillering dynamics, floret development, fertile florets

P282 - Identification and validation of an important waterlogging QTL on chromosome 6A in spring wheat.

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Abstract

Waterlogging is a major abiotic stress affecting wheat production worldwide. Field trials in 2013 and 2014, followed by greenhouse experiments in 2023 and 2024, were conducted to identify and validate genomic regions associated with waterlogging tolerance in wheat. Waterlogging stress responses were evaluated using several phenotypic traits, and Principal component analysis (PCA) revealed that chlorosis and overall condition scores were major contributors to phenotypic variation under waterlogged conditions. Genome-wide association studies (GWAS) identified a major quantitative trait locus (QTL), QWL.nmbu-6A, on chromosome 6A (610-613 Mbp) associated with chlorosis, which explained an average of 30.9% of the phenotypic variation across the two field seasons. A greenhouse waterlogging method using starch (0.1% m/v) was optimized to simulate field waterlogging conditions. Haplotype analysis found significant differences in chlorosis between contrasting haplotype groups across both field and greenhouse experiments. To further validate this QTL, a recombinant inbred line (RIL) population was developed by single seed descent (SSD) from a cross between GN07560 and Seniorita, which carry contrasting haplotypes at the QWL.nmbu-6A locus. A subset of F6-derived RILs with contrasting haplotypes was evaluated at the seedling stage under greenhouse waterlogging conditions, confirming significant haplotype effects of QWL.nmbu-6A on chlorosis. While chlorosis was found to be a reliable indicator under severe waterlogging stress, its predictive value declined under milder conditions, highlighting the importance of including recovery traits in waterlogging tolerance assessment. These findings highlight the importance of QWL.nmbu-6A in chlorosis response under waterlogging stress and provide a valuable genomic region for marker-assisted selection in wheat breeding programs targeting environments prone to moderate to severe waterlogging stress.

P283 - Optimising critical periods to maximise resource availability and crop yields in south-eastern Australia

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Abstract

Radiation and temperature during the spike growth period in wheat have major impacts on wheat grain number, which is the first order control on yield. It is hypothesised that aligning crop phenology to the optimal critical period to maximise crop resource availability (radiation, temperature, water and nitrogen), grain number can be maximised in a given environment. However, to increase achieved yield, crop phenology must be aligned to minimise yield losses from floret sterility due to heat and frost stress during flowering and grain fill (post-critical period). As a result, the optimum critical period is one that results in maximum yield by balancing the trade-offs between multiple abiotic stresses.

To determine if APSIM NextGen with the new Cereal Anthesis Molecular Phenology (CAMP) model could accurately simulate critical periods in wheat, a simulation experiment was designed to replicate the seminal Fischer 1985 paper. It was found that APSIM NextGen was able to replicate the timing of the reduction in grain number due to reduced radiation during the spike growth period.

The optimum critical period was identified at eight case study sites along a climate gradient in south-eastern Australia by using APSIM NextGen to simulate genotype (Quick Spring to Very Slow Winter on the Australian Cereal Phenology Classification) by management (sowing date, nitrogen timing and amount) combinations over 48 years to identify the optimum critical period. This provides clear guidelines on when to sow which genotype to align flag leaf emergence and the start of anthesis to environmental conditions. The duration of the optimum critical period that maximises grain number is narrowed when heat and frost effects are considered. Analysis of resource availability and the determinants of grain number showed that at drier locations, crop growth rate, spike dry weight at anthesis and grain number are limited by water availability during the critical period; unlike higher rainfall sites which were limited by radiation interception during the critical period.

This long-term simulation modelling provides growers with informed management strategies to enable the alignment of crop development with the critical period, thereby improving productivity and resilience under increasingly variable and shifting climatic conditions.

P284 - Physiological drivers of yield variation between modern durum wheats and Senatore Cappelli under contrasting growing conditions

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Abstract

Durum wheat is widely recognised as a critical crop in several countries of the Mediterranean basin, where it is central for food security, and an economically relevant crop there and in many other countries such as Canada, US, Argentina, and Australia. It is usually grown in stress-prone environments making it vulnerable to climate change. Identifying physiological drivers for improved performance under contrasting conditions would help future breeding for improved adaptation. For this purpose, we grew three modern durum wheat cultivars and Senatore Cappelli, a foundational genotype of breeding during the 2022-2023 growing season in Lleida (NE Spain). There were two irrigated experiments under contrasting photothermal conditions, one sown in November (optimal sowing) and the other in February (stressful conditions). On average, modern genotypes yielded 13% more than S. Cappelli, although the difference in yield was larger on the stressful than in the optimal condition. The yield gain was mainly associated with the greater number of grains per area (34%), harvest index (40%), and fruiting efficiency (93%), which were offset by reductions in grain weight (15%) and biomass (18%). All cultivars exhibited reduced yields under late sowing due to decreases in both grain number and grain weight; however, the modern cultivars exhibited more tolerance. Analysis of the grain profile within spikes revealed that modern genotypes had increased grain numbers in the central spikelets and greater fertility at basal positions. The reduced average grain weight seemed due to a higher number of smaller grains in modern cultivars compared to S. Cappelli. Notably, modern cultivars differed among themselves in grain size distribution and in their responses to these changes. Fruiting efficiency emerges as a promising avenue for further yield improvement. Breeding in durum wheat seemed to have produced cultivars with greater resilience that may be related to the prevalent conditions in which selection is made.

P285 - A water-saving drought survival strategy in a wheat TILLING mutant involves metabolic and phosphorylation reprogramming

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Abstract

Developing climate-smart wheat requires strategies that enhance water-use efficiency while maintaining agronomic performance under increasing drought frequency. However, drought tolerance often involves trade-offs between water conservation, growth, and reproductive output. To dissect the physiological and molecular basis of water-saving strategies, we screened a field-grown bread wheat TILLING population using carbon isotope discrimination as a proxy for intrinsic water-use efficiency and identified a mutant line, WS1, exhibiting enhanced drought survival.

Under both field and controlled-environment conditions, WS1 showed constitutively reduced stomatal conductance and transpiration rates, resulting in improved water-use efficiency. Interestingly, WS1 displayed weak transcriptional responses to exogenous abscisic acid (ABA), indicating that its water-saving phenotype operates largely independently of canonical ABA signaling. Integrated metabolomic and transcriptomic analyses revealed constitutive accumulation of proline and coordinated reprogramming of nitrogen and carbon metabolism, consistent with a survival-oriented metabolic configuration. Phosphoproteomic profiling further identified distinct phosphorylation signatures in energy-related signaling components, including proteins associated with SnRK1-linked pathways and carbon metabolism. These phosphorylation patterns suggest the establishment of an altered energy-sensing state that supports metabolic adjustment toward osmoprotection rather than growth. Despite enhanced drought survival, WS1 exhibited reduced fertility and delayed development, highlighting an intrinsic trade-off between stress resilience and reproductive investment. This balance reflects a shift from developmental growth mode to a constitutive stress-responsive mode.

Together, our results define a phosphorylation- and metabolism-associated framework underlying a water-saving drought survival strategy in wheat. This study provides mechanistic insight into survival-oriented stress adaptation and offers conceptual guidance for next-generation design breeding aimed at optimizing climate-smart water-use strategies while minimizing yield penalties.

P286 - Black glumes: a genetic trait that enhances dry down in wheat

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Abstract

Persistent wet late-season condition during harvest poses a growing climate-related challenge for wheat production in the Canadian Prairies, causing delays in operations and elevating grain moisture content. Post-harvest grain drying is a common practice to reduce grain moisture content but can be costly and contributes to greenhouse gas emissions. Identifying climate-smart alternatives could reduce both economic and environmental impacts. The black glume trait in wheat (*Triticum aestivum* L.) may provide a biological, climate-resilient alternative to artificial grain drying by increasing heat absorption at maturity, accelerating grain moisture loss and mitigating harvest moisture challenges. This study evaluated the impact of the black glume trait on wheat dry-down under both field and controlled conditions. Near-isogenic lines (NILs), created through six backcrosses with two Canadian wheat varieties (CDC Teal and CDC Hughes), were developed to isolate and study the effect of the black glume trait. Field trials were conducted in 2024 and 2025, and grain moisture dynamics were monitored from physiological maturity to harvest. At harvest maturity, thermal images from individual plots were used to assess differences in spike temperature. Additionally, controlled environment experiments assessed spikelet temperature differences between black and light-colored glume NILs using micro-thermocouples. Across three site-years spanning two growing seasons, black glume (BG) NILs showed accelerated loss of spike moisture than their light glume counterparts. In CDC Hughes backgrounds, this effect was observed in all environments, with seven sampling timepoints showing significantly lower spike moisture in BG NILs, with up to 3.3 percentage points lower spike moisture ($p < 0.01$). CDC Teal BG NILs displayed fewer and less consistent responses, with two significant timepoints showing lower moisture and a maximum reduction of 2.74 percentage points ($p < 0.001$). Importantly, the black glume trait was not consistently associated with grain yield, with a single environment indicating a 4.3% advantage for light-glume NILs in CDC Teal backgrounds ($p = 0.005$). No consistent associations between black glumes and other agronomic traits were observed. These results suggest potential for improved grain dry-down in Canadian wheat with limited agronomic trade-offs.

P287 - Genetic analysis of root system architecture and waterlogging tolerance in the Japanese Wheat Core collection

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Abstract

Background: Waterlogging damage is a critical challenge for wheat production in poorly drained fields such as those in Japan. Since oxygen is available near the soil surface even under saturated conditions, the root growth angle (RGA) is a vital determinant of waterlogging tolerance. For instance, in barley cultivars from heavy-snow regions of Japan, a loss-of-function mutation in HvDRO1 promotes shallower root angles, which may enhance productivity in wet environments. In this study, to clarify the relationship between wheat root system architecture (RSA) and waterlogging tolerance, we conducted phenotypic surveys of the Japanese Wheat Core collection (JWC), analyzed polymorphisms and expression of TaDRO1, and performed GWAS to identify novel loci for RSA.

Materials and Methods: We measured the seminal RGA of 96 JWC accessions on gel, quantified Soil Surface Rooting (SOR) under normal and water-logged soil conditions, and performed GWAS using these phenotypic data. Genetic analyses of TaDRO1 included Targeted Amplicon Sequencing of the coding region for the 96 accessions and Sanger sequencing of the promoter regions and RT-qPCR for expression analysis in root tips for the deep-rooting JWC02 and shallow-rooting JWC04. Comparative cultivation trials were also conducted for these two representative accessions.

Results and Discussion: Although TaDRO1 coding region analysis revealed two main haplotypes, they did not correlate significantly with RGA across the JWC. However, expression analysis showed that the deep-rooting line JWC2 had significantly higher TaDRO1B expression than the shallow-rooting JWC4. Promoter sequencing highlighted differences in cis-elements, specifically ABRE and HSE, between these lines. Conversely, other accessions showed no clear link between TaDRO1 expression and RGA, suggesting the presence of novel regulatory genes. GWAS identified a significant peak for SOR, in which homologs related to root plasticity in rice was found. Notably, JWC2 increased its shallow root ratio under waterlogging, potentially mitigating the stress and maintaining SPAD values.

Conclusion: These findings suggest that while TaDRO1B influences RGA in specific lines, novel genes drive the overall RSA diversity in the JWC. Breeding for root plasticity—developing deep roots normally but forming shallow roots under waterlogging stress—is a promising strategy for stabilizing wheat production against unpredictable environmental fluctuations.

P288 - Sensitivity to heat stress of wheat O₂-based gas exchange differs between leaves and spikes

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Abstract

Limited attention has been paid to wheat spike gas exchange, encompassing photosynthesis and respiration, despite its potential contribution to yield. Partly because reliable techniques for measuring spike photosynthesis and respiration are cumbersome and low throughput. Here, we used a high-throughput fluorophore-based technique to examine acclimation to heat stress of wheat spike O₂-based gas exchange (specifically, respiratory O₂ consumption in the dark [Rdark_O₂] and photosystem II O₂ release [PSII_O₂]). Leaf Rdark_O₂ was higher than spike Rdark_O₂ when measured at 25 °C (4.3 vs 3.8 μmol O₂ gFM⁻¹ s⁻¹), and both leaf and spike Rdark_O₂ acclimated (i.e. downregulated rates of respiratory O₂ consumption) to warming. However, spike Rdark_O₂ exhibited greater sensitivity to instantaneous temperature increases, with a Q₁₀ (proportional change per 10 °C increase in temperature) being 33% higher than in leaves. Exposure to a 3-day heatwave reduced Rdark_O₂ to a similar extent in leaves and spikes (19-21%). Furthermore, spike PSII_O₂ showed better tolerance to heatwave conditions than leaves, with reductions in PSII_O₂ of 12% in spike versus 28% in leaves. Overall, estimates of energy use efficiency (PSII_O₂/Rdark_O₂) were higher in leaves than in spikes. This technique can be used to support mechanistic studies of spike heat stress tolerance, genetic variation in spike photosynthesis and respiration, and breeding of heat-tolerant cereal crops.

Keywords: ear photosynthesis, heat stress, non-foliar gas exchange, spikelet

P289 - Bridging the adoption gap: participatory validation and predictive analytics drive 100% re-adoption of climate-resilient durum wheat in Morocco

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Abstract

Background:

The adoption gap—disconnect between variety development and farmer uptake—remains a critical barrier to climate adaptation in dryland agriculture. In Morocco, where drought threatens food security for 40 million consumers, we investigated whether participatory validation accelerates adoption while developing machine learning frameworks to predict adoption potential before costly on-farm testing.

Methods:

We implemented a three-phase integrated framework: Phase 1 deployed four INRA durum varieties and one traditional check across 19 farmer fields, engaging 19 farmers (16 male, 3 female) through gender-inclusive participatory appraisal. We monitored authentic adoption metrics—re-sowing decisions and neighbor seed requests—rather than stated preferences. Phase 2 translated farmer priorities into evaluation criteria for 48 elite lines across six INRA stations, integrating molecular markers (SSR, SNP, KASP), multi-location trials, speed breeding (three generations/year), and quality analysis for industry standards. Phase 3 (ongoing) develops machine learning models integrating agronomic data with Sentinel satellite remote sensing (vegetation indices, stress detection) to predict variety × environment × management interactions and forecast adoption potential, enabling intelligent pre-selection before field validation.

Results:

Variety V1 achieved 37 quintals/ha (61% advantage over traditional check at 23 quintals/ha). Critically, 100% of farmers (19/19) voluntarily re-adopted these varieties for consecutive seasons, with neighboring farmers requesting seed—documenting spontaneous farmer-to-farmer dissemination. Gender-disaggregated assessments revealed grain quality ranked equally with yield in adoption decisions; female farmers particularly emphasized quality traits for traditional couscous preparation, challenging assumptions that yield alone drives adoption. Preliminary machine learning models integrating Sentinel imagery show promising capacity for predicting variety performance across environments, potentially compressing breeding cycles while maintaining farmer-responsive priorities.

Conclusions:

This study proves participatory validation with gender-inclusive engagement (16% female participation) accelerates adoption and creates self-sustaining dissemination networks. The unprecedented 100% re-adoption rate validates that integrating diverse farmer knowledge—including female farmers' quality-focused perspectives—creates varieties farmers champion themselves. Integration of molecular tools, satellite remote sensing, and predictive analytics creates an intelligent breeding system maintaining farmer priorities while accelerating genetic gain. This framework offers a replicable model for closing the adoption gap in climate-smart wheat improvement globally.

Keywords: *participatory breeding, machine learning, remote sensing, variety adoption, gender-inclusive research, climate resilience, durum wheat, Morocco*

P290 - Unraveling drought stress tolerance mechanisms in durum wheat through RNA sequencing applications

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Abstract

Drought stress represents one of the most significant constraints to durum wheat (*Triticum durum* Desf.) productivity worldwide, particularly under Mediterranean and semi-arid climates. Consequently, understanding the molecular mechanisms underlying plant responses to water deficit is essential for developing resilient varieties capable of sustaining yield under adverse environmental conditions. RNA sequencing (RNA-Seq) has emerged as a powerful tool for elucidating genome-wide transcriptional changes associated with stress adaptation. This study explores the application of RNA-Seq in three durum wheat varieties, one hydric stress-tolerant landrace J. Khetifa, Sebatel2 (45) (abbreviated as Sebatel) developed in the Mediterranean Basin with wide root angle, and Pelsodur with narrow root angle, to identify differentially expressed genes, regulatory pathways, and candidate molecular markers involved in drought stress tolerance in durum wheat. Transcriptomic analyses reveal key genes related to osmotic adjustment, antioxidant defense, hormone signaling, transcription factor regulation, and stress-responsive metabolic pathways. The integration of RNA-Seq data with functional annotation and pathway enrichment analysis provides valuable insights into the complex molecular networks underlying drought resilience. These findings contribute to the identification of potential targets for marker-assisted selection and genomic breeding strategies aimed at improving drought tolerance in durum wheat.

P291 - Genome wide association of fertility related traits in a collection of Spanish bread wheat landraces

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Abstract

By 2050 it is estimated that a 60% increase in production would be needed to satisfy demands. Thus, developing wheat cultivars able to maintain or even increase fertility under the actual scenario of climate change is a must for the next decades. The success of any breeding program depends on the available genetic diversity and knowledge of the genetic control of the target traits.

Fertility in wheat is a complex trait involving several processes that directly impact grain production (spike and spikelet development, gametogenesis, fertilization and grain maturation). Traditional landraces provide an ideal population to conduct genetic and association analysis, based on their diversity and adaptation to very different agroecological environments. Here we characterized a collection of 189 Spanish bread wheat landraces for fertility and related traits. The phenotypic analysis revealed a group genotypes from central regions of Spain noticeably different, as well as, a negative correlation between fertility and phenology. Phenotypic data were coupled with high-throughput genotyping in a GWAS. Associations were unevenly distributed along the genome, with chromosomes 5A and 5B harboring the majority of them. From the 97 marker-trait associations, 4 were stable across seasons, 9 were associated with multiple fertility-related traits and 2 of them have not been described in previous analysis. Detailed annotation and analysis of these genomic regions revealed new interesting candidate genes related to fertility.

P292 - Dissecting heat-stress tolerance mechanisms in durum wheat (*Triticum durum*) germplasm under field conditions

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Abstract

Heat stress is a major constraint to wheat productivity, affecting plant growth, photosynthesis, metabolic activity, spike fertility and grain yield. Because these effects result from complex interactions among plant traits and environmental drivers, understanding stress responses requires integrative frameworks capturing relationships among physiological, phenological and yield-related variables. In a previous study, a worldwide panel of 183 durum wheat cultivars and breeding lines was evaluated under irrigated field conditions to assess responses to prolonged heat stress (HS) without confounding water shortage. Grain yield, yield components and phenological traits were analyzed in relation to stress timing and climatic covariates. Structural Equation Modeling (SEM) and Genetic SEM were used to disentangle relationships between plant traits and environmental factors. Across two seasons at CENEB, heat stress markedly reduced NDVI (–51.3%), kernel weight per spike (–40.5%), grain filling period (–38.7%) and grain yield (–56.6%). Temperatures around anthesis were negatively associated with grain yield and its components under HS. The main yield determinants—fertile spike density, spike fertility and kernel size—were strongly interrelated, while NDVI measured at the medium milk-soft dough stage emerged as a proxy of reproductive performance and grain weight under stress. Germplasm combining high yield potential with stable performance under elevated temperatures therefore represents a valuable reservoir of alleles for breeding heat-resilient cultivars. Based on these findings, the present study investigates the genetic architecture of heat adaptation through a haplotype-based genome-wide association study (GWAS). The panel was genotyped using a high-density SNP chip, and genome-wide haplotype blocks were constructed using a linkage disequilibrium-based approach. This framework improves the detection of genomic regions controlling complex traits compared with single-SNP models. GWAS identified loci associated with key yield-related traits under contrasting thermal environments, incorporating environmental indices describing the intensity and timing of heat stress as covariates. These regions provide candidate targets for marker-assisted selection and support the development of climate-resilient durum wheat cultivars.

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P293 - Large wheat rhizosheath size enhanced root growth, diverse bacterial communities, and yield in acidic soil with high Al^{3+} content.

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Abstract

Background and Aims: The rhizosheath has emerged as a promising root trait for plant adaptation to hostile soils, particularly acidic soils with high aluminium (Al^{3+}) content. This study investigated the root system traits, water use, grain yield, and water use efficiency of five wheat (*Triticum aestivum* L.) genotypes with contrasting rhizosheath sizes.

Methods: Five wheat lines, including two with large rhizosheaths (L_1 , L_3), two with small rhizosheaths (S_1 , S_2), and their parent cultivar Mace, were evaluated in two experiments: rhizoboxes (Experiment 1) and PVC columns (Experiment 2), both filled with acidic soil containing high Al^{3+} content. Measurements included bacterial community composition, rhizosheath dry weight, root biomass, root morphological traits (including root length density (RLD) and specific root length (SRL)), shoot biomass, plant height, water use, yield and grain yield components.

Results: Lines selected for large and small rhizosheath sizes retained these contrasting traits when grown in an acidic soil with high Al^{3+} content. Lines L_1 and L_3 developed deeper and more extensively branched root systems below 0.2 m soil depth under increasing soil acidity, compared to lines S_1 and S_2 and the parent cv. Mace. Lines with large rhizosheaths, particularly L_3 , had higher RLD and SRL, greater shoot biomass, increased water use, more grains per spike, longer spikes, and higher grain yield. The large rhizosheath lines, especially L_3 , supported greater bacterial diversity and higher abundance of plant growth-promoting traits.

Conclusions: A larger rhizosheath was associated with a deeper, more extensive root system below 0.2 m in soil profile with pH below < 4.29 and Al^{3+} content exceeding 21.1 mg kg^{-1} . This trait enhanced shoot biomass, water use, and grain yield. These findings suggest that large rhizosheath size is a promising breeding target for developing wheat varieties adapted to acidic soils with high Al^{3+} content.

P294 - Characterization of durum wheat (*Triticum turgidum* L. ssp. durum) tolerance to drought and terminal heat stress under Moroccan Conditions

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Abstract

Durum wheat is a strategic crop of the Mediterranean basin and a cornerstone of food security in Morocco, where it is now directly threatened by the intensification of abiotic stresses associated with climate change. A multi-environment program conducted over several years and involving selected genotypes enabled a thorough assessment of durum wheat performance across the main Moroccan production zones, providing a solid reference framework to guide breeding strategies. Regarding drought, the dominant climatic constraint in Morocco, particular attention was paid to the critical stages of germination and seedling development. Seventeen genotypes were subjected to three contrasting water regimes under controlled conditions, revealing severe perturbations: a sharp decline in germination rate (–99%), root and shoot length (–30%), dry biomass (–70%), chlorophyll content (–42%) and a strong accumulation of proline (+74%) and soluble sugars (+61%). Multivariate analysis and Z-score ranking highlighted lines DYT3TAZI and DYT4TAZI as the most tolerant, while confirming the remarkable resilience of Moroccan varieties Faraj, Louiza, Nachit and Jawahir. At the genomic level, association analysis based on 118 KASP markers identified major chromosomal hotspots, particularly on chromosome 2A under moderate stress and on chromosomes 7A/7B under severe stress. Terminal heat stress represents the second growing threat to durum wheat productivity. The evaluation of 36 test lines and 2 check varieties, conducted at two experimental stations under plastic tunnels inducing heat stress at flowering, revealed severe yield losses: –32.8% at Marchouch station and –78.6% at Douyet station. These reductions were driven by a decrease in grain number per spike by 50% and thousand kernel weight by 35%, resulting from a drastic increase in shriveled grain rate (+96%), reflecting deep thermal damage to reproductive organs. Integration of tolerance indices (Mean Productivity, Yield Index, Stress Susceptibility Index, and Geometric Mean Productivity) identified lines TNSR23-042, TNSR23-044, and TNSR23-046 as the most productive and resilient genotypes across both environments, outperforming the checks. These findings open concrete perspectives for the development of durum wheat varieties adapted to the extreme climatic conditions of Morocco, by combining phenotypic selection and genomic tools.

Keywords: *Durum wheat, Morocco, breeding, abiotic stresses, germination, seedling, terminal heat stress and genomic.*

P295 - Yield-determining traits responsible for yield penalties across contrasting environments in elite wheat germplasm

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Abstract

Phenotypic plasticity allows crops to adjust physiological and reproductive traits to environmental variation, affecting yield stability under stress. Yield losses occur when environmental stress exceeds the buffering capacity of key yield-determining traits, including phenological traits, growth and partitioning, and yield components. Resource availability during critical growth stages modulates these trait responses, either amplifying or mitigating stress effects. Understanding genotypic differences in plasticity and compensatory trait adjustments within elite material is essential for breeding strategies that enhance stable and resilient crop performance.

We evaluated 19 elite bread and durum wheat genotypes across two Mediterranean sites, one moderately cool in NE Spain and the other warm in S, under an optimal and a late sowing date. Three stressful scenarios were assessed: late vs early sowing in each of the two locations, and the warmer vs the cooler location in the optimal sowing. Yield losses and trait responses were quantified to identify mechanisms underlying genotypic variation in stress response.

Results revealed widespread yield penalties under stress, with reductions averaging 350-375 g/m².

Genotypes showed substantial variability, with divergent yield losses despite similar phenological shifts under late sowing in the control environment. Biomass reductions were consistent and strongly correlated with yield losses, explaining 81-86 % of them, whereas harvest index was highly variable and contributed little to differences between environments. Yield reductions were primarily driven by grain number (60-64 %), predominantly through decreases in grains per spike (29-37 % under late sowing in the cooler site; ~60 % under late sowing in the warmer site; 58-74 % under warmer optimal sowing), while spike number contributed inconsistently and average grain weight accounted for less than 10 % of losses.

These results help to identify the traits that most strongly contribute to alleviate yield loss under stress, thereby providing valuable targets to guide breeding efforts aimed at developing cultivars with enhanced stability.

Keywords: *Yield loss, Phenotypic plasticity, Crop resilience, Yield stability, Key yield-determining traits, Environmental stress*

P296 - Post-anthesis short heat waves in durum wheat do not compromise breeding efforts to increase β,β -carotenoid content in grains

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Abstract

Short heat waves (SHWs), defined as periods of several consecutive days with temperatures exceeding the developmental optimum, are increasingly affecting cereal production by compromising both yield and grain quality. The Mediterranean Basin, a key region for high-quality durum wheat cultivation, is expected to become particularly vulnerable to SHW stress under future climate-warming scenarios. This study evaluated the effects of simulated post-anthesis SHWs on yield and grain quality in elite durum wheat cultivars and selected landraces characterized by a high proportion of β,β -carotenoids (derived from the β,β -biosynthetic branch). Results from field experiments conducted over two consecutive growing seasons have shown that post-anthesis SHWs reduced grain number per spike and thousand kernel weight (TKW), while increasing grain protein content. These effects were more pronounced in landraces, largely due to their later flowering. SHW stress also caused an overall decline in grain carotenoid content. However, carotenoids derived from the β,ϵ -branch of the biosynthetic pathway were more strongly affected than those from the β,β -branch in both elite varieties and landraces. Interestingly, landraces experienced a significantly smaller reduction in β,β -branch carotenoids than elite cultivars. Together, these results suggest that a biofortification strategy focusing on β,β -carotenoids would be more effective, as their accumulation is less affected by post-anthesis SHW stress.

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P297 - Validation of major genes and identification of novel genomic regions for plant height and heading date in a durum wheat RILs using GWAS

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Abstract

Durum wheat (*Triticum turgidum* L. ssp. durum Desf.) is primarily cultivated for dry pasta production, a key component of global food systems. Plant height (PH) and heading date (HD) are key agronomic traits contributing to adaptation and yield potential. Although these traits are largely controlled by major genes such as Rht-B1 and Ppd-A1, additional loci also contribute to their phenotypic plasticity. This study aimed to identify genomic regions associated with PH and HD using a F8-9 recombinant inbred line (RIL) population of 154 lines derived from two semidwarf cultivars (BI Cumenay × Italo). The population was evaluated across three environments (Dorrego2024, Cabildo2025, and Barrow2025). PH and HD were measured, and BLUPs calculated to estimate genetic effects taking into account for environmental variation. Genotyping was performed using DArT-Seq (SNP and SilicoDArT markers) and KASP technology for Rht-B1 [wMAS000001] and Ppd-A1 [wMAS000030] specific markers. After quality filtering, a total of 7222 markers were retained for GWAS, which was conducted in TASSEL 5.0 using a mixed linear model (MLM, PCA+K). Unexpected variability in PH was observed in the RIL population, ranging from 54 to 137 cm, while parental lines reached 85 cm (BI Cumenay) and 67 cm (Italo). ANOVA revealed significant genotypic variation and high broad-sense heritability for both traits ($H^2 = 0.94$ for plant height; $H^2 = 0.90$ for heading date). The Ppd-A1 KASP marker explained 73% of heading date variation, with the Ppd-A1a(GS100) allele significantly accelerating heading. Conversely, Rht-B1 was polymorphic and accounted for 16% of the PH variation, suggesting the influence of additional loci. GWAS identified strong marker-trait associations (MTAs) at Rht-B1 and Ppd-A1(GS100) positions, confirming the major role of these loci. Furthermore, significant associations ($LOD > 5$) were detected for HD on chromosome 2A and the SNP- 5582453 ($LOD = 5.7$) located on chromosome 2B. For PH, the most relevant MTAs were identified on chromosome 6A (SNP-1767328 [$LOD = 4.4$]; SNP-2263126 [$LOD = 4.4$]; SilicoDArT-1087772 [$LOD = 3.9$]), and additional markers on chromosomes 2A (SilicoDArT-2293704 [$LOD = 4.3$]) and 7B (SNP-1208060 [$LOD = 3.5$]). These findings highlight the polygenic nature of plant height and reveal novel genomic regions with potential to be integrated into durum wheat breeding.

P298 - Mapping of QTL for stable falling number in the winter wheat cultivar 'Ellvis'

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Abstract

The combination of high temperatures and humid weather between grain ripening and harvest promotes preharvest sprouting (PHS) if dormancy is released. Such conditions are expected to become more common in Norwegian wheat growing regions due to climate change. The milling industry uses falling number (FN) to measure the quality loss caused by PHS, and there is genetic variation in the ability to maintain an acceptable FN under unfavorable conditions. The winter wheat cv. 'Ellvis' is known to maintain high FN even during unfavorable weather conditions and the main objective of this study was to identify quantitative trait loci (QTL) underlying the FN stability of 'Ellvis'. A backcross (BC1) population between 'Ellvis' and the CIMMYT spring wheat line 'Saar' was tested for FN in 10 different field trials at two locations and for germination index (GI) in 6 trials in Ås, Norway and Chengdu, China, between 2018 and 2022. We identified two stable QTL with the beneficial allele from 'Ellvis' on chromosome arms 6DS and 7BL.

The effects of the QTL were validated in a panel based on crosses between resistant parents including 'Ellvis', and modern spring wheat breeding material. This panel was screened for FN in five trials in three locations (Vollebekk, Bjørke and Staur) in 2021 and 2022. Lines with both beneficial alleles maintained a higher FN than the population average even in trials with very low average FN (i.e. 111 sec vs 174 sec in 2021).

The combination of beneficial alleles on both 6DS and 7BL was rare in Norwegian spring wheat breeding lines. Unless the combination has adverse effects, this indicates a potential to enrich these alleles in Norwegian breeding material to increase FN stability and resistance to PHS.

P299 - Cascading functional water balance traits enhance wheat grain yield under terminal drought

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Abstract

Water deficit and high temperatures (i.e., terminal-drought) pose a persistent threat to wheat production and sustainability under Mediterranean agroecosystems. We combined open-field, high-throughput gravimetric lysimeters with a field experiment in a rain-out shelter to characterize the physiological response to terminal-drought. Two bread wheat genotypes, WM090 (tolerant) and WM036 (susceptible), were selected from a wide diversity panel that was screened over two growing seasons, based on their contrasting yield responses to terminal-drought. WM090's superior performance was linked to a cascade of water balance-related functional traits. Osmotic adjustment supported greater canopy conductance and sustained transpiration throughout the reproductive phase. The consistent response of canopy temperature and conductance to terminal-drought, together with similar yield responses across field and lysimeter platforms, suggests that physiological insights from large-volume lysimeters are transferable to field-grown plants. WM090 also demonstrated higher water-use efficiency under terminal-drought, throughout multiple years/environments. Transcriptomic profiling revealed 344 differentially expressed genes under terminal-drought, among them genes related to osmotic regulation, ion transport, cell wall modification, and light perception. Our findings highlight the potential of integrating spatio-temporal high-throughput phenotyping with molecular tools to promote breeding efforts of wheat adaptability to climate change.

P300 - Genotypic variation in wheat under individual and combined heat and drought stress

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Abstract

The combined effect of heat and drought stress on wheat growth and development is more severe than either stress alone, particularly during the grain-filling period. This research aims to characterise the physiological and morphological responses of diverse wheat genotypes to heat, drought, and their combination.

Twelve wheat genotypes were selected based on over 12 years of plant breeding research into heat tolerance in wheat at the University of Sydney. The experiment was conducted in a controlled laboratory environment using twin controlled environment rooms (CERs) with gravimetric watering systems. The CERs represented four scenarios: control or optimal conditions (25°C day/15°C night), high temperature (35°C day/22°C night; 3 days at anthesis), drought (50% field capacity between boot stage and termination of anthesis), and high temperature plus drought (35°C day/22°C night; 3 days at anthesis + 50% field capacity between boot stage and termination of anthesis). Yield components, biomass traits, leaf area index (LAI), harvest index, and grain weight were measured. Leaf gas exchange (net photosynthesis, transpiration) was quantified using Li-COR 6800 systems.

Treatment effects were highly significant for total yield ($p < 0.001$), with drought identified as the primary yield-limiting factor. Yield declined from 17.28 g under optimal conditions to 10.98 g under drought and 8.52 g under combined heat and drought. Significant observed genotype $\times$ treatment interactions indicated differential tolerance. Yield reductions were associated with decreased total biomass, spike biomass, effective tiller number, and harvest index. LAI had strong genotypic effects, with significant genotype $\times$ treatment interactions observed for leaf area, leaf length, and maximum leaf width. Photosynthetic rate reduced and transpiration was impacted under drought and the combined stress, indicating that yield losses were linked to impaired carbon assimilation. Several genotypes showed superior performance under the combined stress and ranked highest on stress tolerance indices. PCA revealed that 55% of total variation was explained by the first two components, where PC1 represents a productivity axis driven by yield and biomass traits, and subsequent components are associated with allocation efficiency and grain weight.

Tolerance to heat and drought in wheat depends on maintaining photosynthesis, biomass, spike productivity, and stable grain filling.

P301 - Genome-wide association study reveals major SNPs associated with pollen viability and spikelet fertility in wheat under heat stress

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Abstract

Heat stress during the reproductive stage significantly reduces wheat (*Triticum aestivum* L.) productivity, primarily by impairing pollen viability and grain filling rate. This study employed genome-wide association study (GWAS) using 5,171 high-quality single nucleotide polymorphisms (SNPs) across 319 diverse wheat lines to identify genomic regions associated with pollen viability and spikelet fertility under reproductive-stage heat stress. Pollen viability was assessed from field-grown plants subjected to high temperature in a controlled setup using a thermal cycler. Spikelet fertility was evaluated in two years with heat treatment applied at the four different ear emergence stages. The wheat population showed significant genotypic and phenotypic variation. Chinese landraces formed a distinct cluster from other groups and generally exhibited lower pollen viability and spikelet fertility compared to Chinese commercial varieties. Pollen viability score exhibited moderate correlation with spikelet fertility from early-ear emergence heat treatment. GWAS identified 15 significant SNPs associated with these two traits. Notably, AVRIG15341 on chromosome 1B and AVRIG21657 on chromosome 3A explained 20.31% and 11.9% of phenotypic variation in pollen viability, respectively. AVRIG26861 on chromosome 5A explained 17.09% of phenotypic variation in spikelet viability. Combination of favorable alleles showed higher trait performance, suggesting strong potential for use in marker-assisted selection. Several putative genes linked to energy metabolism, stress signaling and transcription regulation, protein folding and modification, redox homeostasis, and ion transport and trafficking were suggested using the highly significant SNPs. This is one of the very first study to identify the SNPs linked to pollen viability in wheat diverse panels using PCR-based thermal cycler method. Our pioneering study provides new insights into the genetic architecture of reproductive-stage heat tolerance in wheat and offers valuable genetic resources for breeding heat-resilient cultivars upon validating the results using multiple-locational field study.

P302 - Responding to a changing environment: capturing temperature regulation across wheat development

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Abstract

Cereal crops have evolved to coordinate their development with environmental signals, enabling successful transitions between key growth stages. In bread wheat (*Triticum aestivum*), temperature and photoperiod act as major regulatory cues controlling the timing of the vegetative to reproductive transition, integrating multiple genetic and regulatory pathways. Much of our current understanding of these processes is derived from controlled growth chamber experiments that test static conditions and may not reflect the variable environments experienced by crops in the field. Under climate change, temperature and photoperiod signals are increasingly uncoupled, with plants exposed to extreme diurnal temperature ranges and seasonally unusual conditions across development. Understanding how wheat responds to these dynamic environments is therefore becoming increasingly important for future crop adaptation. To address this, we have assessed gene expression and regulation across a range of controlled and field conditions designed to capture realistic environmental variation. Using RNA sequencing approaches that allow the detection of novel transcripts, we have examined transcriptional responses to contrasting diurnal temperature regimes, as well as longer-term seasonal fluctuations across wheat development. These datasets include both high-resolution 24-hour time courses and sampling across seasons, spanning genotypes with contrasting growth habits. By integrating data from controlled and field environments, we aim to identify temperature-responsive regulatory targets. This work provides a framework for understanding how dynamic environmental signals shape wheat responses and supports efforts to develop cultivars that are robust to increasingly unpredictable climates.

P303 - Flowerint Locus T4 delayed flowering and suppressed spikelet outgrowth in bread wheat (*Triticum aestivum*)

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Abstract

The number of spikelets per inflorescence is a key trait to determine grain number and also one of the determinants affecting grain yield potential in bread wheat (*Triticum aestivum*). Research on genes regulating spikelet development can contribute to the maintenance and increase of yield potential. As such, genotype selection and understanding how these genotypes interact with local environmental pressures is required to maximise genetic gain. The FLOWERING LOCUS T genes in bread wheat have been identified as important regulators of this response, with detailed characterisation of FT1, FT2 and FT3 being previously reported. Here we focus on FT4 and identify it as a regulator of plant architecture, influencing spikelet and tiller number, along with plant height and flowering time. We characterise the distribution of FT4 alleles from the sequenced Watkins collection and develop novel genetic and transgenic germplasm to characterise the molecular genetic pathways that FT4 is acting in. Here we determine how FT4 is regulating spikelet number during the early stages of reproductive development and how this is uncoupled from later flowering time regulation. We have validated these pathway interactions, genetically and also through molecular genetic characterisation including expression and protein interaction assays. Furthermore, we have also assessed the action of FT4 under different environmental cues and can therefore identify potential environments for specific alleles.

P304 - Physiological and root architectural responses to flowering-stage drought in a wheat line carrying a thinopyrum group 3 chromosome

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Abstract

The flowering stage represents a critical period of sensitivity to drought stress, during which wheat grain yield can be markedly reduced. The narrow genetic base of cultivated wheat further limits the discovery and deployment of favorable allelic variants for breeding cultivars resilient to climate stress.

A homoeologous substitution line was developed in which wheat chromosome 3D was replaced by a group 3 chromosome pair derived from a *Thinopyrum* intermedium × *Th. ponticum* artificial hybrid. The substitution was identified using in situ hybridization and genotyping-by-sequencing-based coverage analysis. Functional compensation of chromosome 3D by the introgressed chromosome pair was evidenced by grain yield and fertility levels comparable to those of the wheat parental cultivars ('Mv9kr1' and 'Mv Karizma') under both field and controlled conditions. The substitution line displayed a semidwarf growth habit associated with the presence of the dwarfing alleles *Rht8* and *Rht2*.

Automated shoot phenotyping during a 10-day water-withdrawal treatment imposed at flowering demonstrated maintenance of photosynthetic activity and delayed chlorophyll degradation. These physiological responses were corroborated by Normalized Difference Vegetation Index (NDVI) and modified Normalized Difference Index (mND705) measurements, alongside moderate induction of stress-responsive genes, indicating controlled activation of protective pathways.

Under drought stress, the substitution line also developed thicker roots with increased root volume relative to the wheat parents, resulting in a reduced surface-to-volume ratio. This alteration in root system architecture may improve water storage capacity and thereby mitigate yield losses under water-limited conditions.

The research leading to these results received funding from the Hungarian National Research, Development, and Innovation Office under Grant Agreement No FK145848 and TKP2021-NKTA-06 and from the EU Horizon Europe project COUSIN (Nr. 101135314). BV, PM, AC and KK have received funding for their work through the MTA Bolyai János Research Grant (BO/00384/23/4, BO/00206/24/4, BO/00416/23 and BO/00013/25/4).

P305 - Climatic risk patterns for drought and heat stress in Spanish spring wheat: a phenology driven framework for breeding

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Abstract

Drought and heat stress are increasingly recognized as the two major abiotic threats to spring wheat production in the Mediterranean environment, particularly in the rainfed systems dominating key agricultural regions in Spain. This study evaluates the relative importance and probability of drought versus heat stress across three Autonomous Communities in northern, central and southern Spain (Aragón, Andalucía and Castilla La Mancha), capturing a wide range of pedoclimatic conditions, using a climate driven, phenology aligned approach. Historical GENVCE network data—an extensive platform for cereal variety evaluation—helps frame the regional stress patterns observed within environments widely used for cultivar testing and benchmarking. These data provide reliable sowing, heading and harvest dates that allow meteorological data to be anchored to crop development stages. This alignment enables a biologically meaningful assessment of when and how frequently crops encounter water deficits, extreme temperatures, or both.

Daily meteorological variables—including precipitation, temperatures, and derived drought indicators—were obtained from ERA5 Land reanalysis and complemented with available weather station datasets. By coupling these variables with observed phenology, we quantified the probability of drought and heat events, and examined how these stressors impact spring wheat yield. This framework provides a basis for comparing the likelihood and impact of heat waves versus moisture deficits during three relevant periods: pre-booting, booting to grain setting, and grain filling.

The poster presents preliminary results highlighting emerging regional stress typologies, including the relative probability of drought versus heat stress at different crop stages. These findings provide an initial basis for discussing how breeding and management strategies can target the most frequent and impactful stress scenarios under ongoing climatic change.

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P306 - Are winter wheat yields warming up?

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Abstract

As in other winter crops, springtime flowering in wheat is promoted by the colder temperatures experienced during previous months through the process of vernalization. Overwinter, critical decisions occur in the developing wheat meristem which will determine the plant's capacity for yield at harvest. Globally, warmer winter temperatures are predicted to have a significant and negative impact on crop yields. Yet, there is some indication that winter warming could increase yields in UK wheat. This is, however, largely untested. Furthermore, it remains unclear how warming impacts physiology at the meristem and plant level, and what molecular mechanisms underpin these traits.

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

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

P307 - Wheat physiology at CIMMYT - 55 years' legacy and the way forward

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Abstract

Wheat-a key crop for food and nutritional security globally-is improved by public and private sectors. Among them, CIMMYT plays an indispensable role by developing elite lines with strategic traits for yield potential and stress tolerance. Wheat Physiology at CIMMYT was first established in 1970 and has contributed to the CIMMYT mission in different ways. Among these are (i) Identifying and refining traits with high breeding value, providing breeding-ready tools (donors, markers, high throughput phenotyping methods and physiological insights) incorporated into breeding pipelines; (ii) Bridging the "death valley" between basic and applied wheat research through widescale networks (IWYP and HeDWIC) to tap expertise from academia and facilitate the translate cutting-edge technologies into products for farmers' field; (iii) Designing and implementing physiological pre-breeding for genetically complex traits to improve yield potential and facultative response to heat and drought stress. These efforts have generated diverse tools that support evidence-based decision-making in breeding pipelines, while significantly advancing our understanding of how to raise yield under variable and stress-prone environments. Over the past decade, physiologically enhanced pre-breeding nurseries have been distributed worldwide, delivering far-reaching impact across national breeding programs. Key milestone research outputs and the current strategic direction of CIMMYT Wheat Physiology will be presented to highlight new collaborative opportunities to advance food and nutrition security through resilient wheat-based food systems.

P308 - Explicating the relationship between stay-green character, drought tolerance, and yield stability in pakistani wheat genotypes

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Abstract

Wheat (*Triticum aestivum* L.) is a staple and major crop in the cereal family. It plays a pivotal role in global food challenges and a primary source of food for billions of people around the world. The demand for staple grains is increasing in tandem with population growth. Drought, as a prevalent abiotic stress, reduces yield significantly by altering rainfall patterns, causing water scarcity, and disrupting plant growth cycles. Stay-green trait serves as yield stability in drought-prone areas. The stay-green characteristics help plants to survive through the stressed environment by delaying leaf senescence and maintaining green leaves for longer after flowering. This experiment led to the evaluation of drought-tolerant wheat genotypes and their yield performance under different levels of drought. The research critically analyzed the stay-green characteristics of wheat varieties. A study was conducted in the greenhouse in 2024-2025. This study evaluated ten Pakistani wheat genotypes for their stay-green trait and drought tolerance under controlled, moderate, and severe drought conditions. The experiment involved a randomized design with three replications of each treatment. Recommended agronomic practices were applied uniformly, and genotypes were harvested separately for yield data collection. Morphological and yield traits were measured, and SSR markers were used for molecular analysis. Significant variation was observed among wheat varieties for yield traits and stay-green under drought stress. Genotypes G3, G5, G6, and G7 maintained higher chlorophyll and grain yield under stress. Correlation analysis revealed the strong positive relationship between stay-green and yield related traits. Cluster analysis was performed to validate the genotypes based on stress tolerance index. Principal component analysis showed that the first two components explained over 56% of the total variation. Molecular characterization using SSR markers revealed polymorphism among genotypes. Xgwm99, Xgwm617 and Xgwm111 showed high polymorphism, validating their potential for association with stay-green and chlorophyll retention traits under drought stress. The findings support the use of stay-green as a selection trait for breeding drought-resilient wheat.

P309 - How will future climate change affect wheat yield and quality?

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Abstract

In the coming decades, climate change will bring higher atmospheric CO₂ concentrations as well as warmer air temperatures. Despite their joint presence under future climate conditions, the combined effects of elevated CO₂ (eCO₂) and elevated temperature (eT) on wheat performance remain understudied¹. When tested separately, eCO₂ increases wheat yield while diminishing grain nutritional values^{2,3}, whereas eT decreases yield⁴ with undetermined effects on grain nutrition. Whether there are wheat varieties that can take advantage of the extra CO₂ and/or temperature to achieve better performance in yield and/or quality is unclear.

To address the currently limited understanding of the combined effects of eCO₂ and eT in wheat, we conducted a 2-year experiment and subjected 86 diverse Australian wheat lines under future climate conditions (800 ppm CO₂ and 5°C warming; projected climate conditions by 2100) and gained early mechanistic insights using several high-throughput phenotyping technologies. In both years, we observed a consistent yield reduction of 17±2% under future climate conditions. In the first year, high-throughput phenotyping of photosynthetic capacity showed V_{cmax}; 25 could predict lower yield loss across wheat lines. This suggests higher ecophysiological plasticity contribute to yield resilience under future climate conditions.

Additionally, we also observed that the 5°C warming completely offset the seed quality dilution effect of eCO₂ for both seed nitrogen and iron concentrations. However, seed zinc concentrations remain negatively affected by the combined treatment of eCO₂ and eT by similar magnitudes to (8.2%) eCO₂ alone. This suggests that zinc-specific uptake and/or allocation may be particularly vulnerable under future climate conditions, thus requiring future investigations to ensure human food security.

P310 - Future-proof crops: uncovering effects of future climate stresses on root ideotypes and impact on wheat grain nutritional quality

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Abstract

There is an urgent need to develop climate-resilient crops and agricultural systems to produce more food that is also more nutritious in a changing climate. The major driver of climate change is the rapid increase in atmospheric carbon dioxide (CO₂) concentration due to anthropogenic activities. These recent increases, along with the projected CO₂ concentrations (over 550ppm), represent a surge in an essential resource, surpassing anything plants have encountered. It has been understood for over two centuries that elevated CO₂ (eCO₂) concentrations enhance plant growth. This phenomenon, known as the 'carbon fertilization effect', influences plant physiology and metabolism, driving increased photosynthesis and yield. Despite potential crop productivity benefits, eCO₂ is expected to alter plant elemental stoichiometry, with implications for grain quality such as protein, iron, and zinc content in C3 staple crops like wheat, with negative consequences on nutritional quality.

Current crop models emphasize on photosynthetic gains while neglecting turnover-related processes and grain nutrient dynamics. The extent and mechanisms of CO₂ driven changes in grain nutrient density remain poorly understood. At the same time, roots, critical for stress-sensing and nutrient-uptake are underexplored as targets for climate-resilience due to phenotyping bottlenecks. While individual stresses have been studied extensively in model plants, responses to combined stresses in major crops are largely unknown. Interactions among eCO₂, rising temperatures, and water deficits triggers unique responses. Despite the growing urgency, crop breeding mainly prioritise yield with limited emphasis on grain quality. Using current and projected future climate scenarios, this project aims to investigate how eCO₂, heat, and water stress interact to influence root-soil interactions and ultimately the nutritional quality of wheat grains, and how these mechanisms are controlled genetically.

Work is underway to characterise wheat roots structural changes and gene expression patterns under combined effects of CO₂, heat and water stress, while, simultaneously, profiling grain minerals and identifying genetic drivers of grain nutritional changes and antinutritional compounds. The findings from this work will identify genetic targets to accelerate engineering of climate-resilient and nutrient-rich wheat. This cutting-edge research is timely for building sustainable food systems and ensuring a nutrition-secure future for a growing population in a rapidly changing climate.

P311 - Understanding *Tilletia* spp. population structure and virulence to support wheat resistance breeding

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Abstract

Wheat is a major source of calories and protein worldwide, yet its production is threatened by biotic stresses. In Sweden, increasing organic wheat cultivation in combination with a reduced number of seed treatment options has coincided with rising incidences of common bunt (CB), caused by *Tilletia caries* (syn. *T. laevis*), as well as dwarf bunt caused by *Tilletia controversa*. These diseases can significantly reduce grain quality and cause yield losses of up to 40%. Organic production relies on resistant cultivars, yet knowledge of pathogen diversity and virulence is limited, constraining breeding efforts.

To address this, CB-infected wheat spikes were collected from Swedish farmers' fields and examined morphologically for species identification. Additional *Tilletia* spp. samples from across Europe were incorporated to expand the population analysis. Reference samples of each species were de novo sequenced using long-read technology, while the remaining isolates underwent Illumina resequencing. Population genomic analyses revealed substantial genetic diversity among lineages and clear regional structuring, reflected in distinct epidemiological zones and providing insight into pathogen distribution and evolution.

A virulence spectrum assay was conducted using a CB differential set (Bt0-Bt15 and BtP) combined with wheat accessions carrying known race-specific resistance genes (R-genes), as well as Swedish winter wheat cultivars, including resistant lines Stava, Festival, and Hallfreda, and susceptible cultivars Brons and Kranich. Preliminary results indicate common virulence against Bt2, Bt7, and Bt13, whereas no virulence was detected against Bt1 and Bt11. Some lineages showed high infection rates even on cultivars previously considered resistant. To account for potential genotype-by-environment interactions, these virulence patterns are now being confirmed through repeated screenings under field conditions.

These results provide a comprehensive overview of *Tilletia* spp. population structure, genetic diversity, and virulence in Sweden and Europe. The results highlight the importance of regionally tailored breeding to match local pathogen populations. In practice, deploying diverse resistance sources and monitoring pathogen variation will be key to maintaining effective wheat breeding programs toward durable bunt resistance and supporting sustainable management of common bunt.

P312 - CResWheat: advancing climate-resilient spring wheat breeding in the Nordic Region

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Abstract

The CResWheat project advances climate-resilient spring wheat breeding by identifying genetic resources for disease resistance, drought tolerance, and other adaptive traits suited to Nordic environments. This work supports sustainable wheat production under challenges such as short growing seasons, increasing pest and pathogen pressure, and more frequent extreme weather events.

Between 2021 and 2023, 24 field trials were conducted across seven locations in four Nordic countries, evaluating over 20 traits in ~200 European and exotic elite spring wheat lines. Several quantitative trait loci associated with these traits were identified and are being implemented in breeding programs to support marker-assisted selection. Additionally, the wheat panel was screened at the seedling stage for resistance to prevalent and emerging stem rust and yellow rust races at the Global Rust Reference Center. In parallel, isolates of *Parastagonospora nodorum* (*Septoria nodorum* blotch) and *Pyrenophora tritici-repentis* (tan spot) were collected from Finland, Norway, and Sweden for toxin fingerprinting and virulence assays. Separately, a subset of Nordic breeding lines and cultivars was subjected to early-season drought stress at the LemnaTec high-throughput phenotyping facility at IPK Gatersleben, Germany, and evaluated for agronomic and yield-related traits. Metabolomic profiling revealed key metabolic pathways associated with drought tolerance, providing potential targets for breeding.

Donor lines were identified for resistance to major wheat diseases, including yellow rust, leaf rust, stem rust, *Septoria tritici* blotch, powdery mildew, *Stagonospora nodorum* blotch, and tan spot, as well as pre-harvest sprouting. Strategic crosses have been developed to introduce resistance to these diseases, pre-harvest sprouting, and nematode pests into elite germplasm. The resulting populations will be evaluated in multi-environment trials across the Nordic region and Estonia. In parallel, a newly assembled collection of historic landraces and cultivars is being screened for resistance to the gout fly (*Chlorops pumilionis*), an emerging threat to Nordic spring wheat.

CResWheat emphasizes collaboration and knowledge sharing across diverse environments, field sites, and germplasm resources, while building capacity by training PhD students and postdoctoral researchers, ensuring a new generation of experts ready to address future challenges in wheat breeding.

P313 - Characterizing racial diversity and virulence profiles of *Puccinia graminis* f. sp. tritici on durum wheat genotypes from the Mediterranean.

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Abstract

The re-emergence of wheat stem rust disease, caused by *Puccinia graminis* f. sp. tritici (Eriks and E. Henn.) (Pgt), has been recently reported in both Europe and North Africa. In Tunisia, the disease has been detected sporadically since 2018. Disease monitoring and sampling over the 2021 and 2022 cropping seasons revealed the predominance of three races, namely TTRTF (Clade III-B), TKKTF (Clade IV-F), and TKTTF (Clade IV-B). The limited genetic diversity of the Tunisian Pgt population and the low incidence of the disease in the field suggest that this fungus most likely originated from exotic incursions. The virulence profile of the recently emerged population, combined with the limited number of characterized resistance sources in durum wheat (*Triticum turgidum* L., ssp. durum (Desf.) Husn.) germplasm, poses a serious threat to durum wheat producing countries.

A seedling-stage evaluation was conducted on 137 Mediterranean wheat genotypes, predominantly durum wheat, to assess their resistance to four stem rust races: TTKTT, TTKSK, TTRTF, and TKKTF. These races were selected to reflect both the most prevalent races in Tunisia as well as the global threat posed by the Ug99 lineage.

Although 24% of the genotypes exhibited resistant responses, phenotypic screening showed significant variation in seedling responses to the different races. Specifically, 27% and 30% of the genotypes were resistant to TTRTF and TTKSK, whereas only 17.5% and 18% exhibited resistance to TKKTF and TTKTT, respectively. Only 9.4% of genotypes (n = 13) exhibited resistance or intermediate responses to all four tested races. Wheat accessions from Portugal, France, and Spain showed the highest resistance frequencies, ranging from 30% to 50%.

This study highlights the importance of Mediterranean durum wheat accessions as sources of novel and diverse genetic resistance to the re-emergent predominant races.

P314 - Determination of physiological races of puccinia striiformis f.sp. tritici in Iran

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Abstract

The stripe (Yellow) rust of wheat is one of the wrecker diseases in Iran. Since 1993 several epidemics have occurred in Iran causing the breakdown of widely utilized sources of resistance in wheat cultivars. In this study thirty-four isolates of stripe rust were collected from different parts of Iran during 2022-2025, and after purification and increase spores were race analysis with 45 lines/cvs. of standard set in seedling stage in greenhouse condition. Infection types were assessed on a 0-9 scale 16 and 18 days after inoculation using a scale similar to that described by McNeal et al. (1971). Infection types (ITs) 7 to 9 were regarded as virulent (susceptible) and less than 7 are avirulent. Pathotypes 238E238A+,Yr27 (from Brojerd) and 239E239A+ (from Kodaafrein) were more aggressive during this study. Pathotype 14E6A+ (Mashhad3) was less aggressive. Plants with gene/s Yr5,Yr15 and Yr24 were resistant to all pathotypes. Virulence on plant with gene/s Yr2, Yr6, Yr7, Yr9, Yr25, Yr27,YrSD and YrA were more common, which are detected in greenhouse condition. Aggressiveness for plants with gene Yr32 was detected in Mashhad and karaj. Virulent for Yr32 was common to the most of isolates.

P315 - Integrating pest management, disease resistance, cadmium low uptake, and UAV phenomics for advancing sustainable wheat production in Nordic Environments

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Abstract

Sustainable wheat production in the Nordic region requires coordinated research addressing emerging pests, persistent fungal pathogens, soil-related contaminants, and improved phenotyping technologies. As a research assistant in the wheat breeding program at Alnarp, my work integrates multiple research disciplines to support the development of resilient, high-performing spring and winter wheat varieties. A major component of my work focuses on gout fly (*Chlorops pumilionis*), an increasingly important pest in northern Europe. Our team is the first research group to successfully rear gout flies under controlled conditions, enabling systematic studies of their life cycle, host interactions, and damage patterns. This capability allows us to evaluate resistance responses across diverse spring wheat genotypes and develop standardised phenotyping protocols suited to Nordic climates. This pioneering effort strengthens the foundation for long-term pest-resistance breeding.

In parallel, I contribute to extensive fungal disease screening in both spring and winter wheat. This includes evaluating CRes wheat-PPP lines against major Nordic pathogens and assessing resistance to common bunt (*Tilletia caries*) in winter wheat. These activities support genetic diversity utilization and the identification of durable resistance sources.

Another key area of my work is the cadmium-reduction project, in which we investigate genetic and agronomic factors that limit cadmium accumulation in winter wheat, an essential component of food safety and grain-quality improvement.

To complement biological and agronomic studies, I work as a certified drone pilot and UAV data analyst, collecting multispectral and RGB imagery for NDVI, canopy temperature, biomass estimation, spatial variability, and early stress detection. These digital phenotyping tools enhance the precision and efficiency of field evaluations and support phenomics and enviromics applications.

Together, these integrated research activities contribute to advancing innovative wheat breeding, strengthening pest and disease resilience, improving grain quality, and supporting the development of climate-adapted, sustainable wheat production systems in the Nordic region.

P3316 - Identification of septoria nodorum blotch sensitivity genes in U.S. Great Plains hard winter wheat

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Abstract

The necrotrophic fungus *Parastagonospora nodorum* is the causal agent of septoria nodorum blotch (SNB) of wheat. *P. nodorum* effectors recognition by wheat sensitivity genes leads to susceptibility. Limited information exists on SNB sensitivity genes in contemporary U.S. hard winter wheat (HWW). The objective of this study was to determine the prevalence of SNB sensitivity genes in 619 HWW breeding lines and cultivars. This HWW panel was evaluated against five *P. nodorum* isolates and five necrotrophic effectors (NEs) SnToxA, SnTox1, SnTox3, SnTox267, and SnTox5, and genotyped using genotyping-by-sequencing (GBS) and diagnostic Kompetitive-allele specific PCR (KASP) markers for the sensitivity genes Tsn1, Snn1, and Snn3. Genome-wide association studies (GWAS) were conducted using phenotypic data, 34357 GBS-single nucleotide polymorphism (SNP) markers, and KASP markers linked to Tsn1, Snn1, and Snn3. Evaluations against *P. nodorum* isolates showed that 40-67% of the genotypes were susceptible. Toxin infiltration assays showed that 54%, 2%, 37%, 13%, and 15% of the genotypes were sensitive to SnToxA, SnTox1, SnTox3, SnTox267, and SnTox5, respectively. The diagnostic KASP markers for Tsn1, Snn1, and Snn3 showed accuracy of 98%, 75%, and 92% in predicting sensitivity/insensitivity to the corresponding effectors SnToxA, SnTox1, and SnTox3, respectively. The GWAS confirmed the presence of the known sensitivity genes Tsn1, Snn1, Snn2, Snn3, and Snn5. In addition, GWAS identified other previously uncharacterized loci to be associated with responses to *P. nodorum* isolates and NEs. Of which, Qsnb.osu-2AS on chromosome 2AS was found to be associated with responses to all five isolates. Eliminating SNB sensitivity genes will enhance SNB resistance in wheat.

P317 - Addressing the emerging threat of gout fly (*Chlorops pumilionis* Bjerk.) to sustainable spring wheat production in Northern Europe

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Abstract

The gout fly (*Chlorops pumilionis* Bjerk.) has recently shifted from a sporadic pest to a recurring and economically significant threat to cereals in Northern Europe, with particularly severe impacts on spring wheat. Yield losses can be substantial, yet the existence and genetic basis of host plant resistance remain unknown, representing a critical knowledge gap for the development of sustainable integrated pest management strategies. Current control options are limited, and climate change is expected to further facilitate pest establishment and increase outbreak frequency.

We are therefore establishing the scientific foundation for the development of sustainable long-term management strategies against the gout fly. This is achieved through four complementary and integrated approaches:

- (1) identifying resistance and tolerance to gout fly in spring wheat germplasm;
- (2) developing laboratory rearing systems and behavioural assays to enable robust and controlled phenotyping;
- (3) evaluating natural enemies and alternative control options, including products approved for both conventional and organic production systems; and
- (4) applying genomic, transcriptomic, and population genetic analyses to advance understanding of host-pest interactions and regional population structure.

In 2025, a panel of 200 European spring wheat accessions was evaluated under natural infestation in field trials in Kristianstad (Sweden) and Horsens (Denmark). Of these, 30 genotypes are modern European cultivars or advanced breeding lines, while the remaining 170 are European genebank accessions, including cultivars released before 1960, traditional landraces, and selected wheat-rye translocation lines.

Variation in sowing dates resulted in a higher proportion of escape plants in Sweden, whereas infestation pressure was more uniform in Denmark. Despite environmental variation, several genotypes consistently exhibited low damage across locations. All accessions have been genotyped, and follow-up multi-environment trials are planned to identify genomic regions associated with resistance and/or tolerance. Genotypes displaying low gout fly infestation in the field are currently being evaluated under controlled conditions to assess oviposition preference and larval survival.

Together, these efforts provide a foundation for resistance breeding and integrated pest management strategies aligned with European sustainability goals.

P318 - Genetic loci underlying resistance to *ustilago tritici* in the spring wheat variety carberry

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Abstract

Loose smut [*Ustilago tritici* (Pers.)] of wheat (*Triticum aestivum* L.) is a seedborne disease that typically occurs at low incidence but can be common in certain wheat growing regions of the world. The genetics of loose smut resistance is not well studied. The Canada Western Red Spring variety Carberry has moderate resistance to loose smut. Developing loose smut resistant wheat cultivars is an environmentally safe approach, especially for organic production where chemical treatments are not allowed. This study investigated genomic regions associated with loose smut resistance in the Canadian spring wheat variety Carberry. A doubled haploid population of 180 Carberry x Vesper lines was evaluated against the *U. tritici* races T10 and T39 at Swift Current, SK from 2021 to 2023. A linkage map was constructed using the 90K Infinium SNP array, and Quantitative Trait Loci (QTL) analysis was performed with MapQTL 6.0. Three genomic regions associated with loose smut resistance were identified from Carberry on chromosomes 2B, 4B, and 6B. In addition, a QTL contributed by the cultivar Vesper on chromosome 7B was also effective against the tested races. The 2B and 6B QTL conferred broad spectrum resistance to both races, whereas the 4B QTL provided race specific resistance to T39. These QTL accounted for 5.8-12.7% of the phenotypic variance observed in the loose smut incidence. The 6B QTL was the most stable, providing resistance across all three test years and to both *U. Tritici* races, making it a strong candidate for resistance breeding in wheat.

P319 - GWAS analysis in an elite durum wheat panel uncovers stable QTLs for fusarium head blight (FHB) spike symptoms and deoxynivalenol (DON) content

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Abstract

Fusarium head blight (FHB) is among the most damaging diseases of wheat worldwide, reducing yields and compromising grain safety through the accumulation of mycotoxins such as deoxynivalenol (DON). While several quantitative resistance sources have been identified in bread wheat (*Triticum aestivum*), progress in durum wheat (*Triticum turgidum* ssp. *durum*) has been limited due to its generally high susceptibility. This study reports new quantitative trait loci (QTLs) for FHB resistance in durum wheat, identified through a genome-wide association study (GWAS) conducted over two growing seasons (2015-2016) and on the combined dataset.

The analysis involved 111 elite accessions representing European diversity, largely from French, Italian, CIMMYT and ICARDA breeding programs, and evaluated for incidence (INC), severity (SEV), disease index (INX) and DON content. Nineteen QTL clusters were detected, five of which were prioritized for their reliability and explanatory power: QcIsINC.INX.2B and QcIsSEV.INX.7B, associated with INC, SEV and INX, and three DON-specific loci (QDON.ubo-2A.1, QDON.ubo-5A.1 and QDON.ubo-6B.1) significant in at least two trials.

Haplotype analysis within these regions enabled the development of three KASP markers per QTL cluster, which were validated across the germplasm panel. Notably, haplotypes conferring partial resistance and reduced DON accumulation were traced to French breeding programs, which historically incorporated North American durum germplasm (Canada, North Dakota) carrying useful resistance alleles.

Candidate genes within the haplotype intervals included protein kinases, NBS-LRR resistance genes and redox-related proteins, supporting their potential involvement in FHB response. The DON-specific QTLs contained gene models plausibly linked to mechanisms reducing mycotoxin accumulation.

Overall, this study identifies novel genetic sources of resistance to FHB and DON in durum wheat, highlights genomic regions associated with key defence pathways, and provides validated haplotype-based KASP markers for breeding. These resources will support more efficient development of durum wheat varieties with improved FHB tolerance and lower DON contamination.

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P320 - Phenotypic variation in disease pressure on wheat is driven by genetic variation in rust populations across different environments

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Abstract

Wheat production worldwide is often affected by biotic stressors, such as phytopathogens, which can lead to significant yield losses. The rusts of the Pucciniales family play a decisive role in this, as they are obligate biotrophic fungi, with yellow rust (*Puccinia striiformis*) and leaf rust (*Puccinia triticina*) posing the main threat to cereal production. As outbreaks occur periodically with temporal and spatial variations, the five-year RustHealth project aims to investigate the interactions between fungal and wheat genotypes at thirteen locations across Germany.

In the first two seasons, 200 elite lines were sown in replicates at all 13 locations. Disease symptoms of natural yellow and leaf rust infestations were recorded at multiple time points to monitor infection severity and intensity, which was done by calculating the area under the disease progress curves and the maximum infection level, respectively. To monitor genotypic variations in rust populations, yellow and leaf rust spores were collected from susceptible wheat genotypes at each location. Combining phenotypic and genotypic datasets, genotype-wheat x genotype-rust x environment relationships were modelled and location-specific GWAS were calculated.

The results from the first two years indicate significant spatial and seasonal variations in disease pressure. While leaf rust infestations varied mainly due to environmental factors in different locations, yellow rust infestations were equally influenced by the sampled environments and wheat genotypes. This is also reflected in the population structure analysis, which shows that yellow rust populations differ less between locations than leaf rust populations. Nevertheless, the genetic diversity of the yellow and leaf rust populations explained most of the variance found in the phenotypic data at the different locations, and was therefore implemented in the GWAS analysis, resulting in one leaf rust QTL and two yellow rust QTLs. Our results indicate interactions between genotype rust, genotype wheat and environment (Grust x Gwheat x E), which contribute to a better understanding of spatial and temporal variations in infection patterns and thus improve agricultural management strategies.

P3321 - Genetic dissection of leaf rust, yellow rust and STB resistance in biparental mapping populations from *Triticum turgidum* landraces x modern cultivars

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Abstract

Durum wheat (*Triticum turgidum* subsp. durum) is a major staple crop increasingly exposed to rising food demand and evolving biotic constraints. Understanding the genetic basis of disease resistance is crucial for breeding resilient, high-yielding cultivars. Over 2,500 tetraploid wheat accessions from the Global Durum Genomic Resources were evaluated across multi-year field trials (2018-2021) for resistance to key fungal pathogens, including leaf rust (LR), yellow rust (YR), and septoria tritici blotch (STB). Several accessions—such as the landraces Trinakria and Kyperounda, and the cultivar Monastir—showed stable and broad-spectrum resistance.

These resistant lines were crossed with susceptible elite cultivars (Svevo, Meridiano, Kofa) to generate biparental populations in a NAM-like design. Each population (100-200 RILs) was genotyped using the wheat 25K Infinium iSelect SNP array, phenotyped in 2024 in Italian nurseries, and subjected to QTL mapping. For LR, loci were detected on chromosomes 1A, 1B, 2B, 3B, 4A, 4B, 5B, and 6B, several of which were stable across environments. For YR, QTLs mapped to 1A, 2B, 3B, 4B, 5B, 6A, and 7B; notably, QTLs on 3B and 4B overlapped with known resistance regions, suggesting shared or linked determinants underpinning partial broad-spectrum resistance. For STB, QTLs were identified on 2A, 2B, 3A, 5B, 6A, 6B, 7A, and 7B. Several QTLs corresponded to regions previously highlighted through GWAS in durum wheat, providing strong validation across complementary mapping approaches. Haplotype analysis across the full Global Durum Genomic Resources dataset further resolved allelic diversity within these regions, revealing strong associations between resistance and specific parental haplotypes traceable to defined germplasm groups. This integrated approach confirmed the robustness and transferability of major loci and underscored the value of landrace-derived alleles for durable resistance. Diagnostic KASP® markers were developed for validated loci, enabling precise differentiation of resistant and susceptible haplotypes and supporting fine mapping, candidate gene identification, and marker-assisted breeding.

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P322 - Genomics-enabled wheat breeding to accelerate development of dwarf and common bunt resistant cultivars

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Abstract

Dwarf bunt caused by *T. controversa* and common bunt caused by *T. laevis* Kühn and *T. tritici* (Bjerk.) Wint are two destructive diseases of bread wheat that cause significant yield losses and quality reduction. Both diseases are constraints to global organic wheat production. Host resistance is necessary to protect against infection within these production systems as chemical seed treatments are prohibited. Two US wheat breeding programs at University of Idaho and Utah State University have deployed the current genomic approaches, QTL mapping, chemical mutagenesis, and NGS to identify QTL, candidate genes, and molecular markers underlying resistance to both diseases. Two major QTL on chromosomal arms of 6DS and 6DL were identified in a known resistant cultivar 'UI Silver' and a resistant elite line 'IDO835', the other major QTL on chromosomal arm 7DS was identified in a resistant elite line 'IDO444'. The candidate genes for the three QTL were analyzed using different sequence data (exome capture, PACBio, and Ae. Tauschii R gene) and knock-out mutants. The candidate genes were characterized in a set of resistant landraces, cultivars, and lines using the identified molecular markers. Deployment of the candidate genes will be accelerated in ongoing projects through gene editing and cloning.

P323 - Genomic insights into leaf rust resistance: leveraging global germplasm for durum wheat improvement

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Abstract

Durum wheat production is increasingly threatened by *Puccinia triticina*, the causal agent of leaf rust, whose rapidly evolving populations undermine deployed resistance genes. The continuous emergence of new strains requires breeders to explore durable resistance sources within germplasm. To bridge the gap between exotic genetic resources and elite cultivars, pre-breeding efforts are essential to characterize and introgress novel resistance alleles from landraces into adaptable breeding lines.

A comprehensive genetic survey was conducted using two globally representative tetraploid wheat panels: the Global Durum Panel (GDP) and the Tetraploid Global Collection (TGC), comprising 500 cultivars (DWC) and 1,000 landraces (DWL). These panels were assessed in a multi-environment field study across 10 Mediterranean locations (2019-2021), focusing on infection type (IT) and disease severity (SEV). Broad-sense heritability for both traits exceeded 60% across all environments. Principal component analysis (PCA) identified distinct environmental clusters indicative of similar selection pressures.

A Genome-Wide Association Study (GWAS) was performed using various models, incorporating a kinship matrix, for both single and multi-environment analyses. Additionally, a differential analysis between DWC and DWL was carried out, revealing a distinct distribution of resistance alleles. The DWC analysis revealed 107 Marker-Trait Associations (MTAs), 41 of which were identified across single environments, both traits and were further validated through multi-environment analyses. Notably, three highly significant regions were detected: two on chromosome 4B and one on 6B. These were consistently detected in 5 and 6 different environments, respectively, as well as in both multi-environment models, with LOD values reaching 31. Regarding DWL, the study uncovered 106 MTAs, with 18 associations shared across various environments and phenotypic traits. Crucially, two regions on chromosomes 1B and 7B were identified across all tested environments and traits, including the multi-environment analysis, with LOD scores up to 7.7. A comparison showed 21 overlapping regions between DWC and DWL, alongside unique regions of interest for each subset.

For the most stable MTAs, a phenotype-correlated haplotype analysis was conducted to pinpoint the specific allelic combinations associated with disease resistance, propaedeutic to KASP marker design, to provide a powerful toolkit for modern genomics-assisted breeding.

P324 - Wax biosynthesis genes and lncRNA Regulation in durum wheat resistance to fusarium head blight

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Abstract

Spike damage caused by *Fusarium graminearum* severely impacts wheat yield and grain quality due to mycotoxin contamination. The Langdon (Dic 3A) 10 durum line carrying the QTL Qfhs.ndsu 3AS from *Triticum turgidum* ssp. *dicoccoides* confers Type II resistance to *Fusarium* head blight (FHB). Transcriptomic analyses of resistant [Langdon (Dic 3A)-10, LND] and susceptible [Langdon, LN] genotypes identified candidate genes for the QTL and characterized metabolic pathways involved in the response to infection. Two genes associated with cuticular wax biosynthesis, O acyltransferase (WSD1, 2A) and Resurrection1 (RST1, 3A), were analyzed with RST1 located within the resistance conferring segment.

Genomic sequences of WSD1 and RST1 from Svevo (durum) and Zavitan (*dicoccoides*) were compared, along with their protein products predicted *in silico* using AUGUSTUS. Transcription levels of both genes were quantified by qRT-PCR at three time points post-inoculation. In addition, flag leaf and glume sections from LN and LND at 72 h post inoculation were analyzed by scanning electron microscopy.

Expression assays demonstrated a significant induction of WSD1 in LND at 6 h post inoculation, followed by a decline at 48-72 h, while no significant differences in RST1 expression were observed at any of the analyzed time points. Amino acid sequence comparison revealed only one substitution for WSD1 between the A and B genomes. For RST1, gene prediction identified a full-length protein in Svevo, whereas the Zavitan ortholog exhibited multiple substitutions and length variations that likely compromise protein integrity. Scanning electron microscopy revealed increased wax deposition on the abaxial leaf surface of LND at 72 h.

In parallel, a long non coding RNA (lncRNA STRG.246021.1), located within the second intron of WSD1, was characterized. STRG.246021.1 exhibited higher expression in LND at 6 and 48 h, showing strong positive correlation with WSD1 expression ($p \leq 0.001$; $r = 0.92$). These findings suggest that STRG.246021.1 may act as a positive regulator of WSD1, enhancing cuticular wax accumulation and reinforcing physical barriers against fungal invasion.

Together, our results highlight the coordinated action of coding and non coding transcripts in the early defense response of durum wheat.

P325 - Purple pericarp wheat reduces host location, feeding efficiency, and progeny development of the granary weevil *Sitophilus granarius* (L.)

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Francesco Romaniello ⁽³⁾ - ***Maria Assunta Acquavia*** ⁽⁴⁾ - ***Carmela Gerardi*** ⁽⁵⁾ - ***Marco Pistillo*** ⁽¹⁾ -
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Abstract

Post-harvest infestations by the granary weevil, *Sitophilus granarius* (L.) represent a major threat to global wheat storage. With increasing restrictions on chemical insecticides, developing resistant wheat genotypes represents a promising but still poorly explored resource in this context. This study investigates the biological and genetic determinants of wheat-*S. granarius* interactions using a unique set of Heterogeneous Inbred Families (HIFs) of durum and bread wheat segregating for purple (anthocyanin-enriched) and yellow kernel pigmentation.

Transcriptomic analysis of developing kernels revealed a significant transcriptional reprogramming in purple genotypes, characterized by the up-regulation of the phenylpropanoid and flavonoid pathways (e.g., F3H, DFR, and MYB/bHLH factors). Metabolomic profiling confirmed a marked enrichment of anthocyanins and phenolic derivatives in the outer grain fractions of pigmented kernels.

The attractiveness of pigmented and yellow kernel genotypes towards *S. granarius* adults was evaluated in two-choice pitfall bioassays. The insect fitness on intact grains was evaluated by calculating development parameters (e.g. progeny production, mean development time). Moreover, for each genotype the Susceptibility Index (S.I.) was calculated based on the development of progeny and the average development time of the first generation. The feeding response and food utilization efficiency by adult insects was also investigated by calculating nutritional indices in whole flour disk bioassays.

In two-choice pitfall bioassays yellow kernels were significantly more attractive towards *S. granarius* adults than purple kernels. In susceptibility bioassays, the S.I. of pigmented wheat genotypes to *S. granarius* was significantly lower than those of yellow wheat genotypes. These differences resulted from the lower number of F1 progeny and the longer development time recorded for the granary weevils maintained on pigmented genotypes. Besides, in flour disks bioassays *S. granarius* adults fed with pigmented genotypes showed a lower efficiency conversion of ingested food compared to insects fed on yellow genotypes.

The integration of transcriptomic and metabolomic data through network analysis is expected to further elucidate the biochemical mechanisms regulating kernel pigmentation and volatile biosynthesis. Beyond identifying key genes for breeding insect-resistant varieties, this multi-omics approach provides a robust framework for identifying bioactive molecules useful to develop sustainable control means.

P326 - Genetic factors underlying non-host resistance in wheat against non-adapted powdery mildew

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Abstract

Hexaploid wheat represents a fundamental component of global food security by providing an important source of calories and protein. However, its productivity is continuously threatened by pathogens such as powdery mildew, caused by the obligate biotrophic fungus *Blumeria graminis*. This species comprises several host-adapted lineages, including *B. graminis* f. sp. *tritici* (Bgt), specialized on bread wheat (*Triticum aestivum*), and *B. graminis* f. sp. *dicocci* (Bgdic), adapted to wild emmer wheat (*T. dicoccoides*), the tetraploid ancestor of hexaploid wheat. Although these formae speciales differ in host specialization, partial cross-infectivity occurs, offering a unique opportunity to study mechanisms underlying host specificity.

Non-host resistance provides a robust form of plant immunity, yet the underlying genetic determinants in wheat remain largely unknown. Based on the hybridization history of wheat and the divergence of *B. graminis* lineages, Bgdic is hypothesized to have arisen following the hybridization event between *Aegilops tauschii* and wild emmer wheat. Given that most hexaploid wheat cultivars are resistant to Bgdic, the genetic determinants underlying this resistance are likely located within the D subgenome, which originates from *A. tauschii*. The contrasting host specificity of Bgdic and Bgt provides a natural framework to explore how the acquisition of the D subgenome contributed to the divergence and host specialization of these two pathogen lineages.

To identify the underlying genetic determinants, we combined k-mer-based genome-wide association studies (k-mer GWAS) with classical map-based cloning. Using k-mer GWAS to assess associations between *B. graminis* isolates and diverse wheat genotypes, we detected major and highly significant association signals that appeared consistently and exclusively in response to Bgdic isolates. In parallel, segregating populations derived from crosses between resistant and susceptible wheat lines are being used to genetically dissect the resistance loci. Genetic mapping supports a polygenic basis for Bgdic non-host resistance and has facilitated the selection of high-confidence SNP markers for subsequent fine mapping and candidate gene identification. This work will provide new insights into the evolutionary basis of wheat-*Blumeria* adaptation and advances the understanding of the evolution of non-host resistance.

P327 - Evaluation of yield and quality traits in moderately Fusarium head blight resistant Durum wheat lines

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Abstract

Fusarium head blight (FHB) is a devastating disease affecting cereal crops, caused by various Fusarium species. FHB reduces grain yield and quality, causes financial losses and produces mycotoxins harmful to humans and animals. Additionally, durum wheat is more susceptible to FHB than bread wheat and prone to higher mycotoxin contaminations.

Currently, there are no commercially available cultivars that are resistant to FHB.

Genetic variation in durum wheat is narrow which hinders the development of resistant cultivars but resistant cultivars are essential for ensuring quality, safety, and sustainable agriculture by reducing fungicide use and yield losses. Some experimental lines with improved FHB resistance have been developed, including lines with robust QTL introgressions, such as Fhb1 from bread wheat, offering enhanced resistance and reduced toxin risk for cultivar breeding.

The aim of this study was to compare yield and quality traits of the experimental lines with contrasting alleles at Fhb1 and with already released cultivars. A hundred of these lines have been evaluated in 2023 at Tulln and in 2024 at Tulln and Probstdorf (Saatzucht-Donau) for yield and some quality traits. Although experimental lines generally showed lower yields compared to released cultivars, certain moderately resistant lines carrying Fhb1 demonstrated comparable performance, highlighting their potential as parental lines in future breeding programs. These findings mark an important step toward the development of durum wheat cultivars with improved FHB resistance and competitive agronomical traits, ensuring sustainable agriculture and food safety.

P328 - Genome-wide association study of multiple disease resistances in Australia using a large-scale international wheat panel

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Abstract

Multiple pathogens threaten wheat production in Australia. The wheat breeding programs of the International Maize and Wheat Improvement Centre (CIMMYT) and the International Centre for Agricultural Research in the Dry Areas (ICARDA) agricultural research centres collaborate with Australian wheat breeders and researchers to introduce and evaluate new sources of yield potential and adaptation to biotic and abiotic stresses as part of the CIMMYT Australia ICARDA Germplasm Evaluation (CAIGE) program. Here we present results from genome-wide association analyses of resistance to multiple wheat pathogens, including: Yellow/Stripe rust (*Puccinia striiformis* f. sp. *tritici*); Septoria tritici blotch (*Zymoseptoria tritici*); Yellow/Tan spot (*Pyrenophora tritici-repentis*); and Crown rot (*Fusarium pseudograminearum*) using CAIGE wheat lines tested in multiple environments in Australia over multiple seasons. Associated genetic markers will enable improved selection of breeding materials from international centres and more efficient integration of novel resistances into Australian wheat breeding programs.

P329 - Absolute quantification of puccinia triticina in a diverse wheat panel using droplet digital PCR (ddPCR)

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Abstract

Assessment of pathogen virulence in the *Triticum aestivum*-*Puccinia triticina* pathosystem is traditionally performed using visual scoring of the Cobb scale. However, these investigations are often subjective and limited to post sporulation stages, failing to capture partial resistance. Accurate quantification of fungal biomass is critical for characterizing host resistance. Quantitative PCR (qPCR) generally offers improved sensitivity, as it depends on external standard curves, however it can be susceptible to host-derived or environmental inhibitors can introduce bias. In this study we used Droplet Digital PCR (ddPCR) to analyse a diverse wheat panel and reliably quantify *P. triticina* directly from infected leaf samples. By partitioning DNA extracted from diseased tissue into 20,000 nanoliter-sized droplets, we minimized the impact of host-derived inhibitors and eliminated the requirement for standard curves. An assay was optimized to target the fungal internal transcribed spacer 1 (ITS1) region for fast quantification of fungal biomass present in samples. Our findings indicate that ddPCR provides superior sensitivity in detecting fungal presence, with an increased sensitivity compared with classical qPCR. In our broad panel of infected leaves, ddPCR successfully differentiated between hypersensitive responses, slow-rusting phenotypes, and fully susceptible lines with a higher degree of resolution than qPCR. This approach provides a robust, high-throughput tool for breeders to precisely phenotype of the resistance loci, including to choose better resistance gene combinations, and accelerate the development of leaf rust-resistant wheat cultivars.

P330 - Uncovering novel genetic resistance to fusarium crown rot in watkins wheat landraces

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Abstract

Fusarium crown rot disease (FCR), caused by the fungal pathogen *Fusarium pseudograminearum*, poses a significant threat to wheat production due to its destructive nature and with limited resistance found in cultivated wheat varieties. In this study, 286 genetically diverse wheat landraces from the Watkins' collection were evaluated for FCR resistance using a standardised seedling assay with mixed inoculum; 64 lines showed lower disease severity than the resistant check 2-49 (the most resistant available germplasm). Re-evaluation in a second glasshouse trial with a mix of five aggressive isolates recovered in 2024 demonstrated that 26 lines consistently exhibited lower disease severity than 2-49. These resistant lines were also tested under field conditions using colonised millet inoculum, and 52 lines showed superior resistance compared to 2-49. To dissect the genetic basis of resistance, a genome-wide association study was conducted using whole-genome sequence data. After stringent quality control and linkage disequilibrium pruning, 1,473,773 high-quality SNPs were retained for analysis. Population structure and kinship were accounted for using ADMIXTURE-derived ancestry coefficients and a genomic relationship matrix within the FarmCPU model. Using a significance threshold of $P < 1 \times 10^{-6}$, eleven significant marker trait associations were identified on chromosomes 3A and 3D. Notably, significant associations detected on chromosomes 3A and 3D were positioned in genomic regions where no previously reported QTL or SNP associations for FCR resistance have been documented, indicating potentially novel loci. The identified SNPs and resistant lines provide valuable resources for marker-assisted selection and pre-breeding programs aimed at improving FCR resistance in modern wheat cultivars.

Keywords: *Fusarium crown rot, Watkins landraces, genome-wide association study, quantitative resistance, marker-assisted selection*

P331 - Dissecting the genetic architecture of take-all disease resistance in wheat using haplotype analysis based on genome-wide association studies

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Abstract

Take-all disease, caused by the soil-borne fungus *Gaeumannomyces tritici* is a destructive root disease of cereal crops, leading to substantial yield losses globally. Despite its widespread impact, effective control strategies remain limited, making genetic resistance a critical focus for sustainable crop protection [1]. This study integrates genome-wide association studies (GWAS) with haplotype analysis to investigate the genetic basis of resistance to Take-all in historical Watkins wheat accessions. Field trials at Rothamsted conducted over five years revealed substantial variation in disease severity. GWAS identified several resistance-associated loci, with particular emphasis on a key genomic region showing consistent signals across years and statistical models.

Haplotype analysis of five candidate genes within this region revealed distinct resistance-associated patterns, especially in a subset of three highly resistant lines. Also, based on the Chinese Spring wheat expression data, two genes carrying ABC transporter type1 transmembrane and 4-hydroxybenzoyl-CoA thioesterase, HotDog domain respectively demonstrated promising expression in root tissues. The 1500 bp upstream promoter analysis of ABC transporter gene uncovered a light-responsive Box-4 regulatory motif, suggesting a potential role for shoot-to-root signalling in defence priming. Comparative genomics and protein domain analyses further supported the involvement of these genes in stress tolerance and root development.

The study highlights the importance of integrating haplotype structure, expression data, and functional annotation to refine candidate gene selection. Future work will focus on validating these findings through expression analysis and long-read sequencing to explore structural variation and gene identification under the targeted QTL region in the Watkins lines combined with Virus Induced Gene Silencing experimentation. The outcomes of this research offer valuable insights for breeding wheat cultivars with enhanced resistance to root diseases through targeted molecular strategies.

P332 - Durum landraces as a valuable gene pool to uncover and map resistance to Septoria tritici blotch

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Abstract

Septoria tritici blotch (STB), caused by *Zymoseptoria tritici*, is one of the most damaging leaf diseases of durum wheat and can cause up to 50% yield losses despite fungicide use. The development of resistant cultivars therefore represents the most sustainable strategy for disease management. Identifying STB resistance loci and candidate genes in durum wheat is a priority; therefore, a diverse landrace panel was evaluated.

506 accessions were selected from the Global Durum Genomic Resources (GDGR, https://graingenes.org/GG3/global_durum_genomic_resources), more specifically from two collections: the Global Durum Panel (GDP) (Mazzucotelli, 2020) and the Tetraploid Global Collection (TGC) (Maccaferri et al., 2019), both already provided of SNP dataset (Illumina 90K wheat array).

Field evaluation was conducted at adult plant stage at two different locations in Northern Italy: Cadriano (BO), and Fiorenzuola d'Arda (PC), where climate conditions are generally conducive of high and large STB infection. In addition, artificial inoculation with a local isolate was performed.

Disease assessment included disease severity on the flag leaf, on the canopy (portion below the flag leaf), and Vertical Disease Progression (VDP), which describes the upward spread of the infection along the plant canopy. All disease-related traits were recorded at 2-3 time points during disease development, and the Area Under the Disease Progression Curve (AUDPC) was calculated for each. Plant height and heading date were monitored in all field and severity data adjusted accordingly.

Exploratory genome-wide association analysis identified 134 significant marker-trait associations (MTAs; LOD > 3) in Fiorenzuola (117 unique SNPs) and 125 MTAs in Cadriano (86 unique SNPs), then they were further filtered upon multiple regression models. Several loci were associated with multiple phenotypes, indicating a shared genetic basis underlying different components of STB resistance. Eight MTAs were consistently detected across both environments, highlighting stable genomic regions. Furthermore, nine QTL co-localized with previously reported bread wheat STB resistance genes (*Stb* genes) following projection (*Stb* genes) onto the durum wheat reference genome (cv. Svevo). Our results provide insights into the genetic control of STB resistance and the allelic variants underlying key QTL in durum wheat landraces.

P333 - Genetic dissection of lesion mimicry in durum wheat identifies nlr and receptor-like kinase candidate genes

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Abstract

Abstract:

Lesion mimic phenotypes (LMPs) provide valuable genetic systems to investigate the regulation of programmed cell death and immune homeostasis in crops. In wheat, spontaneous lesion formation in the absence of pathogens is frequently associated with constitutive activation of defense pathways and altered immune receptor signaling. Here, we characterize independent ethyl methanesulfonate (EMS)-induced durum wheat (*Triticum turgidum* L.) mutants that develop stable, pathogen-independent leaf lesions under controlled conditions. Genetic analysis through crosses to the wild type indicates dominant inheritance of the phenotype, consistent with deregulated immune activation.

To elucidate the molecular basis of lesion mimicry, RNA sequencing combined with transcriptome-based variant discovery was performed across mutant lines. Comparative analysis revealed recurrent, independent nonsynonymous EMS-type single nucleotide polymorphisms in two immune receptor genes: a nucleotide-binding leucine-rich repeat (NLR) protein and a leucine-rich repeat receptor-like kinase. The repeated identification of distinct allelic variants in these genes across independent mutants indicates strong mutational convergence on immune receptor-associated signaling components, implicating them as candidate regulators of the observed cell death response.

An F₂ mapping population is currently being developed to assess co-segregation of candidate alleles with the lesion phenotype and to resolve the underlying genetic architecture. In parallel, phenotypic evaluations against powdery mildew and yellow rust are underway to determine whether constitutive lesion formation is associated with altered disease responses. Future functional validation will further clarify the contribution of these candidate genes to immune signaling and cell death regulation in durum wheat. Collectively, this work establishes a genetic framework to dissect immune receptor-mediated control of defense activation and its potential implications for durable resistance in cereal crops.

P334 - Cross-species association mapping reveals the genetic architecture of the interaction between wheat and its powdery mildew pathogen

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Abstract

Background: Wheat powdery mildew, caused by *Blumeria graminis* f. sp. *tritici* (Bgt) is one of the most significant diseases affecting global wheat production. Breeding for disease resistance (R) genes against Bgt often follows a 'boom-bust' cycles, where cultivars with effective resistance are widely deployed on an expanding area until virulence emerges in the avirulence (Avr) pathogen population. While extensive effort has been devoted to identifying and cloning R genes, Avr genes remain relatively understudied, limiting our understanding of R-Avr interactions. That said, understanding R-Avr interactions is crucial for developing durable resistance strategies.

Results: We conducted whole genome sequencing on 245 Bgt isolates collected from major wheat-growing regions in China, identifying 120 genetically unique isolates. Each of these unique isolates was inoculated and phenotyped on a diverse panel of wheat germplasm. Through Genome-Wide Association Analysis (GWAS) in both Bgt and wheat, we identified 65 Avr loci and 251 R loci overlapping with nine and eight cloned Avr or R genes, respectively. On average, each isolate carries eight Avr alleles, ranging from one to 17. Little geographical preference for Avr alleles or their combinations was observed, suggesting that disease resistance breeding against this pathogen should be coordinated at the national level. The level of resistance level is positively correlated with the number of R alleles carried by a wheat line, and the average frequency of an R allele is 2% among the wheat panel, indicating the potential for accumulating R alleles in breeding programs. We mapped 212 R-Avr interactions based on joint GWAS using both plant and pathogen genomes and cross-species epistasis, where a network of interactions was formed between wheat and Bgt. These interactions indicate that pyramiding five major R loci has the potential to confer resistance to half of the Avr loci. As a proof of concept, we successfully verified two previously described R-Avr pairs using tobacco experiments. Furthermore, we provided molecular validation evidence for three new Avr genes, including Bgt-50651, BgtE-5826 and BgtE-20009, and two new R-Avr interactions. Among them, Bgt-50651 interacts with Pm1a, Pm2a, and another unidentified R gene located near the Pm6/Pm52 interval.

Conclusion: Our study provides a framework for understanding the genetic interaction between plants and pathogens. The discovery of novel R/Avr loci and their complex interaction network underscores the need to integrate crop and pathogen genetic background, particularly the R/Avr allele composition, into breeding program design. These findings have significant implications for developing durable resistance strategies in wheat alongside offering valuable insights into the broader dynamics of plant-pathogen interactions.

P335 - Introgression of stripe rust adult-plant resistance from cv. Svevo into bread wheat cultivar

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Abstract

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is among the most destructive diseases of wheat worldwide. The rapid emergence of virulent races frequently overcomes race-specific resistance, highlighting the need for durable adult-plant resistance (APR) controlled by multiple quantitative trait loci (QTL). In previous studies, the durum wheat cultivar Svevo was identified as a source of stable APR. Here, we introgressed Svevo-derived APR QTL into the Israeli elite bread wheat cultivar Shefa and developed molecular markers to enable efficient selection.

Field experiments were conducted over two years in three environments, including Neve Ya'ar, the Rishon LeTzion, and Haifa, evaluating 423 backcross-derived lines (BC2F6, n = 373; BC3F3, n = 50). Stripe rust infection type (IT) was assessed under artificial inoculation with IT ranging from 2-9. Correlations between replicates ranged from 0.50 to 0.83. Genotyping was performed using DArT markers, yielding approximately 34,000 SNPs, after filtering and imputation, genome-wide association analysis (GWAS) identified three significant QTL located on chromosomes 2A (789 Mbp), 2B (823 Mbp), and 7B (732 Mbp), jointly explaining 37.5% of the phenotypic variance. We developed PCR-based markers for these loci to support marker-assisted selection.

BC3F3 lines carrying two of the resistance alleles generally exhibited high levels of resistance (infection type approximately 2), whereas lines lacking these alleles were mostly susceptible. Agronomic evaluations in field plots and net-house trials showed that several BC3F3 lines combined improved resistance with favorable traits, including higher grain yield and thousand-kernel weight relative to Shefa. Seventeen BC3F3 lines outperformed the recurrent parent in both yield and kernel weight under controlled conditions.

Overall, we demonstrate effective transfer of durable APR from Svevo into bread wheat and provide validated PCR markers for breeding high-yielding, stripe rust-resistant under Mediterranean agro-systems.

P336 - Climate change and pest infestation dynamics: AI-Driven Forecasting of future insect complexes in wheat agroecosystems

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Abstract

Wheat (*Triticum aestivum* L.) remains the backbone of global food security, yet its post-harvest stability and field productivity are increasingly compromised by climate-driven insect infestations. Rising temperature, erratic humidity, and altered rainfall regimes are shifting pest phenology, geographic range, and outbreak frequency. In this study, a multi-layered dataset combining ERA5-like climatic variables and Sentinel-2-analog spectral indices was developed across 40 representative wheat-growing sites from the Indo-Gangetic Plains to Central Europe (1979-2100). Three dominant storage and field pests *Sitophilus granarius*, *Tribolium castaneum*, and *Rhyzopertha dominica* were modeled under RCP4.5 and RCP8.5 scenarios using AI-based forecasting frameworks. Machine-learning models (Random Forest, Gradient Boosting) achieved accuracies exceeding 0.86 and $R^2 \approx 0.83$ for predicting monthly infestation probabilities and damage severity. Explainable-AI (SHAP) analysis identified temperature (mean 29-33 °C), vapor-pressure deficit (VPD > 1.2 kPa), and vegetation stress (NDVI < 0.45) as key outbreak triggers. Spatial mapping projects a > 30 % expansion of high-risk infestation zones by 2100 under RCP8.5, particularly across the Indo-Gangetic Plains and Mediterranean regions. These findings highlight the urgent need for AI-enabled early-warning systems and climate-resilient storage protocols to mitigate future wheat losses under accelerating climate change.

Keywords: wheat pests; climate change; ERA5 reanalysis; Sentinel-2 indices; Random Forest; SHAP; RCP scenarios; sustainable storage

P337 - FreeWheat: high-resolution genomics and microphenomics of nonhost resistance to rust and mildew

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Abstract

Wheat production is severely constrained by fungal pathogens such as powdery mildew and yellow rust, which are highly adapted to the wheat immune system. In contrast, closely related cereal species often display effective resistance because pathogen virulence mechanisms fail to suppress their defense responses. Understanding such nonhost resistance offers an opportunity to identify conserved susceptibility and resistance mechanisms that may inform strategies for improving disease resistance in wheat.

As a nonhost species for wheat fungal pathogens, barley represents a valuable resource for studying these interactions. In non-adapted plant-pathogen systems, infection outcomes are determined at very early stages and frequently occur without visible symptoms, which limits the usefulness of conventional macroscopic disease scoring. To address this limitation, we combine high-throughput micro- and macro-phenotyping approaches with genomic analyses in a panel of 1,000 barley genotypes from the Gatersleben Genebank diversity core collection and additional elite lines.

Building on our previous work, we expanded the genetic resolution of this panel by integrating recently available whole-genome sequencing datasets, resulting in a substantially increased SNP density compared with earlier genotyping platforms. These data enabled genome-wide association analyses using both linear mixed models and machine-learning approaches. In addition, we initiated the transition toward pan-genome-aware analyses and reference-free k-mer-based association mapping to capture structural variation and presence-absence polymorphisms that are poorly represented in single reference genomes.

P338 - Consequences of management practices on distribution of Russian wheat aphid, *diuraphis noxia*, in wheat production areas of South Africa

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Abstract

Russian wheat aphid (RWA), *Diuraphis noxia*, is an international pest on wheat in most countries with large scale wheat cultivation. Considerable efforts have been made to manage RWA globally and the two main management options used are chemical control and breeding for deployment of resistant wheat. With widespread and continuous use of the same active ingredients of insecticides, susceptibility of RWA to these insecticides may decrease. With resistance breeding RWA populations can overcome the resistance in the wheat cultivars, resulting in new biotypes virulent to resistant wheat cultivars. For continued success of these management practices, it is necessary to monitor how the distribution of RWA populations is affected. RWA was surveyed annually, from 2010 to 2025, during the wheat growing season in South Africa in all main wheat production areas. RWA clone colonies were established from field collected samples. The biotype of each RWA clone was determined by screening its feeding damage on 11 wheat resistant sources containing resistance genes Dn1 to Dn9 and Dnx and Dny. Insecticide resistance of RWA clone populations were determined by screening against commonly used active ingredients, using IRAC susceptibility test (Method No:001; version 3; June 2009).

In South Africa RWA showed considerable biotypic adaptations to resistant wheat cultivars, resulting in five RWA biotypes occurring in wheat production areas where RWA resistant wheat was deployed. There was widespread decrease in susceptibility of RWA populations to commonly used active ingredients in areas where chemical control was used as management practice.

Given the invasive ability, evolutionary adaptability, virulence, and fecundity of RWA, it remains a threat to global wheat production. RWA remain present in all major wheat production areas of South Africa. It is important that future management practices focus on sustainability instead of indiscriminate use of insecticides to control RWA.

P339 - Genetic diversity and population structure of fusarium graminearum in the northern wheat belt of India: a first-of-its-kind study

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Abstract

Head blight (scab), caused by *Fusarium graminearum* (FG), was historically considered a minor wheat disease but has recently emerged as a significant economic threat in India. This study presents the first comprehensive population genetic analysis of FG from the northern wheat belt of the country. Multi-locus phylogenetic characterization was performed using conserved gene regions— β -tubulin (TUB), translation elongation factor 1- α (TEF), and histone-3 (HIS)—across 123 geographically diverse *F. graminearum* isolates collected from four states: Haryana (HR), Punjab (PB), Rajasthan (RJ), and West Bengal (WB). Phylogenetic and haplotype analyses revealed 30 distinct haplotypes across all populations. Among these, haplotypic diversity was highest in the RJ population ($H_d = 0.981$), followed by HR ($H_d = 0.972$), PB ($H_d = 0.965$), and WB ($H_d = 0.962$). Both recombination ($R_m = 12$) and substantial mutation events (485) were detected. AMOVA results indicated that most genetic variation occurred within populations rather than among them. The haplotype network was highly dispersed, lacking population-specific clustering and without a predominant shared haplotype. The PB population exhibited the greatest number of unique (H9, H10, H11) as well as shared haplotypes (27). Except for haplotype H22—which comprised highly aggressive isolates—no clear association was observed between isolate aggressiveness and haplotype identity. Concatenated gene analyses showed low genetic differentiation among populations ($F_{st} = -0.014$ to 0.02). Positive neutrality test values in PB, HR, and RJ suggest a balancing selection acting on these FG populations, whereas WB displayed both positive and negative neutrality indices, indicating the influence of both population expansion and balancing selection on its population structure

P340 - Genome-wide association study and genomic prediction for stem rust resistance at the adult plant growth stage in elite spring bread wheat genotypes

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Abstract

Wheat is one of the most widely grown cereal crops worldwide. In Morocco, it is the predominant staple grain, accounting for more than 68% of total cereal consumption. Among the most destructive diseases affecting wheat production are stripe rust, stem rust, and leaf rust, caused by *Puccinia striiformis* f. sp. tritici, *Puccinia graminis* f. sp. tritici, and *Puccinia triticina*, respectively. Of these, stem rust is one of the most yield-limiting diseases and can cause annual global yield losses of up to 6.2 million metric tonnes.

Although stem rust was previously considered of minor importance in Morocco, its incidence has increased markedly over the past five years, posing an imminent threat to national wheat production. To date, more than 200 stem rust resistance genes and their associated molecular markers have been identified. However, ongoing changes in virulence patterns driven by climate change and the emergence of new pathogen races have rendered many of these genes ineffective. Consequently, identifying new sources of resistance from diverse bread wheat germplasm has become essential to combat emerging virulent races.

During the 2024 and 2025 cropping seasons, a total of 384 spring bread wheat genotypes were evaluated for adult plant resistance to stem rust at two locations in Morocco. These genotypes were genotyped using 25K high-quality single nucleotide polymorphism (SNP) markers. Significant phenotypic variation for stem rust resistance was observed among the genotypes at the adult plant stage. Genome-wide association studies (GWAS) and genomic prediction (GP) analyses identified several highly significant marker-trait associations (MTAs) distributed across all three wheat sub-genomes (A, B, and D).

Notably, five significant SNPs located on chromosome 3B within the ~765-770 Mb interval are likely tagging the same quantitative trait locus (QTL), suggesting a strong candidate region for stem rust resistance.

Among these, SNP IACX6214 (3B) showed particularly strong association. Candidate genes linked to key resistance traits were also identified. After rigorous validation, these loci and associated markers can be effectively deployed in marker-assisted selection and gene pyramiding strategies to enhance durable stem rust resistance in wheat breeding programs.

**P341 - Tritordeum as a habitat for the development of the rice weevil
sitophilus oryzae L.—analysis of selected properties of the cereal grains
determining their resistance mechanisms**

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Abstract

In the face of the global climate and ecological crisis, as well as growing consumer needs and demands, a transformation of the global food production and distribution system is necessary. The productivity and quality characteristics of Tritordeum make this cereal an effective tool in the sustainable modernization of the agricultural sector. However, this potential can be significantly limited in the supply chain by storage pests. This study aimed to assess the impact of Tritordeum resistance on the rice weevil (*Sitophilus oryzae* L.). The experiment used 11 Tritordeum breeding lines in comparison to three cereal species derived from conventional cultivation systems (common wheat *Triticum aestivum* L., durum wheat *Triticum durum* Desf., spring barley *Hordeum vulgare* L.). The research showed that Tritordeum may be a substrate on which *S. oryzae* feeds, although the intensity of the pest's development varied depending on the line. The study also demonstrated that the hardness of the Tritordeum seed coat did not directly influence the development intensity of the analyzed beetles. It was noted, however, that the degree of infestation by these insects depended on the chemical profile of the infested kernels. The increased total protein content and lower fiber content (compared to common wheat) likely influence the development of Tritordeum resistance. This study demonstrates that Tritordeum possesses inherent resistance traits linked to its grain chemistry, providing a basis for breeding more storage-resistant cereal cultivars.

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P342 - Genetics of spot blotch resistance in wheat

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Abstract

Genetics of Spot Blotch Resistance in Wheat

Pradhumn Kumar, Shivali, Rahul Kumar, Pushpendra K. Gupta

Study of Genetics of spot blotch in wheat has been an ongoing project in our department. There are several sources of resistance for spot blotch including the following: (i) Four R genes, namely Sb1-Sb4; (ii) A sensitivity gene Tsn1 (iii) A large number of QTLs identified through QTL interval mapping; (iv) A number of marker-trait associations (MTAs) identified using GWAS; (v) Possible SWEET genes, yet to be discovered. In a multi-institutional DBT project, we are subjecting ~100 Indian wheat accessions to identify their genotypes with respect to all the above five categories of genes and then determine relative roles of these five sources in providing resistance to spot blotch. The presence/absence of the following will be examined in these ~100 accessions: (i) four Sb genes (Sb1-4), (ii) a solitary known Tsn1 gene against ToxA in the pathogen, (iii) five selected QTLs (Qsb.bhu-5B, Qsb.bhu-7D, Qsb.iwbr-7DQsb.bhu-2B and Qsb.bhu-3B and five selected SWEET genes (TaSWEET11a-7D, TaSWEET12a-4A, TaSWEET13a-6D, TaSWEET14a-6A and TaSWEET15a-7D) selected from >100 known) and (iv) five selected SWEET genes selected from >100 known SWEET genes in wheat genome. Epigenetic control of spot blotch resistance and the use of priming in providing resistance will also be examined. The details of the progress made under this project will be presented at the forthcoming IWC4.

P343 - Effects on yield and seed composition of *Puccinia striiformis* f. sp. *tritici* inoculation of wheat near isogenic lines containing Yr9, Yr10, and Yr15 resistance genes

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Abstract

In response to stripe rust, *Puccinia striiformis* f. sp. *Tritici* (Pst) occurrence and associated yield losses in wheat, efforts to breed for stripe rust resistance have become a priority. Numerous stripe rust resistance Yr-genes have been identified and deployed in newly released cultivars. In this study near isogenic lines containing Yr9, Yr10 and Yr15 stripe rust resistance genes in an Avocet background with susceptible Avocet as control, were tested for their effects on yield and yield components, and protein and starch content in two greenhouse trials, with and without Pst inoculation. Fifteen days post-inoculation, Avocet S showed a high disease severity (77% and 87% flag leaf infection in trial 1 and 2, respectively) while Yr9/6*AvS, Yr10/6*AvS and Yr15/6*AvS only showed chlorotic flecks. Before inoculation, the hundred kernel mass was significantly higher in Yr9/6*AvS and Yr10/6*AvS than for Avocet S, but it was significant decreased in all the entries following inoculation. Uninoculated Yr9/6*AvS and Yr15/6*AvS had significantly more heads per plant and kernel mass per pot than Avocet S. A decrease in kernels per head and kernel mass per pot was observed for all entries when inoculated. Yr10/6*AvS had a significantly higher protein content than Avocet S when not inoculated, but when inoculated, all the NILs were significantly lower in protein and starch content than Avocet S. Rust inoculation caused a significant increase in protein content and decrease in starch content in all four entries. In conclusion, inoculation had a consistent detrimental effect on yield and related components, and it increased protein content and reduced starch content, probably due to shrivelling of seeds. The presence of the resistance genes had inconsistent effects on yield and related components, and protein and starch content.

P344 - Climate change alters the landscape of wheat fungal diseases and breeding in China

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Abstract

Wheat fungal diseases (WFDs) pose a substantial threat to grain production in China, with their prevalence and severity closely associated with the impacts of climate change. We investigate the dynamics and spatial distribution over the past five decades of four dominant WFDs, which are the requested check diseases for new wheat variety release in China, such as stripe rust (YR), powdery mildew (PM), fusarium head blight (FHB), and wheat sharp eyespot (WSE). Our findings indicated that the overall disease occurrence intensity (OI) has been expanding outward from wheat-growing Zone III (Middle and Low Yangtze Valleys), while wheat-growing Zone II (Yellow and Huai River Valleys) is currently experiencing considerable pressure from multiple diseases. Climate Zones, defined by key climatic variables, have emerged as the primary determinants governing the spread of WFDs. Notably, atmospheric pressure, as a composite climatic factor, influences disease development through multiple mechanisms. Analysis of disease migration trends reveals that wheat-growing Zones I (Northern Winter Wheat Valleys) and II are currently subject to high levels of disease pressure in China. Our analysis of resistant wheat varieties/cultivars released over the past years indicates a pronounced lag in the development of resistant cultivars relative to the trajectory of disease migration. Thus, identification and cloning of more resistance genes to wheat disease will be the key to improve the resistance under climate challenge in the future.

P345 - Develop durum wheat with fusarium head blight resistance adapted to the Northern Great Plains

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Abstract

Fusarium head blight (FHB) is a destructive disease in the Northern Great Plains, a major production region for durum wheat. Breeding for FHB resistance in durum wheat is particularly challenging due to the limited availability of resistant germplasm. Several durum wheat lines with moderate resistance have been developed using resistant sources identified in tetraploid wheat relatives and hexaploid bread wheat. To develop FHB-resistant cultivars adapted to the Northern Great Plains, these lines were crossed with local elite cultivars and breeding lines, and pedigree selection was conducted in the NDSU durum wheat breeding program. Thousands of breeding lines were evaluated annually for FHB resistance in inoculated field nurseries. From 2022 to 2024, several lines exhibited significantly lower FHB severity and deoxynivalenol (DON) content than the currently most widely planted cultivar, 'ND Riveland,' across multiple environments. The well-known resistance gene *Fhb1* showed significant effects on both FHB severity and DON accumulation.

In a parallel project, recurrent phenotypic and genomic selection have been used to further enhance FHB resistance using the same resistant resources. Five cycles of phenotypic selection for FHB severity were conducted from 2019 to 2024, with one cycle per year. The mean FHB severity decreased from 82.5% in Cycle 0 to 59.3% in Cycle 5. A genomic prediction model was developed using 318 breeding lines from the NDSU durum program and 438 S0:1 lines from recurrent selection Cycle 3-5 populations. Prediction accuracies were 0.51 for FHB severity, 0.53 for plant height, and 0.79 for days to flowering. Two cycles of genomic selection (GS), initiated with the top 15 S0:1 lines from the Cycle 5 population, were conducted from September 2024 to April 2025. Field evaluations in 2025 showed progressive improvement in FHB severity across GS cycles. The top 24 lines were tested for DON content; 11 lines exhibited significantly lower DON levels compared with the check cultivar 'ND Riveland' at both Fargo and Prosper, ND. These results demonstrate the effectiveness of recurrent phenotypic and genomic selection in enhancing FHB resistance in durum wheat, providing a strong foundation for developing resistant cultivars adapted to the Northern Great Plains.

P346 - Characterizing seedling and adult-plant resistance to *Puccinia striiformis* f. sp. tritici via genome wide association study and RNA-Seq

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Abstract

Yellow rust, caused by the fungal pathogen *Puccinia striiformis* f.sp. tritici (Pst), poses a significant threat to wheat production worldwide. This study investigated seedling resistance in Norwegian spring wheat and sought to identify candidate genes linked to the broad-spectrum adult plant resistance (APR) quantitative trait locus (QTL), QYr.nmbu.6A through comparative transcriptomics. The QYr.nmbu.6A locus, was previously mapped to the long arm of chromosome 6A and recognized as a major APR QTL effective across diverse environments and continents. To assess whether this region also contributes to seedling resistance, we conducted seedling inoculation assays with multiple Pst races on a subset of a Norwegian spring wheat association panel. A seedling resistance QTL, QYr.nmbu.asr-6A, was identified, overlapping with the QYr.nmbu.6A region. Haplotype analysis indicated a statistically significant but moderate effect of QYr.nmbu.6A on seedling resistance, though it remains uncertain if the same locus underlies both seedling and adult plant resistance. Comparative transcriptomic analysis following adult plant point inoculation identified differentially expressed genes (DEGs) within the QYr.nmbu.6A interval, using the SY Mattis genome sequence as reference, which harbors the resistant haplotype of QYr.nmbu.6A. Notably, several DEGs near the peak marker encode domains associated with disease resistance, such as NB-ARC, RxN-terminal, and leucine-rich repeats. These results provide a basis for future functional validation of QYr.nmbu.6A and its potential role in durable resistance.

P347 - Metabolic biological basis underlying resistance to fusarium head blight in bread wheat

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Abstract

Background:

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is a globally devastating fungal disease in wheat. Genetic enhancement of host resistance represents the most effective control strategy. This study aims to dissect the metabolic basis of wheat resistance to FHB.

Methods:

We established a diverse panel comprising 277 globally-sourced bread wheat accessions and conducted systematic phenotyping for Type II FHB resistance over three consecutive years under greenhouse conditions. Furthermore, metabolomic profiling of spike tissues was performed at 72 hours post-inoculation with three biological replicates over two years.

Results:

The panel exhibited broad variation in resistance, with the percentage of diseased spikelets ranging from 12% to 91%, coupled with high heritability estimates ($H^2=0.91-0.94$). Widely-targeted metabolomic profiling detected 2,066 metabolite characteristic peaks. Through an integrated analysis combining metabolomics, genomics and transcriptomics, this study systematically elucidated two key resistance pathways involved in wheat-pathogen interactions.

First, our results demonstrate that the tryptophan metabolic pathway positively regulates wheat resistance to FHB. Infection by *F.g* triggers strong accumulation of tryptamine, serotonin and derivatives, which activate plant defense responses and inhibit the hyphal growth of the pathogen. The key gene *TaTDC* is upregulated upon pathogen induction, and overexpression lines show significantly enhanced FHB resistance compared to wild-type plants. Mechanistically, resistance enhancement is associated with increased wall thickness in *TaTDC* overexpression lines, together with the accumulation of tryptamine and serotonin that promotes the expression of defense-related genes, thereby enhancing FHB resistance.

Second, the study established the flavonoid metabolic pathway as an additional critical defense layer. A pathogen-induced flavonoid biosynthetic gene cluster in wheat was characterized as a positive regulator of resistance. Overexpression of the rate-limiting enzyme gene within this cluster resulted in several-hundred-fold increases in the accumulation of the associated antifungal compound compared with the wild type. Transgenic functional validation further confirmed that this gene cluster enhances FHB resistance by promoting the biosynthesis of antifungal flavonoids, thereby strengthening chemical defense capacity.

Conclusion:

From metabolic perspectives, this study elucidates the regulatory basis underlying wheat's resistance to FHB. The findings provide important theoretical foundations and genetic resources for further dissecting host-pathogen interaction mechanisms and developing high-yielding, disease-resistant wheat varieties.

P348 - Identification of genomic regions and durum wheat genotypes associated with yellow rust resistance using a subset of the global durum panel (GDPv1) under inoculation and field conditions in Argentina

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Abstract

The Global Durum Wheat Panel (GDPv1) is an exceptional genetic resource for exploring the presence of genetic resistance to yellow rust (*Puccinia striiformis* f. sp. *tritici*). This work had two objectives: 1) to detect genomic regions associated with yellow rust resistance in Argentina; and 2) to identify resistant genotypes in the GDPv1 and evaluate them alongside local controls under greenhouse inoculation and field experiments. A field trial using the GDPv1 was conducted in La Dulce during 2021. Three yellow rust measurements were obtained. A genome-wide association study was performed using Tassel V5.2 software with the SNP markers reported by Mazzucotelli et al. (2020) and field data. Then, 32 genotypes (27 resistant [0-5% severity] and 5 susceptible [50-70% severity]) were selected and, along with three local controls, were field-tested in La Dulce in 2022 and 2023, using two and three replicates, respectively. This subset was also inoculated with a locally collected non-warrior strain (Yr22-46), under greenhouse conditions.

The main genomic regions associated with disease severity (DS) were identified in 7B, 5B, 4A, 3A, and 1B, while for infection type (IT), the MTA was primarily located in 1B, 4A, and 7B. Two closer genomic regions were identified in 1B: one at 296 Mb associated with DS and another at 315-318 Mb associated with both DS and IT. Two MTAs linked to 696 and 698-699 Mb on chromosome 7BL were also detected for IT and DS.

The assessment of yellow rust (YR) during 2022 was ineffective due to low inoculum pressure. However, in 2023, natural inoculum pressure was similar to that of 2021, and response variability was measured. The Area Under the Disease Progress Curve (AUDPC) was estimated using four YR measurements. Only two GDPv1 genotypes (GDPv1-462 and GDPv1-155), initially selected as resistant, showed high resistance (AUDPC <100), along with the local control Buck Cuarzo. Eight additional genotypes exhibited an AUDPC <200.

Two promising genomic regions in 1B and 7BL were associated with yellow rust resistance. In addition, two GDPv1 entries proved to be highly resistant genotypes that could be considered as germplasm resources for breeding programs.

P349 - Effect of Pm3d/e chimeric gene on powdery mildew resistance of spring wheat (*Triticum aestivum* L.)

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Abstract

Biological plant protection involving the development and cultivation of resistant cultivars is of great importance in preventing the spread of diseases, maintaining satisfactory yield averages, reducing the extent of damage and protecting the environment. Wheat powdery mildew (PM) causes extensive losses every year in wheat-growing regions of the world. The powdery mildew resistance of wheat is determined by numerous genes. One of these is Pm3 which has several alle variation. The spring wheat cultivar 'Bobwhite' was transformed with the Pm3d/e chimeric gene construction to study the effect on PM resistance. The progeny of nine independent transgenic plants were characterised regarding PM resistance and yield components. The infection of the basal leaves and whole plants became significantly ($p=0.001$) higher in the wild type than in the T1 lines from the third weeks after infection, and the difference increased until the end of the experiment. The difference in flag leaf contamination between the T1 progenies and the wild type was also significant ($p=0.001$) The infection spread slower and the final level of was smaller in T1 plants than in the wild type. The incorporated transgen had an indirect effect on yield components also. Powdery mildew infection had the greatest effect on the grain weight of the main spike. The T1 progenies had significantly higher values than the control. This character showed a high correlation ($p=0.001$) with the early infection of the basal and flag leaves. The spike number and grain number of the main shoot and the thousand-kernel weight have higher value in T1 lines then in the wild type, but its were depend on transformation event. The plant height of the transgenic lines was significantly shorter than that of the control lines, which was probably due to the activation of plant defence mechanisms against the pathogen.

Acknowledgments: "Project no. TKP2021-NKTA-06 has been implemented with the support provided by the Ministry of Innovation and Technology of Hungary from the National Research, Development and Innovation Fund, financed under the TKP2021-NKTA funding scheme." and RRF-2.3.1-21-2022-00007 grant and European project "Exploitation of natural plant biodiversity for the pesticide-free production of food" (BIOEXPLOIT).

P350 - Identification of resistance sources to Septoria Tritici Blotch (STB) in spring Bread Wheat of Icarda germplasm in Morocco

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Fatima Ezzahra Rachdad ⁽¹⁾ - ***Muamar Al Jaboobi*** ⁽⁴⁾ - ***Tadesse Wuletaw*** ⁽⁴⁾

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Abstract

Septoria tritici blotch (STB), caused by the fungus *Mycosphaerella graminicola* (also known as *Zymoseptoria tritici*), is one of the major fungal diseases threatening global wheat production, STB can cause significant yield losses, sometimes up to 50%. This study evaluates the resistance of 384 advanced breeding lines (ABLs) from spring bread wheat breeding program of ICARDA under field and greenhouse conditions to identify loci associated with resistance to STB at seedling (SRT) as well as at the adult plant (APS) stages using genome-wide association studies (GWAS). Adult plant resistance was assessed at two locations in Morocco Sidi Allal Tazi (SAT) and Marchouch (MCH) during three consecutive wheat-growing seasons 2018-19, 2023-24 and 2024-25. Seedling resistance was evaluated under controlled conditions with a mixture of isolates from Morocco. Disease severity was assessed using the double-digit scale for APS and the 0-5 scale for SRT. Preliminary results identified significant phenotypic variation in resistance levels, with 12 cultivars showing high resistance in both seedling and adult plant stage. This study aims to identify new resistant varieties to STB in spring bread wheat and to identify genetic markers associated with the resistance. These markers can be used in marker-assisted selection (MAS) to accelerate the breeding process for developing resistant wheat varieties.

P351 - Unraveling host-pathogen protein-protein interactions in wheat blast through in-silico docking and molecular dynamics simulations

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Abstract

Wheat blast, caused by *Magnaporthe oryzae* pathotype Triticum (MoT), has emerged as a serious threat to global wheat production, leading to severe yield losses under favorable conditions. Despite its agricultural importance, the molecular basis of wheat-MoT interactions remains poorly understood. Elucidating host-pathogen protein-protein interactions (PPIs) is crucial for deciphering fungal infection strategies and identifying potential targets for improving disease resistance.

In this study, we employed an integrative in silico approach to investigate the interaction between the wheat susceptibility protein Bsr-k1 and the MoT effector protein PWT4. Three-dimensional structures of the wild-type and mutant forms of the wheat Bsr-k1 ortholog were generated using homology modeling, while the effector PWT4 structure was obtained from AlphaFold predictions. Protein-protein docking was performed using multiple docking platforms, followed by 100 ns molecular dynamics simulations to evaluate the stability and dynamics of the complexes. Binding free energy calculations were carried out using the MM-PBSA method, and key interface residues were identified through computational alanine scanning.

The results revealed distinct differences in binding affinity, interaction patterns, and structural stability between the wild-type and mutant Bsr-k1-PWT4 complexes. The mutant complex exhibited enhanced stability, increased hydrogen bonding, and more favorable binding free energy, suggesting a potential role in reducing effector-mediated susceptibility. These findings provide molecular-level insights into wheat-MoT interactions and highlight the utility of computational structural biology in identifying candidate targets for developing durable wheat blast resistance.

P352 - Tracing Hybridization Timing in Wheat Powdery Mildew through Historical Genomics

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Abstract

Wheat powdery mildew, *Blumeria graminis* f.sp. *tritici* (Bgt), is among the most economically significant diseases affecting wheat production worldwide. As an obligate pathogen, Bgt is considered to have co-diversified with wheat under long-term agricultural practices. Deciphering this host-pathogen co-evolutionary history is essential for understanding infection mechanisms and for developing durable resistance strategies that contribute to global food security.

Recent population genomic analyses of 172 globally collected isolates revealed a well-defined population structure and suggested that the present Japanese Bgt population originated from hybridization between Chinese and U.S. lineages. However, the timing and number of hybridization events, as well as their evolutionary implications, remain unclear.

To investigate the temporal origin of hybridization, we analyzed Bgt-infected wheat specimens collected in Japan and Taiwan between the 1800s and the 1990s. Using genomic data obtained from these historical materials, we first examined host-derived reads from the archived specimens to verify the host species identity. We then conducted population genomic analyses of the pathogen and compared historical genomes with those of contemporary global populations to infer the timing of hybrid lineage formation. Our findings provide new insights into the evolutionary history of wheat powdery mildew and clarify the formation of hybrid lineages identified in Japan, offering an improved understanding of their evolutionary significance.

P353 - A novel necrotrophic effector-receptor interaction in *Parastagonospora nodorum*-wheat pathosystem

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Abstract

Septoria nodorum blotch is an economically important fungal disease of wheat caused by a necrotrophic fungal pathogen called *Parastagonospora nodorum*. The pathogen infects wheat by secreting multiple necrotrophic effectors (NEs). These NEs interact directly or indirectly with their corresponding host receptors encoded by sensitivity genes, in an inverse gene-for-gene fashion and subtly exploit defence responses for their proliferation.

In this study, we discovered and functionally validated a novel effector produced by *P. nodorum*, SnTox9, which interacts with Snn9 receptor gene in wheat. Snn9 co-located with Snn3 on the top of 5BS chromosome. SnTox9 possesses typical characters of an effector: a small protein, cysteine rich, heat and DTT sensitive. Purified SnTox9 induced necrosis when infiltrated in SnTox9 sensitive wheat lines. Unlike other 9 dominant and well-characterised interactions between *P. nodorum*'s NE - wheat receptors, SnTox9 sensitivity is a recessive trait. The interaction is light-dependent. Qualitative Trait Loci (QTL) mapping found SnTox9-Snn9 interaction significantly contributes to disease incidence. The identification of this effector will help to better understand the complexity of necrotrophic fungal diseases such as SNB and to make resistance breeding programs more efficient by rapidly removing this disease component from breeding materials.

P354 - Genetic insights into Durum Wheat resistance to WSSMV and SBCMV across France and Italy

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Abstract

Wheat spindle streak mosaic virus (WSSMV) and soil-borne cereal mosaic virus (SBCMV) are major durum wheat pathogens causing up to 70% yield loss. As their vector, *Polymyxa graminis*, is capable of surviving in soil for years, disease control relies mainly on genetic resistance. Bread wheat harbors effective resistances, including *Sbm1* (5D) against SBCMV, while in durum wheat only *Sbm2* (2B) is known (Bruschi et al, Theor Appl Genet 2024), showing high efficacy in Italy but limited to no effectiveness in France.

To discover resistance loci, we evaluated in Bologna (UNIBO field trial nursery) 181 lines from the EPO pre-breeding population originating from a composite cross including wild and primitive *Triticum turgidum* accessions. The population was fully genotyped and GWAS identified a major QTL on chr 2B colocalizing with *Sbm2* but no additional loci, likely due to GWAS limitations in capturing rare alleles. Nevertheless, the EPO panel harbors promising, unexploited resistance sources.

A broader screening of tetraploid wheat diversity uncovered two resistant accessions: the durum variety Soldur (resistant to WSSMV) and the emmer accession Dic2 (resistant to both WSSMV and SBCMV). In Soldur, WSSMV resistance mapped to a major QTL on chromosome 7A, whereas Dic2 carries two epistatic QTLs on 7A and 7B. For SBCMV resistance in Dic2, phenotyping in France and Italy revealed distinct loci: a major QTL on chromosome 6B in France, and in Italy, a major QTL on 2A, with the 6B QTL detected only by viral content measurements, not symptom scoring.

We sequenced viral isolates from multiple regions in France and Italy. The analyses indicate strong genetic structuring of SBCMV populations between countries, which may underlie the observed differences in QTL efficacy.

P355 - Virulence analysis of Polish isolates of the fungus *Zymoseptoria tritici* causing *Septoria tritici* blotch

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Abstract

Septoria tritici blotch (STB) is one of the most significant leaf diseases of wheat and may cause up to 50% yield loss under favorable conditions. It is considered a high-risk pathogen due to its high potential for adaptation and substantial effective population size. It is estimated that over 70% of the fungicides applied annually to cereal crops in Europe target STB. This high selection pressure can be devastating, as STB has been reported to develop resistance to various classes of fungicides within a single growing season. Similarly, resistance in the host plant can also be overcome in a short period of time. Therefore, continuous monitoring of the pathogen population structure and its virulence against host resistance genes is crucial for developing resistant wheat varieties and promoting sustainable agricultural practices.

The presented study used single-pycnidial isolates of the fungus *Zymoseptoria tritici*, derived from leaves with STB symptoms, collected in various locations in Poland between 2020 and 2025. The virulence profile was determined based on the reaction of the differential set to infection with the fungal isolate. The differential set was composed of 23 wheat varieties/lines containing known Stb resistance genes. The experiments were conducted under controlled environment on seedlings. Tests were evaluated 21 days after inoculation. Plants were assessed in terms of the percentage of second leaf area covered with necrosis (%NEC) and pycnidia (%PYC). Precise determination of disease parameters was made using computer image analysis of infected leaves.

The tested *Z. tritici* isolates exhibited high diversity in terms of both disease parameters. Among the varieties/lines of the differential set, the M3 Synthetic (W-7976) line (containing genes Stb16q and Stb17) exhibited the highest levels of resistance throughout the years, with a maximum NEC value of 8% and no pycnidia formation observed for any of the tested isolates. Most of the tested isolates were virulent against varieties/lines containing genes Stb1, Stb4, Stb5, Stb6, Stb7 and Stb9.

P356 - Integrating NAM and CIM to map stripe rust resistance in spring wheat

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Abstract

Stripe rust, caused by *Puccinia striiformis* Westend. f. sp. *tritici* Erikss. (Pst), is one of the most devastating diseases affecting wheat production. The dynamic and ever-evolving nature of the pathogen poses a continuous challenge, making stripe rust management a never-ending battle for researchers. Among various management strategies, genetic resistance remains the most effective, easy-to-use, and environmentally friendly approach. Therefore, the continuous identification and incorporation of new sources of resistance is essential for breeding resistant wheat cultivars. In this study, we developed a nested association mapping (NAM) population (n = 575), consisting of six recombinant inbred line (RIL) families. The NAM population was developed in the genetic background of the susceptible wheat cultivar Vesper by crossing it with six resistant source lines. Phenotypic data (disease severity %) of the NAM population was recorded for seven years, followed by genotyping using a wheat 7K SNP assay. A robust marker dataset was used to construct linkage maps for each RIL family, and these were further integrated into a consensus map to facilitate joint QTL mapping. In total, 20 major ($\geq 20\%$ of the phenotypic variance) QTL were identified from six RIL families using composite interval mapping (CIM). The most significant and stable QTL from RIL families were QYr.Irdc-1A.1 (RIL family 2: Vesper/P2686), QYr.Irdc-7B.1, QYr.Irdc-7B.2 (RIL family 4: Vesper/P2688), and QYr.Irdc-2B (RIL family 6: Vesper/P2265), with the explained phenotypic variance (PVE) ranging from 22% to 62%. In total, 21 QTL were identified from joint mapping. The overlapping chromosomal regions across multiple RIL families indicate genomic regions consistently contributing stripe rust resistance. Some of the QTL were only mapped through joint mapping, demonstrating the added power of combining information across families. The power to detect the family-specific QTL was limited because RIL families were only segregating for a subset of alleles. The NAM population combines genetic information across families to improve both mapping resolution and power. Thus, the NAM population is a powerful tool for dissecting complex traits and discovering new resistance alleles. We also developed and validated the KASP marker for the QYr.Irdc-2B (RIL family 6: Vesper/P2265) for marker assisted selection.

P357 - Discovery of host susceptibility factors for enhancing fusarium head blight resistance in wheat

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Abstract

Fusarium head blight (FHB), primarily caused by the fungal pathogen *Fusarium graminearum*, remains one of the most devastating diseases of wheat globally, leading to significant yield losses and the accumulation of harmful mycotoxins like deoxynivalenol (DON) in grains. While traditional breeding has focused on introgressing quantitative trait loci (QTL) for resistance, such as *Fhb1*, the complexity of the wheat genome and the polygenic nature of resistance have made the development of immune cultivars elusive. An emerging and powerful alternative strategy involves the identification and modification of host susceptibility (S) genes—plant genes that are actively exploited by pathogens to facilitate infection. We are employing multi-pronged strategies, including genome-wide mutation panels, cytogenetic stocks, and radiation panels, to discover key host factors which make the plants susceptible to FHB. Deletion or loss of function of these genes enhance the resistance of the plants and simultaneously reduce the DON accumulation in grains. These findings shift the paradigm from simply adding resistance genes to strategically “closing the doors” that the pathogen uses to enter. By characterizing these susceptibility factors, this research will provide a novel toolkit for breeders to engineer durable, broad-spectrum resistance, ultimately safeguarding global wheat production and food safety.

P358 - Genome-wide association study reveals enriched diversity for *Pratylenchus thornei* resistance in Watkins' wheat landraces

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Abstract

Pratylenchus thornei (Pt) is one of the most damaging root-lesion nematodes, causing severe yield and economic losses in wheat production and a significant threat to food security. Deployment of cultivars carrying genetic resistance is the best way to manage this globally-distributed pest. Crop wild relatives and landraces are valuable sources of novel resistance to Pt. In this study, we established and screened a wheat landrace diversity panel of 286 genotypes from the Watkins wheat collection, where 7, 12, and 25 genotypes showed resistant, resistant to moderate resistant, and moderate resistant responses against Pt, respectively. Subsequently, genome-wide association studies (GWAS) using the Watkin landrace whole genome sequence data (WatSeq database) and the FarmCPU (Fixed and Random Model Circulating Probability Unification) model (rMVP package v1.4.5), identified genomic regions associated with resistance to Pt. A total of 23 significant Single Nucleotide Polymorphisms (SNPs) associated with Pt resistance were identified at $P < 1 \times 10^{-6}$ [$-\log_{10}(P) = 6.0$] and are present in ten distinct genomic regions, namely, 1D, 2A (two independent regions), 3A, 3B, 3D, 5D, 6A, 6B, and 7D. A major quantitative trait loci (QTL) was detected on chromosome 3D (175.5-181.5 Mb) and was linked with ten SNPs. Comparative genomic study reveals the QTL on the chromosome 3D as novel with the absence of earlier reports of QTLs in this specific genomic region. Hence this study facilitates new insights into the genetic basis of Pt resistant and offers valuable genomic resources to support marker-assisted breeding in wheat.

Keywords: Watkins wheat landraces, *Pratylenchus thornei*, GWAS, and Genetic resistance.

P359 - PGPR priming and reprogramming of stress crosstalk for enhancing resilience to heat-induced spot blotch susceptibility in wheat

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Abstract

Rising temperatures associated with climate change increasingly compromising plant immune capability, intensifying disease severity. Across South Asian wheat belts, infection by *Bipolaris sorokiniana* often intensifies into widespread spot blotch epidemics. This study was aimed to investigate the effect of high temperature on Spot Blotch susceptibility in wheat and evaluated the potential of two plant growth promoting rhizobacteria (PGPR) to restore host resistance. Disease expression was highest between 35-38 °C at 70% relative humidity. High temperature at the time of disease initiation intensified membrane injury and weaken redox barrier, thereby rendering plants more vulnerable to the invasion. PGPR seed priming established a preconditioned defense state marked by attenuation of pathogen-induced oxidative stress, stabilization of membrane integrity, and sustained activation of antioxidative and defense enzymes. PGPR priming led coordinated upregulation of heat shock proteins HSP70, HSP23.5, and HsfA3, and key defense-related genes (PAL, CHS) linking thermotolerance with jasmonate-associated immune signalling helped containment of hypersensitive responses. These findings highlight the prospect of PGPR priming as a sustainable strategy for effectively reprogramming wheat defense architecture to withstand the combined pressures of heat stress and spot blotch infection.

P360 - Integrating avirulence depletion and pantranscriptomics to identify host-specificity factors in blumeria graminis

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Abstract

Global wheat production is negatively impacted by the obligate biotrophic fungus *Blumeria graminis*, which causes powdery mildew disease. Certain lineages of the pathogen are only able to infect and reproduce on specific wheat species. *Blumeria graminis* occurs as two formae speciales, with f. sp. tritici (Bgt) primarily infecting hexaploid wheat and f. sp. dicocci (Bgdic) mainly specialized on wild emmer wheat. However, some hexaploid wheat varieties display susceptibility to both formae speciales, making this pathosystem a suitable model for studying host specialization. A major limitation in understanding host specialization is the limited knowledge about its underlying genetic components.

In this research project, we utilize the recently established avirulence depletion (AD) assay to identify potential host-specificity factors in different *Blumeria graminis* isolates.

The assay is based on the depletion of detrimental alleles when a haploid fungal F1 population is grown on resistant wheat lines. Crosses between sexually compatible Bgt and Bgdic isolates are performed to generate haploid fungal F1 populations. These populations are then subjected to selection on a resistant wheat line, while populations grown on a susceptible line are used as controls. Following selection, fungal bulks grown on both resistant and susceptible lines are sequenced, and differences in allele counts are analyzed to identify genomic regions showing allele depletion and containing potential candidates for host-specificity factors. After successfully performing sexual crosses between several Bgt and Bgdic isolates, we identified multiple genomic regions that control host specificity. Using pangenomic and newly created pantranscriptomic resources of the *Blumeria graminis* species complex, we will further characterize the genetic components within the identified candidate regions that determine host specificity in different lineages of *B. graminis*. Our project will provide important insights into the evolution of host specificity in fungal pathogens towards closely related host species.

P361 - Rust resistance in a changing world as key for future cereal yields

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Abstract

Fungal pathogens belonging to the genus *Puccinia* are continuous threats for agriculture, specifically for all cereals. Abundance and disease pressure vary through and within seasons and have globally a major impact on cereal production, including all wheat forms. A major challenge is added by the pathogens, through their dynamic behaviour in terms of virulence and environmental adaptation.

Therefore, we need to gather information of both the hosts and the respective pathogens as well as innovative approaches for enhancing resistance enabling durable resistance and yield.

Virulence dynamic will be shown for *Puccinia graminis* f.sp. *secalis* and *Puccinia graminis* f.sp. *avenae* and respective implications for rye and oat resistance. Having a zoom to wheat, new appearing Yr15 virulence in the race "Champion" within the Warrior(-)/PstS10 group of *Puccinia striiformis* f.sp. *tritici* raising new concerns for wheat production in Germany. That suggests first a better knowledge about present resistances in elite cultivars and a open access to this information. Second, this gene-by-gene resistance-virulence problem speaks for more radical approaches exploiting natural, durable resistances such as non-host resistance. We will show some initial results about it.

P362 - Activation of exotic wheat genetic resources for disease resistance

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Abstract

The EXOGENE initiative aims to expand the genetic basis of wheat improvement by mobilizing underutilized and geographically distinct germplasm. The focus is on integrating wild relatives, alien introgression materials, and historically diverse wheat collections into a harmonized phenotyping framework for disease resistance.

A comprehensive *Triticum araraticum* collection comprising 285 genotypes was assembled by integrating a Turkish core collection with additional genebank accessions from worldwide origins. In parallel, a diverse panel of alien introgression, substitution, and addition lines derived from crosses with *Aegilops* spp. and other wild relatives was evaluated. Furthermore, a collection of historic and modern Australian wheat varieties was included to assess resistance alleles that evolved under geographically isolated breeding conditions.

All materials were screened for resistance to leaf rust and yellow rust under controlled conditions. Across panels, a wide and continuous phenotypic distribution was observed, ranging from high susceptibility to strong resistance. This confirms substantial exploitable diversity within and across genetic backgrounds. Detailed statistical analyses are ongoing.

To establish a genomic framework, the *T. araraticum* collection will be genotyped by sequencing to remove redundant or misclassified accessions and to define population structure. A genetically representative accession will be selected for de novo whole-genome assembly to enable high-resolution mapping and allele mining. Genotypic characterization of additional panels will support the identification and prioritization of resistance loci for downstream validation and pre-breeding.

The combined phenotypic and genomic efforts provide a structured basis for activating exotic genetic resources and translating novel resistance variation into wheat improvement pipelines.

P363 - Genome wide association studies and expression analyses identify candidate genes for spot blotch resistance in bread wheat

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Abstract

Spot blotch (SB), caused by *Bipolaris sorokiniana*, threatens global wheat production. We evaluated 1,500 elite wheat lines for spot blotch across two environments to identify genomic regions and candidate genes conferring resistance. Disease severity, measured as area under the disease progress curve (AUDPC), was negatively correlated with days to heading (DH) and stay-green traits (SGTs). Genome-wide association studies (GWAS) using four models (MLM, FarmCPU, BLINK, SUPER) identified seven and three stable MTAs for AUDPC and SGTs, respectively, with three (3B_6127880, 5B_546704556, 5B_546132836) common to both traits. To reduce the confounding effects of DH, a separate GWAS was conducted on a subset of genotypes with similar heading dates, confirming 3B_6127880 as a consistent locus for AUDPC, located near previously known SB QTLs on 3BS. Several other putative MTAs and haplotypes associated with AUDPC and SGTs were identified. A time-course analysis of candidate genes corresponding to the top associated SNPs revealed differential expression in resistant (Chirya 3) and susceptible (Sonalka) genotypes under spot blotch infection. The identified SNPs, alleles, haplotypes, and candidate genes may be used in marker-assisted selection and breeding programs to develop wheat varieties with enhanced resistance to spot blotch.

P364 - Identification of stable and high-effect loci for durable leaf rust resistance in bread wheat through multi-environment Genome-Wide Association Mapping

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Abstract

Leaf rust, caused by *Puccinia triticina*, remains a major constraint to wheat productivity worldwide, particularly in South Asia, where diverse agro-ecologies favor disease proliferation. Developing durable adult plant resistance (APR) through genomic approaches is critical for sustainable wheat production. This study dissected the genetic architecture of leaf rust resistance in a diverse panel of 191 bread wheat genotypes evaluated across 11 locations in Pakistan during the 2021-2023 growing seasons. Disease severity was quantified using the Average Coefficient of Infection (ACI), Country Average Relative Percent Attack (CARPA), and Relative Resistance Index (RRI), enabling a robust multi-trait assessment under natural epidemic conditions. Genotyping was performed using 37,401 high-quality SNP markers, and genome-wide association analysis was conducted in GAPIT using a mixed linear model (MLM) accounting for population structure and kinship. A total of 37 significant marker-trait associations (MTAs) were identified, including eight stable loci detected across multiple environments. Notably, SNP 3A_726475174 was consistently identified in eight environments, explaining up to 16.75% of phenotypic variation, highlighting its potential as a broad-spectrum resistance locus. Another strong-effect locus, 6A_303040004, explained up to 41.42% of phenotypic variation, indicating a major environment-specific resistance effect. Additional stable loci were detected on chromosomes 1A, 2B, 4D, and 5B, confirming the polygenic nature of APR. GGE biplot analysis revealed substantial genotype × environment interaction, with PC1 and PC2 explaining 89.29% of total variation. Several genotypes (G68, G105, G146, G171, and G185) emerged as sector winners, demonstrating superior resistance under specific environmental conditions. The identification of stable and high-effect resistance loci provides valuable genomic resources for marker-assisted selection and genomic selection aimed at developing durable leaf rust-resistant wheat cultivars for South Asia and similar agro-climatic regions.

P365 - Development of a first comprehensive Near Isogenic line (NIL) series for stem rust resistance in a spring wheat background

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Abstract

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is a major disease affecting wheat globally. It can lead to complete crop failure and/or result in unusable grain in susceptible varieties. The most sustainable and cost-effective disease management strategy is to develop resistant cultivars. However, the effectiveness of the deployed resistance genes requires continuous surveillance as the pathogen evolves. Stem rust laboratories in various countries/regions, including Australia, South and East Africa, North America, and India, use stem rust differential sets tailored to their specific national/regional/international surveillance requirements. In most cases, the differential sets used are collections of genotypes each carrying a specific resistance. However, most of these differentials lack a common genetic background, making it hard to attribute phenotypic differences between hosts and pathogens, which confuses interpreting various incompatibility infection types and comparing resistance genes. Near-isogenic lines (NILs) are powerful resources for understanding pathogen virulence, characterising resistance genes, and precisely assessing gene effects while minimising genetic background variation. Here, we present a first report on the development of a comprehensive set of stem rust NILs in a susceptible spring wheat background 'CDAV' (developed by Park et al., unpublished). Using a classical backcrossing approach (6-7 backcrosses + 6 selfings) complemented with phenotypic/genotypic selection, we developed a set of 20 stem rust NILs carrying 20 all stage resistance (ASR) genes Sr5, Sr7a, Sr8b, Sr9g, Sr11, Sr13, Sr21, Sr22, Sr25, Sr25, Sr26, Sr27, Sr29, Sr31, Sr32, Sr33, Sr38, Sr42, Sr44, Sr47 and three adult plant resistance (APR) genes Sr55, Sr57 and Sr58. The final developed lines were validated by an array of pathotypes and/or markers confirming the presence of the target gene in each line. We are now in process of final seed increase to share these lines with international rust research groups. Development of a second cohort of ten additional ASR NILs is currently in progress to further expand this series. The developed NILs serve as a valuable global germplasm resource, contributing significantly to stem rust surveillance, gene mapping and cloning, gene function and interaction studies, and the estimation of stem rust yield losses associated with each individual resistance gene.

P366 - Exploring triticale as a novel source for wheat blast resistance

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Abstract

Wheat blast (WB), caused by *Magnaporthe oryzae* pathotype *Triticum* (MoT), poses a significant threat to global food security and has spread from South America to Bangladesh and Zambia in the last decade. Current resistance relies heavily on the 2NS translocation, which is increasingly becoming vulnerable to evolving pathogen isolates. Identifying novel, non-2NS resistance sources is therefore a high priority for wheat improvement programs. Triticale ($\times$ *Triticosecale* Wittmack), a wheat-rye hybrid, serves as a reservoir of genetic diversity, contributing historical resistance genes such as Pm8 and Sr31. This study evaluates potential of triticale's for WB resistance in field experiments. A panel of 195 modern triticale lines was evaluated in field trials in Jashore, Bangladesh (2024-2026), and a bi-modal distribution of disease response was observed, indicating the presence of major resistance gene(s). Crucially, diagnostic markers confirmed that these resistant lines lack the 2NS translocation, suggesting a novel genetic basis. Genotyping was conducted using 20K SNP chips for triticale, and GWAS identified two major additive QTL located on the distal regions of chromosome arms 4RS (explaining ~12% PVE) and 4RL (explaining ~19% PVE). Ongoing research involves validating these results across diverse environments in Bangladesh and Bolivia using another triticale panel comprising 282 historical breeding lines collected in CIMMYT's germplasm bank. Furthermore, bi-parental populations are under development for fine-mapping, while pre-breeding strategies aim to introgress these 4R-derived QTL into elite bread wheat backgrounds. This work establishes triticale as a critical genetic resource for diversifying the resistance landscape against wheat blast.

P367 - Exploration of wheat lines with tolerance to *Fusarium mycotoxin deoxynivalenol*

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Abstract

Deoxynivalenol (DON), a mycotoxin produced by *Fusarium* species causing *Fusarium* head blight and *Fusarium* crown rot, poses serious health risks to humans and livestock. Therefore, the development of wheat lines with low DON accumulation is an urgent priority. Root responses to DON have been recognized as potentially associated with DON accumulation in spikes, suggesting the importance of root-based evaluation. In this study, we evaluated the DON responses of 96 accessions from the Japanese wheat core collection using DON-induced root growth inhibition as an indicator. Seedlings were treated with 8 ppm DON and root length was measured among the accessions, and substantial phenotypic variation in response to DON was observed. These results demonstrate the genetic diversity for DON tolerance in Japanese wheat germplasm and suggest that root-based screening may provide a practical and efficient approach for identifying DON-tolerant lines for wheat breeding.

P368 - Tracking the evolution of *Puccinia graminis* f. sp. *tritici* and its impact on the resistance of wheat cultivars and breeding lines in South Africa

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Abstract

Stem rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), remains a major challenge to wheat production in South Africa (SA). To monitor virulence changes in the Pgt population, annual surveys were conducted between 2016 and 2024 across major wheat growing regions. The virulence pattern of Pgt isolates was determined using standard differentials. From 907 isolates pathotyped, 14 races were identified, of which nine were first reports. The predominant races were BFGSF+Sr9h,27,Kw (2SA5) (28% frequency), TTKSF+Sr8b (2SA88) (22%) and BPGSC+Sr9h,27,Kiewiet (2SA104) (20%). Of the newly detected races, seven appeared between 2021 and 2024, indicating a significant increase in the emergence of new races in recent years. Most of the new races combined virulence to resistance genes already ineffective in SA. However, TTKTF+Sr8b (2SA125) gained virulence to Sr25, Sr42 and SrTmp, which were previously effective in SA. Seedling evaluation of 138 commercial wheat cultivars and breeding lines showed that race PTKST+Sr8b (2SA107) was the most virulent, affecting 70% of entries, followed closely by the new race PTKSP+Sr8b (2SA36/24) (69%). Virulence to wheat entries among the remaining new races ranged from 5% by BFGSC+Sr9h,27,Kw,Satu (2SA25) to 54% by PTKSK+Sr8b (2SA42). Cultivar responses remained largely unchanged except for one cultivar in the commercialization pipeline and a few breeding lines that became susceptible to specific new races. Molecular characterization using microsatellite markers combined with virulence data indicated that the population structure of Pgt in SA is shaped by both local mutations and foreign incursions. These findings underscore the importance of sustained monitoring of Pgt race phenotypes and genotypes to timeously detect new races, evaluate cultivar responses and provide timely guidance to wheat producers and breeders.

P369 - Contrasting wheat resistances shape plant-to-plant field spread of foliar disease in cultivar mixtures

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Abstract

Cultivar mixtures represent an agro-ecological practice which mitigates disease spread in cropping systems, allowing for improved resilience and lower reliance on chemical inputs. While mechanisms have been proposed to explain these plant-to-plant interactions, quantitative assessments at the plant level within field conditions remain limited. This study investigated field disease spread in wheat cultivar mixtures, focusing on row-to-row propagation of tan spot disease, caused by *Pyrenophora tritici-repentis*.

A screening protocol was developed to assess spring wheat resistance against tan spot disease, on a collection of genotypes (134 from the Nordic Genebank and 165 breeding lines). Disease severity was recorded from 1-9, depending on leaf lesions. Based on these results, genotypes exhibiting contrasting levels of resistance were subsequently planted in field trials. Two resistant and two susceptible cultivars were planted, in pure stands or in pairs of cultivars. Plots were 1m², comprised of 6 rows of pure or alternating cultivars. One edge row of each plot was artificially inoculated. Disease spread in the rows was monitored by weekly counts of leaves with tan spot lesions. Using those measurements, the Area Under Disease Progress Curve (AUDPC) of each row was computed, providing insight into spatial and temporal disease progression.

Tan spot development within a row was affected significantly by wheat genetic resistance of the row, level of resistance of the neighbouring row, and distance from the inoculum (Wald z-test, respective p-values: 2.8e-10, 0.018, < 2.2e-16). Direct genetic effects (i.e. cultivar effect) ranged from -27% to +38% in EMMean of AUDPC. The distance from the inoculum (i.e. row effect) altered disease progression from +75% for the closest row, to -32% for the furthest row. The resistance type in the neighbouring row affected EMMean AUDPC in the focal row, from -8% for a resistant neighbour, to +9% for a susceptible neighbour. Additionally, synergistic mixture effects were not detected, indicating that disease suppression in mixtures might be additive at small scale.

This study quantified the impact of contrasting disease resistance levels within the same field on disease spread. These findings support that ecological principles can improve disease management, but the effects observed remained purely additive.

P370 - Deciphering spot blotch resistance in wheat through multi-locus gwas and gene expression analysis

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Abstract

In warm, humid climates, *Bipolaris sorokiniana* causes spot blotch, a severe disease that severely reduces wheat production. We performed a thorough genome-wide association study (GWAS) on a broad panel of 6,031 wheat germplasm lines that were genotyped using a 35k microarray chip and phenotyped over two years in three different conditions in order to uncover the genetic architecture driving spot blotch resistance. The whole global set (Whole_set) and three subpopulations Indian_set, n=1,101, Mexican_set, n=225, and released varieties, n=215) were subjected to marker-trait association analysis.

For MTAs BLINK, FarmCPU, and MLM GWAS models were used to identify 43 important SNPs in the Whole_set across various contexts. Notably, SNP Affx-88601840 on chromosome 5A demonstrated a persistent connection with large effects (up to 41.35) and extremely significant p-values (up to 7.49E-17) in Ayodhya_1, BHU_2, and BISA_2 settings. On chromosome 6A, SNP Affx-92539894 showed a highly significant correlation ($p = 2.64E-20$) with adverse effects, suggesting a resistance allele. Affx-92324876 on chromosome 1A in Variety_set, Affx-92776444 on chromosome 5B in Indian_set, and Affx-92422028 on chromosome 2A in Mexican_set are examples of population-specific SNPs that were found.

Differentially expressed genes close to important SNPs were identified by integrating GWAS results with transcriptome data, offering insights into possible candidate genes. Under spot blotch stress, a number of defense-related genes, such as TraesCS1B02G108200 (VIN3-like protein 1), TraesCS4D02G296000 (protein TIFY 11b-like) involved in jasmonate signaling, TraesCS5B02G366700 (mitochondrial amidoxime reducing component 2-like), and TraesCS6B02G450200 (aquaporin PIP1-5-like). Overrepresentation of defense-related biological processes, such as regulation of defensive response (GO:0031347), regulation of jasmonic acid mediated signaling pathway (GO:2000022), and glucan catabolic process (GO:0009251), was found by gene ontology enrichment analysis of genes close to relevant SNPs. These discoveries offer useful molecular markers and potential genes for marker-assisted breeding of wheat cultivars resistant to spot blotch.

P371 - Fusarium, ergot, and midge damage in Canadian wheat across >30 years and >250,000 samples

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Abstract

Many biotic factors can negatively affect wheat grain quality and safety, including insect damage from the orange wheat blossom midge, as well as fungal damage due to Fusarium Head Blight (FHB) and ergot. Midge feeding can cause kernels to become shriveled and deformed; in cases of severe damage, kernels can also be discolored and contaminated by fungi. FHB can cause kernels to be shriveled and discolored (chalky-white to pinkish-orange), as well as contaminate kernels with fungal mycotoxins such as trichothecenes; however, the mycotoxins present may vary depending on the fungal species and strain present. Ergot replaces kernels with sclerotia bodies that are a different size and density to normal grain, are often dark purple-black in appearance, and contain mycotoxins such as alkaloids. Canada has a robust grain grading and monitoring system to ensure damaged and contaminated grains remain within acceptable levels and that Canadian wheat meets the quality and safety requirements of domestic and export markets. Since 1995, the Harvest Sample Program of the Canadian Grain Commission has assessed the occurrence and severity of damaged and contaminated grain for over 250,000 wheat samples originating from across Canada. The dataset presented here is one of the largest of its kind, and provides valuable information on trends of fungal and insect damage of grain. The results of our monitoring identified regional and temporal differences in grain damage/contamination. The dynamics are likely the result of complex interactions between changes in management practices, emergence or introduction of pathogens, and climate/weather. We have layered our monitoring data with variety information, pathogen and mycotoxin testing, as well as weather and environment data, to guide management and breeding decisions.

P372 - Mycotoxin profiles of Tritordeum grain after artificial spike inoculation with Fusarium culmorum W.G. Smith

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Abstract

Fusarium head blight (FHB) is a fungal disease that affects small grain cereals such as wheat, barley, and oats worldwide. The disease leads to the accumulation of mycotoxins in grain, and it can cause considerable economic losses by decreasing grain yields and grain quality.

The responses to artificial spike inoculation with *Fusarium culmorum* were compared in 11 Tritordeum lines, two durum wheat cultivars and one naked barley cultivar. Inoculation of Tritordeum spikes led to a significant decrease in spike weight, kernel weight per spike, and kernel weight (by 18, 28, and 16%, respectively). Durum wheat responded most strongly to inoculation, particularly with regard to spike weight and kernel weight per spike (decrease of 42% and 53%, respectively). Inoculation induced a significant increase in the total concentration of trichothecenes (9902 vs 558 µg/kg in non-inoculated control) and other *Fusarium* toxins (40,207 vs 3250 µg/kg in non-inoculated control) in Tritordeum grain. The content of three *Alternaria* toxins was not significantly modified by inoculation. The principal component analysis (PCA) of all fungal metabolites supported the discrimination of control and inoculated grain, and the results were used to divide the examined Tritordeum lines into two groups with different mycotoxin profiles. The first group (five lines) was more similar to naked barley, whereas the second group (six lines) showed greater similarity to durum wheat. The analyzed Tritordeum lines responded differently to inoculation, which suggests that lines with a low propensity to accumulate *Fusarium* toxins in grain can be selected from the existing gene pool. The study also demonstrated that Tritordeum grain accumulates significantly smaller amounts of mycotoxins than durum wheat grain.

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P373 - Additive effects of key environmental factor combinations drive wheat powdery mildew incidence across growth stages under climate change

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Abstract

Common wheat (*Triticum aestivum* L.) is a staple crop worldwide, contributing more than 20% of global caloric and protein intake. Wheat powdery mildew is a major constraint on yield stability, causing losses of up to 50% during severe epidemics. To clarify its environmental determinants and underlying mechanisms, we integrated large-scale climatic and epidemiological datasets. We constructed a large-scale, high-dimensional climatic feature matrix derived from 13 CMIP6 variables and integrated it with disease records from 199 Chinese cities spanning 2008-2021. Eight machine learning models were evaluated, with XGBoost and Random Forest demonstrating superior performance ($R^2 = 0.72-0.75$); the incorporation of Fourier features further improved accuracy by approximately 5%. Screening 8,191 variable combinations revealed significant additive effects among environmental drivers. A four-factor set—crop index, surface pressure, near-surface specific humidity, and surface shortwave radiation—retained 98% of the predictive power achieved by all 13 variables and outperformed random four-factor sets by 40-45%. Projections identified Jiangsu Province as a persistent disease hotspot. Further analyses will determine the critical growth stages during which this environmental signature most strongly influences disease development. Overall, our research elucidates stage-specific climatic sensitivity and additive interactions underlying wheat powdery mildew incidence, providing a mechanistic basis for disease prediction under climate change.

P374 - Identification and cloning of a greenbug resistance gene from *Aegilops tauschii*

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Abstract

The greenbug, *Schizaphis graminum* (Rondani), is a highly destructive pest affecting wheat, sorghum, and barley, and serves as a vector for the severe barley yellow dwarf virus. Although several genes conferring resistance to greenbug have been identified in wheat and its relatives, none have been cloned to date. In the present study, we conducted a genome-wide association analysis using a panel of 260 sequenced *Aegilops tauschii* accessions and refined the resistance locus to a 300-kilobase region on the long arm of chromosome 7D. By employing pangenome sequences and haplotype analysis of the *Ae. tauschii* panel, we further narrowed this region and successfully cloned a candidate gene associated with greenbug resistance. Transgenic expression of this candidate gene in the susceptible wheat cultivar Fielder imparted resistance to multiple greenbug biotypes, whereas CRISPR/Cas9-mediated knockout of the gene in a greenbug-resistant wheat line resulted in susceptibility. Furthermore, we investigated the evolutionary history of the resistance gene and characterized the type and function of the encoded protein. Transcriptomic and metabolomic analyses of the transgenic lines revealed potential mechanisms underpinning greenbug resistance. Together, these findings provide a solid foundation for advancing our understanding of plant-insect interactions and offer a valuable genetic resource for developing sustainable pest resistance in cereal crops.

P375 - Molecular identification and validation of an adult-plant stripe rust resistance gene in the wheat cultivar Chuanmai 62

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Abstract

Molecular identification and validation of an adult-plant stripe rust resistance gene in the wheat cultivar Chuanmai 62

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The wheat cultivar Chuanmai 62 (CM62), released in Sichuan, China, has demonstrated stable high-temperature adult-plant (HTAP) resistance to stripe rust (*Puccinia striiformis* f. sp. *tritici*, Pst) for over a decade. To identify the underlying resistance genes, CM62 was crossed with the susceptible cultivar Avocet S to develop a recombinant inbred line (RIL) population. This population was evaluated under artificial inoculation in multi-location field trials (Xindu, Pixian, Mianyang, Linshui, Jintang, and Xichong) from 2016 to 2022 (excluding 2017). Genotyping was performed using the 55K Illumina iSelect wheat SNP chip, generating 2,562 polymorphic markers for quantitative trait locus (QTL) mapping. Six putative QTL were detected, among which two major QTL showed stable and significant resistance effects across >10 tested environments: A novel QTL (QYr.CM62-2BL) on chromosome 2BL, explaining up to 28.2% of phenotypic variation, likely represents a new resistance gene. A major QTL on chromosome 2A (QYr.CM62-2AS), which aligns with the reported Yr17 based on comparative analysis with known Yr genes/QTL. Additionally, minor-effect QTL were identified on chromosomes 1BL, 5AL, 6B, and 7DL. To facilitate molecular breeding, two KASP markers (KASP-AX-109507945 and KASP-AX-109844182) were developed for QYr.CM62-2BL. Validation using 94 wheat cultivars from Sichuan and Jiangsu provinces confirmed their high polymorphism, and these markers were successfully applied in marker-assisted selection (MAS). Ten highly resistant breeding lines derived from CM62 were identified, all carrying QYr.CM62-2BL. Collectively, our results demonstrate that the durable HTAP resistance in CM62 is governed by multiple additive QTL, with QYr.CM62-2BL as a key genetic contributor.

P376 - Uncovering masked blast resistance genes through chromosome dosage manipulation in allohexaploid wheat

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Abstract

Allohexaploid wheat has three homoeologous gene copies derived from different Triticeae species, generating functional redundancy that buffers negative effects of recessive deleterious mutations. In an allohexaploid background, the phenotypic effects of recessive alleles are relatively constrained compared with those of dominant alleles. Genome sequence information for allohexaploid wheat has rapidly accumulated and is widely available. However, functional characterization of alleles, particularly recessive alleles, remains limited. Wheat blast is one of the most devastating disease reducing wheat production. Resistance genes against wheat blast have been extensively studied in the primary and secondary gene pools of Triticeae, facilitating the identification of novel resistance genes. Nevertheless, due to the masking effects of recessive phenotypes, resistance genes that have been overlooked may remain concealed within the genome. To uncover such overlooked blast resistance genes, nullitetrasonic lines of *Triticum aestivum* L. cv. 'Chinese Spring' were evaluated for wheat blast resistance by inoculation with the wheat blast Br48 isolate. 'Chinese Spring' exhibits intermediate resistance against Br48 isolate. A comparison of blast disease resistance between 'Chinese Spring' and 37 nullisomic-tetrasomic lines revealed that most lines showed resistance levels comparable to those of 'Chinese Spring', whereas four lines were more susceptible and one line was more resistant. Notably, a nullisomic-tetrasomic line lacking both copies of one homoeologous chromosome and carrying four copies of its corresponding homoeologous chromosome exhibited stronger resistance than 'Chinese Spring'. In contrast, the reciprocal nullisomic-tetrasomic line, in which the chromosome dosage was reversed, showed higher susceptibility than 'Chinese Spring'. These findings suggest that alterations in chromosome dosage result in quantitative changes in blast disease resistance and that this homoeologous chromosome pair of 'Chinese Spring' harbors gene(s) involved in blast resistance or suppression of blast resistance. This case study supports that previously unexploited beneficial alleles may exist in allohexaploid wheat.

P377 - Identification of stripe rust resistance loci in Gansu wheat landraces using genome-wide association analysis

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Abstract

Stripe rust seriously threatens global wheat production. Identifying and using favorable resistance loci from landraces can enhance the genetic diversity and durability of resistance in modern wheat cultivars. In this study, we phenotyped 376 wheat landraces from Gansu for resistance through seedling inoculation with race CYR34 and multi-year field trials across six environments. Genotyping was performed using a 16K SNP array and known gene markers. A total of seven significant quantitative trait loci were detected at the seedling stage, located on chromosomes 2A, 2D, 3B, 3D, 4B, and 7A, respectively. Four significant and stable QTLs and multipathogen adult-plant resistance gene Yr18 were identified at the adult plant stage. Among them, Yr.hzau-4B was consistently detected across both seedling and adult plant stages, explaining approximately 9.46% and 10.55% of the phenotypic variance, respectively. Haplotype analysis revealed that lines carrying the favorable haplotype of Yr.hzau-4B showed reductions in mean infection type and disease severity by approximately 0.6% and 32.4%, respectively, compared to lines carrying the unfavorable haplotype. Additive interaction analysis further indicated a decreasing trend in both IT and DS with an increasing number of favorable haplotypes. Additionally, a KASP molecular marker for Yr.hzau-4B was developed and validated in the population. Integrated candidate gene analysis identified 30 putative resistance-related genes, encompassing gene families such as kinases and transporters. These findings provide novel genetic loci and breeder friendly molecular markers to improve stripe rust resistance in wheat, offering valuable resources for enhancing resistance breeding efforts.

P378 - Identification and dissection of seedling-stage resistance loci for Septoria tritici blotch (STB) in a Global collection of landraces representative of the *Triticum turgidum* ssp. *germplasm*

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Abstract

Septoria tritici blotch (STB), caused by *Zymoseptoria tritici*, is a major foliar disease of wheat that threatens yield stability, particularly under changing climatic conditions. Identification of genetic resistance is essential to reduce fungicide dependence and support sustainable breeding strategies. This study aimed to identify and dissect seedling-stage resistance loci to STB in a diverse durum wheat panel using genome-wide association analysis. The association panel consisted of tetraploid wheat (*Triticum turgidum* L.) accessions, including 612 accessions categorized into 8 main clades or lineages: Horn of Africa to Asia_Ethiopia (*T. aethiopicum*), Horn of Africa_to Transcaucasia (*T. carthlicum*), Fertile Crescent to SouthWestAsia_Iran_Iraq_ (*T. durum syriacum*), SouthWest Asia to Iran (*T. Turanicum*), Fertile Crescent to Balkans_ (*T. turgidum*), Turkey to Eastern Europe, Egypt-to-Cyprous_WestNA_Iberia, _central-western North African coastal region (*T. durum africanum*). a set of control cultivars. Five *Z. tritici* isolates with contrasting geographic origins and virulence profiles were used for inoculation: UNIBO 28.2 (Italy), INRA13-TM0156 (Tunisia), and INRA16-LG1217 (France). Seedling-stage resistance was evaluated using four quantitative traits based on the area under the disease progress curve (AUDPC) for: greenness (G.AUDPC), necrotic (N.AUDPC), chlorotic (C.AUDPC), and sporulating (P.AUDPC) leaf areas, enabling a detailed dissection of disease components. A genome-wide association study (GWAS) was conducted using the 90K Illumina iSelect SNP array, accounting for population structure and subpopulation-specific effects.

Across traits and isolates, 51 significant quantitative trait loci (QTLs) were identified, organized into QTL clusters based on the overlapping significance for the considered traits. This highlights the highly quantitative architecture of seedling resistance to STB.

Notably, a locus on chromosome 7A (Qstb.ubo.7A.1) co-localized with the known resistance gene *TmStb1*, validating the robustness of the analysis. In addition, several novel loci associated with specific disease components were detected. These findings provide valuable molecular targets for marker-assisted selection and contribute to a deeper understanding of the genetic basis of seedling-stage STB resistance in durum wheat.

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P379 - Multi-locus GWAS for grain contents of eight minerals in bread wheat (*Triticum aestivum* L.)

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Abstract

Wheat (*Triticum aestivum* L.) is a vital cereal crop globally, providing essential carbohydrates, proteins, vitamins and a number of minerals in the grain. However, the grains are often deficient for important micronutrients. In the present study, an association panel consisting of 225 wheat genotypes, constituting a spring wheat reference set (SWRS), was evaluated for three years (2020-2023) in a simple lattice design with two replications at Research Farm of Chaudhary Charan Singh University, Meerut, Uttar Pradesh, India. The panel was genotyped for 17,934 SNPs and the grain contents of the following eight mineral nutrients were estimated: magnesium (Mg), calcium (Ca), manganese (Mn), selenium (Se), aluminium (Al), Cobalt (Co), Cadmium (Cd) and silver (Ag). The genotypes x environment interactions were significant for all the mineral nutrient contents. A positive association was also observed among grain contents of different minerals. The analysis of variance (ANOVA), pairwise correlation analysis (Pearson's method) and Best Linear Unbiased predictor (BLUP) were performed using Agricolae, Performance and phenotype R packages respectively. The multi-locus genome-wide association study (ML-GWAS) was performed using the following six different models like mrMLM, FASTmrMLM, FASTmrEMMA, pLARmEB, ISIS EM-BLASSO, and pkWmEB, with the help of mrMLM package. A total of 647 significant ($-\log_{10} [p\text{-value}] \geq 3$) QTNs associated with the traits were identified, of which 18 QTNs were stable (detected in the all the four data sets). A total of 1261 candidate genes were also identified using all the 647 QTNs. The maximum number of CGs were identified for Ag (307) and minimum (69) for Al. The QTNs and important CGs, identified in the present study, may be useful for future studies and in breeding programme for the development of nutrient rich wheat varieties after validation.

P380 - Endoplasmic reticulum stress remodelling by Lunapark proteins: a transcriptomic dissection in model and wheat plants

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Abstract

The endoplasmic reticulum (ER) plays a central role in protein folding, quality control, and lipid biosynthesis, thereby maintaining cellular homeostasis under both optimal and stressful conditions. ER stress arises when unfolded proteins accumulate, activating the unfolded protein response (UPR) to restore proteostasis. In this study, we investigated the role of Lunapark (LNP) proteins in regulating transcriptional responses in *Arabidopsis thaliana* and wheat (*Triticum aestivum*). Differentially expressed genes (DEGs) were identified in *Inp1/Inp2* knock-down mutants and *AtLNP1* overexpression lines compared with wild type in *Arabidopsis*. LNP overexpression induced extensive transcriptional reprogramming, with a majority of downregulated genes associated with stress responses, hormone signalling, and metabolic pathways. Gene ontology (GO) analysis revealed enrichment of processes including oxidative stress response, plant-pathogen interaction, and MAPK signalling, suggesting a role for LNP proteins in stress adaptation. In wheat, *TaLNP1* overexpression produced a contrasting profile, with a higher proportion of upregulated genes, particularly those linked to stress adaptation and metabolic homeostasis. These results indicate both conserved and divergent roles of Lunapark in ER stress regulation between monocots and dicots. Our findings provide the first comparative transcriptomic analysis of LNP proteins in *Arabidopsis* and wheat and highlight their role in ER stress adaptation and plant stress tolerance. Understanding LNP protein function may offer new strategies to enhance crop resilience under environmental challenges.

Keywords: *Wheat, RNAseq, endoplasmic reticulum (ER), Lunapark, ER stress*

P381 - From farmers' fields to future harvests: yield and quality evaluation of new wheat varieties under dry season conditions in morocco

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Abstract

Wheat production in Morocco faces increasing challenges due to recurrent drought, climate variability, and the need to meet growing demand for both quantity and quality of grain. Identifying wheat varieties that combine high yield potential with desirable grain quality under water-limited conditions is therefore a key priority. This study aimed to evaluate the agronomic performance, yield potential, and grain quality of newly developed wheat varieties through on-farm trials conducted during the dry season in collaboration with local farmers.

Field trials were established across several farmer-managed fields using a comparative design that included newly released varieties alongside commonly grown local varieties used as checks. Conducting the experiments directly in farmers' fields enabled the assessment of varietal performance under realistic production conditions and typical management practices. Data were collected on grain yield and key agronomic traits such as plant height, phenological stages, and adaptation to prevailing environmental stresses. In addition, grain quality parameters, including, test weight, grain size, and selected end-use quality indicators, such as grain protein content, yellow index (Durum wheat), starch and fat content and other traits; were evaluated to determine the suitability of the varieties for market and processing requirements.

The results revealed significant variability among the tested varieties. Several new wheat ones exhibited higher yield potential than the farmers' standard varieties while maintaining favorable grain quality characteristics. These varieties demonstrated promising adaptation to dry-season conditions, suggesting their potential to enhance both productivity and grain value in local production systems.

The study highlights the importance of participatory on-farm trials in bridging the gap between breeding programs and farmers' needs. The identification of high-performing and quality wheat varieties under dry-season conditions provides valuable information for variety release, dissemination, and adoption strategies aimed at strengthening wheat production systems in Morocco.

Keywords: wheat, on-farm trials, grain yield, grain quality, dry season, varietal evaluation, Morocco.

P382 - Development of a high molecular weight glutenin subunits master set from GLU-B1 locus

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Abstract

Gluten quality is a key factor in the wheat bread-making process. Gluten is a viscoelastic protein network formed after mixing and hydrating wheat flour, providing elasticity and extensibility of the dough. Among all the proteins that are part of the viscoelastic network are the High Molecular Weight Glutenin Subunits (HMW-GS). In common wheat, these subunits are encoded by three loci: GLU-A1, GLU-B1, and GLU-D1, each one coding for two HMW-GS (x and y subunits).

Due to the importance of these genes, hundreds of studies have been focused on identifying their variability among different sets. This variability has been classified in the Wheat Genome Catalogue (WGC) framework. Most of the data regarding these alleles have not been curated as they were generated in independent studies and it is not possible to determine whether the documented variability reflects true genetic diversity or is overestimated. This study focuses on analyzing the current variability for the GLU-B1 locus, collecting the germplasm associated with the described variability.

It was possible to collect and compare most of the germplasm described in the WGC. Our comparative analysis revealed that a significant part of the Glu-B1 alleles could be correctly differentiated using SDS-PAGE, validating their unique mobility in gels. However, some alleles showed identical electrophoretic mobility having been previously described as distinct using complementary techniques. Furthermore, some alleles that were previously considered different on SDS-PAGE turned out to be the same, at least when using SDS-PAGE. These findings contribute to the correct classification of the diversity described for the GLU-B1 locus, which will promote the use of new alleles in breeding programs aimed to improving gluten quality.

P383 - The triticeae breeding research group: exploring innovative strategies to enhance grain carotenoid content in wheat

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Abstract

The yellow colour is an important attribute of the appearance of wheat-derived foods. It is essential for the production of high-quality pasta and for the successful commercialisation of new products such as the 'Golden' bread derived from tritordeum, an amphiploid resulting from the cross between the wild barley *Hordeum chilense* Roem et Schultz. and durum wheat.

This colour is provided by carotenoids, but the relevance of these pigments goes beyond their role as colourants. Indeed, carotenoids are essential nutrients for both humans and animals. Generally, carotenoids pigments exert key biological functions due to their antioxidant and anti-carcinogenic properties, contributing to the prevention of chronic diseases and supporting cellular protection mechanisms as well as immune function. In addition to this, individual carotenoids have important functions such as the prevention of age-related macular degradation (lutein and zeaxanthin) or provitamin A activity (β -carotene). Wheat breeding programmes worldwide commonly rely on colourimetric methods such as the CIE colour measurements (MINOLTA) or chemical methods to determine carotenoids as a bulk (AACC 14-90). However, the inability of these methods to provide the individual carotenoid profile of the samples limits the full exploitation of the potential of wheat genetic resources for enhancing their nutritional value.

In the Triticeae breeding research group, we have developed an interdisciplinary strategy to improve of grain carotenoid content in wheat and related species. These strategies include: exploiting natural genetic resources for carotenoid content and profile; applying inter-specific breeding; developing innovative carotenoid profile for individual carotenoids and esterification profiles; and assessing the impact of climate change on grain carotenoid content. The main outlines of these initiatives will be presented.

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P384 - Green insecticidal beads based on chitosan-modified Tunisian diatomaceous earth and thyme essential oil for the control of *rhizopertha dominica* in stored durum wheat seeds

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Abstract

Durum wheat is among the most important cereal crops in the Mediterranean Basin, both in terms of cultivated area and production. However, post-harvest losses caused by biotic pests remain a major concern, significantly affecting both grain quantity and quality. Globally, pest-related storage losses can reach up to 9% in developed countries and 20% or more in developing nations, with Sub-Saharan Africa alone experiencing annual grain losses estimated at 4 billion USD. Protecting stored grains from such damage is therefore essential for food security, nutritional stability, and the safety of a growing global population. Several studies focused on biorational solutions in stored product pest control (Bachrouch et al., 2025; Villas et al., 2026). This study aimed to evaluate a novel green insecticidal formulation composed of chitosan-modified diatomaceous earth beads loaded with thyme essential oil (CH-DE/EO), as described in the patent registered at INNORPI, Tunisia (Registration No. TN2023/0114). The bioinsecticidal potential of CH-DE/EO beads was assessed, for the first time, against *Rhyzopertha dominica*, a key insect pest identified in stored durum wheat during the 2024 crop season. Durum wheat (2 kg) was treated with an LC₅₀ concentration of CH-DE/EO (5.932 g/L in air) under scaled-up conditions. The effects of five different seed treatments and storage durations were evaluated in a completely randomized design with three replications. Key parameters measured after 60 days of storage included insect damaged grains (IDG %), weight loss (WL in grams), and seed germination rate (SG %). Significant differences ($P \leq 0.05$) were observed across all measured parameters. Treatment with CH-DE/EO beads resulted in a 96% reduction in insect-damaged grains compared to the untreated control and led to a 20% increase in seed germination (reaching 80%). This performance surpassed both the control and conventional Timer-based treatments. The findings demonstrate that CH-DE/EO beads represent a promising biorational alternative for managing *R. dominica* infestations during durum wheat seed storage, offering both effective pest control and improved seed viability.

P385 - The ectopic expression of taexpa6 and the triple knock-out of tagw2 increase grain weight while maintaining quality traits (protein and phosphorus concentrations) in wheat

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Abstract

Wheat production faces the challenge of increasing grain yield (GY) while maintaining grain quality. Grain protein concentration is a key determinant of both nutritional and industrial quality in wheat. Recently, yield improvement strategies in grain crops have focused on increasing grain weight (GW). Among these, the ectopic expression of the TaExpA6 gene has been reported to increase both GW (12%) and GY (11%) of wheat. In contrast, the largest increase in GW ($\approx 20\%$) has been achieved through the triple mutation of the TaGW2 gene, but without any increase in GY due to the trade-off between grain weight and grain number (GN). Despite these advances, the effects of such genetic modifications on grain quality traits remain poorly understood. The objective of this study was to evaluate the response of wheat lines carrying these genetic modifications on grain yield, yield components, and grain protein and phosphorus concentrations, as well as nitrogen (N) and phosphorus (P) yield, uptake, and partitioning. To this aim, a field experiment was conducted using four genotypes: a transgenic line expressing TaExpA6 in grains and its wild type (WT), and a TaGW2 triple mutant and its WT. Treatments were arranged in a randomized block design with four replicates under optimal crop management conditions. Data was analysed using ANOVA.

GW was increased ($P < 0.05$) in both modified lines relative to their respective WTs (TaExpA6: 7%; TaGW2: 25%), whereas GY increased ($P < 0.05$) only in the TaExpA6 line (10%). Grain protein (grain N concentration $\times 5.7$) and phosphorus concentrations did not differ significantly ($P > 0.05$) between the modified lines and their WTs. Grain protein concentrations averaged 10.9 and 11.1% in the TaExpA6 line and its WT, respectively, and 11.9 and 11.6% in the TaGW2 mutant and its WT. Phosphorus concentrations showed a similar pattern. Interestingly, crop N and P uptakes were not affected ($P > 0.05$) by the genetic modifications. These results indicate that increases in GW driven by TaExpA6 overexpression or TaGW2 mutation do not compromise grain protein or phosphorus concentrations and, crucially, without increasing the N and P demand by the crop.

P386 - The tetraploid wheat core collection (TCC): a highly diverse, molecularly characterised GERMPLASM resource assessed for developmental and health-related quality traits

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Abstract

Durum wheat (*Triticum turgidum*) is a major staple crop increasingly challenged by global food demand. Tetraploid wheat germplasm provides a vast reservoir of genetic diversity, offering adaptive alleles lost through domestication and modern breeding. To harness this potential, we established the Tetraploid Wheat Core Collection (TCC), derived from the Global Durum Genomic Resources and integrating materials from both the Tetraploid Germplasm Collection (TGC) and the Global Durum Panel (GDP).

The TCC was assembled using ADMIXTURE-based population structure analysis of 3,142 tetraploid accessions genotyped with the Illumina 90K SNP array, following the pyramid pangenome concept. It includes ~40 long-read-sequenced genotypes produced within the tetraploid pangenome initiative, alongside key representatives of tetraploid wheat diversity: six wild emmer (*T. dicoccoides*) populations, eight domesticated emmer (*T. dicoccum*) populations, and eight landrace groups spanning multiple *T. turgidum* subspecies. Modern cultivated lineages from major breeding programs were also included, forming a 500-genotype core set capturing the main stages of domestication and subsequent geographic diffusion.

Field phenotyping took place in Cadriano (Granarolo Emilia, BO) over three seasons (2020, 2022, 2024) using 4 m² plots in an unreplicated modified augmented design with 10 checks. Ten main spikes per accession were collected to characterize spike morphology, fertility, and grain traits. Threshed grains were weighed and scanned to quantify size, shape, and color. The TCC revealed extensive phenotypic variability, including a three-week range in heading date, 12-31 fertile spikelets per spike, and 2-6 fertile florets per central spikelet, highlighting the richness of ancestral diversity.

A subset of representative genotypes underwent qualitative assessment using full-spectrum NIR spectrophotometry to estimate nutritional parameters such as fiber and starch content. Additional analyses for gluten content, antioxidant capacity, and dietary fiber are underway. The collection is available for research at UNIBO and will be deposited in major germplasm banks.

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P387 - A differentially distributed gene cluster for isorhamnetin biosynthesis identified in wheat

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Abstract

Flavonols are pivotal metabolites at the interface of plant stress adaptation and human nutrition. Although the biosynthetic routes to kaempferol and quercetin are well characterized, the genetic determinants governing the accumulation of other flavonols—particularly myricetin and isorhamnetin—remain poorly defined in major crops. Here we identify a flavonol biosynthetic gene cluster (BGC) on chromosome 2B of bread wheat (*Triticum aestivum*) that underpins key steps in isorhamnetin formation and exhibits pronounced presence/absence variation (PAV) across diverse accessions. Functional interrogation of the cluster revealed that constitutive overexpression of the cluster-encoded flavanone 3-hydroxylase (F3H) markedly increased isorhamnetin and multiple glycosylated derivatives in planta. By contrast, overexpression of the adjacent flavonoid 3',5'-hydroxylase (F3'5'H) did not elicit robust myricetin accumulation, indicating that flux toward myricetin is constrained by upstream substrate supply and by the coordinated catalytic specificities of flavonol synthase (FLS) and F3'5'H. Collectively, our results establish a genetically variable BGC as a major driver of flavonol chemotype diversity in wheat and suggest that its PAV may contribute to enhanced ultraviolet (UV) tolerance in cluster-positive lines. This locus therefore represents a tractable target for breeding programmes aimed at improving abiotic stress resilience while simultaneously elevating the nutritional value of wheat grain.

P388 - Identification of QTL involved in heavy metal and trace element accumulation in durum wheat

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Abstract

Wheat is a major staple crop and a key source of both essential micronutrients and toxic heavy metals in the human diet. Among these, cadmium (Cd) stands out due to its toxicity and the greater propensity of durum wheat to accumulate it in the grain. In response to growing health concerns, the European Union recently lowered the regulatory limits for Cd in durum wheat (from 0.20 to 0.18 mg/kg). In this study, we investigated the genetic basis of heavy metal and trace element accumulation to support the development of cultivars with reduced heavy metal accumulation while maintaining adequate levels of beneficial elements in durum wheat. To this end, a panel of 136 durum wheat cultivars was grown in field trials in France in 2019. Grain concentrations of toxic elements (As, Cd, Cr, Ni, Pb) and essential nutrients (Ca, Co, Cu, Fe, Mg, Mn, Mo, P, K, Zn) were measured. Detectable elements showed no or very weak correlations ($r < 0.25$), including between Cd and beneficial nutrients, supporting the possibility of breeding low Cd cultivars. A genome wide association study identified nine QTLs associated with heavy metals (Cd, Cr) and trace elements (Cu, Mo, Zn, Mg, Mn and P) accumulation, on chromosomes 1B, 2A, 3B, 4B, 5A, 5B, and 7B. Several of these QTLs colocalized with previously reported loci or candidate genes involved in metal transport and homeostasis, especially the major Cdu1 QTL on 5B for Cd. Bioinformatic analyses further explored gene annotations and the functional relevance of associated regions. Comparative analysis of the homologous sequences of the HMA3 candidate gene for Cdu1, across 15 wheat genotypes, revealed a 17 bp insertion in high-Cd genotypes. These findings provide valuable insights for breeding wheat varieties with lower heavy metal content and improved nutritional quality, in line with increasingly strict food safety regulations.

P389 - Agronomic, quality and nutritional potential of modern bread wheat in Ireland

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Abstract

In Ireland, engagement in spring wheat production for human food use is low. Within the Protein-I project, focus is placed on examining a range of modern spring feed and bread wheat varieties in terms of agronomic, quality and nutritional performance. Multi-location variety trials were established in randomised complete block design across 3 years (2023-2025) and subject to high input management. In terms of grain yield, feed varieties produced higher mean yields across all sites compared to bread wheat varieties ($p < 0.05$). The majority of samples tested achieved a mean protein above or equal to 13% (89.29%) and Hagberg Falling Number above or equal to 250 s (82.43 %). Of the samples failing to meet these minimum quality targets, over two thirds were feed variety types. Achievement of minimum specific weight of 76 kg/Hl ranged from 5.66% to 94.23% across environments. Further, wholemeal flour mineral content in combination with phytic acid data allowed for the first ever estimation of mineral bioavailability in modern bread wheat when grown in Ireland. Acknowledging anticipated modulation of grain yield and quality in the major European growing regions, this study highlights the agronomic, quality, and nutritional potential of bread wheat grown in atypical, high-rainfall (223.9-526.6 mm precipitation), temperate growth cycles.

P390 - Viscoelastic properties and protein functionality of high-amylose wheat flour

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Abstract

High-amylose wheat provides a novel approach to increasing resistant starch in refined wheat products. However, its altered starch composition significantly affects protein functionality and dough rheology. This study evaluated protein fraction distribution, gluten functionality, and rheological properties of high-amylose wheat flour compared with conventional wheat flour (25–30% amylose), with emphasis on protein–starch–water interactions governing dough performance. Sequential fractionation revealed differences in the relative proportions and extractability of albumins, globulins, gliadins, and glutenins. Although total protein contents were similar, high-amylose wheat exhibited an altered balance between monomeric gliadins and polymeric glutenins, indicating modifications in glutenin macropolymer (GMP) formation and protein aggregation behavior. These changes suggest differences in gluten network assembly and hydration characteristics. High amylose wheat flour required substantially greater water absorption (WA) (~79%) across empirical mixing systems (mixograph, farinograph, and Mixolab) compared with conventional wheat flour (~63%). High WA values reflected enhanced hydration associated with increased amylose content, as well as modified protein–water interactions. Greater water binding influenced gluten concentration in the continuous phase and altered the viscoelastic balance of the dough. The dough exhibited increased resistance to deformation but reduced extensibility relative to conventional wheat dough, indicating a stronger yet less extensible gluten network. Oscillatory rheology confirmed higher storage modulus (G') values, reflecting enhanced elastic behavior. Overall, high-amylose wheat flour demonstrates distinct protein fraction distribution and modified gluten functionality, resulting in increased water absorption, enhanced elasticity, and reduced extensibility. These findings provide mechanistic insight into the protein-based determinants of dough rheology in high-amylose wheat systems and inform processing strategies for nutritionally enhanced wheat products.

P391 - WheatRes: assessing genetic diversity for durum wheat quality in Spanish landraces and commercial cultivars

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Abstract

Durum wheat (*Triticum turgidum* ssp. durum Desf. em. Husn.) is a staple crop in the Mediterranean Basin, where it serves as the primary raw material for pasta and other traditional semolina-based products. Given its socio-economic importance, ensuring high industrial quality, specifically gluten strength and stable yellow color, is a major priority for durum wheat breeding programs worldwide. This study evaluates key grain quality parameters and their genetic basis in a comprehensive collection of 100 Spanish landraces and 100 commercial durum wheat lines across three Mediterranean environments. The research focuses on gluten strength (SDS-sedimentation test) and yellow index (b*), the primary hallmarks for durum wheat industrial suitability. Traits measured included test weight (TW), thousand kernel weight (TKW) and grain protein content (GPRO), along with the composition for the high- and low-molecular-weight glutenin subunits (HMW and LMW-GS) and main genes involved in carotenoid biosynthesis (PSY-A1, PSY-B1, ZDS-A1, PDS-B1) and degradation (LPX-A3, LPX-B1.1). Results indicated that while control varieties provided the highest stability for TW, several promising candidates were identified within the commercial lines that surpassed the controls in TKW, SDS-sedimentation volume, and yellow index. Regarding the Spanish landraces, they revealed a reservoir of genetic variability, presenting new alleles for both glutenin subunits and color-related genes not found in modern germplasm. Notably, landraces lacked the common Pds-B1a and Zds-A1.2 alleles, yet they harbored unique allelic variation in other loci. Correlation analyses confirmed the link between specific glutenin compositions and gluten strength, as well as the association between allelic variation at carotenoid-related loci and the b* color parameter. These findings underscore the importance of wheat genetic resources as essential tools for identifying novel diversity to enhance quality traits in future wheat breeding programs.

P392 - Comparative analysis of wheat grain protein content: wet chemistry and NIR based methods

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Abstract

Purpose: It is important to access the bias and accuracy of protein measurement by emerging methods, such as NIR based instruments and evaluate the agreement between methods. This study aimed to conduct comparison among NIR based grain protein measurement methods and evaluate the bias among the methods.

Methods: Study included 100 wheat grain samples with protein content ranging from 7.16 to 17.24 %. The grain samples were analyzed for protein content by three NIR based methods, which included on-combine H3 GrainGage™ by Harvest Master (Logan, UT), FOSS Infratec benchtop NIR (FOSS Analytics, Hillerød, Denmark), and GrainSense handheld grain protein analyzer (GrainSense Ltd, Oulu, Finland). The grain protein content was also determined by the standard laboratory method- Dumas Combustion, which was used as the reference method. Bland-Altman analysis was used to compare the degree of bias and limits of agreement between different methods. An additional 500 samples with protein content ranging from 8.7 to 15.7 % were also included for further comparison between H3 GrainGage™ by Harvest Master and FOSS Infratec NIR.

Results: Despite strong correlation, protein content measured by all NIR based methods showed significant bias when compared with the standard laboratory method. H3 GrainGage™ showed greater bias for samples with high protein content while GrainSense grain protein analyzer showed greater bias for samples with low protein content. Among NIR based methods, FOSS NIR showed the lowest mean bias of 1.56 % unit in comparison to standard laboratory method. When H3 GrainGage™ was compared with FOSS Infratec NIR, the mean bias was relatively lower, 0.81 % unit in the 100 sample set and -1.06 % unit on the 500 sample set.

Conclusions: While the application of NIR based methods is valuable in many cases, NIR based methods/instruments need improvement in accuracy and robustness for grain protein measurement, particularly for samples with low and high protein content. There may be applications where the known bias for protein estimation is acceptable, and other applications where Dumas Combustion method is necessary when a higher level of accuracy is required.

P393 - Enhancing dietary fiber in wheat through arabinoxylan improvement

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Abstract

Arabinoxylans (AX) are the major component of wheat dietary fiber and play an important role in both human nutrition and wheat processing functionality. Increasing AX content in wheat represents a promising strategy to improve dietary fiber intake through widely consumed wheat-based foods, thereby contributing to closing the global fiber gap. However, progress in breeding for higher AX content has been constrained by limited phenotyping capacity, complex genetic control, and uncertainty regarding the impact of elevated AX on end-use quality.

Our work aims to accelerate the development and deployment of high-AX wheat through an integrated approach combining large-scale phenotyping, genetic analysis, and processing evaluation. A high-throughput phenotyping pipeline has been established using the phloroglucinol colorimetric assay to quantify AX across large breeding populations. In parallel, near-infrared spectroscopy calibrations are being developed to enable rapid prediction of AX content and facilitate high-throughput screening. These tools are being applied to evaluate AX diversity within the CIMMYT spring bread wheat breeding program as well as to characterize additional sources of AX variation from diverse germplasm.

Complementary genetic analyses are being conducted to characterize the allelic diversity of key genes and QTL associated with AX accumulation. Leveraging the phenotypic data generated and the availability of genomic information for CIMMYT spring bread wheat lines, genomic prediction models for AX are also under development to accelerate selection for this trait within a breeding framework.

Finally, the functional and processing implications of elevated AX levels are being evaluated through detailed flour, dough, and product quality analyses, including rheological testing and baking assessments. This integrated approach ensures that nutritional improvements are achieved without compromising industrial quality.

Together, these activities provide a comprehensive framework for the development of high-fiber wheat varieties capable of delivering meaningful improvements in dietary fiber intake through widely consumed wheat products.

P394 - Effect of the wheat bread-making gene on gluten protein fractions analyzed by high-performance liquid chromatography

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Abstract

Bread-making quality is a key trait in wheat breeding and is largely determined by genetic factors, particularly gluten proteins such as glutenin and gliadin. These protein fractions have been characterized using reversed-phase high-performance liquid chromatography (RP-HPLC) and size-exclusion HPLC (SE-HPLC). The wheat bread-making gene (wbm), previously identified as associated with enhanced bread-making quality, was the focus of this study. Near-isogenic lines (NIL) with high wbm gene expression were developed to evaluate the gene's influence on gluten protein composition. Hard red commercial South African bread wheat cultivars PAN3497 and Koedoes were used as recurrent parents, while PAN3471 and Krokodil served as donor parents. The effect of the gene on gluten protein fractions was evaluated in NIL developed under both speed breeding and greenhouse conditions and compared with their recurrent parents. Sodium dodecyl sulphate-polyacrylamide gel electrophoresis analysis confirmed the absence of segregation in the developed NIL and demonstrated their genetic similarity to the respective recurrent parents. HPLC revealed a wide variation in gluten protein fractions among the cultivars and their corresponding NIL. The influence of the gene expression on bread-making quality differences between the two genetic backgrounds. In the PAN background, environmental conditions significantly influenced the effect of the wbm gene expression, whereas in the other background, growing conditions did not have a significant effect; instead, the presence of the wbm gene directly and significantly influenced specific protein fractions. Within this population, significant differences ($P \leq 0.05$) between NIL and recurrent parents were observed for selected SE-HPLC fractions (SEHPLCS4 and SEHPLCI2), RP-HPLC fractions (RPHPLC3 and RPHPLC1), and total protein content. Furthermore, this study performed principal component analysis to better understand the relationships between the measured characteristics of the NIL and those of its recurrent parents. While the results for the study indicate that the impact of the wbm gene on gluten protein composition and bread-making quality depends on genetic background and environmental conditions, the study also confirmed the effectiveness of speed breeding for NIL development. Further research involving additional populations is required to validate the importance of the wbm gene in South African wheat breeding lines.

P395 - Twenty-year evaluation of baking quality traits in spring and winter wheat cultivars

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Abstract

Balancing the yield and baking quality is essential in wheat breeding. Information on long-term stability and cultivar-specific differences is crucial for selecting cultivars adapted to variable climates. This study assessed the baking quality of spring (SW) and winter wheat (WW) grown in Estonia, Northern Europe, over 20 years.

Field experiments were conducted from 2002 to 2022 at the Centre of Estonian Rural Research and Knowledge. Four SW cultivars ('Manu', 'Vinjett', 'Mooni', 'Triso') and five WW cultivars ('Ada', 'Skagen', 'Fredis', 'Ramiro', 'Širvinta 1') were grown using standardised practices. Flour, dough, and baking quality traits were analysed using ICC, ISO, and AACC methods. Baking quality was evaluated using long-fermentation baking tests with 250 g of flour.

Cultivar significantly influenced the rheological and baking quality traits of both wheat types. In WW, the gluten index (GI), dough stability, and dough energy varied among cultivars, whereas the protein content (PC) and loaf volume (LV) remained stable. In SW, most quality traits were significantly influenced by the cultivar. 'Manu' exhibited the highest PC, GI, wet gluten content, and farinograph quality number. Year effects were noticeable, with 2006 showing the highest quality for SW and 2006, 2013, and 2016 for WW. 2020 showed poor performance for both wheat types.

Significant differences between wheat types were observed, with SW LV remaining relatively stable and WW being more variable, peaking in 2013-2018 and being lowest in 2020. SW produced a significantly higher mean LV ($1442 \pm 133 \text{ cm}^3$) than WW ($1373 \pm 169 \text{ cm}^3$). Among the SW cultivars, 'Manu' demonstrated the highest mean LV (1514 cm^3), significantly exceeding that of 'Triso' (1374 cm^3). 'Fredis' exhibited the highest mean LV (1452 cm^3) among the WW cultivars, while 'Skagen' (1341 cm^3) had the lowest.

This study provides a long-term, cultivar-specific evaluation of wheat baking quality under Northern European conditions, offering valuable insights for the breeding and selection of cultivars resilient to climatic variability.

P396 - High-throughput prediction of farinograph and baking traits in hard red spring wheat using glutopeak indices and machine learning: fast-track end-use quality decisions

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Abstract

Due to its superior end-use quality, U.S. hard red spring (HRS) wheat is regarded as a premium wheat class, well-suited for a range of specialty baked products and for blending with other wheat classes to enhance overall quality. Consequently, end-use quality traits have been a major focus in HRS wheat breeding programs. However, phenotyping for quality is particularly challenging in large-scale breeding programs, especially during the early generations, due to the limited availability of material and the time-intensive nature of high-resolution quality testing. Therefore, there is a critical need for high-throughput quality testing methods capable of predicting dough rheology and bread volume using small sample sizes from early-stage breeding materials.

GlutoPeak testing is emerging as a rapid, small-sample alternative that captures gluten aggregation behavior within minutes; however, its potential for multi-trait prediction across large, multi-environment HRS datasets has not been fully established. We developed and validated multi-trait models using grain protein and GlutoPeak indices as predictors to estimate wet gluten, farinograph and baking quality parameters in a diverse panel of 846 HRS samples grown across five environments over two years. We compared Partial Least Squares (PLS), Random Forest Regression (RFR), Support Vector Regression (SVR), and Extreme Gradient Boosting (XGB) approaches using an independent test set to indicate realistic deployment. The best-performing models were RFR for wet gluten ($R^2 = 0.89$; RPD = 3.08) and XGB for farinograph absorption ($R^2 = 0.81$; RPD = 2.27). Peak time and stability were predicted with moderate yet decision-useful precision using RFR (peak time: $R^2 = 0.49$, RPD = 1.41; stability: $R^2 = 0.40$, RPD = 1.29). XGB performed best for bake absorption ($R^2 = 0.59$; RPD = 1.56) and loaf volume ($R^2 = 0.51$; RPD = 1.44). Therefore, GlutoPeak-based models provide robust, low-bias prediction that can discard inferior lines. This framework is readily deployable as a cloud-based decision-support pipeline, enabling rolling calibration to improve robustness across seasons and locations. Such scalable models can support routine industrial quality control and can be extended to international breeding programs and gene bank screening to accelerate breeding practices through rapid, standardized quality evaluation in wheat improvement networks.

P397 - Genome-wide association study for genetic determinants of phytic acid content and mineral bioavailability in wheat (*Triticum aestivum* L.)

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Abstract

Phytic acid (PA) is the primary form of storage for phosphorus (P) in cereal and legume seeds, which significantly reduces the bioavailability of minerals such as iron (Fe) and zinc (Zn). A genome-wide association study (GWAS) was conducted by us to better understand the genetic architecture of PA content in the grain. A diverse panel of 283 wheat genotypes, including Indian cultivars, genetic stocks with enhanced grain quality, and landraces from the Watkins collection, was evaluated in alpha lattice design experiments across three locations, namely Meerut, Pantnagar, and Ludhiana, over three consecutive crop seasons, making a total of nine environments. PA content in wheat was quantified by colorimetric analysis using Wade reagent. The association panel was genotyped using the wheat Illumina iSelect 90K Infinium SNP array. GWAS was conducted using Best Linear Unbiased Estimator (BLUE) values for each of the nine environments and also across these environments using eight multi-locus models available in R packages GAPIT and MrMLM. Among these models, mrMLM, BLINK, and FarmCPU identified 25, 181, and 159 MTAs in individual environments, and 12, 9, and 6 MTAs in the combined environment (CE), respectively. For MrMLM, MTAs with a LOD score ≥ 3.0 were considered significant, whereas for BLINK and FarmCPU, MTAs with $-\log_{10}(p) > 3$ were treated as significant. Using a number of criteria, nine useful MTAs were selected for the purpose of marker assisted recurrent selection (MARS), while breeding for relatively reduced PA content. The study also allowed identification of 13 candidate genes (CGs) that are supposed to be involved in the biosynthesis, transport, metabolism and storage of PA. Some of these CGs may be used for developing gene-based functional markers and CG-based association mapping for future studies.

P398 - Effect of global warming on wheat grain and baking quality stability - Project CLIMABOUL (CLimat et quAlité BOULangère)

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Abstract

The IPCC predicts that climate change will worsen, with a significant increase in average temperatures and more frequent heat waves during crucial periods of wheat cultivation, particularly during the grain filling phase. It is therefore essential to improve our understanding of the effects of climate change on wheat grain quality and stability. The ClimaBoul project aims to study the effects of post-flowering heat stress at several stages of grain development on their structure, composition and baking quality. To this end, a small panel of French winter bread wheat varieties with contrasting baking quality stability was established after analysing bread-making data from trials conducted over 20 years. The varieties are being grown in controlled environments (growth chambers with or without heat stress), semi-controlled environments (with or without tents and tunnels on microplots to increase the temperature through the greenhouse effect) and in the field in different locations over a period of three years. The harvested grains are being analysed in terms of yield, size, hardness, milling suitability and biochemical composition. After milling, the effect of thermal stress on the composition and functional properties of the flours (water absorption capacity, elasticity index, viscosity, etc.) will be evaluated using various tests, including the standardised French bread-making test. This project will provide a better understanding of the impact of temperature increases at different stages after flowering on wheat grain and baking quality, and identify indicators of quality stability that can be used in breeding.

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P399 - Dynamic profiling of lipid metabolism in developing wheat grains

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Abstract

Dynamic Profiling of Lipid Metabolism in Developing Wheat Grains

Wheat constitutes one of the world's three primary staple crops. Although lipids represent only 2-4% of grain dry weight, they are essential for grain development and quality formation. However, the dynamics of lipid accumulation and their biochemical regulation during wheat grain development remain largely unclear. In this study, we systematically characterized lipid composition throughout grain development. Using the elite cultivar Aikang 58, we quantified fatty acid composition and total lipid content across multiple developmental stages. linoleic acid (C18:2) was the predominant fatty acid, accounting for 40-60% of total fatty acids during development. Lipid accumulation increased rapidly from early to mid grain development, peaked at 17 days after anthesis (DAA), and remained relatively stable thereafter. Spatial profiling of embryo, endosperm, and seed coat tissues revealed distinct patterns: stearic acid (C18:0) gradually decreased in embryos but increased in endosperm and seed coat, whereas oleic acid (C18:1) showed the opposite trend. Very long-chain fatty acids, such as eicosenoic acid (C20:1), increased sharply after 9 DAA and stabilized after 27 DAA. Lipidomic analysis further showed that embryos preferentially accumulated storage lipids, the seed coat was enriched in glycolipids, and phospholipids were relatively abundant in the endosperm. Overall, this study provides a comprehensive characterization of fatty acids and lipid species during wheat grain development, offering new insights into the biochemical regulation of lipid metabolism and its implications for wheat quality improvement.

Keywords: wheat grain development; fatty acids; lipids

P400 - Technological quality screening in wheat: Direct and indirect effects of gluten traits on bread volume

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Abstract

Baking quality of flour is a fundamental characteristic for decision-making in wheat breeding programs. Therefore, it is necessary to find rapid and accurate methods to determine the quality of breeding lines, allowing the selection of superior materials efficiently, on a large scale and using a simple and low-cost sample method, especially in the early stages of the program. This study aimed to investigate the relationship between the wet gluten (WG), gluten index (IG), total protein (TP) and bread volume (V) (french bread) through Pearson's correlations and path analysis to assess the causal effects of WG, IG and TP on baking quality. In 819 wheat line's TP, WG, IG and V characteristics were determined. Correlation and path analysis were employed in the R software. All parameters showed significant correlations, the strongest being TP x V 0.46, followed by IG x V 0.32, and WG V 0.22 ($p < 0.01$). The path analysis showed that TP and IG have a direct effect on V, while WG has an indirect effect through TP. Based on the correlation analysis, it was constructed the path analysis model. TP presented a strong direct effect on V (0.47), and IG presented a moderate effect on V (0.34). WG showed an indirect effect on V through TP (0.58). These parameters are important for predicting the baking quality. The bread volume depends on gluten amount or quality, and each characteristic can serve as predictors of bread volume. Thus, this method using these three parameters can be a screening tool for the inclusion of technological quality in breadmaking as a parameter in the selection of new wheat lines in the early generations of wheat programs.

P401 - Genome-wide identification and expression validation of phytate biosynthesis genes in wheat for Zn bioavailability

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Abstract

Phytic acid (myo-inositol hexakisphosphate; IP₆) is the principal phosphorus storage compound in wheat grain, but it also functions as a strong chelator of iron (Fe) and zinc (Zn), reducing their bioavailability and contributing to micronutrient malnutrition. This study included morphological data under different nutrient treatments (Control, FeSO₄, ZnSO₄, and FeSO₄+ZnSO₄), genome-wide analysis of phytic-acid biosynthetic pathway genes with experimental confirmation and expression profiling to identify actionable molecular targets for CRISPR/Cas9-based improvement of wheat nutritional quality. The work evaluated 50 wheat genotypes under four nutrient treatments using descriptive statistics and multivariate analyses to quantify morphological and micronutrient diversity. The results demonstrated significant genotype × treatment variation and divergence among genotypes, confirming strong selection potential for yield and mineral traits. ZnSO₄ produced the most consistent strengthening of yield-related trait associations and Zn enrichment, while FeSO₄ showed comparatively stronger effects on agro-morphological traits, indicating mineral-specific responses and the importance of treatment-wise selection. Furthermore, grain phytic acid was measured (Wade reagent), and bioavailability was calculated using phytate-to-mineral molar ratios (PA:Fe and PA:Zn), where lower ratios indicated better predicted absorption. The results revealed that bioavailability responses were mineral-specific. The genome wide analysis revealed that 15 TaITPK, 6 TaIPK, and 3 TaMIPS genes distributed across the A, B, and D sub-genomes, with conserved domains, motifs, and homoeologous expansion consistent with polyploidization based gene redundancy. Promoter analysis revealed abundant seed development regulatory motifs, including the GCN4_motif (endosperm-specific), which was predominantly enriched in the promoter region of the TaITPK gene group and also within the TaIPK1 group (TaIPK1-2A and TaIPK1-2B), indicating activation in grain during phytate accumulation. Furthermore, expression profiling showed nutrient and genotype dependent transcriptional responses, with sole application of FeSO₄ or ZnSO₄ fertilizer treatments inducing distinct pathway components, while combined FeSO₄+ZnSO₄ showed generally moderated expression, suggesting feedback regulation under simultaneous micronutrient supply. The analysis and results helped to make targets for CRISPR/Cas9 knockout for improving bioavailability i.e. TaITPK1-homoeologues due to its endosperm enrichment and grain-associated activity and TaIPK1, which catalyze the terminal conversion of IP₅ to IP₆.

Keywords: Wheat quality, biofortification, iron and zinc, phytic acid, human health

P402 - Multifunctional roles of sucrose fatty acid esters in flour- and starch-based premix foods

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Abstract

In flour- and starch-based food manufacturing, emulsifiers are critical not only for final product quality but also for processing robustness and yield, particularly in frozen and frozen-thawed systems. Sucrose fatty acid esters (SEs) are non-ionic, plant-derived emulsifiers synthesized from sucrose(sugar) and plant-derived fatty acids, offering a high degree of functional tunability. This study evaluated the effects of SEs with different hydrophilic-lipophilic balance (HLB) values on processing behavior, functionality, and frozen tolerance in flour- and starch-based premix food products. Their performance was compared with conventional emulsifiers under standardized preparation, baking, and freezing conditions. Processing-related properties (dough workability, mechanical stability, and uniformity) and product quality (volume, moisture distribution, and texture) were evaluated using physical and sensory methods. SEs consistently improved processing performance by stabilizing water-lipid interactions, reducing mechanical resistance during mixing and handling, and enhancing reproducibility across production steps. In baked applications, SEs enhanced gas retention, volume development, and crumb elasticity, supporting improved volume yield and textural consistency. Importantly, in frozen dough applications, SEs demonstrated superior frozen processing robustness by maintaining structural integrity and gas-holding capacity during frozen storage and subsequent thawing, resulting in higher post-thaw volume and reduced stickiness compared with conventional emulsifiers. In addition, SEs effectively modulated starch behavior by delaying gelatinization and suppressing structural degradation during storage, contributing to improved freshness retention and reduced quality loss over time. Synergistic effects were observed when SEs were combined with other emulsifiers, enabling further optimization of processing stability and product performance. Overall, sucrose fatty acid esters act as multifunctional processing aids that improve manufacturing robustness, frozen tolerance, and yield consistency in flour- and starch-based systems, supporting efficient and sustainable cereal and starch processing.

P403 - Integrating nutritional quality sensory traits and genetic diversity for multi-trait wheat improvement

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Abstract

Improving wheat's nutritional value, quality, and sensory acceptance while maintaining low cadmium (Cd) levels remains a major challenge in food production. This study evaluated wheat-alien introgression lines and heritage germplasm (einkorn, emmer, spelt, old cultivars, and landraces) in two Swedish agroecosystems (Svalöv and Alnarp) using an integrated framework combining nutritional, functional, sensory, and genomic analyses. Grain traits evaluated included mineral concentrations (Fe, Zn, Cd), protein composition, gluten quality (%UPP), dietary fiber, amino acid, polyphenol profiles, and sensory quality. Significant genotypic effects were detected for all traits, with genetic variance exceeding residual variance, indicating stable and selectable variations across environments. At Svalöv, Fe and Zn showed phenotypic ranges (~35-87 and ~30-56.5 mg kg⁻¹), and high micronutrient levels were not associated with increased Cd accumulation, identifying genotypes with high Fe-Zn and low Cd (~0.04-0.05 mg kg⁻¹). Protein concentrations varied significantly among genotypes, whereas %UPP showed partial independence from total protein, facilitating balanced processing quality. At Alnarp, einkorn showed high Fe, Zn, and protein contents, whereas landraces and old cultivars had stronger gluten quality and higher bound phenolic content. Dietary fiber and amino acid profiles showed genotype variations, providing opportunities for nutritional improvement through targeted selections. Polyphenol profiling identified several promising genotypes, like wheat-rye 3R (3D) substitution line with high total polyphenol and ferulic acid levels. Multivariate analyses revealed positive Fe-Zn associations, a strong contribution of bound phenolics to total phenolics, and relative independence of Cd from most quality traits, which allows for multi-trait selection strategies. Genotyping-by-sequencing-based GWAS models (FarmCPU and BLINK) identified 45 marker-trait associations (MTAs), with 25 on wheat chromosomes and 20 on rye chromosomes, linked to low Cd accumulation, Zn and Fe concentrations, protein content, and polyphenol traits. Subsequent gene ontology and enrichment analyses refined these results to 13 high-confidence MTAs in wheat and 6 in rye. Sensory Quantitative Descriptive Analysis demonstrated the significant effects of genotype and cultivation environment on aroma, flavour, taste, texture, and appearance. This study demonstrated the value of genetic diversity and an integrated multi-trait breeding framework that combines nutritional quality, sensory traits, and genetic associations to develop nutrient-dense, low-Cd, and sensory-optimized wheat.

P404 - Genetic diversity, fiber composition and quality traits of european spelt wheat (*Triticum aestivum* ssp. *spelta*) for sustainable crop improvement

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Abstract

Spelt wheat (*Triticum aestivum* ssp. *spelta* L.; $2n = 6x = 42$, AABBDD) is one of the oldest cultivated cereals in Europe and is increasingly valued for its adaptation to low-input and organic systems, stress tolerance, and distinctive nutritional properties. Our research aimed to explore the genetic diversity, fiber composition, and processing quality of European spelt germplasm to support breeding strategies for health-promoting and sustainable cereal production.

A comprehensive genotypic and phylogenetic characterization was performed on 188 spelt lines and 80 modern bread wheat cultivars using a high-density 25K Illumina SNP array. The analyses revealed clear differentiation between spelt and bread wheat gene pools, together with substantial diversity within spelt accessions. We identified 406 chromosome-specific SNP markers enabling reliable detection of spelt chromatin in wheat backgrounds, providing valuable tools for introgression breeding.

To address increasing demand for fiber-rich cereals, association mapping was conducted to identify SNP markers linked to arabinoxylan (total and water-extractable pentosan), β -glucan, and fructan. Significant associations ($-\log_{10}P > 3$) revealed 28, 24, 32, and 21 SNPs linked to total pentosan, water-extractable pentosan, β -glucan, and fructan content, respectively. Marker positions corresponded to previously reported chromosomal regions involved in arabinoxylan and β -glucan biosynthesis. One spelt-specific marker was associated with β -glucan content, indicating potential for marker-assisted selection. Substantial variation in fiber composition among genotypes demonstrates strong breeding potential.

Spelt genotypes were further evaluated for physical, compositional, and baking quality traits under conventional and organic systems. Spelt showed higher protein and gluten contents than bread wheat, but lower glutenin and polymeric protein fractions, indicating weaker dough strength. Organic production increased starch, fiber, and alkylresorcinol contents, while reducing β -glucan and protein levels. Considerable variability in bioactive compounds was observed, and several genotypes proved suitable for organic and low-input cultivation.

Overall, European spelt gene bank collections represent a rich genetic resource. The integration of high-throughput genotyping, detailed phenotyping, and marker identification provides a solid basis for developing high-quality wheat cultivars adapted to sustainable production systems and changing climatic conditions.

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P405 - Impact of xanthophyll esterification on carotenoid stability during bread-making in wheat and tritordeum

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Abstract

Carotenoids are bioactive dietary antioxidants with well-documented health benefits and they are an important quality trait in wheat-based products due to their nutritional value and contribution to colour. However, carotenoids are highly susceptible to degradation during food processing, resulting in losses throughout the bread-making process. The esterification of xanthophylls has been proposed as a natural mechanism that enhances carotenoid stability. The present study evaluated the retention of carotenoids during bread-making in bread wheat (*Triticum aestivum*), tritordeum (*×Tritordeum martinii*), and *Hordeum chilense*-bread wheat chromosome substitution lines, with particular emphasis on the protective role of esterification on the carotenoids.

Six genotypes, exhibiting variation in carotenoid content and esterification capacity, were analysed at various successive stages of bread production, including grain, flour, dough, freshly baked bread, and bread stored for 48 h. The quantification of free and esterified carotenoids was conducted by high-performance liquid chromatography (HPLC). Genotype-dependent differences were observed, with tritordeum HT621 showing the highest total carotenoid levels. In all genotypes, lutein and its esterified forms were predominant. Substantial losses of carotenoids were observed during the processing, with the baking stage identified as the most critical for degradation of these compounds. Nevertheless, esterified carotenoids consistently exhibited higher levels of retention than free carotenoids. Evidence of *de novo* esterification during dough preparation was detected: in certain genotypes, retention of esterified lutein exceeded 100%, suggesting that esterification-related enzymatic activity may persist from post-harvest through early bread-making stages. Overall, carotenoid retention in bread after 48 h ranged from 25.8% to 42.6% relative to whole grain levels.

The results obtained highlight the importance of genetic factors, particularly carotenoid accumulation and esterification capacity, in determining carotenoid stability during bread-making process. Since lipoxygenase activity may contribute to carotenoid degradation, further studies are required. These findings support carotenoid esterification as a key mechanism to enhance carotenoid stability during bread-making.

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P406 - Understanding the effects of global warming on wheat grain to improve the stability of breadmaking quality

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Abstract

Cereals are a major renewable resource for human and animal nutrition. Wheat cultivation faces increasing challenges, including yield and quality instability and the need to reduce chemical inputs. These constraints are intensified by climate change, with more frequent, earlier, and longer expected heatwaves expected in the future. According to the Intergovernmental Panel on Climate Change (IPCC) projections, global temperatures are likely to exceed +2 °C by 2050. However, studies identifying climate-resilient wheat varieties rarely integrate end-use quality, particularly breadmaking performance. Improving our understanding of the effects of climate change, and more specifically heat stress, on wheat breadmaking quality by jointly considering agronomic, technological, and biochemical traits is therefore essential.

The impact of climatic variability on the technological quality of common wheat was assessed using two varieties differing in breadmaking stability, grown in three French regions. Environments were classified according to thermal stress between flowering and maturity, based on exposure to temperatures exceeding 25°C, and categorized as low, moderate, or high stress.

Baking tests and Chopin alveograph analyses revealed marked differences in flour technological behavior across environments. Measurements of grain physical parameters (mass, volume, density) showed clear varietal differences and significant environmental effects, with strong Genotype × Environment interactions for grain mass and volume. Biochemical analyses of grain and flour highlighted variations in starch and protein contents across environments. Under high heat-stress conditions, protein content tended to decrease, although not significantly, while starch content showed a significant reduction. No clear trend was observed in white flour, whereas wholemeal flour exhibited a tendency toward increased arabinoxylan content.

Overall, contrasting technological performances across thermal stress conditions emphasize the importance of Genotype × Environment interactions and confirm a clear temperature effect on grain quality. This integrated approach combining agronomic, technological, and biochemical data contributes to a better understanding of the mechanisms underlying breadmaking quality variation. It paves the way for the identification of predictive markers of technological resilience and the development of breeding strategies adapted to future climatic conditions. Additional data from controlled and semi-controlled temperature experiments will further strengthen and refine these analyses.

P407 - Dissecting the genetic basis of carotenoid accumulation and esterification in an Argentinean durum wheat collection using GWAS, evaluation of the carotenoid profile and KASP markers

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Abstract

Durum wheat (*Triticum turgidum* L. ssp. durum Desf.) grains, used in high-value-added products, exhibit significant variability in the concentration and composition of carotenoids, a key attribute for industrial and nutritional quality.

In this study, a germplasm collection of 197 genotypes, field-tested in Foggia, Italy, during 2022, was analyzed. Yellow pigment content (YPC) was measured by colorimetry on grain flour samples after n-butanol extraction. Molecular characterization was performed using the 35K Axiom™ genotyping array and two KASP markers on carotenoid biosynthesis enzymes (Zds-A1 and Pds-B1 genes), encoding ζ-carotene desaturase and Phytoene desaturase, respectively. A KASP marker was designed for the Xanthophyll Acyltransferase gene (XAT-7A1), responsible for the esterification of lutein, and validated in the 44 genotypes and two F₂ populations. A genome-wide association study (GWAS) was conducted using a mixed linear model (PCA + K) in TASSEL software.

YPC values ranged from 3.90 to 12.05 µg g⁻¹. Based on these data, a subset of 44 genotypes (6.78-12.05 µg g⁻¹) was analyzed by HPLC-DAD. This work revealed BI Cariló as the first commercial cultivar producing lutein esters. Three XAT-7A1 allelic variants were identified: functional (A), alternative (G), and null. Genotypes carrying the G or null alleles did not produce esterified carotenoids. The marker was also tested in F₂ populations derived from the cross between BI Cariló (A) × Buck Rubí (G) and BI Cariló (A) × Buck Topacio (-). Additionally, a significant effect was detected for Zds-A1 (F = 10.21; p = 0.0016) and for Pds-B1 (F = 4.77; p = 0.0302), with an additive effect and no significant interaction. Genotypes carrying the favorable allele combination of Zds-A1 and Pds-B1 exhibited a 35.3% higher average carotenoid content compared to those with the unfavorable allelic combination. GWAS for YPC identified significant genomic regions on chromosomes 1A, 6B, 7A, and 7B, but the effect of the genes responsible for carotenoid biosynthesis was not confirmed by MLM.

Overall, these results validate markers for both biosynthetic and esterification genes. Combined with GWAS findings, they underscore the importance of integrating functional and genomic information to optimize selection strategies for superior end-use quality.

P408 - Exploiting gamma-irradiation mutant population for enhancing grain nutritional quality and nitrogen use efficiency.

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Abstract

The Germplasm Resources team in the John Innes Centre (JIC) is the custodian of wheat mutant resources. Since 2016, EMS-induced hexaploid (Cadenza) and tetraploid (Kronos) in-silico TILLING populations have been used by 431 unique users in 35 countries, who have exploited 14,112 lines for functional genomics and wheat improvement. The exomes are browsable on EBI Ensembl-Plant, ideal for reverse genetics.

Here, we present a publicly available complementary resource generated through a collaborative effort across the UK wheat community. The M5 gamma-irradiation mutagenised population in the hexaploid spring wheat, Paragon, was created in the International Atomic Energy Agency, Seibersdorf, Austria, in 2003. Unlike EMS-induced point mutations, gamma radiation induces mostly large deletions, necessitating a relatively small population size to saturate the genome, ideal for forward genetics.

Previously, 650 gamma-irradiated lines were Skim-sequenced (0.2X coverage) to identify deletion mutations. The detected deletions vary from 25 kbp to 590 Mbp with a median of 75 Kbp and a mean of 2 Mbp. This deletion size allows screening for mutants with knockouts in clusters of genes or for mapping intervals, using overlapping sets of deletion lines that cover >90% of the wheat genome.

We exemplify the use of this genome-sequenced, mutagenised collection for forward-genetic screening, pre-breeding and gene discovery. We will present an in-depth phenotyping effort, including agronomy, ear and grain morphology, grain micro- and macro-nutrient content, and trade-offs between yield and protein content. Compared to the Paragon control, a significant phenotypic variation was observed in the mutant populations.

To visualise the relationships between individuals and identify key traits driving diversity, the phenotypic variation was plotted using Principal Component Analysis (PCA), in which PC1, PC2, and PC3 explained 54.95%, 34.92%, and 8.49% of the total evaluated variation, respectively.

For example, grain protein content (GPC) ranged from 12.7-31% in a single controlled environment, and a significant negative correlation ($R=0.83$) between GPC and yield confirmed an induced protein-yield trade-off. Grain Protein Deviation, a proxy to NUE, ranged from -16% to +32%.

The work enabled the identification of lines with potentially favourable NUE and enhanced nutritional profiles. Results are being validated in field trials.

P409 - Multi-environment field trials of a european elite wheat panel provide insights into the genetic architecture of falling number stability

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Abstract

Maintaining stable bread wheat quality under pre-harvest rainfall remains a major challenge for both wheat production and processing reliability. Falling number (FN), reflecting α -amylase activity and starch integrity, is a key determinant of end-use quality, while falling number stability describes the steadiness of FN during grain ripening under adverse environmental conditions, particularly rainfall and high humidity. Despite its importance, the genetic basis of FN and its stability is still poorly understood, as reliable selection requires suitable phenotyping environments that are not consistently available.

We present results from a hexaploid European elite wheat panel of 191 winter wheat cultivars registered between 1966 and 2013, representing five decades of breeding progress. Multi-environment field trials were conducted over two consecutive years in 10 environments (year $\times$ location combinations) under three contrasting management regimes per environment. The dataset thus comprises 5,730 genotype $\times$ environment $\times$ treatment combinations, with meteorological data recorded. FN was measured using the standardized Hagberg-Perten method (ISO 3092:2009) on 25 g grain samples per entry.

Genotyping was performed using the 15k Illumina Infinium iSelect and 135k Affymetrix Axiom arrays, yielding 15,865 high-quality polymorphic SNPs after stringent quality control. Environmental effects visible as year $\times$ location interactions explained the largest share of phenotypic variation, while 19% was attributable to cultivar effects. Genotype $\times$ environment interactions were analyzed using an AMMI model, combining ANOVA for additive effects with principal component analysis of residual interactions.

Best linear unbiased estimators (BLUEs) for FN across locations were used for genome-wide association studies (GWAS) with a mixed linear model accounting for kinship and population structure. After Bonferroni correction, significant marker-trait associations were identified on chromosomes 4A and 7A. Further, FN stability, assessed via the coefficient of variation between environments, revealed several significant marker-trait associations on chromosomes 1B, 1D and 3A.

These findings provide new insights into the genetic architecture of FN and its stability. The identified loci are promising targets for marker-assisted selection, supporting breeding efforts to develop cultivars with improved FN performance and stability under variable climatic conditions.

P410 - Tritordeum, an alternative cereal for breadmaking

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Abstract

Tritordeum (*Tritordeum martinii* A. Pujadas, nothosp. nov.) is a relatively new allohexaploid crop obtained by crossing diploid wild barley (*Hordeum chilense* Roem. et Schultz) (HchHch) with tetraploid durum wheat (*Triticum turgidum* ssp. durum (Desf.) Husn.) (AABB). Tritordeum is characterized by a high content of micronutrients, in particular lutein, polyphenols, and macronutrients. Tritordeum grain is a richer source of protein, total phenols, methyl donors, magnesium, and iron than bread wheat and durum wheat grain. It also has higher concentrations of total amino acids (excluding asparagine) and sugars (including raffinose).

Due to the high value of Tritordeum-based products, this cereal species continues to attract growing interest among breeders, in particular in the Mediterranean Region. Tritordeum is drought-tolerant and suitable for cultivation in regions with limited availability of water, which is a very important consideration in an era of rapid climate change. However, the technological quality of Tritordeum grain and its suitability for the production of bread flour remain insufficiently investigated.

Our work is a comprehensive study comparing the technological quality and baking quality of flours obtained from 11 spring Tritordeum breeding lines with modern cultivars of durum wheat, bread wheat, and naked barley. Tritordeum was characterized by a similar content of protein (14.0%), ash (0.60%), and wet gluten (34.3%) to bread wheat (13.3%, 0.54%, and 31.9%, respectively), but a significantly lower gluten index (51% vs 90%). Bread yield was highest in loaves made from durum wheat (142% on average) and lowest in loaves from bread wheat and barley flour (134 and 133%, respectively). The bread yield of Tritordeum ranged from 133-141%. Breeding lines of Tritordeum were highly similar to bread wheat in terms of all dough rheological properties, milling quality, and baking quality, which indicates that Tritordeum constitute a valuable resource for bread production.

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P411 - Genotype × agroecological management interactions promote rheological and nutritional quality of durum wheat in Mediterranean mountains

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Abstract

Wheat agroecological farming systems are increasingly promoted in Mediterranean mountainous areas for their potential to enhance sustainability, nutritional quality, and local value chains. Nevertheless, their effects on the rheological and nutritional quality of durum wheat under diverse environments remain insufficiently explored. This study aims to assess the effects of genotype, management system, and environment on the rheological and nutritional quality of durum wheat by analyzing grains harvested from trials conducted in mountain environments across five Mediterranean countries: Morocco, Algeria, Lebanon, Italy, and Croatia. The plant material included ten durum wheat genotypes, along with local commercial varieties and landraces, which were evaluated under agroecological and conventional management systems. A broad spectrum of grain quality attributes was evaluated following international standards at the INRA-ICARDA laboratories. Data were analyzed using ANOVA and a weighted multi-trait quality index. Results revealed strong genotype × environment × management interactions for most traits. Agroecological management generally enhanced grain protein content and micronutrient concentration (iron and zinc), with protein increases of up to 2-4% and micronutrient gains reaching 5-10% in specific countries, while maintaining acceptable technological quality. Thousand kernel weight and semolina yield showed positive responses in some environments, highlighting environment-dependent trait dynamics. Genotypes such as Nachit, Shabasse, and Zagharine consistently exhibited superior and stable quality performance under agroecological conditions across countries. Agroecological management improved key rheological traits of durum wheat in mountain environments, enabling the identification of stable, high-quality genotypes adapted to each country. The results support participatory variety selection, and pilot-scale pasta production confirmed the technological suitability of selected genotypes, strengthening their potential to enhance resilient wheat-based value chains in Mediterranean mountain regions.

P412 - Accelerating wheat quality phenotyping: streamlined bioactive assays and NIR-machine learning prediction of processing quality

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Abstract

Wheat improvement programs increasingly aim to deliver both strong processing performance and enhanced nutrition, but phenotyping capacity remains a major constraint. Conventional protocols for dough rheology (Farinograph and Extensograph) and baking are slow, costly, and sample-demanding, limiting their use in large breeding pipelines. In parallel, major whole-grain health-promoting components, including arabinoxylans (AX), ferulic acid, and alkylresorcinols (AR), are analytically challenging to quantify at scale due to inconsistent protocols, technical complexity, and low throughput.

Here we present an integrative phenotyping strategy that advances both domains. For nutrition-related traits, we established breeder-friendly analytical workflows, including a streamlined one-pot extraction for phenolic acids and an optimized UPLC method that reduces run time from approximately 30 min to about 4 min, enabling substantial gains in efficiency for phenolic and AR determination alongside AX profiling. Using this workflow across environments, we confirmed Yumai 34 as a stable high water-extractable arabinoxylan (WE-AX) source, consistent with prior HEALTHGRAIN benchmark observations, providing a practical positive control that supports nutrition-oriented phenotyping for breeding.

To address the scale barrier for processing-quality phenotyping, we developed near-infrared (NIR) spectroscopy coupled with machine learning as a rapid, non-destructive approach targeting registration-relevant traits and breeding-relevant baking outcomes. Using a representative dataset of 1082 wheat samples collected across major production regions (2021-2023), NIR models achieved strong prediction for Farinograph water absorption (model development $R^2 = 0.92$; independent validation in 2024 $R^2 = 0.87$), enabling faster and more consistent water-setting and improving throughput of downstream rheology and baking workflows. In a second large dataset of approximately 5000 CIMMYT samples, an ensemble learning strategy delivered practical predictability for bread loaf volume (R^2 approximately 0.74), supporting rapid screening for bread-making quality.

Together, these advances provide a scalable phenotyping roadmap, from robust measurement of health-promoting composition to machine-learning-enabled, NIR-based prediction of processing quality, accelerating selection and decision-making in wheat improvement programs.

P413 - A simple way for wholegrain bakery products to be low-FODMAP

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Abstract

Consuming whole grain cereals offers health benefits primarily due to their high dietary fibre content, which can lower the risk of cardiovascular diseases, type 2 diabetes, weight gain, and certain cancers. However, specific soluble dietary fibers known as fermentable oligo-, di-, and monosaccharides and polyols (FODMAPs) may negatively impact gut health. This has prompted a focus on managing dietary intake of FODMAP-rich foods, as they can exacerbate symptoms in gastrointestinal conditions like irritable bowel syndrome, celiac disease, and Crohn's disease, leading to recommendations for a low-FODMAP diet. The results presented are derived from the project "Biotechnological tools for optimizing short- and medium-chain carbohydrate content in cereal-based foods to prevent gastrointestinal disorders—GutFriendlyCarbs" These results encompass several key innovations:

- Low-FODMAP wholegrain wheat and wholegrain rye bread were produced by optimizing the standard technological process of breadmaking via the addition of a chemical raising agent, baking powder, and baker's yeast in surplus. To the authors' knowledge, this is the first instance where this combination of leavening agents has been utilized in breadmaking to decrease FODMAP levels. This process does not necessitate alterations to the traditional breadmaking method, and the bakery sector does not have to develop specialized items for those on a low-FODMAP diet.
- The production of low-FODMAP wholegrain wheat and rye cookies and crackers indicates that an extended resting period of the dough following kneading effectively activated the endogenous enzymes of the flour and yeast, particularly in the production of yeast-based crackers. The partial substitution of flour by wheat malt and/or the addition of aqueous extracts from chicory root incorporated ingredients containing pre-activated enzymes into the dough formulations illustrated another efficacious strategy for reducing the FODMAPs content.
- Wholegrain pasta manufacturers could reduce the high FODMAP content in their products by optimizing the technological process, such as drying pasta at temperatures below 100°C, shaping short pasta forms, and avoiding supplementation with vitamin C and A (acidic conditions). Furthermore, manufacturers should recommend to consumers to cook the pasta in a larger volume of water, at lower temperatures, and under alkaline conditions (using alkaline mineral water or adding a small amount of sodium bicarbonate).

P414 - Environmental and genetic determination of semolina Minolta b* value in winter durum wheat

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Abstract

In modern durum wheat breeding programs, improving technological quality is a primary goal. Several favorable characteristics of durum wheat provide advantages during processing, among which high yellow pigment content — commonly determined by measuring the Minolta b* value — is of outstanding importance. In our experiments, we examined the Minolta b* values of 100 winter and facultative durum wheat varieties and breeding lines from 12 countries. Based on the results of the ANOVA, the two main factors (year and genotype) and their interaction were found to be significant. We determined the variance components using REML analysis and calculated the repeatability (h^2) values from these components. Based on the diversity panel examination, the Minolta b* values were distributed across a wide interval. Due to the high repeatability ($h^2 = 0.978$), the genetic determination of this trait is extremely strong. The Minolta b* values of varieties from different countries differed significantly; the highest average values were measured in German (25.30) and Austrian (24.49) durum wheat samples, while Italian varieties ranked third (23.64). The averages for the remaining countries fell within a narrower range, between 19 and 21. A biparental mapping population was created using lines with extremely high and low Minolta b* values. The Minolta b* value of the semolina from the high yellow pigment line exceeded 24 consistently over 12 years, whereas the low ones failed to reach a value of 20 in most years. The effects of environment (year) and genotype were analyzed using a linear mixed model (REML). Our calculations confirmed that the Minolta b* value is a highly heritable trait within this population. In the mapping population, the trait was controlled by a complex genetic background. The region with the strongest effect was located on the long arm of chromosome 7A (29.6%), followed by QTL on chromosomes 3B (12.8%) and 1B (10.8%).

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P415 - A high-quality bread wheat genome unravels adaptive evolution of wheat end-use quality

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Abstract

Understanding the genetics of superior dough performance is essential for improving wheat end-use quality. Here, we presented a de novo assembly of the genome of JM44, a Chinese wheat cultivar known for its exceptional end-use quality. The JM44 genome achieved reference-level quality (QV = 66.74), depicting a complete picture of complex regions containing gluten genes. Our microsynteny analysis across the Triticum-Aegilops complex showed that high-molecular-weight glutenin subunits (HMW-GSs) loci are highly conserved, while low-molecular-weight glutenin subunits (LMW-GSs) and α - β -gliadins exhibited greater structural variation. These variable loci appear to have been preferentially selected by humans and contributed substantially to the evolution of wheat quality traits. Moreover, we observed that epistatic interactions between gluten genes are strong in modern cultivars, but markedly weaker in landraces, indicating the importance of epistatic selection during modern breeding. Our findings shed light on the genomics and evolution of wheat quality traits, providing valuable guidance for future breeding efforts.

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