



4th International Plant Genetics
and Genomics Conference

IPGG 2026

21-25 September 2026

*Advancing Genomics
for Future Crop
Improvement*

Book of Abstracts

4th International Plant Genetics and Genomics Conference (IPGG 2026)

Book of Abstracts

Edited by

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Welcome Message

Welcome to the 4th International Plant Genetics and Genomics Conference (IPGG 2026)

Dear Colleagues, Researchers, Students, and Industry Partners,

On behalf of the organizing committee, it is our great pleasure to welcome you to the 4th International Plant Genetics and Genomics Conference (IPGG 2026), held virtually from 21-25 September 2026.

This year's conference brings together leading scientists, breeders, geneticists, genomic researchers, plant pathologists, computational biologists, and students from around the world to discuss recent advances in plant genetics, genomics, breeding, biotechnology, and crop improvement. As agriculture faces increasing challenges from climate change, emerging diseases, environmental stresses, and growing global food demands, scientific innovation is more important than ever.

IPGG 2026 provides an international platform for sharing cutting-edge research, fostering collaborations, and promoting discussions on innovative strategies that accelerate genetic gain and sustainable crop improvement. The conference program features distinguished keynote speakers and emerging researchers presenting their work across a wide range of topics, including abiotic and biotic stress resistance, molecular breeding, genomics-assisted selection, artificial intelligence in plant breeding, gene editing, and modern crop improvement technologies.

We sincerely thank all keynote speakers, presenters, participants, reviewers, sponsors, and partners for their valuable contributions and continued support. Your participation is essential to the success of this conference and to advancing scientific discovery in plant genetics and genomics.

We wish you a productive and inspiring conference experience and look forward to the exchange of ideas that will contribute to the future of plant science and global food security.

Prof. Dr. Ahmed Sallam

Conference Chair

4th International Plant Genetics and Genomics Conference (IPGG 2026)

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The Conference

The 4th International Plant Genetics and Genomics Conference (IPGG 2026) will be held online via Microsoft Teams.
September 21-25, 2026

Awards

1. Best Talks and Poster Presentation Awards
2. The Young Researchers Award

Contact Information

For inquiries regarding the conference, abstracts, registration, or the Young Researchers Award, please contact:

Email: mgb17@aun.edu.eg

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Official Website: <https://mgbsonline.wixsite.com/mgb17>

Mailing list: <https://forms.gle/F5917McCSaKhd2DQ79PE/edit>

Previous events:

<https://www.mgb17-ipgg.com/previous-events>

Citation

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Conference Program

International Plant Genetics and Genomics Conference (IPGG 2026)

21-25 September 2026 | Virtual Conference

All times are listed in Cairo, Egypt (GMT+3)

Day I: Monday, 21 September 2026

Registration and Opening

Time	Activity
13:00-13:30	Registration
13:30-13:40	Opening and Welcome Speech Prof. Dr. Ahmed Sallam
13:40-14:00	Opening Scientific Address <i>From Genomics to Genetic Gain: Accelerating Crop Improvement for a Changing World</i> Prof. Dr. Rajeev Varshney (Murdoch University, Australia)

Session 1: Genetics and Breeding for Abiotic Stress Tolerance Moderators: Prof. Dr. Dina Abdel Moneam & Prof. Dr. Ahmed Sallam

Time	Presentation	Page
14:00-14:40	Keynote Lecture 1: <i>Recent Advances in Developing Salt-Tolerant Crop Varieties: Linking Genetic Identity to Nutritional Traits.</i> Prof. Dr. Jutta Papenbrock (Leibniz University Hannover, Germany).	1
14:40-15:20	Keynote Lecture 2: <i>Peduncle Trait Variation and Its Genetic and Phenotypic Association with Spike Productivity in Wheat under Contrasting Water Regimes.</i> Prof. Dr. Ahmed Sallam (Assiut University, Egypt).	2
15:20-16:00	Keynote Lecture 3: <i>Development and Delivery of Stress-Tolerant Crops for Marginal Environments.</i> Prof. Dr. Mark Tester (KAUST, Saudi Arabia).	3
16:00-16:20	Coffee Break	

16:20-16:40	Oral Presentation 1: <i>Identification and Validation of Novel Genes Associated with Lead Tolerance in Spring Wheat at the Seedling Stage.</i> Shrouk Abd Al-Twab Abd Al-Moneim (Assiut University, Egypt).	4
16:40-17:00	Oral Presentation 2: <i>Comparative Transcriptomic Meta-Analysis of Male Reproductive Heat Stress Responses in Plants.</i> Neeta Lohani (TIET, India).	5
17:00-17:20	Oral Presentation 3: <i>Unravelling Critical Phenological Windows of Heat Stress Resilience in Bread Wheat Through Temporal NDVI and Canopy Temperature Dynamics.</i> Narain Dhar (Ch. Charan Singh University, India).	6
17:20-17:35	Poster Presentation 1: <i>Transcriptomic Response of the Wild Plant Mesembryanthemum forsskalii Hochst. ex Boiss to Salinity Stress: De Novo Assembly, Functional Annotation, and Transcription Factor Profiling.</i> Dr. Sumayah I. Alsanie (IAU, Saudi Arabia).	7

Day II: Tuesday, 22 September 2026

Session 2: Advances in Molecular Plant Breeding and Genetics Moderators: Prof. Dr. Mohamed Ali & Prof. Dr. Diaa Abdel Moneam

Time	Presentation	Page
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10:40-11:20	Keynote Lecture 5: <i>Translational Genomics for Wheat Breeding.</i> Dr. Awais Rasheed (CIMMYT, China).	9
11:20-12:00	Keynote Lecture 6: <i>Induced genetic diversity through mutagenesis in wheat gene pool and significant use of SCoT markers to underpin key agronomic traits.</i> Dr. Mohammed Ali (Maryout Research Station, Egypt)	10
12:00-12:20	Coffee Break	
12:20-12:40	Oral Presentation 4: <i>Genetic Dissection of Grain Zinc Concentration Reveals Novel QTL on Chromosome 6AS From</i>	11

Synthetic Hexaploid Wheat.
Youshaa Danyal (CAAS, China).

12:40-13:00	Oral Presentation 5: <i>Genetic Diversity of Azerbaijani Wild Cherry Plum (<i>Prunus cerasifera</i> Ehrh.): Molecular Characterization.</i> Shahmar R. Hajiye (Azerbaijan State Agricultural University, Azerbaijan).	12
13:00-13:20	Oral Presentation 6: <i>Population Structure and Migration Patterns of Cashew (<i>Anacardium occidentale</i> L.) Revealed by Genome-Wide SNP Analysis.</i> Oliver Johns (University of Lisbon, Portugal).	13
13:20-13:35	Poster Presentation 2: <i>Map-Based Cloning of the Grain Zinc Concentration Gene TaNAS10-6D in Common Wheat.</i> Mengjing Sun (CAAS, China).	14
13:35-13:50	Poster Presentation 3: <i>Genome-Wide Identification of Zn/Fe Homeostasis Genes and Association Mapping for the Candidate Gene TaZIP14-3A in Common Wheat.</i> Huichun Ye (CAAS, China).	15

Session 3: Legume Breeding and Genetics

Moderators: Prof. Dr. Ahmed Sallam & Dr. Daa Daghma

Time	Presentation	Page
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16:40-17:20	Keynote Lecture 8: <i>Faba Bean Pan-Omics.</i> Prof. Dr. Stig Andersen (Aarhus University, Denmark).	17
17:20-18:00	Keynote Lecture 9: <i>Structural Variation and Breeding Trade-Offs Underlying Disease Resistance in Pea.</i> Dr. Sanu Arora (John Innes Centre, UK).	18
18:00-18:20	Coffee Break	
18:20-18:40	Oral Presentation 7: <i>Genome-Wide Association Mapping Highlights Stable SNP Markers Associated With Yield-Related Traits in Faba Bean.</i>	19

	Salwa Mohammed Mahmoud (Assiut University, Egypt).	
18:40-19:00	Oral Presentation 8: <i>Dissecting the Genetic Basis of White Mold Resistance in Common Bean Through Genome-Wide Association Analysis.</i> Neha G. Paserkar (McGill University, Canada).	20
19:00-19:15	Poster Presentation 4: <i>Genetic Diversity Assessment of Portuguese Cowpea Germplasm: A Foundation for Next-Generation Breeding.</i> Graça Pereira (INIAV, Portugal).	21

Day III: Wednesday, 23 September 2026

Session 4: Genetics and Breeding for Biotic Stress Resistance

Moderators: Dr. Shams-Eldeen Eltaher & Dr. Amira Mourad

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10:40-11:20	Keynote Lecture 11: <i>Advances in Disease and Pest Resistance in Faba Bean.</i> Prof. Dr. Diego Rubiales (Spain).	23
11:20-12:00	Keynote Lecture 12: <i>Beyond Conventional Breeding: Protoplast-Based Technologies and Genome Editing for Sustainable Citrus Disease Management.</i> Dr. Ahmad A. Omar (University of Florida, USA).	24
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12:20-12:40	Oral Presentation 9: <i>Identification and Validation of a Novel Stripe Rust Resistance Locus on Chromosome 6BL Using Genome-Wide Association Analysis in Common Wheat.</i> Yirga Kindie Wasihun (CAAS, China).	25
12:40-13:00	Oral Presentation 10: <i>Viral Discovery and Genomic Surveillance Reveal Emerging Plant Virus Threats in the Southeastern United States.</i> PhD Candidate Abdelaal H. A. Shehata (Auburn University, USA).	26

13:00-13:20	Oral Presentation 11: <i>Exploring Genetic Variation and Stripe Rust Resistance in ICARDA's Spring Bread Wheat Using GWAS in the WANA Region.</i> Alaa Youssef (ICARDA, Egypt).	27
13:20-13:35	Poster Presentation 5: <i>Map-Based Cloning and Functional Validation of the Adult-Plant Resistance Locus QPmjbr.caas-6BL to Powdery Mildew in Common Wheat.</i> Xiaowan Xu (CAAS, China).	28
13:35-13:50	Poster Presentation 6: <i>Characterization and Fine Mapping of a Major Adult-Plant Resistance Locus on Wheat Chromosome 4BL for Powdery Mildew in Cultivar Zhongmai 30.</i> Bingyi Liu (CAAS, China).	29

Day IV: Thursday, 24 September 2026

Session 5: AI-Accelerated Precision Plant Breeding

Moderators: Dr. Diego Jarquin & Dr. Mohamed Ali

Time	Presentation	Page
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14:40-15:20	Keynote Lecture 14: <i>From Data to Seeds: Digital Technologies Driving Innovation in Plant Breeding and Farming.</i> Dr. Ana Garcia-Oliveira (INIAV, Portugal).	31
15:20-16:00	Keynote Lecture 15: <i>Genomic AI Prediction Framework Assisted by Proximal and Remote Sensing Data: Examples and Methods.</i> Dr. Diego Jarquin (University of Florida, USA).	32
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Moderators: Dr. Diaa Daghma & Prof. Dr. Ahmed Sallam

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10:00-10:40	Keynote Lecture 16: <i>CRISPR-Based Genome Editing for Climate-Smart Agriculture.</i> Prof. Kailash Bansal (NAAS, India).	33

	Keynote Lecture 17: <i>Functional Validation of the MYB4-12 Homolog to Modulate PAL2-Mediated Phenylpropanoid Flux Toward Capsaicin Biosynthesis in Capsicum annuum L.</i>	
10:40-11:20	Dr. Diaaeldin Daghma (JKI, Germany).	34
	Keynote Lecture 18: <i>New Breeding Tools to Enhance Crop Quality and Sustainability.</i>	
11:20-12:00	Dr. Domenica Nigro (University of Bari Aldo Moro, Italy).	35
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12:20-13:00	Prof. Dr. Goetz Hense (CPGE, Heinrich Heine University Düsseldorf, Germany).	36
	Poster Presentation 7: <i>Novel Mitochondrial Genome Editing Reveals Cytoplasmic Male Sterility in Tobacco and Seedless Fruit Traits in Tomato.</i>	
13:00-13:15	Caitlin C. Kestell (North Carolina State University, USA).	37
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Session 1

Genetics and Breeding for Abiotic Stress Tolerance

Day I: Wednesday, 21 September 2026

Keynote Lecture 1

Recent Advances in Developing Salt-Tolerant Crop Varieties: Linking Genetic Identity to Nutritional Traits

Andre Fussy¹ & Jutta Papenbrock^{1,*}

¹Institute of Botany, Leibniz University Hannover, Hannover, Germany

*Presenting author: Jutta.Papenbrock@botanik.uni-hannover.de

Abstract

Soil salinization, freshwater scarcity, and climate change pose significant challenges for modern agriculture. Salt-tolerant crops like *Salicornia*, *Sarcocornia*, and *Arthrocnemum* offer a smart solution for farming on saline soils. These plants thrive where conventional crops fail, enabling food production without competing for valuable freshwater or arable land. Accurate and reliable species identification is crucial to ensure consistent quality for breeding, farming, and marketing. In a recent study on European *Salicornia*, we applied morphological analysis, nuclear DNA content measurements, standard DNA barcoding markers including diagnostic ETS polymorphisms, and microsatellite profiles. ETS-based markers proved a straightforward, low-cost method for species identification, while microsatellite length variation distinguishes subspecies. The current research investigates whether these species differ in their nutritional value and bioactive compounds. Under controlled hydroponic conditions, phenolic profiles, macronutrients (proteins, fats, and fiber), essential minerals, and biomass yield were analyzed. Phenolics serve as antioxidants with potential health benefits. It was hypothesized that certain species accumulate unique phenolic acids or other bioactive substances, in parallel with favorable nutrient profiles and yields, making them suitable for foods, animal feed, or pharmaceuticals. Linking genetic identity to nutritional traits and productivity will enable targeted selection of promising halophytic species and subspecies for sustainable agriculture on marginal lands.

Keywords: *Salicornioideae*, barcoding, molecular phylogeny, phenolic compounds, saline agriculture.

Keynote Lecture 2:

Peduncle Trait Variation and Its Genetic and Phenotypic Association with Spike Productivity in Wheat Under Contrasting Water Regimes

Ahmed Sallam^{1,*}, Mostafa Hashem¹, Asmaa A. M. Ahmed¹, Saleh M. Ismail², P. Stephen Baenziger³, Andreas Börner⁴

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² Soils and Water Department, Faculty of Agriculture, Assiut University, Assiut, Egypt.

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⁴ Department of Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

*Presenting author: amsallam@aun.edu.eg

Abstract

The peduncle stem is critical for resource allocation and water transport to wheat spike grains under normal conditions, yet its role under drought stress remains underexplored. This study investigates peduncle traits—length (PL), diameter (PD), and weight (PW)—and their associations with spike productivity to uncover drought mitigation mechanisms in wheat. A diverse panel of 198 highly homozygous spring wheat varieties was evaluated under normal and drought conditions across two growing seasons. Key traits measured included peduncle dimensions (PL, PD, PW), spike attributes (spike length [SPL], spikelets per spike [NSPS], grains per spike [GNPS], grain yield per spike [GYPS]), and thousand-kernel weight (TKW). Results showed PD and PW, unlike PL, exhibited strong, significant correlations with spike traits and grain weight under both conditions. Genome-wide association studies (GWAS) revealed distinct genetic architectures: no shared stable markers linked peduncle and spike traits, highlighting independent control mechanisms. Notably, contrasting genotypes identified key SNPs, including one in a highly expressed peduncle/spike gene model. Cultivars with superior PD and PW consistently outperformed low-trait counterparts in yield-related metrics, especially under drought. This is the first study demonstrating PD and PW as pivotal adaptive traits mitigating drought effects on spike productivity. PL showed no such associations. Selecting for high PD and PW offers a promising strategy to boost wheat yield stability amid genotype-environment interactions. Seven elite genotypes with combined high peduncle and spike traits are recommended for breeding drought-tolerant cultivars, advancing genomic-assisted selection.

Keywords: Peduncle traits, Drought stress, Wheat productivity, GWAS, Spike yield, Distinct SNP

Keynote Lecture 3:

Development and Delivery of Stress-Tolerant Crops for Marginal Environments

Mark Tester^{1,*}

¹*The Food Mission, King Abdullah University of Science & Technology, Saudi Arabia.*

*Presenting author: mark.testter@kaust.edu.sa

Abstract

In the process of trying to deliver outcomes of our research on salinity tolerance, we are developing a series of new hybrid allotetraploid lines that greatly increase yield and profitability. This approach also provides a new method for rapidly stacking complex multigenic tolerance traits to produce strong hybrid allotetraploid rootstocks. The primary target materials are tomato rootstocks, but we are now broadening this approach to a range of crops, including woody perennials. To deliver our research, we have now established a small series of companies, where we combine engineering and plant science to develop and use saltwater-based agricultural systems to reduce the water and carbon footprint of modern agriculture, and to do this in an environmentally sustainable and economically viable.

Keywords: salinity tolerance; genetics; neo-domestication; sustainable food security; plant physiology; ion transport

Oral Presentation 1:

Identification and Validation of Novel Genes Associated with Lead Tolerance in Spring Wheat at the Seedling Stage

Shrouk Harb^{1,*}, Sara Baghdady², Mohamed T. Mourad³, Ahmed Sallam^{1,2}, Andreas Börner⁴, and Amira M.I. Mourad^{3,4}

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Abstract

Lead (Pb) contamination threatens wheat production and food safety, yet the genetic basis and stability of Pb tolerance across stress intensities remain poorly understood. This study used complementary discovery and validation populations to identify robust genomic regions controlling Pb tolerance in wheat seedlings. Initially, 103 diverse spring wheat genotypes were evaluated under control and Pb-contaminated soil (65.81 mg kg⁻¹). Genome-wide association analyses using 25K-SNP-array and genotyping-by-sequencing datasets detected 222 significant marker–trait associations. An independent panel of 106 genotypes was subsequently evaluated under control (2.93 mg kg⁻¹), moderate (180.31 mg kg⁻¹), and high (318.35 mg kg⁻¹) Pb concentrations to validate these associations. Significant genotypic variation and moderate-to-high broad-sense heritability were detected for seedling traits. Pb exposure primarily reduced root growth and biomass accumulation, with stronger effects at the highest concentration. Single-marker analysis validated 27 and 24 previously identified SNPs under moderate and high Pb stress, respectively. Seven markers on chromosomes 2B, 6A, 7A, and 7B were consistently associated with Pb-responsive traits across all three concentrations. Multivariate and allele-effect analyses confirmed significant phenotypic differentiation between their alleles, although marker effects varied with stress intensity. Five stable markers located within genes encoding stromal cell-derived factor 2, a transmembrane protein, nucleolar GTP-binding protein 1, an arginine–glutamic acid repeat protein, and a Mediator complex subunit. Functional enrichment implicated transcriptional regulation and GTP-binding processes. These validated markers and candidate genes provide promising resources for functional characterization and marker-assisted improvement of Pb tolerance in wheat across different Pb-contaminated agricultural environments.

Keywords: Lead tolerance; wheat (*Triticum aestivum* L.); heavy metal stress; GWAS; SNP markers; candidate genes; gene expression; seedling growth; marker-assisted selection.

Oral Presentation 2

Comparative Transcriptomic Meta-Analysis of Male Reproductive Heat Stress Responses in Plants

Madhav Takkar¹, Neeta Lohani^{1,*}

¹Department of Biotechnology, Thapar Institute of Engineering and Technology, Patiala, Punjab, India.

*Presenting author: neeta.lohani@thapar.edu

Abstract

Rising global temperatures threaten crop productivity, and the male reproductive phase is among the most thermosensitive stages of the plant life cycle. Individual transcriptomic studies typically examine a single species, genotype, or developmental stage, making it difficult to separate responses fundamental to thermotolerance from those specific to a single experimental context. We reanalyzed 312 publicly available and in-house RNA-sequencing runs from male reproductive tissues of eight species (*Arabidopsis thaliana*, *Brassica napus*, *Cucumis sativus*, *Zea mays*, *Glycine max*, *Nicotiana tabacum*, *Solanum lycopersicum* and *Triticum aestivum*) through one uniform pipeline (STAR, StringTie, DESeq2), and integrated 31 heat-versus-control contrasts by orthology (OrthoFinder). We identified 57,924 differentially expressed genes (30,703 up- and 27,221 down-regulated) and, using Gene Ontology and KEGG enrichment, resolved the response into three modules. Module 1 defined a compact, deeply conserved core of protein homeostasis and redox control: of 25,931 heat-responsive orthogroups, 147 were recruited in all eight species and were dominated by heat-shock proteins and chaperones, including small heat-shock proteins, BAG6 and HSA32. Module 2 distinguished thermotolerant from thermosensitive genotypes of *T. aestivum*, *S. lycopersicum* and *G. max*, and tolerant genotypes were marked by endoplasmic-reticulum protein quality control and ER-associated degradation, whereas sensitive genotypes showed signatures of oxidative damage. Module 3 revealed a large lineage- and stage-specific periphery, with 49% of orthogroups restricted to a single species. The genotype-associated thermotolerance signature barely overlapped the conserved core (under 3%), showing that the determinants of differential thermotolerance lie in the peripheral fraction rather than the universal chaperone machinery. These results provide a unified framework and a prioritised catalogue of candidate genes for breeding heat-resilient crops.

Keywords: Heat stress, Male reproduction, Pollen thermotolerance, Comparative transcriptomics, Meta-analysis, Orthology, Heat-shock proteins.

Oral Presentation 3

Unravelling Critical Phenological Windows of Heat Stress Resilience in Bread Wheat Through Temporal NDVI and Canopy Temperature Dynamics

Narain Dhar^{1,2,*}, Pradeep K. Sharma¹, Pradeep K. Bhati², Manish K. Vishwakarma²

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²Borlaug Institute for South Asia (BISA) New Delhi India

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Abstract

Heat stress during the terminal phase increasingly threatens wheat productivity, but the critical phenological window for heat tolerance remains unidentified. We have tested 230 genotypic entries (225 germplasms and five check varieties), generating 240 field plots in two years, three locations, and contrasting normal and late sowing conditions. Time-series NDVI and Canopy temperature (CT) were recorded at anthesis, grain filling, and maturity phases, and their relationship with grain yield and thousand-grain weight (TGW) were analyzed using BLUEs, correlation, Random Forest, and path analysis. Late seeding caused the temperature to rise by about 5.5-8.8°C during grain filling and shortened the reproductive period, which put the crop under heat stress. NDVI at anthesis phase ($r = 0.71$) and maturity ($r = 0.76$) were highly positively correlated with grain yield, while CT at anthesis showed high negative correlation ($r = -0.68$). Using the Random Forest technique, NDVI and CT variables in the time-series between anthesis and grain filling were the most significant physiological traits predicting of grain yield under terminal heat stress. Path analysis further showed that CT exhibited a negative direct effect on grain yield ($\beta = -0.196$) and TGW ($\beta = -0.214$), whereas maturity NDVI showed a positive direct effect on grain yield ($\beta = 0.485$). Time series physiological traits identified the elite genotypes, which were G12051, G12072, G12031, G12007 and G12037, having desirable canopy characteristics and heat tolerance potential. This study shows that heat stress is a temporal phenomenon and that time-series NDVI-CT profiling has emerged as an effective tool to identify critical physiological windows and develop climate-resilient wheat germplasm.

Keywords: Bread wheat; Terminal heat stress; NDVI; Canopy temperature; Phenological window; Grain yield; TGW; Heat resilience.

Poster Presentation 1

See poster on the next page

Transcriptomic Response of the Wild Plant *Mesembryanthemum Forsskalii* Hochst. Ex Boiss to Salinity Stress: *De Novo* Assembly, Functional Annotation, and Transcription Factor Profiling

Sumayah I. Alsanie^{1,*} and Faten Dhawi ²

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²Agricultural Biotechnology Department, College of Agricultural and Food Sciences, King Faisal University, Al- Hofuf, Saudi Arabia.

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Abstract

Halophytes such as *Mesembryanthemum forsskalii* Hochst. ex Boiss. are well-adapted to harsh environments characterized by high salinity and drought, offering both nutritional and medicinal benefits. However, the genetic and molecular basis of salinity tolerance in *M. forsskalii* Hochst. ex Boiss remains largely unexplored. This study aimed to generate novel genomic resources and identify the genes, pathways, and transcriptional regulators that associated with salt stress tolerance. Plant samples were treated with NaCl at 150 mM and 400 mM, resulting in transcriptomic sequencing yielding over 50 million reads for each concentration. Differential expression analysis revealed 5,606 and 665 significantly upregulated and downregulated genes, respectively, in plants irrigated with 150 mM NaCl (C vs S1), while 10,730 DEGs were identified under 400 mM NaCl (C vs S2), of which 9,970 were upregulated and 760 downregulated. De novo assembly indicated that a substantial proportion of transcripts encoded novel or functionally unknown proteins. Approximately 29% and 21% of transcripts under 150 and 400 mM NaCl were functionally annotated in UniProt, GO, and KEGG databases. The most enriched molecular functions included manganese ion binding and oxidoreductase activity. Transcription factor families, including bHLH (127 and 161 unigenes), NAC (104 and 132 unigenes), and MYB-related (95 and 111 unigenes), were highly represented among the functionally annotated DEGs under 150 and 400 mM NaCl, respectively. These results provide a salinity-focused transcriptomic resource for *M. forsskalii* and identify candidate pathways involved in ion homeostasis, redox regulation, RNA processing, and growth-stress trade-offs.

Keywords: De novo transcriptome assembly; Salinity Tolerance; *Mesembryanthemum forsskalii*; Differentially expressed genes (DEGs); Transcription factor (TF) families.

See the poster on the next page

Transcriptomic response of the wild plant *Mesembryanthemum forsskalii* Hochst. ex Boiss to salinity stress: de novo assembly, functional annotation, and transcription factor profiling

Sumayah I. Alsanie¹ and Faten Dhawi²

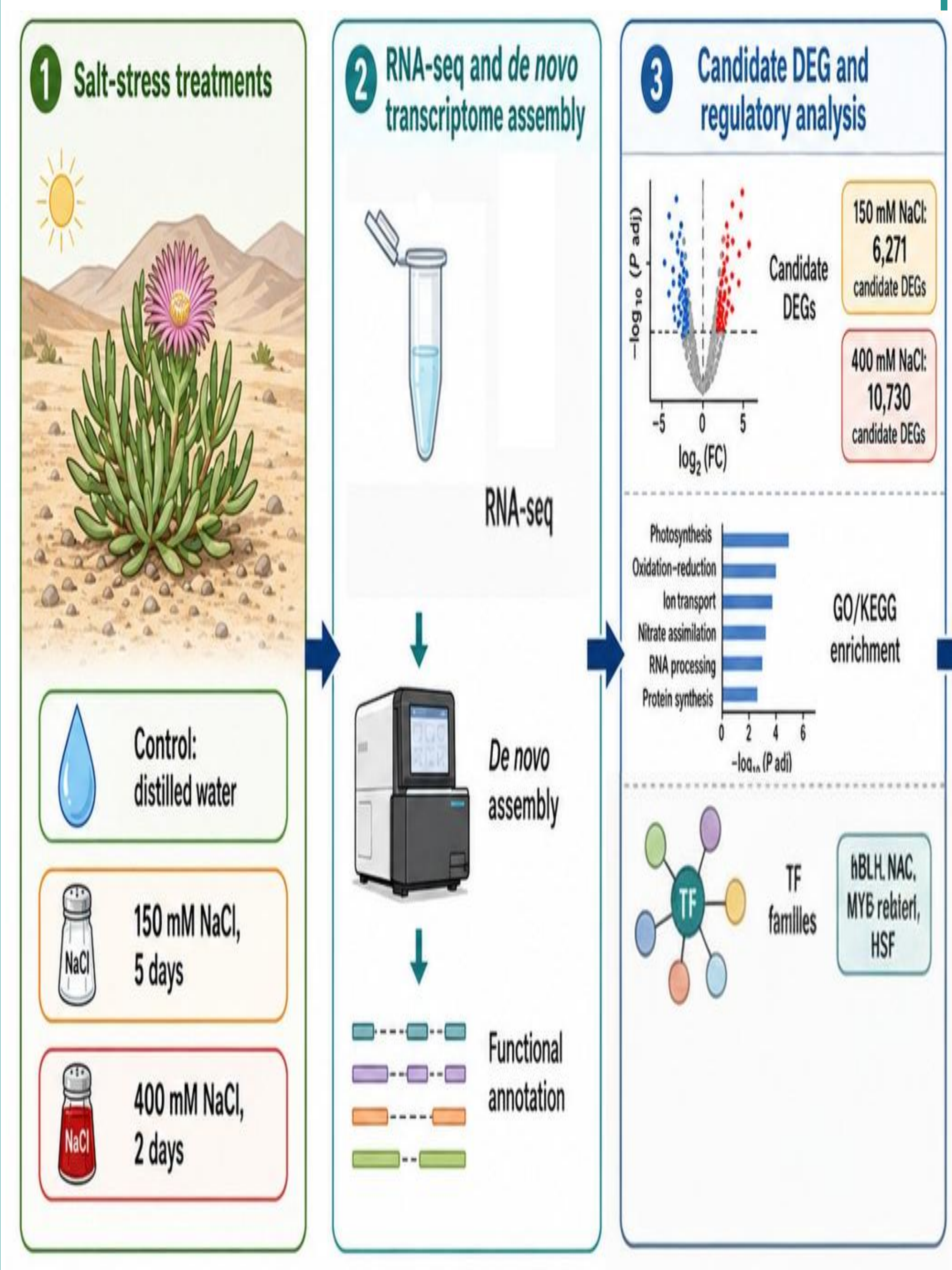
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Abstract

Halophytes such as *Mesembryanthemum forsskalii* Hochst. ex Boiss. are well-adapted to harsh environments characterized by high salinity and drought, offering both nutritional and medicinal benefits. However, the genetic and molecular basis of salinity tolerance in *M. forsskalii* Hochst. ex Boiss remains largely unexplored. This study aimed to generate novel genomic resources and identify the genes, pathways, and transcriptional regulators that associated with salt stress tolerance. Plant samples were treated with NaCl at 150 mM and 400 mM, resulting in transcriptomic sequencing yielding over 50 million reads for each concentration. Differential expression analysis revealed 5,606 and 665 significantly upregulated and downregulated genes, respectively, in plants irrigated with 150 mM NaCl (C vs S1), while 10,730 DEGs were identified under 400 mM NaCl (C vs S2), of which 9,970 were upregulated and 760 downregulated. De novo assembly indicated that a substantial proportion of transcripts encoded novel or functionally unknown proteins. Approximately 29% and 21% of transcripts under 150 and 400 mM NaCl were functionally annotated in UniProt, GO, and KEGG databases. The most enriched molecular functions included manganese ion binding and oxidoreductase activity. Transcription factor families, including bHLH (127 and 161 unigenes), NAC (104 and 132 unigenes), and MYB-related (95 and 111 unigenes), were highly represented among the functionally annotated DEGs under 150 and 400 mM NaCl, respectively. These results provide a salinity-focused transcriptomic resource for *M. forsskalii* and identify candidate pathways involved in ion homeostasis, redox regulation, RNA processing, and growth-stress trade-offs.

Keywords: De novo transcriptome assembly; Salinity Tolerance; *Mesembryanthemum forsskalii*; Differentially expressed genes (DEGs); Transcription factor (TF) families.

Methodology



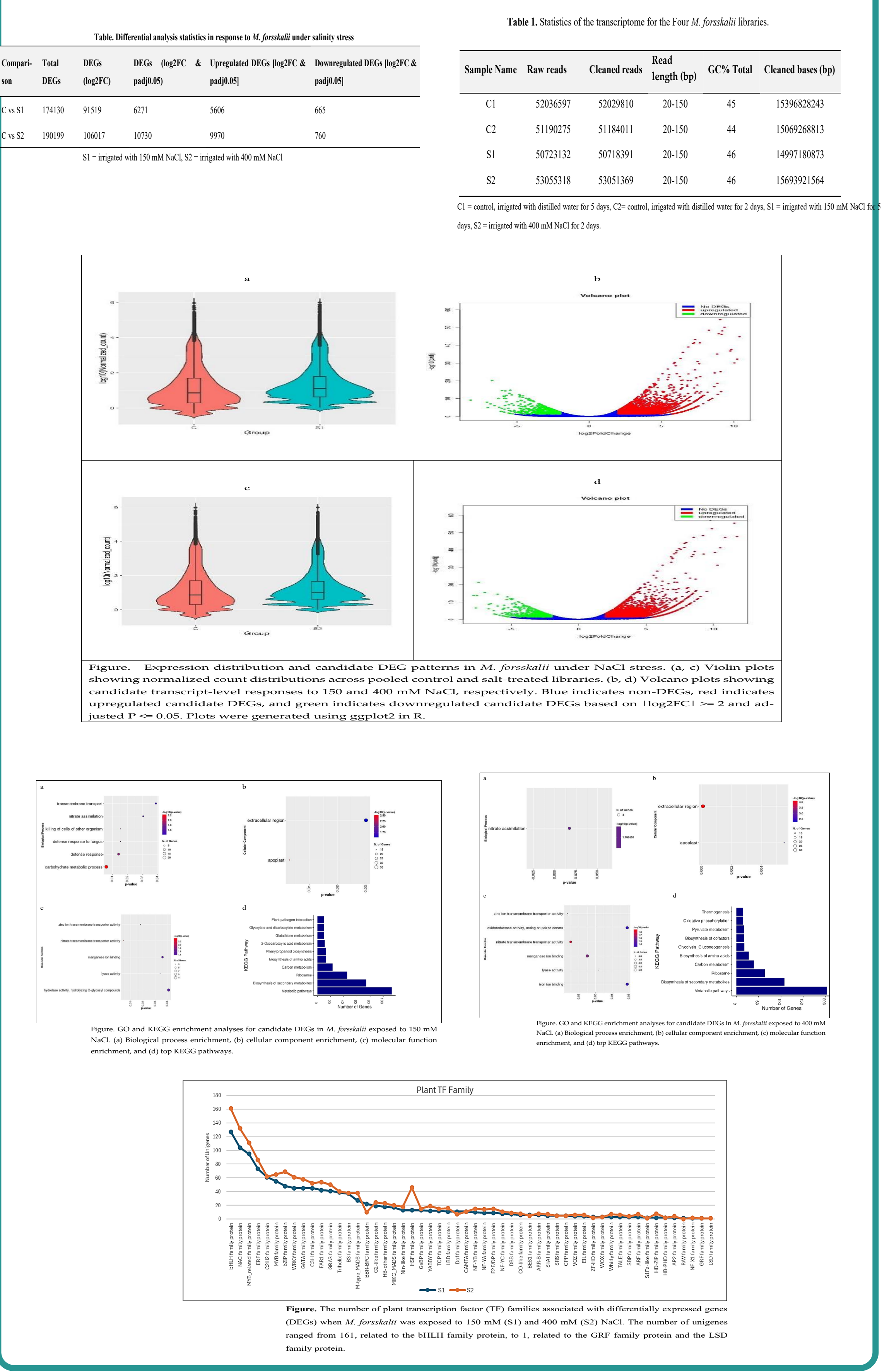
Discussion

Salinity induced substantial transcriptional reprogramming in *M. forsskalii*, with a stronger response under 400 mM NaCl. At this concentration, 9,970 genes were upregulated and 760 were downregulated. Enrichment analyses indicated that upregulated genes were mainly associated with ion transport, osmoprotectant and cutin biosynthesis, peroxisome activity, antioxidant and defense responses, and transcriptional regulation, whereas downregulated genes were largely related to photosynthesis, glutathione metabolism, and growth-related processes. Manganese and iron ion binding, oxidoreductase activity, and metabolic pathways were among the most prominent molecular functions and pathways, suggesting an important role for metal-dependent antioxidant mechanisms in mitigating salinity-induced oxidative stress [49–56]. Nitrate assimilation was also significantly enriched, indicating its potential contribution to nitrogen regulation under salt stress. Several transcription factor (TF) families, particularly bHLH, NAC, MYB-related, ERF, C2H2, MYB, bZIP, WRKY, and HSF, were consistently induced under both salinity treatments. NAC, bHLH, and MYB-related TFs showed the highest expression changes, suggesting their potential roles in regulating ion homeostasis, ROS detoxification, osmotic adjustment, and stress signaling [57–62]. In contrast, BBR-BPC TFs showed a concentration-dependent response, being induced at 150 mM but suppressed at 400 mM NaCl, potentially reflecting a shift from growth-related processes toward severe stress adaptation [63–69]. Overall, these findings indicate that *M. forsskalii* employs a multilayered transcriptional response involving ion homeostasis, antioxidant defense, metabolic adjustment, and stress-responsive TF networks. As the RNA samples were pooled and physiological traits were not quantitatively assessed, the identified DEGs and TFs should be considered candidate mechanisms requiring further physiological and molecular validation.

Introduction

Salinity is a major environmental stress that negatively affects plant growth and productivity by causing osmotic stress, ionic toxicity, nutrient imbalance, and excessive production of reactive oxygen species (ROS) [1–11]. Plants employ several adaptive mechanisms to cope with salt stress, including osmotic adjustment, ion compartmentalization, accumulation of compatible solutes, and regulation of Na⁺ and Cl⁻ transport [12–20]. Recent advances in next-generation sequencing and RNA-Seq technologies have significantly improved our understanding of the molecular mechanisms underlying plant responses to salinity and have enabled the identification of salt-responsive genes and pathways [21–27]. Halophytes are naturally adapted to saline environments and represent valuable genetic resources for understanding stress tolerance and improving crop resilience [28–32]. *Mesembryanthemum forsskalii* Hochst. ex Boiss. (Samh) is an annual succulent halophyte naturally distributed in arid and semi-arid environments [33–36]. Its seeds have nutritional and economic value and are traditionally used as food in northern Saudi Arabia [37–42]. However, despite its ecological importance and natural adaptation to stressful environments, the molecular mechanisms underlying salinity tolerance in *M. forsskalii* remain poorly understood. Therefore, this study aimed to investigate salinity-responsive transcriptional regulation in *M. forsskalii* through de novo transcriptome analysis and to identify candidate genes, pathways, transcription factor families, and hub genes associated with NaCl stress responses.

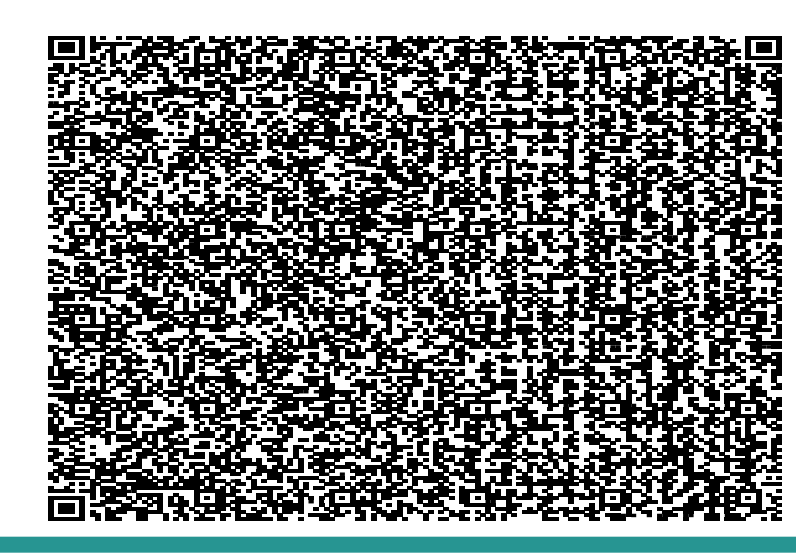
Results



Conclusion

This study a salinity-focused transcriptomic resource for the wild halophytic plant *M. forsskalii* (locally known as Samh). Integrating de novo assembly, exploratory differential expression screening, transcription factor profiling, and PPI network analysis revealed candidate salinity-responsive genes and pathways associated with transcriptional and post-transcriptional regulation, metabolic adjustment, antioxidant defense, and growth-stress trade-offs. Approximately 29% of candidate DEGs under 150 mM NaCl and 21% under 400 mM NaCl were linked to UniProt, GO, and KEGG annotations. Enriched functions and pathways included manganese ion binding, oxidoreductase activity, nitrate assimilation, metabolic pathways, spliceosome, ribosome, glutathione metabolism, and circadian rhythm-related regulation. The top transcription factor families included bHLH, NAC, and MYB-related proteins, with treatment-associated variation in HSF and BBR-BPC families. The hub-gene network highlighted candidates related to ribosomal protein L15, an RRM domain-containing protein, glutathione transferase, and COL1. Collectively, these findings support the view that *M. forsskalii* responds to salinity through coordinated transcriptional, post-transcriptional, metabolic, and redox-related adjustments. However, the conclusions are constrained by the pooled RNA-seq design, the absence of quantitative physiological measurements, and the lack of experimental validation of candidate genes. Future research should validate the identified candidates using qRT-PCR and functional genomics, include independent biological replicate libraries, measure ion accumulation and physiological stress traits, and test responses under combined abiotic stresses such as drought and salinity.

References



Session 2

Advances in Molecular Plant Breeding and Genetics

Day II: Wednesday, 22 September 2026

Keynote Lecture 4

Plant Genetic Resources for Genetic Studies on Abiotic Stress Tolerance

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Abstract

Plant genetic resources for food and agriculture (PGRFA) play a major role for global food security. The most significant and widespread mean of conserving PGRFA is *ex situ* conservation. World-wide 7.4 million accessions are stored in about 1,750 *ex situ* genebanks. With a total inventory of 150,000 accessions from 3,212 plant species and 776 genera, the 'Federal *ex situ* Genebank of Germany' in Gatersleben holds one of the most comprehensive collections worldwide. It comprises wild and primitive forms, landraces as well as old and more recent cultivars of mainly cereals but also other crops. In cereals, mainly wheat and barley, a number of bi-parental mapping populations and association mapping panels have been established to allow for the genetic analysis of various traits. The current focus covers resistance/tolerance to a number of abiotic stresses, in particular drought. Here, we present examples on genome-wide association studies (GWAS) identifying allele(s)/loci which can be used in the breeding crop for adaptation and yield improvement. This promising approach represents a tremendous step forward in genetic analysis of plant genetic resources stored in genebanks world-wide.

Keywords: Plant genetic resources, Wheat, Barley, Abiotic stress, QTL mapping, GWAS.

Keynote Lecture 5

Translational Genomics for Wheat Breeding

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Abstract

The completion of the first reference genome sequence of bread wheat (IWGSC, 2018) was a major leap forward for the wheat scientific community. It was difficult to foresee at that time that within the span of a few years, extensive genome sequencing resources of wheat and its wild relatives around the world would be available. We have outlined at least 26 studies that have characterized large wheat populations at a whole-genome level to answer questions related to wheat evolution, domestication, adaptability, wild introgressions, and breeding (Rasheed et al 2025). Such an advancement in wheat genomics over the past 6 years is unparalleled in any other crop species with a giant genome size such as wheat's. However, the efforts to translate this knowledge for practical crop breeding is slow. We discussed the key barriers and possible solutions to overcome these barriers and designing genomics-enabled tools and resources for practical wheat breeding.

Keywords: *Wheat, Biofortification, KASP markers, Genotyping.*

Keynote Lecture 6

Induced Genetic Diversity Through Mutagenesis in Wheat Gene Pool and Significant Use of SCoT Markers to Underpin Key Agronomic Traits

Ahmed Ali Abdelhameed¹, **Mohammed Ali**², Doaa Bahaa Eldin Darwish^{3,4}, Manal Abdullah AlShaqhaa⁵,
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Abstract

Background: This research explores the efficacy of mutagenesis, specifically using sodium azide (SA) and hydrazine hydrate (HZ) treatments, to introduce genetic diversity and enhance traits in three wheat (*Triticum aestivum* L.) genotypes. The experiment entails subjecting the seeds to different doses of SA and HZ and cultivating them in the field for two consecutive generations: M1 (first generation) and M2 (second generation). We then employed selective breeding techniques with Start Codon Targeted (SCoT) markers to select traits within the wheat gene pool. Also, the correlation between SCoT markers and specific agronomic traits provides insights into the genetic mechanisms underlying mutagenesis-induced changes in wheat. In the study, eleven genotypes were derived from parent varieties Sids1, Sids12, and Giza 168, and eight mutant genotypes were selected from the M1 generation and further cultivated to establish the M2 generation. The results revealed that various morphological and agronomical characteristics, such as plant height, spikes per plant, spike length, spikelet per spike, grains per spikelet, and 100-grain weight, showed increases in different genotypes from M1 to M2. SCoT markers were employed to assess genetic diversity among the eleven genotypes. The bioinformatics analysis identified a correlation between SCoT markers and the transcription factors ABSCISIC ACID INSENSITIVE3 (ABI3) and VIVIPAROUS1 (VP1), crucial for plant development, growth, and stress adaptation. A comprehensive examination of genetic distance and the function identification of gene-associated SCoT markers may provide valuable insights into the mechanisms by which SA and HZ act as mutagens, enhancing wheat agronomic qualities. This study demonstrates the effective use of SA and HZ treatments to induce gene diversity through mutagenesis in the wheat gene pool, resulting in the enhancement of agronomic traits, as revealed by SCoT markers. The significant improvements in morphological and agronomical characteristics highlight the potential of mutagenesis techniques for crop improvement. These findings offer valuable information for breeders to develop effective breeding programs to enhance wheat quality and resilience through increased genetic diversity.

Keywords: Wheat (*Triticum aestivum* L.), Chemical mutagenesis, Genetic diversity, Gene pool, Sodium azide, Hydrazine hydrate, SCoT marker, Agronomic traits, Polymorphism.

Oral Presentation 4

Genetic Dissection of Grain Zinc Concentration Reveals Novel QTL on Chromosome 6AS from Synthetic Hexaploid Wheat

Youshaa Danyal^{1,*}, Mengjing Sun¹, Muhammad A. Qureshi¹, Ye Huichun¹, Bingyi Liu¹, Fugong Ding¹, Xiaowan Xu¹, Awais Rasheed², Zhonghu He^{1,2}, Yuanfeng Hao^{1,**}

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Abstract

Over 30% of the world population is zinc-deficient, while 65% is anemic across all age groups, which is alarming, particularly in developing countries. A sustainable approach to eradicate micronutrient malnutrition is genetic biofortification of staple crops such as wheat. Synthetic hexaploid wheat (SHW) represents high-nutrient donor sources for biofortification. In the current study, an RIL population was developed from a cross between semi-dwarf high-yielding cultivar Zhongmai 30 (ZM30) and an accession of synthetic hexaploid wheat SHW-1. The population and parents were evaluated for grain zinc concentration (GZnC), grain iron concentration (GFeC), plant height (PH), thousand-grain weight (TGW), and days to heading (DH) across four environments over two consecutive seasons and genotyped using 1× re-sequencing. QTL mapping identified two stable QTL for GZnC (6A and 7B) and three for GFeC (4D, 5A, and 7A). GZnC has a significant positive correlation with GFeC ($r = 0.55$, $p < 0.001$). Among these, *QGZnCzs.caas-6A*, *QGFzcs.caas-5A* each explained more than 10% of the phenotypic variance and had no effect on both PH and TKW. Notably, *QGZnCzs.caas-6A*, with a favorable allele from SHW-1, was consistently detected across four environments, explaining up to 17.2% of phenotypic variance with an additive effect of 3.6 mg kg⁻¹. The QTL was located within a 21.93–23.87 Mb interval of chromosome 6AS, where no previous gene or QTL related to GZnC has been reported, indicating its novelty. 41 high-confidence polymorphic genes between the parental lines ZM30 and SHW-1 were retrieved. Among them, 21 genes were identified as differentially expressed based on pan-transcriptomic analysis and expression patterns in wild relatives. Zinc homeostasis-related *TaYSL17-6AS*, *TaHMA-6AS*, and *TaYSL12-6AS* were probable candidates for the 6AS QTL. Their genome sequences were validated using Sanger sequencing. The favorable alleles from SHW-1 differ from those in assembled common bread wheat cultivars, including ZM-30. However, they are identical to sequences from ancestral species such as durum wheat (Langdon, Svevo, Kronos), wild emmer wheat (Zavitan), *Triticum monococcum* (PI306540 and TA299), and *Triticum urartu*, indicating that this locus has not yet been utilized in modern wheat breeding. Micro-collinearity-based synteny analysis revealed largely conserved gene order across cultivars, while SHW-specific and ancestral-specific variations highlighted the evolutionary significance of this region. Collectively, these findings underscore the potential of SHW-1 in reintroducing novel allelic diversity for Zn biofortification in modern wheat breeding.

Keywords: Wheat; Biofortification; Grain zinc concentration; Synthetic hexaploid wheat

Oral Presentation 5

Genetic Diversity of Azerbaijani Wild Cherry Plum (*Prunus Cerasifera* Ehrh.): Molecular Characterization

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Abstract

The primary objective of this study was to investigate the genetic resources of *Prunus cerasifera* Ehrh. in Azerbaijan at the molecular level, assess their genetic diversity, and identify valuable genotypes for use in breeding programs. This species, widely distributed across the country, represents an important component of Azerbaijan's rich wild flora and holds significant potential for genetic improvement and conservation efforts. A total of 100 indigenous cherry plum genotypes were collected from diverse geographical regions of Azerbaijan. Leaf samples were obtained from different populations, and their geographic coordinates were carefully recorded. This sampling strategy enabled a comprehensive evaluation of both genetic relationships and geographic distribution patterns among the genotypes. Molecular analyses were conducted using Inter Simple Sequence Repeat (ISSR) markers, which target genomic regions between microsatellite sequences. ISSR markers are widely recognized for their high level of polymorphism, reproducibility, and technical simplicity, as they do not require prior sequence information. In this study, 20 ISSR primers were employed, most of which consisted of di-nucleotide repeat motifs such as GA, AG, AC, and CT, known to be abundant in plant genomes and associated with high mutation rates. The ISSR analysis generated a total of 157 amplified loci, of which 128 were polymorphic, resulting in an overall polymorphism rate of 81.9%. The number of bands per primer ranged from 5 to 11, with an average of 7.9, while the mean number of polymorphic bands was 6.4. These findings indicate a high level of genetic variability among the studied genotypes. The polymorphism information content (PIC) values ranged from 0.15 to 0.49, with a mean of 0.39. Primers containing GA and AG motifs exhibited particularly high levels of polymorphism and strong discriminatory power. Additional parameters, including effective multiplex ratio (EMR), marker index (MI), and resolving power (Rp), further confirmed the efficiency and robustness of the ISSR marker system in differentiating among genotypes. The genetic diversity index (GDI) ranged from 0.55 to 0.98, with an average value of 0.91, demonstrating that the Azerbaijani cherry plum germplasm is highly diverse and genetically rich. This relatively high level of diversity may be attributed to the region being part of the species' center of origin. Cluster analysis grouped the genotypes into five major clusters; however, the distribution of genotypes did not strictly correspond to their geographic origins, suggesting the presence of gene flow among regions. Nevertheless, genotypes from the Nakhchivan Autonomous Republic formed a relatively distinct group, likely due to geographic isolation and limited genetic exchange. Principal Coordinates Analysis (PCoA) revealed that the first three axes explained only a small proportion of the total genetic variation, indicating that most genetic diversity is distributed within populations rather than among them. This observation was further supported by Analysis of Molecular Variance (AMOVA), which showed that 96% of the total genetic variation occurred within populations, while only 4% was attributed to differences among populations. The low fixation index ($F_{st} = 0.044$) and high gene flow estimate ($N_m = 5.47$) further confirmed weak genetic differentiation and substantial genetic exchange among populations. In conclusion, the results of this study demonstrate that *Prunus cerasifera* genotypes in Azerbaijan possess a high level of genetic diversity, primarily within populations. ISSR markers proved to be effective tools for assessing this diversity. These findings provide a valuable scientific basis for the conservation of genetic resources, the selection of promising genotypes, and the development of future breeding programs.

Keywords: *Prunus cerasifera* Ehrh., genetic resources, genetic diversity

Oral Presentation 6

Population Structure and Migration Patterns of Cashew (*Anacardium occidentale* L.) Revealed by Genome-Wide SNP Analysis

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Abstract

Despite being one of the most consumed tree nuts globally, limited genomic research has been conducted on genetic diversity in cashew. This is particularly the case in West Africa, which accounts for approximately 51% of global cashew production. Understanding population genetic structure and migration pathways is an essential step toward characterising cashew diversity across different regions, providing insights into local adaptation and the conservation of genetic resources. This study analysed a SNP dataset of 77 *Anacardium occidentale* samples from 8 countries, generated through Illumina-based genotyping-by-sequencing (GBS). SNP calling was performed following GATK Best Practices and quality-filtered (including minor allele frequency filtering) using a custom bioinformatics pipeline, retaining 111,744 SNPs for downstream analysis. STRUCTURE population analyses supported three major cashew genetic clusters (K=3) as the optimal number of populations. One cluster was centred in São Tomé and Príncipe, another spanned Cape Verde and Guinea-Bissau, while the third was globally distributed, including populations from West Africa and Guinea-Bissau. Within these, clear country-level substructure was also evident. Beyond this, the results supported two separate migration events from Brazil. The first radiated from Brazil to São Tomé and Príncipe, then through Cape Verde and Southern and East Africa, before diverging into Asia and West Africa. The second seems to be a direct route from Brazil via Cape Verde to West Africa. Notably, evidence of admixture between these two cashew populations was observed in West Africa. These findings help clarify long-standing questions about global cashew migration patterns and offer new insights into the genetic differentiation observed between cashew populations.

Keywords: cashew, Guinea-Bissau, germplasm, genotyping-by-sequencing, diversity

Poster Presentation 2

See poster on the next page

Map-Based Cloning of the Grain Zinc Concentration Gene *Tanas10-6D* in Common Wheat

Mengjing Sun^{1,2}, Yangyang Liu³, Yelun Zhang⁴, Zongjun Pu⁵, Jiangtao Luo⁵, Huichun Ye¹, Bingyi Liu¹, Xiaowan Xu¹, Fugong Ding¹, Zifeng Guo³, Zhongfu Ni², Zhonghu He^{1,6}, Yuanfeng Hao^{1,*}

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Abstract

Zinc (Zn) is an essential micronutrient for human health; grain zinc concentration (GZnC) in wheat, a staple crop worldwide, directly affects human nutritional status. We previously mapped a GZnC locus, QGZnC.caas-6DL, in two recombinant inbred line (RIL) populations and fine-mapped it to a 285-kb interval (462.20-462.48 Mb) containing 14 candidate genes that is highly conserved across wheat genome assemblies. The two haplotypes of the high-zinc and low-zinc parents correspond to *Aegilops tauschii* lineages L3 and L2, respectively. Compared to L2, the L3 haplotype carries at least two insertions of approximately 295 kb and 60 kb of non-coding sequences. Based on gene expression profiles and genome annotation, *TaNAS10-6D*, encoding nicotianamine synthase, was identified as the target gene, and its high-zinc and low-zinc haplotypes differ by 13 non-synonymous mutations. Overexpression of *TaNAS10-6D* **increased grain zinc concentration by up to 55.2% relative to the wild type**. AlphaFold3 structural predictions together with luciferase complementation (LCA) and bimolecular fluorescence complementation (BiFC) assays showed that **the protein encoded by the low-zinc allele has lost its homodimerization ability**, potentially compromising enzyme activity. Future work will focus on enzyme activity assays to determine whether the loss of homodimerization affects catalytic function, and also on the regulatory network of this key gene for zinc homeostasis.

Keywords: Wheat; Biofortification; Grain zinc concentration; Nicotianamine synthase.

See the poster on the next page

Map-based cloning of the grain zinc concentration gene *TaNAS10-6D* in common wheat

Mengjing Sun^{1,2}, Yangyang Liu³, Yelun Zhang⁴, Zongjun Pu⁵, Jiangtao Luo⁵, Huichun Ye¹, Bingyi Liu¹, Xiaowan Xu¹, Fugong Ding¹, Zifeng Guo³, Zhongfu Ni², Zhonghu He^{1,6}, Yuanfeng Hao^{1,*}

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Abstract

Zinc (Zn) is an essential micronutrient for humans. As a staple crop worldwide, wheat grain zinc concentration (GZnC) directly impacts human nutritional status. Previously, we mapped a GZnC locus, *QGZnC.caas-6DL*, in two recombinant inbred line (RIL) populations, and fine-mapped it to a 285-kb physical interval (462.20-462.48 Mb). This interval harbors 14 candidate genes and is highly conserved across wheat genome assemblies. Based on gene expression profiles and genome annotation, *TaNAS10-6D*, encoding nicotianamine synthase, was identified as the target gene. Its overexpression lines showed significantly higher GZnC than wild-type controls, and the premature stop mutant showed significantly lower GZnC than its wild-type control. The gene possesses two haplotypes with 13 non-synonymous mutations. AlphaFold3 structural predictions, luciferase complementation (LCA) and bimolecular fluorescence complementation (BiFC) assays demonstrated that the protein encoded by the low-GZnC allele has lost its homodimerization ability, potentially affecting enzyme activity. The high-GZnC allele (*TaNAS10-6D^{JD8}*) is the dominant haplotype in European germplasm, while low-GZnC allele (*TaNAS10-6D^{AK58}*) is the major haplotype in East Asian germplasm. Ancestral tracing indicated that the *Aegilops tauschii* haplotype corresponding to *TaNAS10-6D^{JD8}* mainly originated from the L3 lineage, while the *TaNAS10-6D^{AK58}* haplotype all came from the L2 lineage. Future work will focus on enzyme activity assays to determine whether the loss of homodimerization affects catalytic function, and also on the regulation network from this key genes for zinc homeostasis.

Materials and Methods

- **Plant materials**
 - 1) Parental materials for QTL mapping: two RIL populations derived from the crosses Jingdong 8 (JD8) × Aikang 58 (AK58) and Zhongmai 175 (ZM175) × Xiaoyan 60 (XY60)
 - 2) Fine-mapping populations: secondary mapping populations derived from residual heterozygous lines of GJA-184 (from JD8/AK58) and ZX91 (from ZM175/XY60)
 - 3) Functional validation materials: *TaNAS10-6D* overexpression lines (OE#1, OE#2, OE#4, OE#13, OE#32), *TaNAS10-6D* premature termination mutants, and F₂ populations
 - 4) Zn treatments: hydroponic conditions with three Zn concentration gradients (0.8, 4, and 20 μM Zn)
- **Methods**
 - 1) Transcriptome sequencing: root samples, to analyze candidate gene expression patterns under Zn concentration gradients
 - 2) Map-based cloning: fine mapping based on recombinant individuals
 - 3) Protein structure prediction: AlphaFold3
 - 4) Protein interaction validation: luciferase complementation assay (LCA), bimolecular fluorescence complementation (BiFC)
 - 5) Grain Zn concentration measurement: ICP-OES

Results

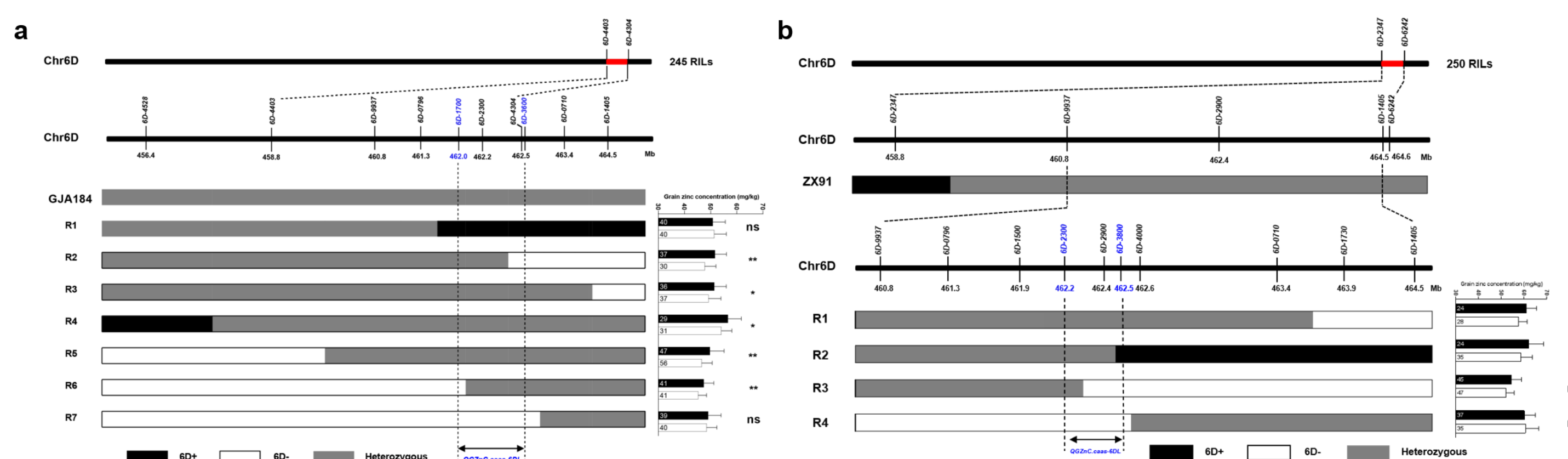


Fig. 1 Fine mapping of *QGZnC.caas-6DL* using residual heterozygous lines GJA184 and ZX91 (a) Fine mapping in GJA184 population; (b) Fine mapping in ZX91 population. Black, white, and gray bars represent 6D+, 6D-, and heterozygous genotypes.

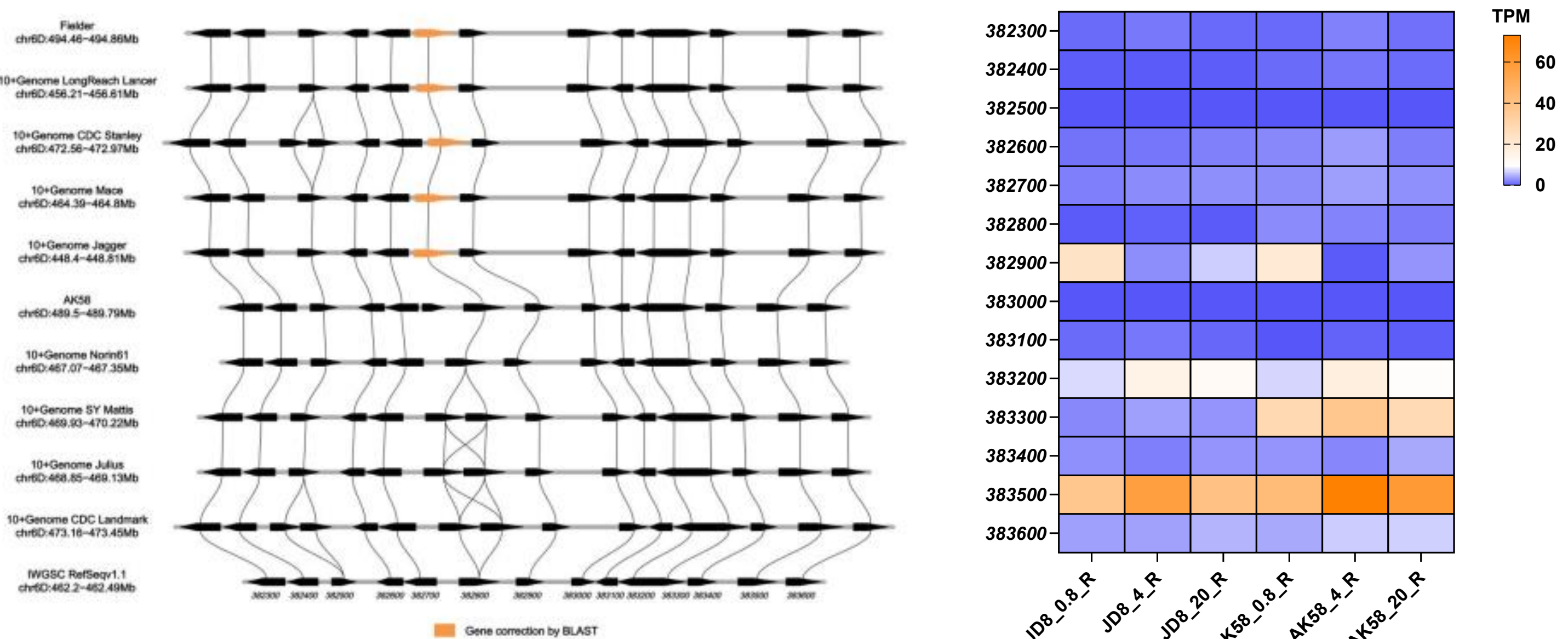


Fig. 2 Synteny analysis of the *QGZnC.caas-6DL* physical interval

Fig. 3 Expression pattern analysis of genes in the *QGZnC.caas-6DL* interval under different zinc concentrations

Acknowledgements

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Results

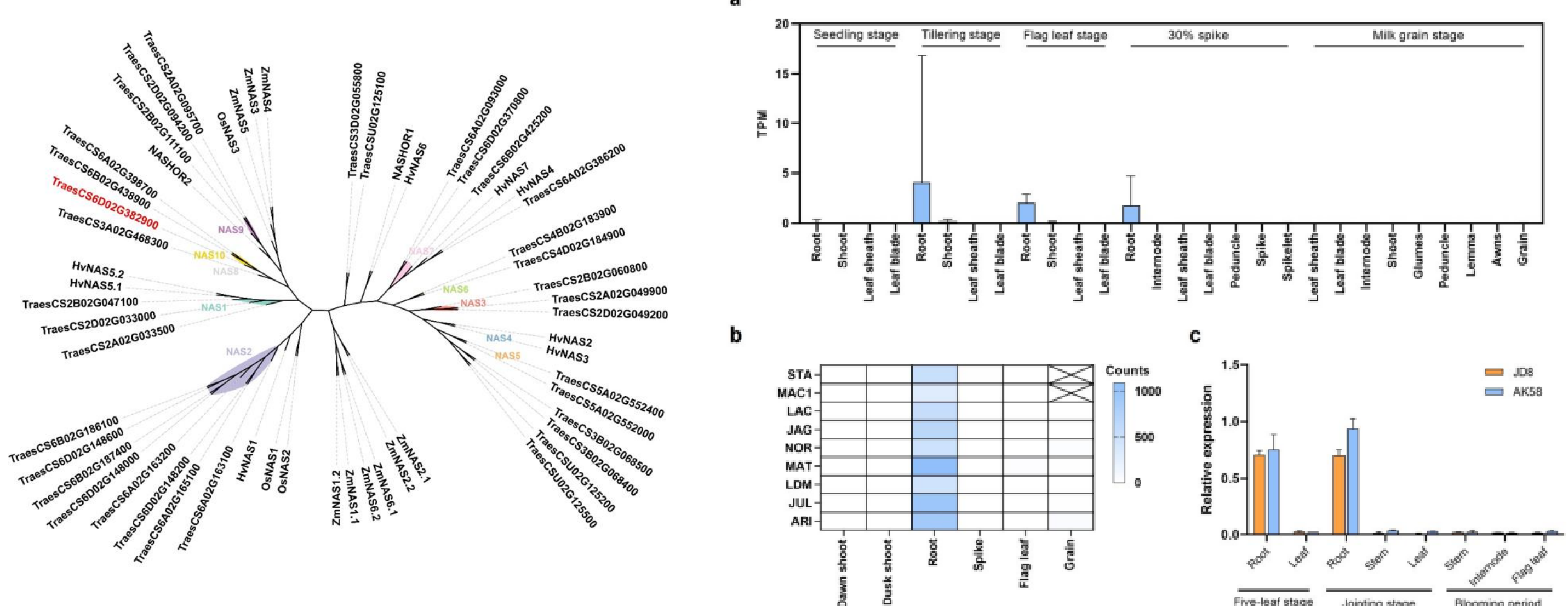


Fig. 4 Phylogenetic tree analysis of NAS proteins

Fig. 5 Expression pattern analysis of *TaNAS10-6D*

(a) Expression pattern of *TaNAS10-6D* across the entire growth period; (b) Expression pattern of *TaNAS10-6D* in the wheat pan-transcriptome; (c) Expression pattern of *TaNAS10-6D* in Jingdong 8 and Aikang 58.

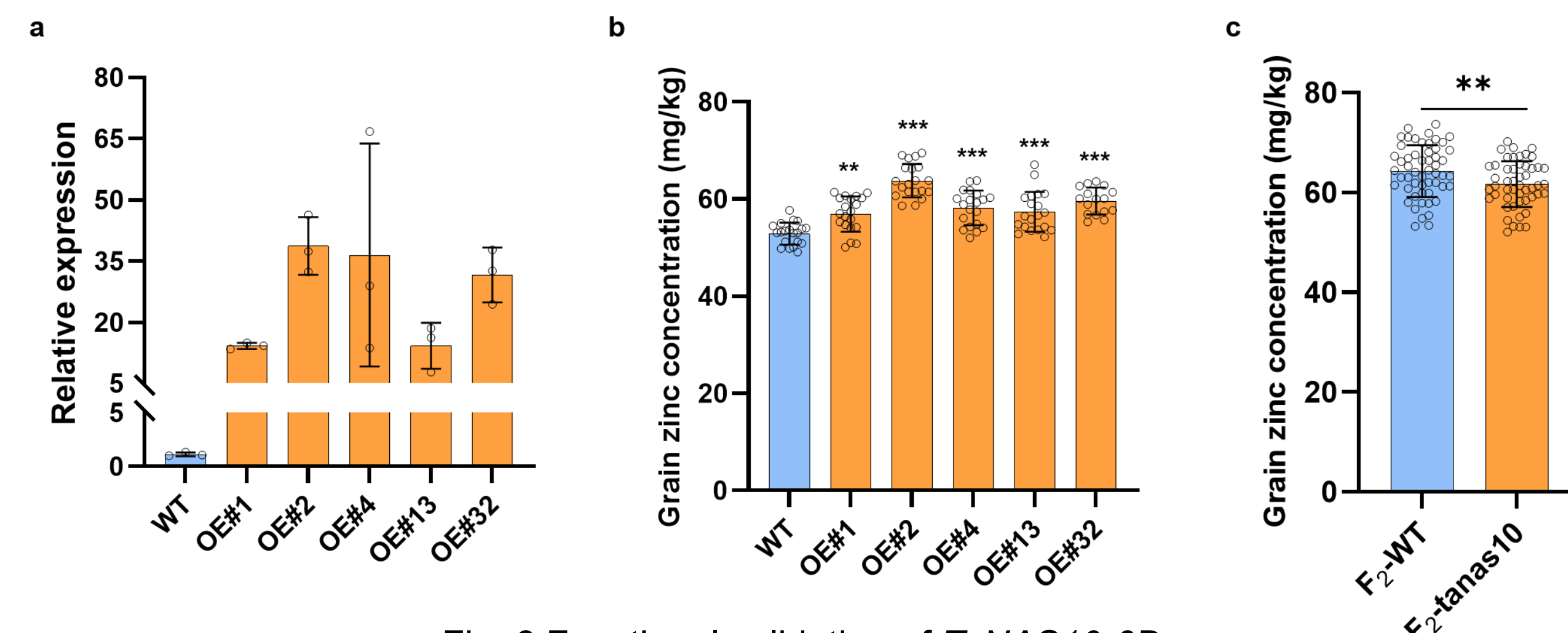


Fig. 6 Functional validation of *TaNAS10-6D*

(a) Expression analysis of OE lines; (b) Phenotype of OE lines; (c) Phenotype of mutants.

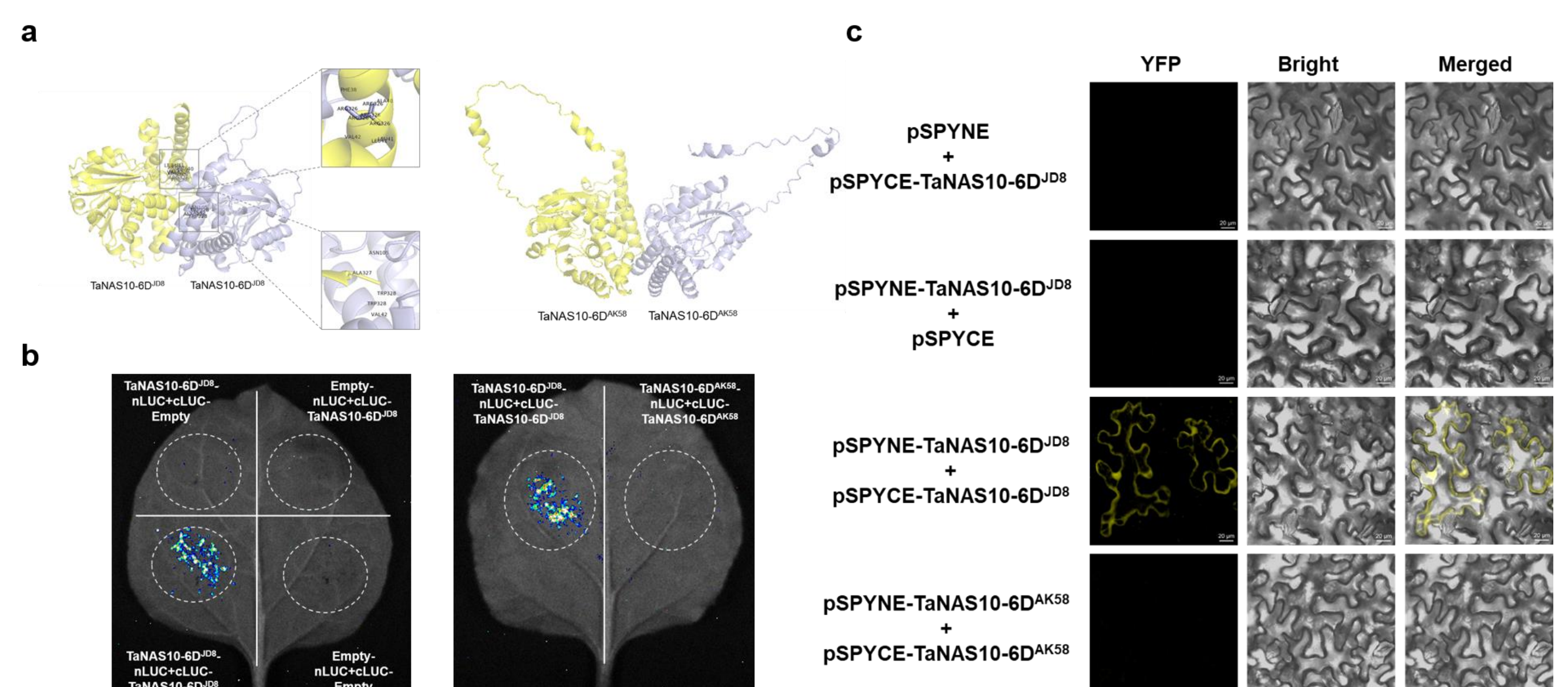


Fig. 7 Analysis of homodimerization ability of the *TaNAS10-6D* protein (a) AlphaFold prediction; (b) LCA analysis; (c) BiFC analysis.

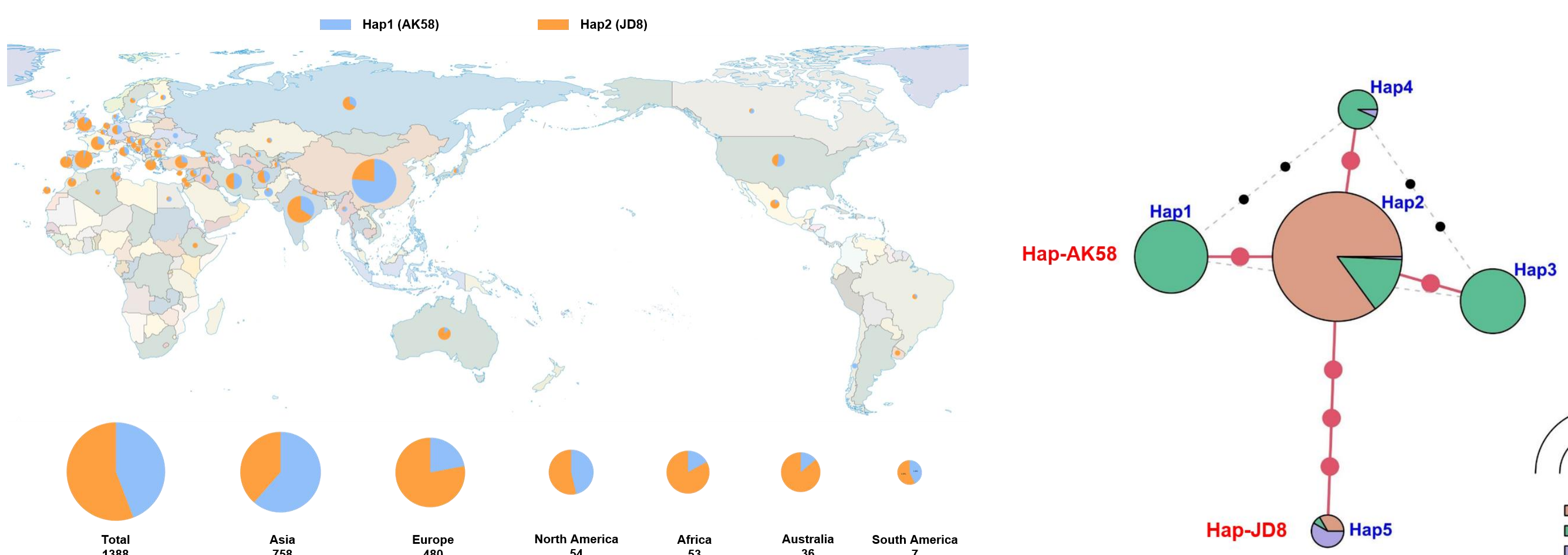


Fig. 8 Genetic variation of *TaNAS10-6D* and global distribution of its major haplotypes in hexaploid wheat

Fig. 9 Evolutionary network analysis of *TaNAS10-6D* in *Aegilops tauschii* accessions

Conclusions

- *QGZnC.caas-6DL* was fine-mapped to a 285-kb physical interval on chr6D
- *TaNAS10-6D* was identified as the key candidate gene controlling grain Zn concentration in wheat, encoding nicotianamine synthase
- Overexpression of *TaNAS10-6D* increased grain Zn; mutants showed significantly lower grain Zn concentration than the wild type
- The low-Zn allele (*TaNAS10-6D^{AK58}*) lost its homodimerization ability due to non-synonymous mutations, potentially affecting enzyme activity

Poster Presentation 3

See poster on the next page

Genome-Wide Identification of Zn/Fe Homeostasis Genes and Association Mapping for the Candidate Gene *Tazip14-3A* in Common Wheat

Huichun Ye^{1,*}, Mengjing Sun¹, Chenyang Hao¹, Yelun Zhang², Bingyi Liu¹, Xiaowan Xu¹,
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***Presenting author:**

Abstract

Zinc (Zn) and iron (Fe) are essential micronutrients whose deficiency affects billions of people, particularly in developing countries reliant on cereal staples. Members of the ZIP, MTP, VIT, and F-bZIP families function in metal ion uptake, transport, storage, and regulation, yet their systematic characterization and natural variation in wheat remain limited. A genome-wide identification of these four families was performed using the Chinese Spring reference genome (RefSeq v1.1) and data from the 10+ Genome Project, followed by analyses of chromosomal distribution, gene structure, and phylogenetic relationships. Association analysis, integrating SNP data from 145 resequenced varieties and grain Zn/Fe phenotypes measured across eight environments, identified 140 members (57 ZIP, 33 MTP, 30 VIT, and 20 F-bZIP) in Chinese Spring, of which 18 showed stable associations across multiple environments. Among them, *TaZIP14-3A*, located at 95 Mb on chromosome 3A, comprises 11 exons and 10 introns, encoding a protein of 436 amino acids. Haplotype analysis revealed that the Hap2 allele of *TaZIP14-3A* conferred significantly higher grain Zn, a trend toward elevated Fe, and no reduction in thousand-grain weight, making it as a favorable Zn-rich haplotype. Functional characterization of this locus is currently underway. Two KASP markers (*Kasp_3AM* and *Kasp_3AP*) were developed and validated in natural populations, enabling marker-assisted selection. These results provide candidate gene resources and diagnostic markers for biofortification breeding in wheat.

Keywords: Grain zinc concentration; Grain iron concentration; Zn/Fe homeostasis; Wheat

Candidate Gene Association Analysis and Haplotype-Based Marker Development for Zn/Fe Homeostasis in Common Wheat

Huichun Ye¹, Mengjing Sun¹, Yelun Zhang², Bingyi Liu¹, Xiaowan Xu¹, Chenyang Hao¹, Xueyong Zhang¹, Zifeng Guo³, Zhonghu He^{1,4,*}, Yuanfeng Hao^{1,*}

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INTRODUCTION

Zinc (Zn) and iron (Fe) are essential micronutrients whose deficiency affects billions of people, particularly in developing countries reliant on cereal staples. Members of ZIP , MTP , VIT and F-bZIP families respectively function in metal ion uptake, transport, storage, and regulation, yet their systematic characterization and natural variations in wheat remain limited

MATERIALS & METHODS

A genome-wide identification of these four families was performed using the Chinese Spring reference genome (RefSeq v1.1) and 10+ Genome assemblies, followed by analyses of chromosomal distribution, gene structure, and phylogenetic relationships. identified 140 members (57 ZIP, 33 MTP, 30 VIT, and 20 F-bZIP) in Chinese Spring. Association analysis, integrating SNP data from 145 resequenced varieties and grain Zn/Fe phenotypes measured across eight environments, which 18 showed stable associations across multiple environments need a table to show these 18 genes,(7 ZIP, 3 MTP, 3 VIT, and 5 F-bZIP) .

RESULTS

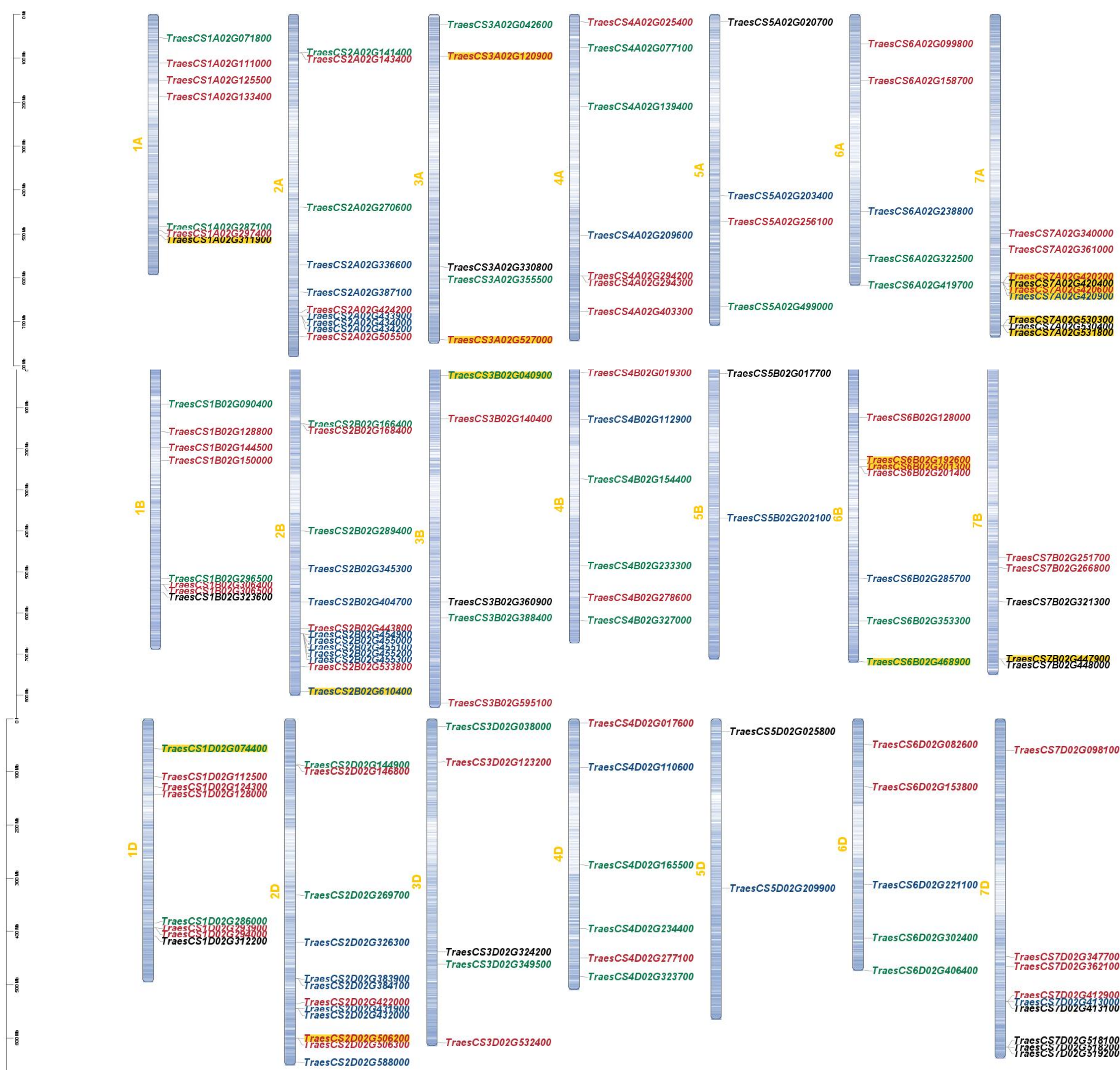


Fig.1 Distribution of the 140 family genes on chromosomes.Red, green, blue, and black represent gene members of the ZIP, MTP, VIT, and F-bZIP families, Yellow-highlighted genes indicate significant associations in the association analysis.

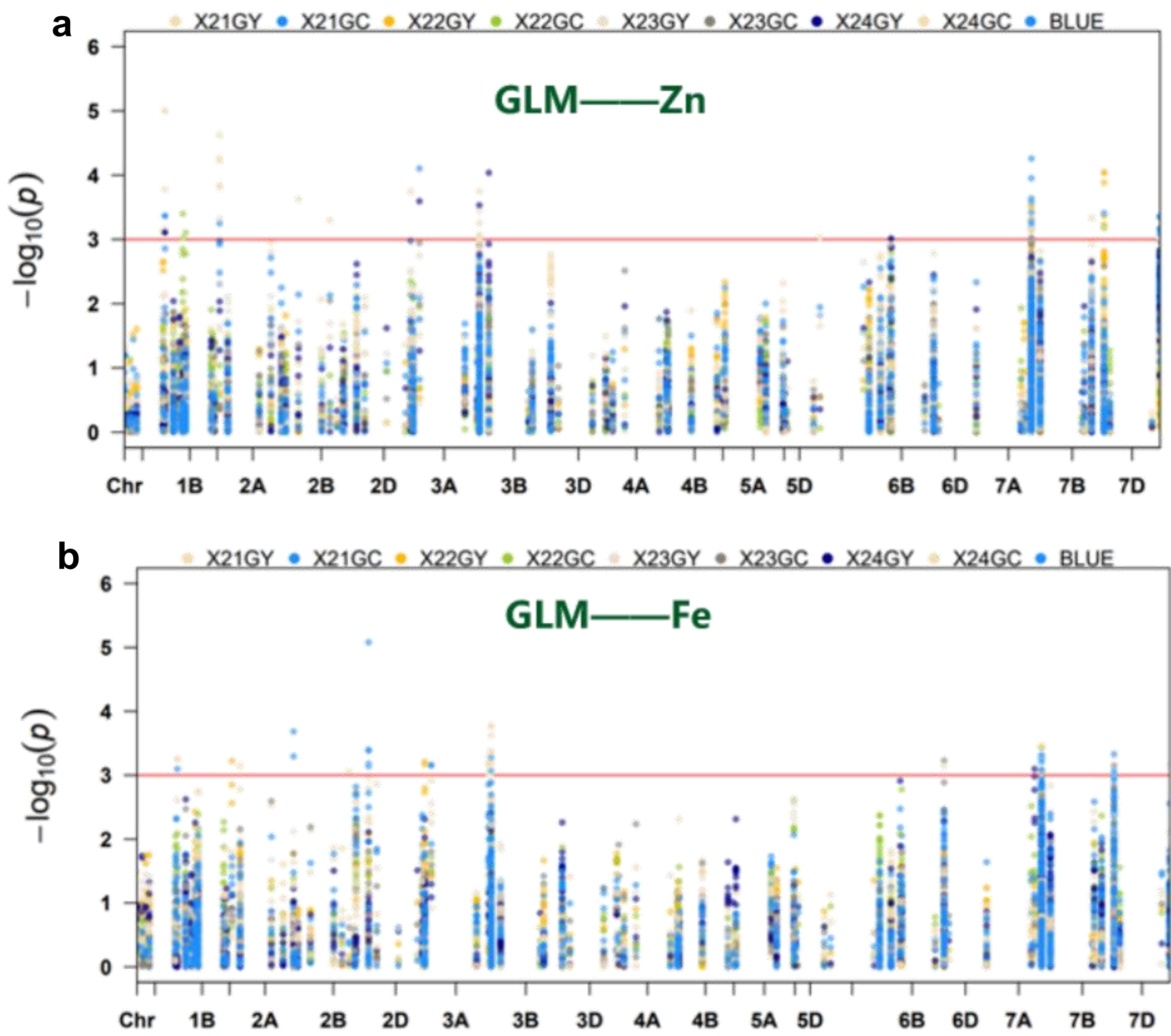


Fig.2 Manhattan plots showing the results of association analysis for candidate genes. (a) Grain zinc content; (b) grain iron content. $-\log_{10}(p) = 3$.

Polymorphic site	95030954	95021415	number	Total
type	upstream_gene_variant	missense_variant		
alleles	T/C	G/A		
Hap1	TT	GG	71	141
Hap2	TT	AA	26	
Hap3	CC	AA	44	

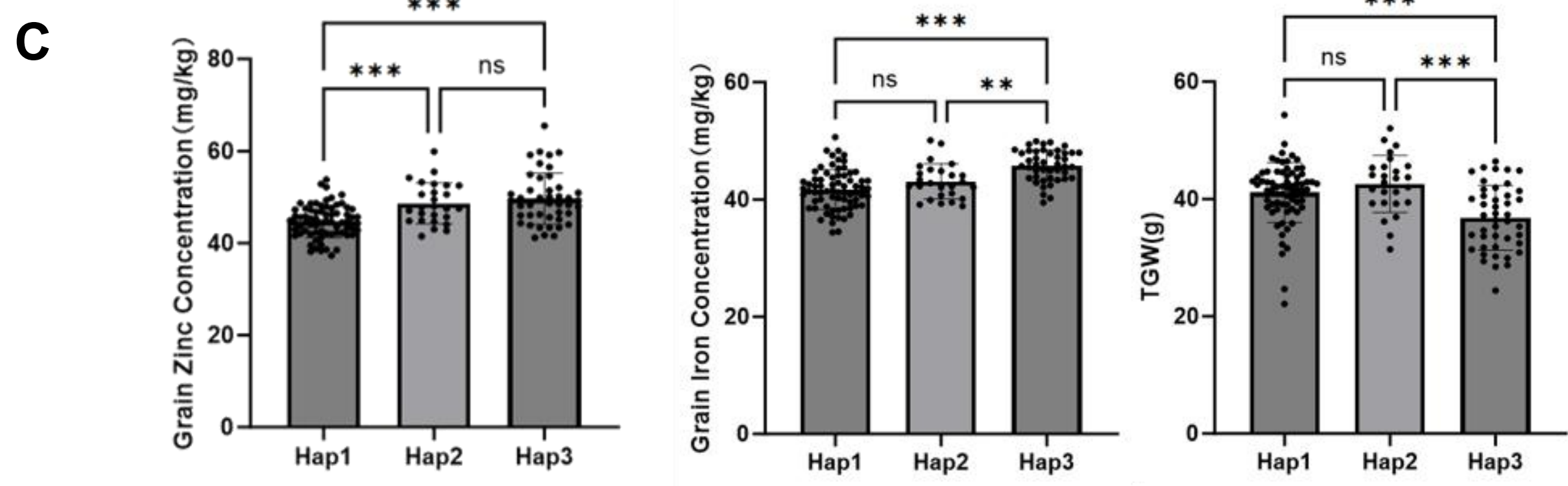


Fig.3 Gene structure and haplotype analysis of *TaZIP14-3A*. (a) Gene structure of *TaZIP14-3A*; (b) Haplotype typing results of *TaZIP14-3A*; (c) Haplotype effects of *TaZIP14-3A* in the 145-accession panel

CONCLUSION

We identified 140 Zn/Fe homeostasis genes and 18 stable association candidates in wheat. The Hap2 allele of *TaZIP14-3A* enhanced grain Zn/Fe with no yield penalty, and two KASP markers were developed for breeding. Functional validation is ongoing.

FUNDING

This work was supported by the National Natural Science Foundation of China.

Session 3

Legume Breeding and Genetics

Keynote Lecture 7

Integrating Breeding and Omics Tools to Address Dry Bean Productivity and Quality

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Abstract

The United States is one of the largest producers of dry beans worldwide, with neighboring states North Dakota and Minnesota accounting for more than 60% of the total production. The North Dakota State University (NDSU) dry bean breeding program is revolutionizing the bean value chain by integrating advanced omics technologies to bridge the gap between initial breeding and final consumption. By leveraging genomics, phenomics, and other areas, the program identifies key genomic regions and markers associated with critical traits such as disease resistance, climate resilience, and nutritional density, among others. To develop a genomic selection pipeline, we designed a trait-based custom 4k SNP chip which allows to discard inferior breeding lines even before field testing, hence increasing selection efficiency. Our research follows a comprehensive "Breeding to Farm to Fork" framework. At the development stage, omics tools accelerate the selection process, allowing for the precise deployment of varieties that thrive in North Dakota's unique environmental conditions. On the farm, these innovations translate to increased yield stability and reduced chemical inputs, enhancing economic sustainability for growers. Beyond the field, the program utilizes metabolomic profiling to address consumer-driven priorities, including improved cooking quality, flavor profiles, and bioavailability of essential minerals such as iron. By identifying the molecular mechanisms that govern bean quality, NDSU is not only optimizing production efficiency but also ensuring the delivery of a superior, nutrient-dense product to the global market. This holistic approach ensures that every link in the bean value chain—from breeder to processor to consumer—benefits from data-driven genetic improvement. This integration of omics tools positions NDSU at the forefront of the bean crop innovation, securing the future of dry beans as a staple of sustainable agriculture and human health.

Keywords: *dry bean, common bean, Phaseolus vulgaris L., omics, crop breeding, phenomics, genomics, crop productivity, crop resilience, nutritional quality.*

Keynote Lecture 8

Faba Bean Pan-Omics

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Abstract

Faba bean (*Vicia faba*) is a globally adapted protein crop with a high yield potential and an exceptional nitrogen fixation capacity. Just a decade ago, faba bean was an orphan crop with scarce genetic and genomic resources. Now, the first reference genomes have paved the way for high-resolution gene mapping and a wide range of omics studies. Combining pan-transcriptome and pan-proteome analysis of faba bean seeds with genotype and seed quality data, we are now dissecting the genetic control of faba bean agronomic and molecular traits. Complementing this trait-level work, we have established the Faba Bean Single-Cell Atlas Consortium, which is characterizing faba bean cells across tissues using single-nucleus and spatial transcriptomics to understand cellular functional specialization.

Keywords: *Vicia faba*, transcriptomics, proteomics, single-cell analysis

Keynote Lecture 9

Structural Variation and Breeding Trade-Offs Underlying Disease Resistance in Pea

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Abstract

Pea (*Pisum sativum*) is a historically important crop species and a major grain legume for sustainable agriculture, yet its productivity is limited by several diseases, including *Fusarium* wilts, root rots and foliar pathogens. Although many resistance traits have been incorporated into breeding programmes through historical selection, their causal genetic variants often remain difficult to identify using a single linear reference genome, particularly when the underlying variation is structural or presence/absence based. Here, I will present how our group uses k-mer association genetics, pan-genome graphs, skim-sequencing imputation and experimental validation to uncover hidden disease-resistance variation in pea. First, I will describe the molecular resolution of the classical Fw locus, which confers resistance to *Fusarium oxysporum* f. sp. *pisi* race 1 and has been used in pea breeding for almost a century. By integrating k-mer GWAS, transcriptomic analysis and transformation-based validation, we mapped Fw to a presence/absence structural variant that is largely missed by conventional SNP-based approaches and contains a previously unannotated transcript. I will also discuss our work on *Fusarium solani* root rot, which revealed an unexpected link between resistance, rhizosphere microbiome recruitment and flower colour. White-flowered pea varieties, historically favoured by breeders and consumers, are generally more susceptible to root rot, whereas purple-flowered lines show stronger resistance. Using recombinant inbred populations, high-throughput root phenotyping, qPCR-based quantification of the dominant rhizosphere fungus and graph-based imputation from skim-sequencing data, we fine-mapped the resistance locus associated with both resistance and microbiome recruitment. Importantly, this locus was genetically separated from the classical A gene controlling flower colour. Together, these studies show how pan-genome-enabled approaches can reveal structural variants missed by reference-based analyses and help convert hidden genetic variation into markers and strategies for durable disease resistance in pea.

Keywords: *Pisum sativum*, *Fusarium* resistance, structural variation, rhizosphere microbiome, pan-genomics.

Oral Presentation 7

Genome-Wide Association Mapping Highlights Stable SNP Markers Associated with Yield- Related Traits in Faba Bean

Salwa M. Mahmoud^{1*}, Mohamed Eslam A. Sayed⁴, Marina N. Abdel-Malak³, Ameer Elfarash¹,
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Abstract

Faba bean (*Vicia faba* L.) is one of the most important legume crops in the Middle East, particularly in Egypt. It serves as a key source of dietary protein and continues to hold significant culinary importance. Enhancing faba bean productivity relies primarily on improving major yield-related traits through effective breeding strategies. Because yield is a complex trait, identifying the genetic determinants of high yield remains a major challenge in breeding new faba bean varieties.

In this study, we evaluated six faba bean yield-related traits—number of pods per plant (PN), number of seeds per plant (SN), 100-seed weight (100SW), seed weight (SW), days to flowering (DTF), days to maturity (DTM), and plant height (PH)—across a set of 128 Egyptian genotypes over two growing seasons (2023/2024 and 2024/2025). High genetic variation was observed among all traits in each season, and highly significant correlations were found among genotypes for all traits. Population structure analysis divided the Egyptian population into five subpopulations.

The faba bean panel was genotyped using single-primer enrichment technology (SPET), yielding 33,165 SNP markers for each season. Genome-wide association mapping was used to identify SNPs associated with the target traits. We identified 249 and 317 significant SNPs in the 2024 and 2025 growing seasons, respectively. Nine common markers associated with the same traits were identified across both seasons. The results of this study provide valuable, stable SNP markers associated with high-yield traits in faba bean. These nine SNP markers could be converted to KASP markers for validation in diverse genetic backgrounds.

Keywords: Faba bean, Genome-Wide Association Study (GWAS), SNPs, Single-primer enrichment technology (SPET)

Oral Presentation 8

Dissecting the Genetic Basis of White Mold Resistance in Common Bean Through Genome-Wide Association Analysis

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Abstract

White mold, caused by the necrotrophic fungal pathogen *Sclerotinia sclerotiorum*, is one of the most destructive diseases of common bean (*Phaseolus vulgaris* L.) and can cause substantial yield losses under favorable environmental conditions. Complete resistance to *S. sclerotiorum* has not been identified in common bean, while available resistance is predominantly partial and quantitatively inherited. Developing cultivars with enhanced genetic resistance therefore represents an important and sustainable strategy for white mold management. In this study, 260 common bean accessions were phenotyped for response to *S. sclerotiorum*. Disease responses showed broad phenotypic variation, spanning the full original 1–9 disease rating scale. For subsequent analysis, the original disease scores were converted to a 1–5 ordinal scale and normalized to account for inter-experimental variation using resistant and susceptible reference genotypes included across experimental batches. Genotype-level normalized means were then used as the phenotype for genome-wide association analysis. Following phenotypic quality control and matching with the genotypic dataset, 255 accessions were retained for GWAS. Phenotypic data were integrated with high-density single-nucleotide polymorphism (SNP) data. Genotypic data were subjected to quality filtering, including minor allele frequency and linkage disequilibrium-based filtering, followed by assessment of population structure and genetic relatedness. Genome-wide association analyses using complementary statistical models are being evaluated to identify genomic regions associated with variation in white mold resistance while minimizing spurious associations. Resulting associations will be further investigated to prioritize genomic regions and candidate genes for subsequent validation. This work will contribute to understanding the genetic architecture of quantitative white mold resistance. It may support marker-assisted and genomics-informed breeding strategies for developing common bean cultivars with improved resistance to *S. sclerotiorum*.

Keywords: *Phaseolus vulgaris*, *Sclerotinia sclerotiorum*, white mold, genome-wide association study, disease resistance, common bean breeding.

Poster Presentation 4*See poster on the next page***Genetic Diversity Assessment of Portuguese Cowpea Germplasm: A Foundation for Next-Generation Breeding**

Graça Pereira^{1,*}, Manuela Meneses¹, Madalena Vaz², Joana Guimarães¹, Cátia Nunes¹,
Fernanda Simões¹, António Cordeiro¹, Ana Luísa Garcia-Oliveira¹

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Abstract

Cowpea (*Vigna unguiculata* (L.) Walp.) is a resilient grain legume with increasing importance for sustainable agriculture under Mediterranean conditions due to its drought/heat tolerance, nitrogen-fixing ability, and high protein content. Portugal hosts valuable local cowpea landraces that represent an important, and yet underexploited source of genetic diversity for crop improvement. These are kept by the Portuguese Plant Germplasm Bank but also by smallholder farmers. The effective conservation and utilization of these genetic resources in National breeding schemes require a comprehensive characterization at the molecular level. Therefore, this study aims to assess the genetic diversity and population structure of more than 100 accessions of Portuguese cowpea germplasm using high-throughput genotyping approaches. A diverse collection of landraces and breeding materials are being analysed to identify genetic relationships, quantify diversity, and detect unique alleles that can be exploited in future breeding efforts. The molecular data will complement existing phenotypic evaluations, facilitating the identification of promising parental lines for traits related to climate resilience, yield stability, and grain quality. Beyond diversity assessment, this work represents the first step toward implementing New Genomic Techniques (NGTs) within the Portuguese cowpea breeding program from INIAV. The generated genomic information will provide the necessary foundation for the identification of candidate genes and genomic regions associated with key agronomic traits, enabling the future application of precision breeding strategies, including genome editing. Integrating genomic resources, conventional and modern breeding will accelerate the development of improved cowpea cultivars adapted to Mediterranean environments while promoting the wider use of cowpea as a sustainable protein-rich intercrop for both human consumption and animal feed. This study establishes a genomic framework for Portuguese cowpea improvement to support the conservation of local genetic resources and promote the adoption of innovative breeding technologies to address future Mediterranean agricultural challenges.

Keywords: Cowpea, Environmental resilience, NTGs, Genotyping by Sequencing, Screening, Heat tolerance.

Genetic diversity assessment of Portuguese cowpea germplasm: a foundation for next-generation breeding

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COWPEA (*Vigna unguiculata* (L.) Walp)

A climate-resilient and sustainable grain legume

- ❖ Well adapted to Mediterranean conditions
- ❖ Drought and heat tolerance
- ❖ Biological nitrogen fixation
- ❖ Protein-rich grain
- ❖ Suitable for crop rotation and intercropping
- ❖ Key in human consumption



COWPEA IN PORTUGAL

- Long tradition as a food crop
- Cultivated at small scale
- Local landraces with high value
- Maintained by farmers over generations
- Conserved in the Portuguese Plant Germplasm Bank
- Important source of genetic diversity



COWPEA BREEDING PROGRAMME at INIAV

Objectives

- Increased crop productivity
- Disease and pest resistance such as ascochyta blight,
- Abiotic stress tolerance such as tolerance to drought and heat
- Higher protein content
- Adaptation to mechanical harvesting
- Synchronized maturity

based on
conventional
breeding

1. Collection of Variability/creation of genetic variation

Use of local landraces, breeding materials and diverse germplasm sources.

2. Selection of the best genetic material

Selection based on agronomic performance, quality traits, and resistance to biotic and abiotic stresses.

3. Field Evaluation and Release of varieties

Field trials and if one genotype is better than the check is recommended for release as new variety.

10-12 Years

Our current goal:

a. Faster early-stage screening

Introduce molecular data in the initial stages of the breeding programme to accelerate the identification of promising material.

b. Link phenotype + genotype

Combine field and genomic data to support Marker-Assisted Selection (MAS)



Molecular data will complement the phenotypic evaluations already carried out at INIAV-Elvas.

Expected outcomes

Generate the knowledge and genomic resources to implement marker-assisted selection in the INIAV cowpea breeding programme and develop of cultivars better adapted to current climatic challenges.

Objective of this study

Assess the genetic diversity and population structure of 120 Portuguese cowpea accessions



GBS – Genotyping-by-Sequencing using high sequencing panels



RESULTS

1. A first batch of cowpea cultivars from diverse African countries were already genotyped (Guimarães et al., 2023)
2. A second batch including Portuguese and Bulgarian landraces and modern accessions are currently being genotyped using high density GBS
3. The genotyping results will be merged and analysed for diversity and structure analysis
4. According with the results and number of markers available we will initiate GWAS analysis



Final message

1. Portugal holds valuable cowpea genetic resources, yet we need to introduce more variability through partnerships
2. Combining conventional breeding and field evaluation with genomic tools, this work aims to transform conserved genetic diversity into useful information for our national breeding program.
3. Support the continuous development of new climate-resilient cowpea cultivars and promote cowpea as a sustainable, protein-rich crop for human consumption, particularly in drought-prone regions.

Session 4

Genetics and Breeding for Biotic Stress Resistance

Day III: Wednesday, 23 September 2026

Keynote Lecture 10

Map-Based Cloning of *Tarlck-2B* Conferring Adult-Plant Resistance to Powdery Mildew in Common Wheat

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Abstract

Powdery mildew poses a significant threat to global wheat production. Consequently, the identification and pyramiding of adult-plant resistance (APR) genes are critical strategies for developing wheat varieties with durable resistance. In this study, we focused on the APR locus *QPm.caas-2BS*, previously identified using the JS16/BN64 recombinant inbred line population and fine-mapped to a 400 kb physical interval (78.01–78.41 Mb). Leveraging the assembled BN64 and JS16 genomes, we determined that this target interval is highly conserved across wheat reference genomes and harbors five high-confidence genes. Among these, *TraesCS2B02G114900*—designated herein as *TaRLCK-2B*—emerged as the primary candidate based on sequence variation, gene expression profiles, and genome annotation. Functional validation via overexpression lines revealed a 45.5%–47.1% reduction in disease severity compared to the wild type, corroborating its role in resistance. The *TaRLCK-2B* gene spans 1,526 bp, comprising two exons that encode a 410-amino acid cytoplasmic receptor-like kinase. Subcellular localization analysis confirms its exclusive presence in the cytoplasm. Phylogenetically, *TaRLCK-2B* clusters within subgroup 7 of the RLCK-VII family, grouping with *Arabidopsis thaliana* kinases PBL31, PBL32, and PBL33, a clade frequently associated with plant defense responses. Furthermore, dual-luciferase reporter assays demonstrated that a single-nucleotide variation in the promoter region drives the differential expression observed between resistant and susceptible parents. The specific regulatory mechanisms governing this gene are currently under investigation.

Keywords: Adult-plant resistance; Powdery mildew; Map-based cloning; Wheat

Keynote Lecture 11

Advances in Disease and Pest Resistance in Faba Bean

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Abstract

Faba bean (*Vicia faba*) is a grain legume widely cultivated in temperate areas for food and feed. As for any crop, its productivity can be constrained by numerous diseases and pests that can be managed by a number of strategies, complemented with the deployment of resistant cultivars in an integrated manner. Faba bean breeders have succeeded in developing resistant cultivars, but progress has been slow as most resistances identified so far are of incomplete expression and in most cases their genetic basis is largely unknown. Diversity is key for the development of durable resistance. This involves diversity at the spatial and temporal gene deployment, and diversity in the genetic basis of resistance. This requires information not only on the genetics of resistance in the plant, but also on deciphering existence of races in the pathogen and monitoring their distribution, which presently is clearly insufficient for most faba bean pathogens. Faba bean resistance breeding will be facilitated by adoption of novel phenotyping and genotyping tools, that although started slowly, have developed fast in the last decade. Reducing genotyping costs is allowing genomic selection on faba bean, that integrated with speed breeding methods already in place, and the adoption of low-cost affordable phenotyping tools will accelerate faba bean improvement.

Keywords: *Vicia faba*, aphids, broomrape, ascochyta blight, rust, chocolate spot

Keynote Lecture 12

Beyond Conventional Breeding: Protoplast-Based Technologies and Genome Editing for Sustainable Citrus Disease Management

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Abstract

The citrus industry faces unprecedented challenges from destructive diseases such as citrus greening (Huanglongbing, HLB), citrus canker, and Phytophthora-induced diseases, which threaten global citrus production and sustainability. Conventional breeding has delivered valuable genetic gains; however, the long juvenile period, high heterozygosity, reproductive barriers, and limited availability of resistant germplasm often constrain the efficient development of improved cultivars. Recent advances in cellular and molecular breeding technologies offer powerful opportunities to accelerate citrus improvement. This presentation will highlight protoplast technology as a versatile platform for citrus innovation. Special attention will be given to somatic hybridization and cybridization, which enable the transfer and combination of desirable nuclear and cytoplasmic genomes across sexually incompatible species and genera. These approaches have facilitated the incorporation of disease resistance traits from wild and related germplasm while preserving the superior horticultural characteristics of elite cultivars and rootstocks. In addition, the presentation will discuss recent progress in citrus genome editing, particularly CRISPR-based technologies, and their application in developing disease-resistant germplasm through targeted modification of susceptibility genes and defense-related pathways. Integrating protoplast-mediated genome editing with regeneration systems offers a promising pathway for producing precise genetic improvements while reducing linkage drag associated with conventional breeding strategies. Examples from citrus breeding and biotechnology programs will illustrate how the combined use of protoplast isolation, somatic hybridization, cybridization, and genome editing is transforming the development of resilient citrus cultivars and rootstocks. Collectively, these technologies represent a powerful toolbox for addressing emerging disease threats and advancing sustainable citrus production. The lessons learned from citrus also provide a model for deploying integrated cellular and genomic breeding approaches in other perennial fruit crops facing similar biotic stress challenges.

Keywords: Citrus biotechnology; protoplast technology; somatic hybridization; cybridization; genome editing; CRISPR/Cas systems; disease resistance; biotic stress resistance.

Oral Presentation 9

Identification and Validation of a Novel Stripe Rust Resistance Locus on Chromosome 6BL Using Genome–Wide Association Analysis in Common Wheat

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Abstract

Common wheat (*Triticum aestivum* L.) is an important cereal crop that ensures global food security. Stripe rust remains the most destructive and devastating fungal disease hindering wheat productivity and grain quality. Here, we assembled a wheat panel including 316 diverse wheat accessions by integrating high-density genotyping with multi environmental stripe rust evaluation to identify adult-plant resistance loci, candidate genes prediction, and development of diagnostic markers for marker-assisted selection. Combined ANOVA revealed highly significant genotypic and genotype by environment interaction effects for resistance in addition to 86.6% broad-sense heritability. Association mapping for diseases severity in three environments and BLUP using the 116340 SNPs and the FarmCPU model in 170 accessions identified eight stable loci comprising five novel (chr 2BS, 6BS, 6BL, 7AL.1 and 7BL.1) and three colocalized QTL (chr 2AL, 7AL.2 and 7BL.2). Among these, *QYr.caas-6BL*, detected on chromosome 6B from 487.14 to 489.45 Mb, exhibited the strongest and most consistent effects across all environments, expressing 10.0–11.8% of phenotypic variance. Three haplotype groups showing significant severity variance and four putative candidate genes have been identified within the LD-defined interval of this locus. Three KASP markers, *K_AX-111671326* (T/C), *K_AX-111757034* (T/A), and *K_AX-110505662* (C/A), were developed from QTL representative SNPs. Alternative alleles (C, A and A) were favorable alleles, presenting a frequency of 37.6%, 34.7% and 33.9% in GWAS association panel, respectively. These favorable alleles were associated with 7.5–8% reduction in disease severity compared with reference alleles. Validation using the remaining 146 accessions confirmed these markers diagnostic potential to classify contrasting disease resistance groups, with resistant genotype frequency of 23.3%, 21.7%, and 17.1% for *K_AX-111671326*, *K_AX-111757034*, and *K_AX-110505662*, respectively. Marker categorized genotype groups showed significant severity variation, confirming developed markers application in marker-assisted selection. *K_AX-111671326* achieved 71.8% diagnostic accuracy, 67.6% sensitivity, and 88.4% specificity, whereas *K_AX-111757034* and *K_AX-110505662* displayed 73.5% and 74.1% diagnostic accuracy, with 74.2% and 80.0% sensitivity and 88.7% and 87.6% specificity, respectively.

Keywords: GWAS, stripe rust, resistance loci, candidate genes, KASP markers

Oral Presentation 10

Viral Discovery and Genomic Surveillance Reveal Emerging Plant Virus Threats in the Southeastern United States

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Abstract

Plant viruses continue to emerge in new hosts, geographic regions, and production systems, underscoring the importance of viral discovery and genomic surveillance for sustainable disease management. Recent studies in Alabama identified four notable virus discoveries that expand our understanding of virus diversity, evolution, and host adaptation in the southeastern United States. First, soybean vein necrosis virus (SVNV) was detected for the first time in peanut in the United States, making peanut a new host for SVNV. Furthermore, RT-PCR detected SVNV-N and TSWV-N in 24 and 26 peanut samples, respectively, providing the first evidence of SVNV and TSWV co-occurrence in peanut, highlighting the need to investigate potential virus interactions. Second, the complete genome of an Alabama SVNV isolate from soybean was assembled using RNA sequencing and rapid amplification of cDNA ends (RACE). Comparative genomic analyses identified numerous nucleotide and amino acid variations relative to the Tennessee reference strain (GCF_004789395.1), providing new insights into SVNV evolution. Third, new resistance-breaking (RB) strains of tomato spotted wilt virus (TSWV) capable of overcoming the widely deployed Sw-5b resistance gene were detected in Alabama tomato production systems. Genomic analyses identified resistance-associated mutations and documented the emergence of locally evolved RB lineages, emphasizing the need for durable management. Finally, grapevine leafroll-associated virus-3 (GLRaV-3), one of the most destructive and economically important viruses of grapevine worldwide, was identified in Alabama grape production for the first time. Molecular characterization and phylogenetic analyses confirmed the presence of GLRaV-3 and underscored the importance of pathogen-free planting material for preventing virus introduction into emerging viticulture systems. Collectively, these discoveries demonstrate the value of integrated field surveillance, molecular diagnostics, and genomic analyses for identifying emerging viral threats and informing management strategies. Continued monitoring of virus populations, host range expansion, resistance-breaking variants, and pathogen introductions will be critical for protecting agronomic crops throughout the southeastern United States.

Keywords: Viral evolution, plant viruses, TSWV, SVNV, GLRaV-3, host range expansion, resistance breaking, and disease management.

Oral Presentation 11

Exploring Genetic Variation and Stripe Rust Resistance in ICARDA's Spring Bread Wheat (*Triticum aestivum* L.) Using GWAS in West Asia and North Africa (WANA) Region

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Abstract

Stripe rust, caused by *Puccinia striiformis* f. sp. tritici, poses a major threat to global wheat (*Triticum aestivum* L.) production and remains a major constraint to wheat improvement in the West Asia and North Africa (WANA) region. This study evaluated adult-plant stripe rust resistance in 154 ICARDA spring bread wheat genotypes across four environments: Izmir, Turkey; Merchouch, Morocco; and Sakha and Sids, Egypt. Disease response was evaluated under natural field infection at the adult-plant stage using the coefficient of infection (CI), with contrasting disease responses observed among genotypes and environments. The mean final CI varied among locations, indicating differences in disease pressure, while 52, 35, 57, and 71 genotypes were classified as resistant at Izmir, Merchouch, Sakha, and Sids, respectively. Genotyping identified 17,692 high-quality SNP markers, and genome-wide association analysis was performed using a mixed linear model (MLM) accounting for population structure and genetic relatedness. GWAS was conducted using the phenotype recorded for each environment, and significant marker–trait associations (MTAs) were subsequently compared across locations to identify consistently associated markers. At a significance threshold of $-\log_{10}(p) > 3.0$, 136 significant MTAs were identified across the evaluated environments. Twenty genotypes, including G101, G117, and G125, exhibited high levels of resistance across all four locations, while 33.77% of the evaluated genotypes were resistant in at least three environments, demonstrating substantial genetic variation for stripe rust resistance within the ICARDA germplasm. Seventeen candidate genes were identified by examining the genomic regions surrounding significant MTAs and their annotated gene models, based on the IWGSC RefSeq v2.1 wheat reference genome. Several associated genomic regions corresponded to previously reported stripe rust resistance loci, including Yr18 and Yr57, whereas others represent potential novel resistance loci. Among the consistently associated markers were AX-109902001 on chromosome 6A, AX-94992026 on 7B, IAAV1650 on 5A, and Excalibur_c37115_306 on 3B. These findings demonstrate substantial genetic variation for stripe rust resistance within ICARDA germplasm and identify resistant genotypes and marker–trait associations of potential value for marker-assisted selection and resistance gene pyramiding in wheat breeding programs targeting the WANA region.

Keywords: *Triticum aestivum*, GWAS, wheat, WANA, stripe rust, SNP marker, and MTAs.

Poster Presentation 5*See poster on the next page***Fine Mapping and Candidate Gene Analysis of the Adult-Plant Resistance Locus *Qpmjbr.Caas-6BL* to Powdery Mildew in Common Wheat**

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Abstract

Wheat powdery mildew poses a severe threat to global crop production, and deploying resistant cultivars remains the most cost-effective and sustainable strategy for disease management. However, all-stage resistance (ASR) genes are often overcome by the rapid evolution of pathogen virulence, making the identification of loci conferring durable adult-plant resistance (APR) a central priority in current breeding programs. We previously mapped a stable APR locus, designated *Qpmjbr.caas-6BL*, to chromosome arm 6BL using a recombinant inbred line (RIL) population. In this study, we further fine-mapped the locus to an approximately 590 kb physical interval through recombinants screening of secondary populations derived from residual heterozygous lines. Alignment to the *de novo* assembled genomes of both parents revealed that this interval is highly conserved at the pan-genome level and contains five high-confidence candidate genes, designated *R1* to *R5*. Analysis of sequence variation and temporal expression profiles of near-isogenic lines across the entire growth period revealed that *R1* and *R3* were either not expressed or expressed at negligible levels, whereas *R2* and *R5* showed neither sequence variation nor expression differences between resistant and susceptible genotypes. Notably, only *R4*, which encodes a serine/threonine protein kinase domain-containing protein, was significantly upregulated in the resistant genotype compared with the susceptible genotype. Expression profiling across the entire growth period further demonstrated that *R4* was expressed at relatively low levels during the seedling stage but was significantly induced at the adult-plant stage. This expression pattern is consistent with the typical characteristics of APR genes, suggesting that *R4* is the most likely candidate gene underlying *Qpmjbr.caas-6BL*. Overexpression and gene-edited lines of *R4* have been generated, and functional validation is currently in progress. The study narrows the locus to a single high-confidence candidate gene and provides a foundation for cloning durable APR genes.

Keywords: Powdery mildew, Adult-plant resistance, Fine mapping, Candidate gene analysis, Common wheat

Fine mapping and candidate gene analysis of the adult-plant resistance locus *QPmjbr.caas-6BL* to powdery mildew in common wheat

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Abstract

Wheat powdery mildew poses a severe threat to global crop production, and deploying resistant cultivars remains the most cost-effective and sustainable strategy for disease management. In this study, a stable APR locus, *QPmjbr.caas-6BL*, was mapped to chromosome arm 6BL using a Jingshuang 16 × Bainong 64 RIL population, with the resistance allele from Bainong 64. A residual heterozygous line from the F₆ RIL population was used to develop a secondary mapping population. After four rounds of recombinant screening, *QPmjbr.caas-6BL* was fine-mapped to a ~590 kb interval using 21 recombinants. Alignment to the assembled genomes of Jingshuang 16 and Bainong 64 revealed that this interval is highly conserved at the pan-genome level and contains four high-confidence candidate genes, designated *R1* to *R4*. Analysis of sequence variation and temporal expression profiles of near-isogenic lines across the entire growth period revealed that *R2* was expressed at negligible levels, whereas *R1* and *R4* showed neither sequence variation nor expression differences between resistant and susceptible genotypes. Notably, only *R3*, which encodes a serine/threonine protein kinase domain-containing protein, showed differential expression, implicating it as the most likely candidate gene. Overexpression and gene-edited lines of *R3* have been generated, and functional validation is currently in progress. The map-based cloning of *QPmjbr.caas-6BL* will deliver a novel gene resource and valuable molecular markers for breeding programs aimed at improving APR to powdery mildew in wheat.

Introduction

Gene Name ^a	Type	Encoded Protein	Cloning Strategy
<i>Pm1</i>	ASR	CC-NBS-LRR	MutRenSeq
<i>Pm2</i>	ASR	CC-NBS-LRR	MutRenSeq
<i>Pm3</i>	ASR	CC-NBS-LRR	Map-based cloning
<i>Pm4</i>	ASR	Serine/threonine kinase	MutChromSeq
<i>Pm5</i>	ASR	CC-NBS-LRR	BSR-Seq
<i>Pm6/Pm52</i>	ASR	PRK-NBS-LRR	Map-based cloning
<i>Pm8</i>	ASR	CC-NBS-LRR	Homology-based cloning
<i>Pm12</i>	ASR	CC-NBS-LRR	Homology-based cloning
<i>Pm13</i>	ASR	MLKL-STK	Map-based cloning
<i>Pm17</i>	ASR	CC-NBS-LRR	Homology-based cloning
<i>Pm21</i>	ASR	CC-NBS-LRR	MutRenSeq
<i>Pm24</i>	ASR	Tandem kinase 3	Map-based cloning
<i>Pm26</i>	ASR	CC-NBS-LRR	Map-based cloning
<i>Pm36</i>	ASR	WTK7-TM	Map-based cloning
<i>Pm38</i>	APR	ABC Transporter	Map-based cloning
<i>Pm41</i>	ASR	CC-NBS-LRR	Map-based cloning
<i>Pm46</i>	APR	Hexose transporter	Map-based cloning
<i>Pm55</i>	ASR	CC-NBS-LRR	Map-based cloning
<i>Pm57</i>	ASR	WTK-vWA	Map-based cloning
<i>Pm60</i>	ASR	CC-NBS-LRR	Map-based cloning
<i>Pm68</i>	ASR	CC-NBS-LRR	Map-based cloning
<i>Pm69</i>	ASR	Rx_N-NBS-LRR	ONT-MutChromSeq
<i>WTK4</i>	ASR	WTK	k-mer-based association mapping
<i>Pm6Sl</i>	ASR	BED-NLR	Map-based cloning

^a Cloned powdery mildew resistance genes

Materials and methods

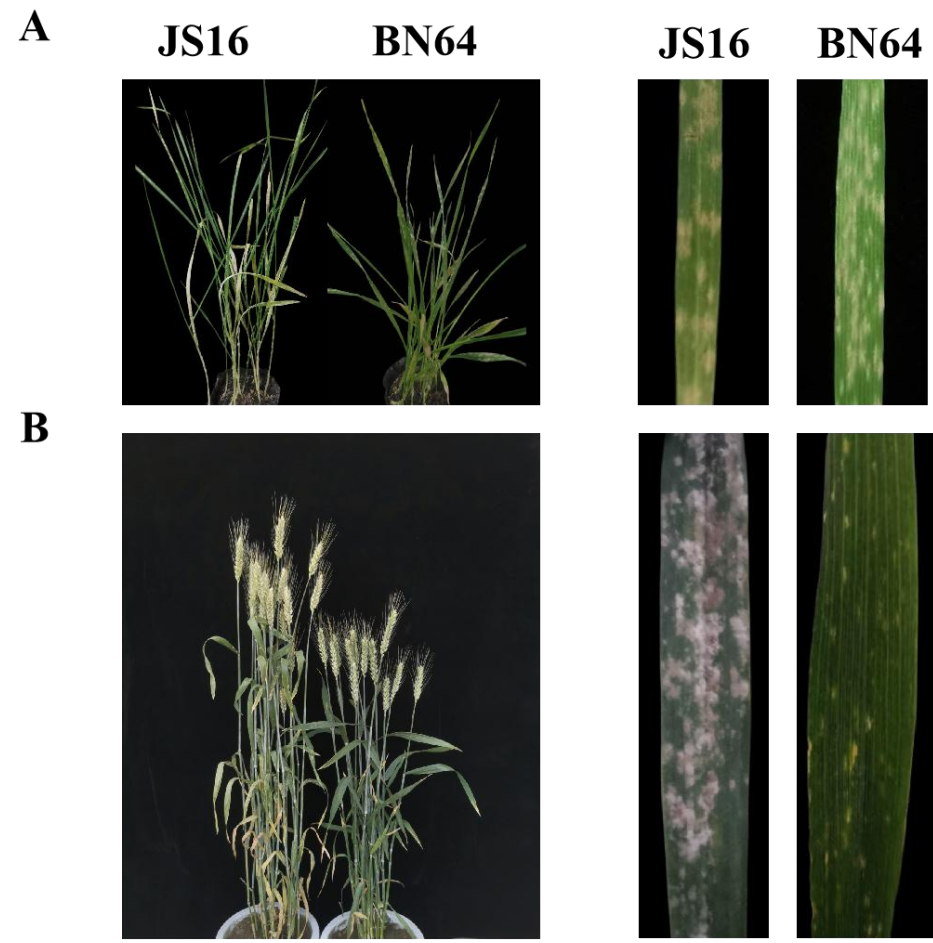


Fig. 1 Responses of Jingshuang 16 (JS16) and Bainong 64 (BN64) to powdery mildew pathotypes E09, E18, E20, E23, and E23-1 at the seedling (A) and adult-plant stages (B).

Mapping population: JS16/BN64 171 RILs
Secondary population: BJRIL54 (a residual heterozygous line at the 6BL locus, derived from the JS16/BN64 RIL population); 5,567 individuals derived from 21 heterozygous recombinant individuals generated by selfing BJRIL54.

QTL mapping of *QPmjbr.caas-6BL*

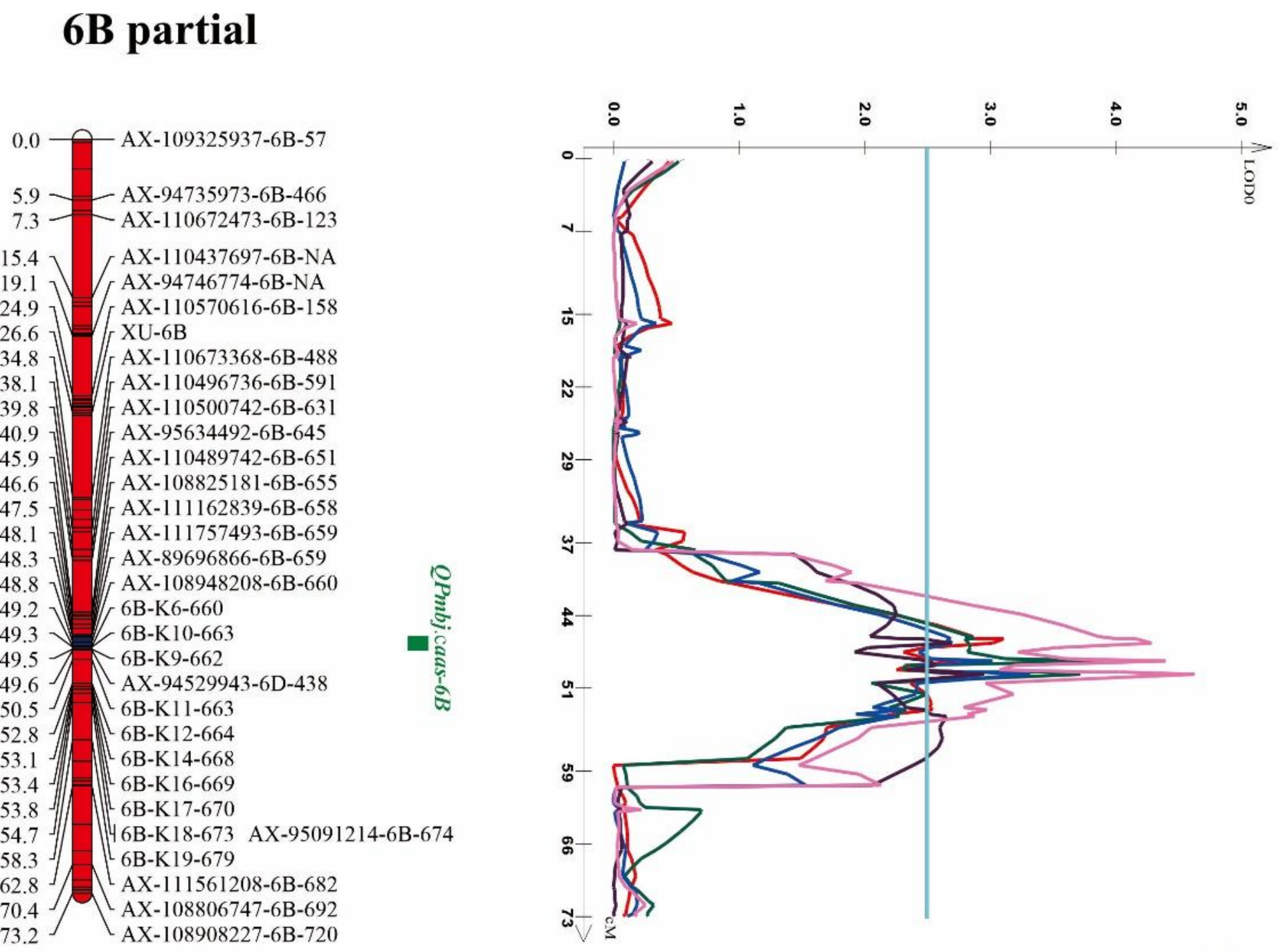


Fig. 2 QTL Mapping of *QPmjbr.caas-6BL* in the JS16/BN64 RIL population

Fine mapping of *QPmjbr.caas-6BL*

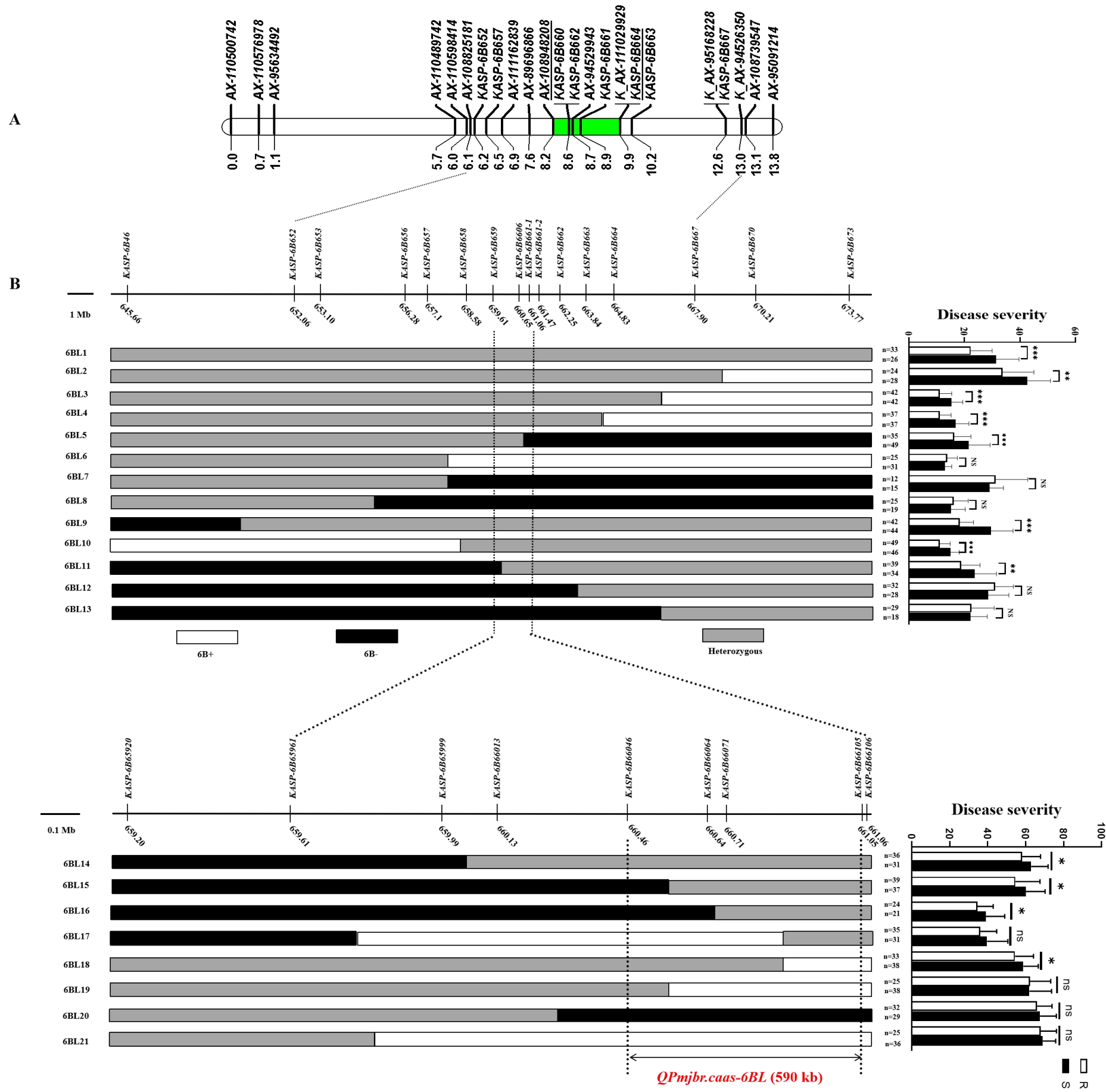


Fig. 3 : Fine mapping of *QPmjbr.caas-6BL*. (A) Genetic linkage map of chromosome 6B, the green region indicates the QTL mapping interval of *QPmjbr.caas-6BL*; (B) Secondary population derived from 21 recombinant individuals.

Genome assembly and annotation

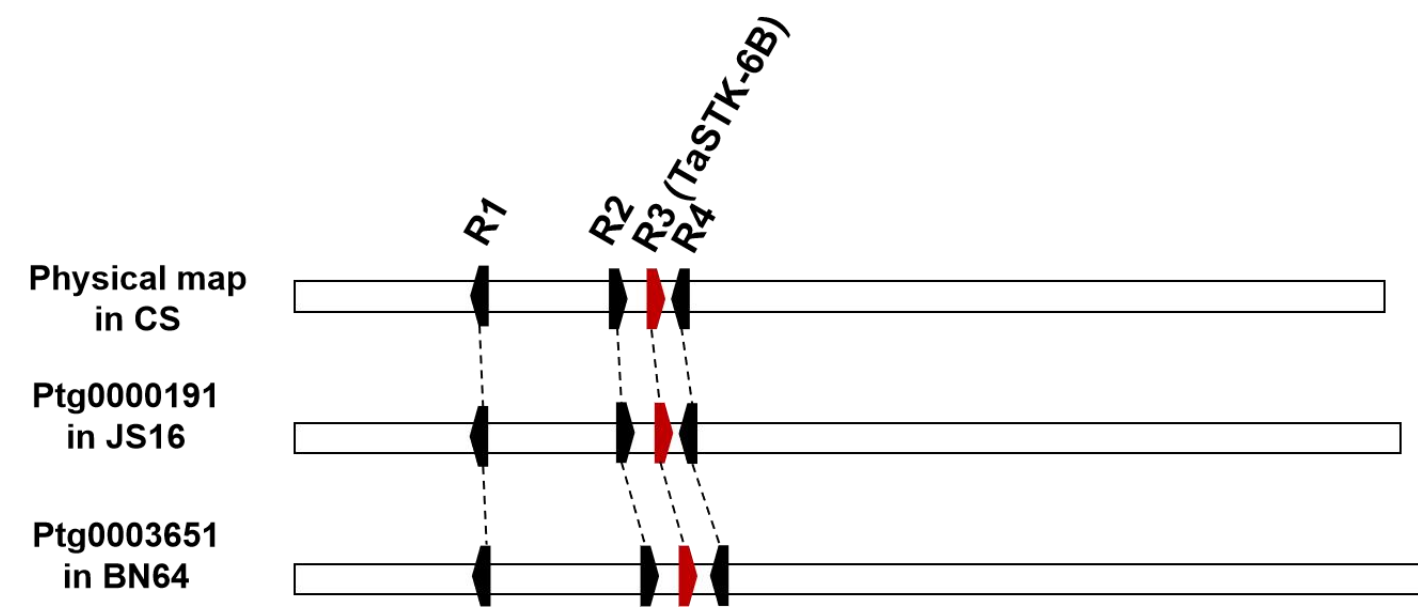


Fig.4 Physical map of the 6BL region in the CS RefSeq v1.1, JS16 genome (contig ptg0000191), and BN64 genome (contig ptg0003651). Four candidate genes were predicted in this region.

Gene	Annotation ^a	Sequence variation ^b
<i>R1</i>	UDP-glucuronate 4-epimerase 4	upstream
<i>R2</i>	F-box protein	upstream+exonic
<i>R3 (TaSTK-6B)</i>	Kinase	upstream
<i>R4</i>	Autophagy-related protein 18	upstream

^aGene annotation based on the CS RefSeq v1.1

^bSequence variations of candidate genes were identified based on PacBio HiFi sequencing

Candidate gene expression analysis

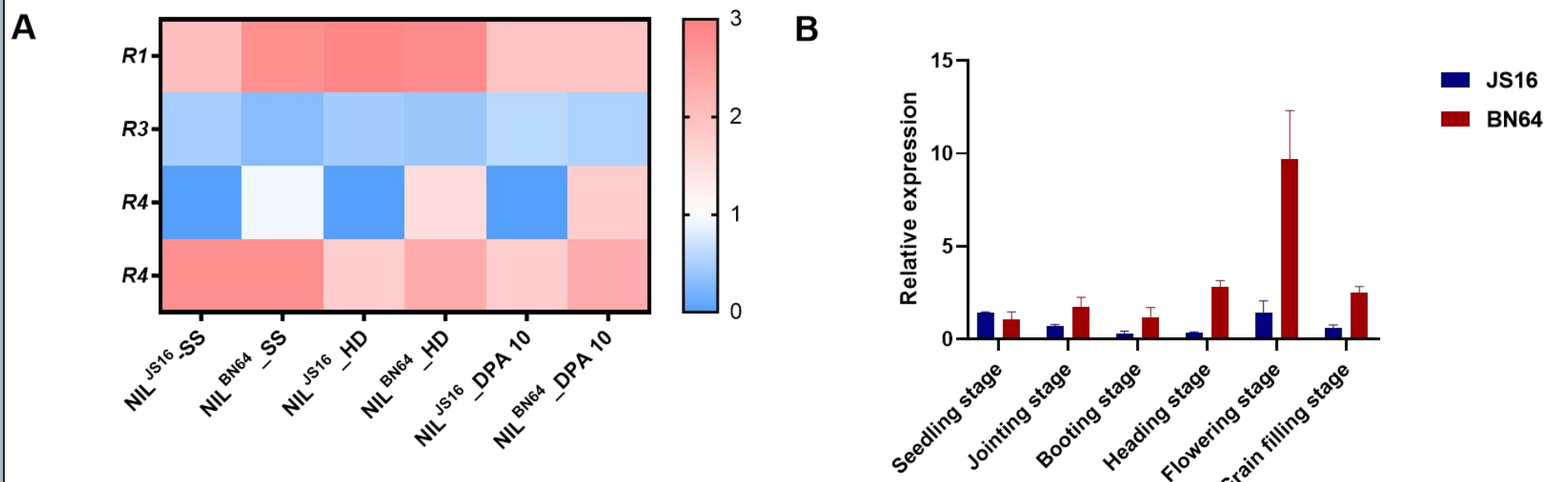


Fig.5 Expression analysis of candidate genes throughout the entire growth period in near-isogenic lines (A) and both parents (B), SS, seedling stage, HD, heading stage, DPA 10, 10 days post-anthesis.

Effects of *QPmjbr.caas-6BL* on yield components

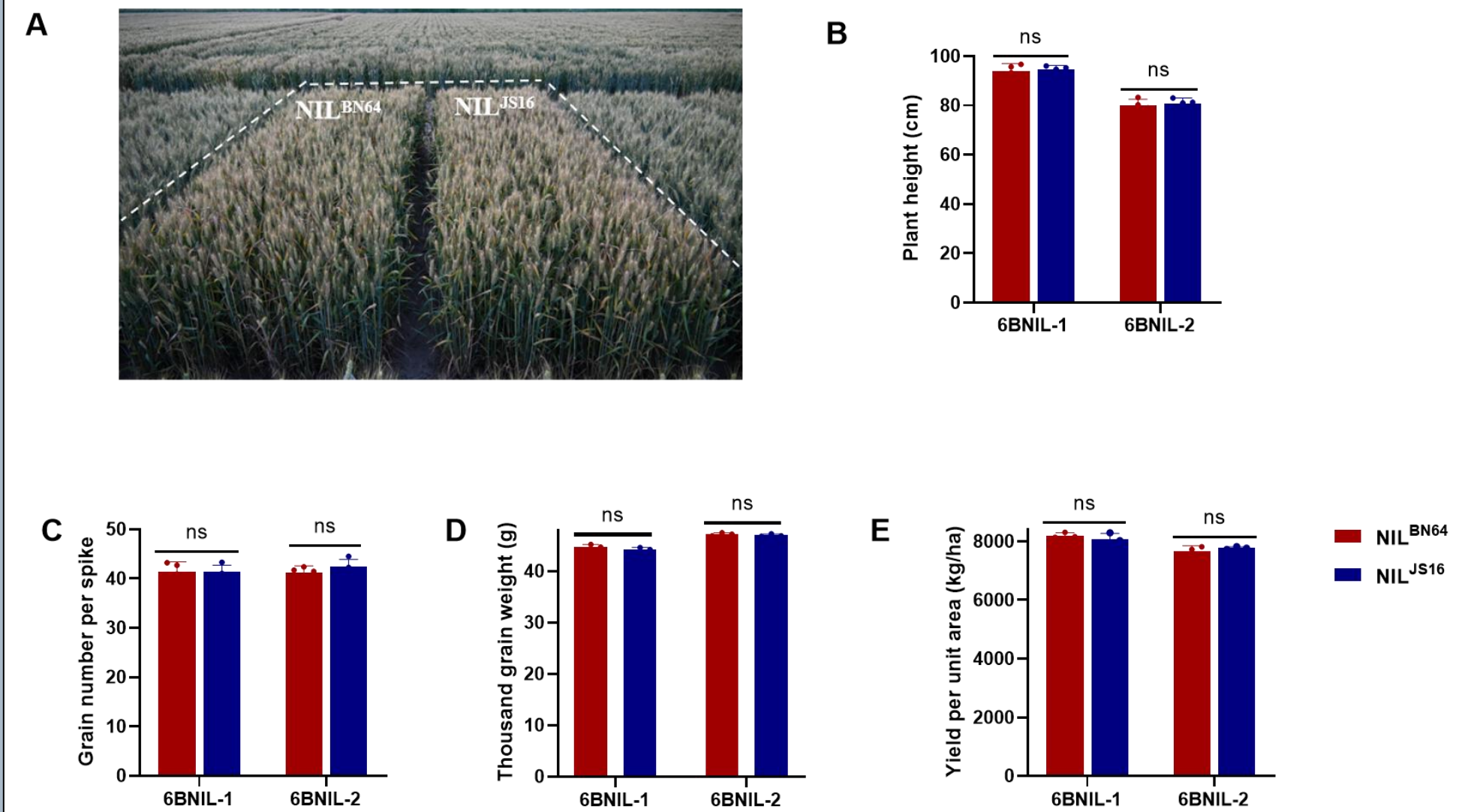


Fig. 6 Phenotypic and yield trait comparison of 6BL NILs. (A) NILs of *QPmjbr.caas-6BL*; (B-E) Comparison of plant height (B), grain number per spike (C), thousand-grain weight (D), and yield per unit area (E) between NIL^{BN64} and NIL^{JS16}.

Functional validation of *TaSTK-6B*

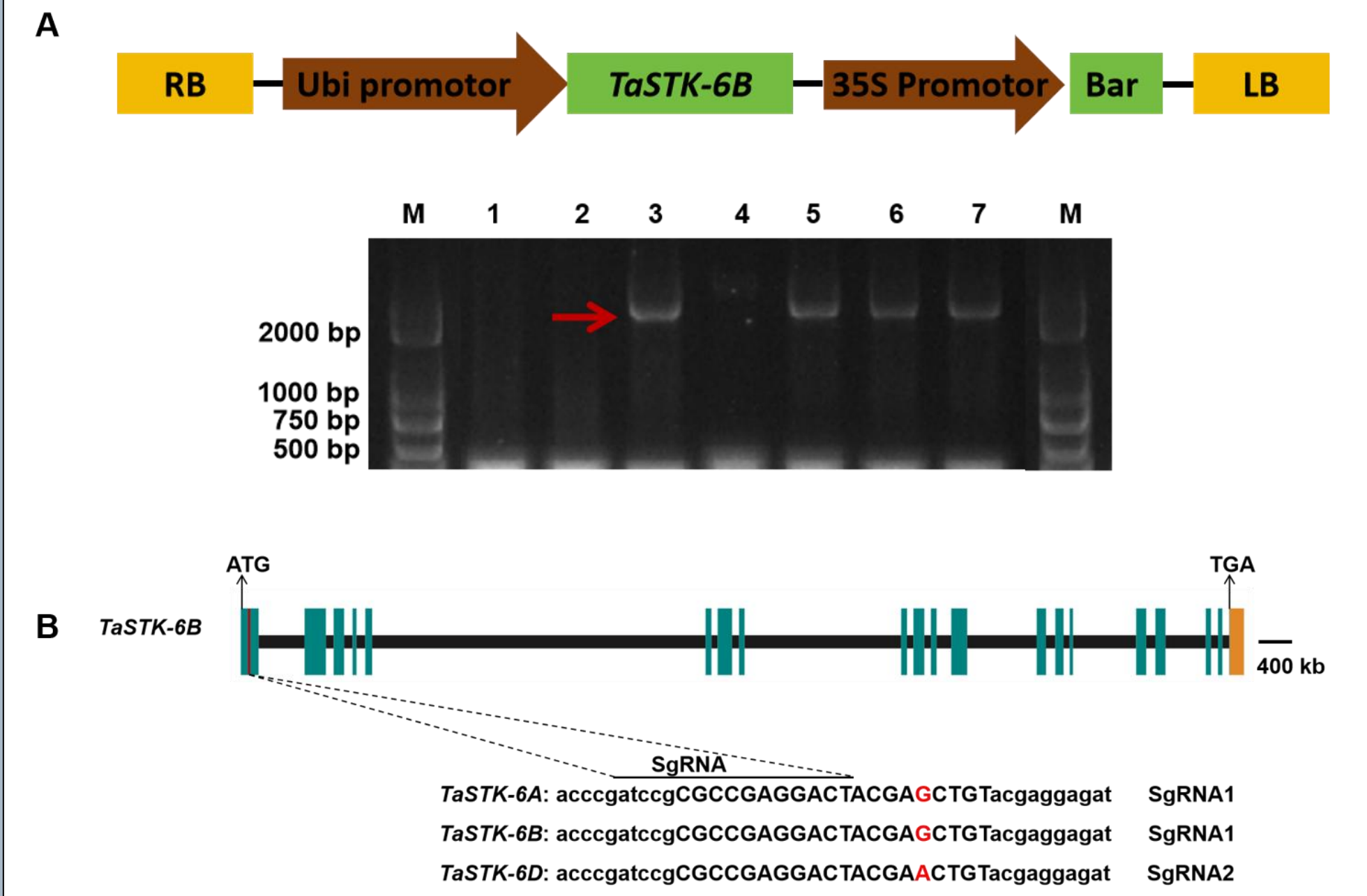


Fig. 7 Functional validation of *TaSTK-6B*. (A) Overexpression of *TaSTK-6B*, M, DL2000 DNA Marker, Lane 1, Fielder; Lane 2, transgenic-negative line; Lane 3, transgenic-positive line; Lane 4, transgenic-negative line; Lanes 5–7, transgenic-positive line; (B) Knockout of *TaSTK-6B*.

References and Acknowledgments

Xu X, Sun D, Ni Z, Zou X, Xu X, Sun M, Cao Q, Tong J, Ding F, Zhang Y, Wang F, Dong Y, Zhang L, Wang J, Xia X, He Z, Hao Y (2023) Molecular identification and validation of four stable QTL for adult-plant resistance to powdery mildew in Chinese wheat cultivar Bainong 64. Theor Appl Genet 136:232

Krattinger SG, Lagudah ES, Spielmeier W, Singh RP, Huerta-Espino J, McFadden H, Bossolini E, Selter LL, Keller B (2009) A putative ABC transporter confers durable resistance to multiple fungal pathogens in wheat. Science 323:1360–1363

Moore JW, Herrera-Foessel S, Lan C, Schnippenkoetter W, Ayliffe M, Huerta-Espino J, Lillemo M, Viccars L, Milne R, Periyannan S, Kong X, Spielmeier W, Talbot M, Bariana H, Patrick JW, Dodds P, Singh R, Lagudah E (2015) A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. Nat Genet 47:1494–1498

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Poster Presentation 6*See poster on the next page***Characterization and Fine Mapping of a Major Adult-Plant Resistance Locus on Wheat Chromosome 4BL for Powdery Mildew in Cultivar Zhongmai 30****Bingyi Liu^{1,*}, Xiaowan Xu^{1,2}, Xinyu Zou¹, Yelun Zhang³, Zhongqiu Ni¹, Mengjing Sun¹, Fugong Ding¹, Huichun Ye¹, Zifeng Guo⁶, Yuanfeng Hao^{1,**}**¹Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing 100081, China²Zhongyuan Research Centre, Chinese Academy of Agricultural Sciences (CAAS), Xinxiang 453519, China³Institute of Cereal and Oil Crops, Hebei Academy of Agricultural and Forestry Sciences, Shijiazhuang 050031, China⁴Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China***Presenting author:** 15729397512@163.com****Corresponding author:** haoyuanfeng@caas.cn**Abstract**

Wheat powdery mildew, caused by *Blumeria graminis* f. sp. *tritici* (*Bgt*), seriously reduces wheat yield. Compared to seedling or all-stage resistance, adult-plant resistance (APR) is more durable and desirable in wheat breeding. The hexaploid cultivar Zhongmai 30 (ZM30) is susceptible to most predominant *Bgt* races in China at the seedling stage, yet it exhibits high to near-immune APR under field conditions. Three RIL populations, each derived from crosses between ZM30 and a susceptible parent (GY18235, JAB42, or JM22), were evaluated for powdery mildew resistance across multiple field environments and genotyped by 1× resequencing. We consistently detected a major QTL on chromosome arms 4BL (*QPmjz.caas-4BL*, 603.58-625.90 Mb) in all three populations, which accounted for 10.8-25.5% of the phenotypic variation. Two additional loci, *QPmjz.caas-1BL* and *QPmgz.caas-5BL*, were identified, with the 1BL locus corresponding to *Pm39/Yr29/Lr46*. ZM30 provided the resistance alleles at all three loci. *QPmjz.caas-4BL* was fine-mapped to 0.99-Mb interval using secondary mapping populations derived from three residual heterozygous lines, and this interval contains 14 high-confidence genes based on the CS RefSeq v1.1 genome assembly. Fine-mapping will continue to narrow the interval to approximately 300 kb, with about five candidate genes expected. Moreover, two KASP markers developed from parental resequencing data validated the 4BL locus in a 343-accession panel; accessions with the ZM30 haplotype exhibited enhanced resistance. The low frequency of this haplotype (9.3%) suggests considerable breeding potential. Our findings identify a stable APR locus on 4BL and provide diagnostic markers for its efficient deployment in breeding.

Keywords: Wheat powdery mildew; Adult-plant resistance; Marker-assisted breeding; 4BL



Mapping and validation of *PmZM30*, a gene conferring adult-plant resistance to powdery mildew in wheat cultivar Zhongmai 30

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INTRODUCTION

Wheat powdery mildew, caused by *Blumeria graminis* f. sp. *tritici* (*Bgt*), causes substantial yield losses worldwide. Adult-plant resistance (APR) is preferred in wheat breeding owing to its higher durability compared with seedling resistance. However, stable APR genes that can be readily used in practical breeding remain limited. The hexaploid wheat cultivar Zhongmai 30 (ZM30) displays excellent field APR to powdery mildew despite seedling susceptibility. This study aimed to dissect the genetic basis of APR in ZM30 and develop usable KASP markers for resistance improvement.

METHODS

Plant materials

Three RIL populations sharing the resistant parent ZM30 were used: GY18235/ZM30 (272 lines), JAB42/ZM30 (94 lines), and JM22/ZM30 (248 lines). A panel of 343 wheat cultivars was employed for QTL validation.

Field phenotyping

Powdery mildew severity was evaluated in multiple field environments using a 0–100% scale, with JAB42 as the susceptible control and spreader. Mixed *Bgt* inoculum collected from six locations was applied. BLUE values across environments were calculated for QTL analysis.

Genotyping and QTL mapping

RILs were genotyped by 1× re-sequencing (and 15K SNP array for JAB42/ZM30), with parental lines at 10× coverage. Linkage maps were constructed using IciMapping and JoinMap, and QTL detection was performed with WinQTLcart. QTL detected in at least two environments were defined as stable loci.

Fine mapping & candidate genes

Three residual heterozygous lines (RHLs) from JAB42/ZM30 were used to develop secondary mapping populations. The 4BL locus was fine-mapped using KASP markers, and candidate genes were predicted based on parental re-sequencing variations and the CS RefSeq v1.1 assembly.

Marker validation

KASP markers tightly linked to the 4BL QTL were developed and validated in the 343-cultivar panel. The 1BL locus was verified using the CAPS marker *csLV46G22* for *Pm39/Lr46/Yr29/Sr58*.

RESULTS

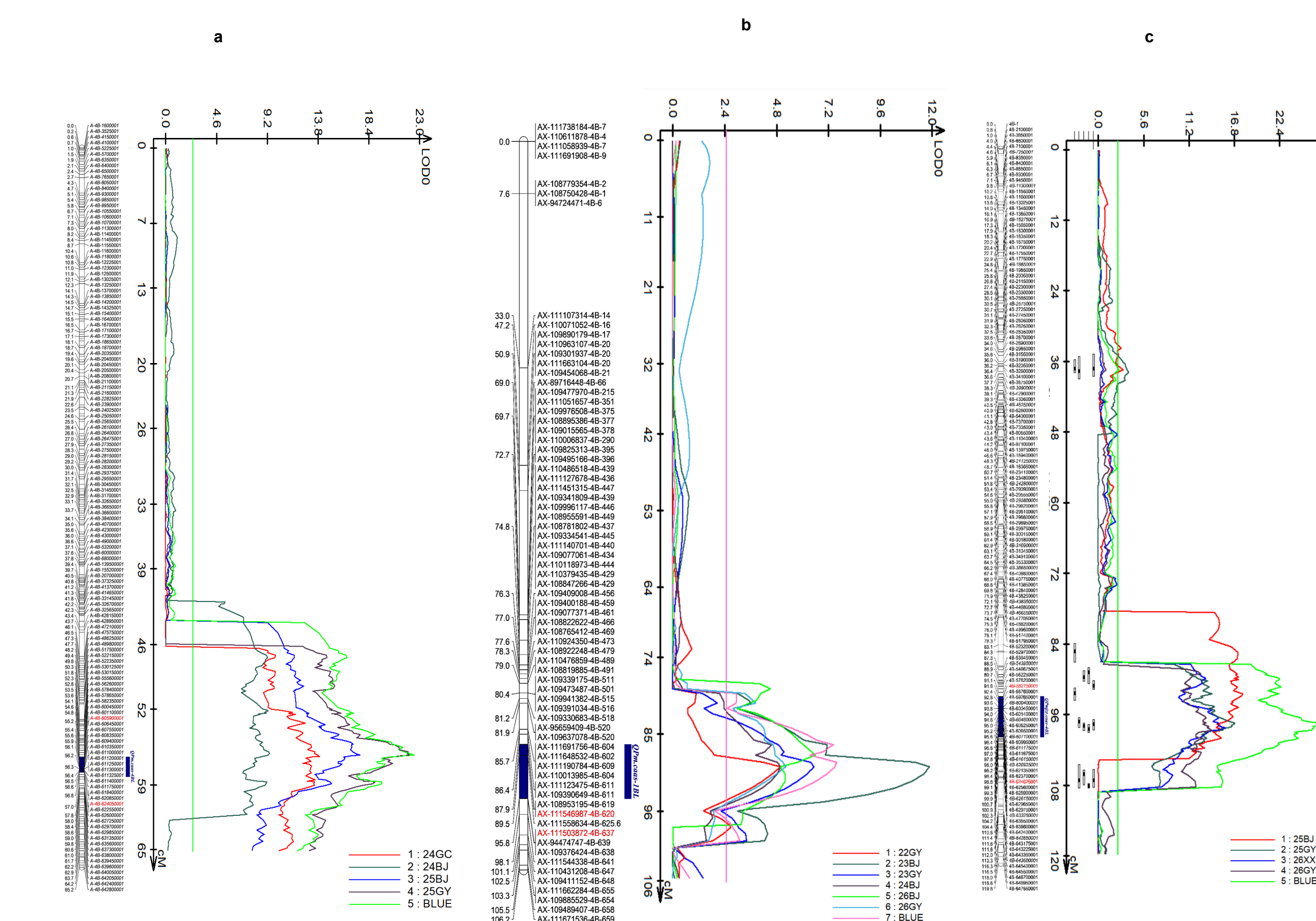


Fig. 1 Stable QTL for APR to powdery mildew were identified on chromosome 4B from ZM30 across all the environments and BLUEs; Markers flanking the QTL are in red. (a) Genetic map of the 4B chromosome in the GY18235/ZM30 RIL population. (b) Genetic map of the 4B chromosome in the JAB42/ZM30 RIL population. (c) Genetic map of the 4B chromosome in the JM22/ZM30 RIL population.

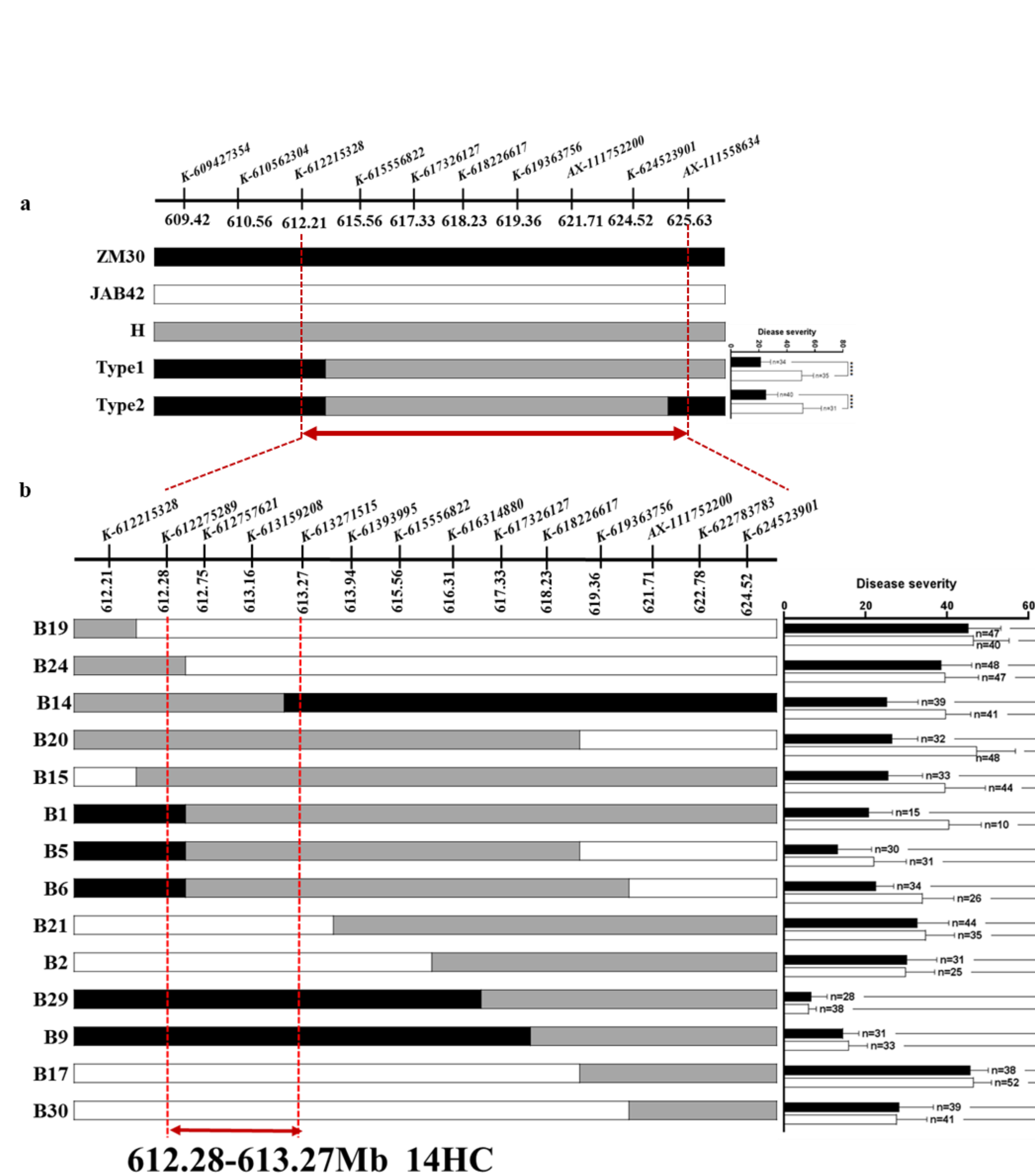


Fig. 2 Fine mapping of *QPmz.caas-4BL* on wheat chromosomal arm 4BL. Black, grey, and white represent homozygous resistant (ZM30), heterozygous (H), and homozygous susceptible (JAB42) genotypes, respectively. (a) Evaluation results in the 2024–2025 growing season; (b) Evaluation results in the 2025–2026 growing season.

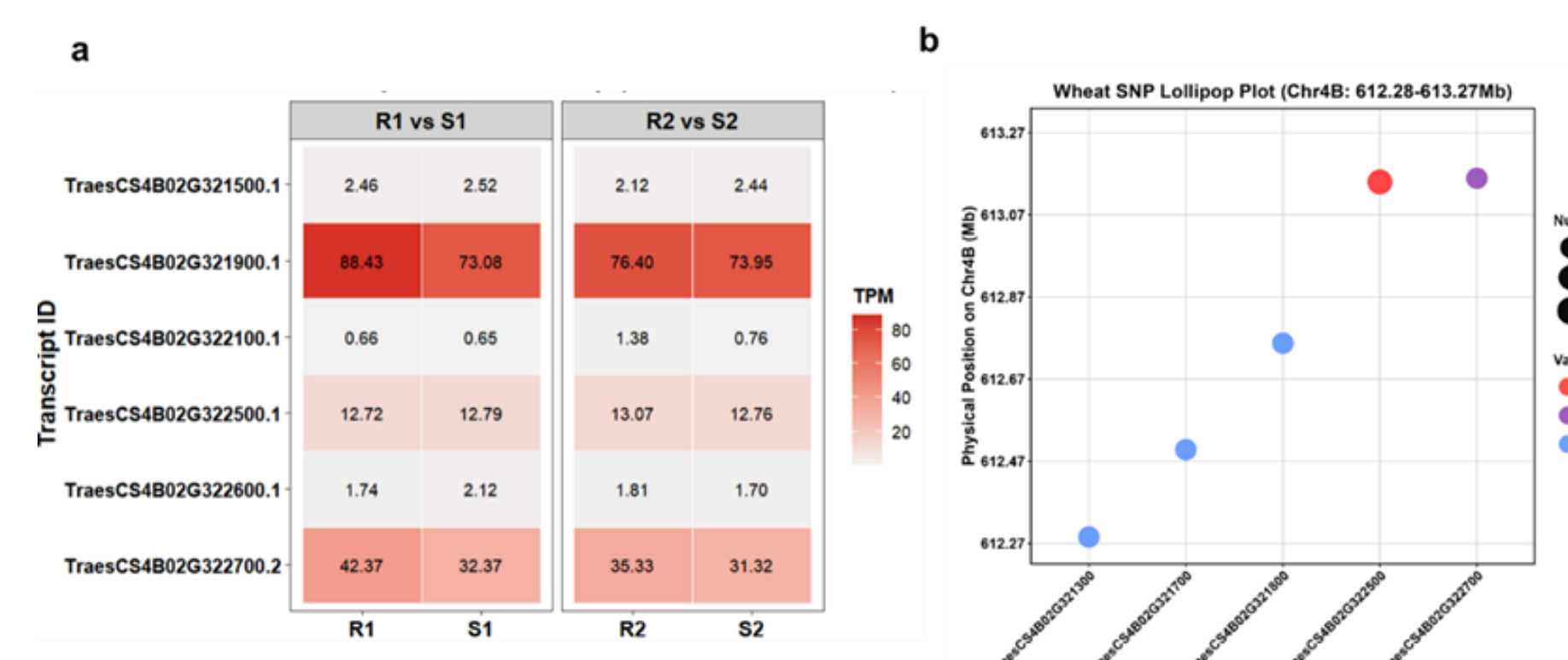


Fig. 3 Gene expression and variant analysis for the 4B target interval (612.28–613.27 Mb). (a) Expression heatmap (TPM) of candidate genes in resistant and susceptible bulks. (b) Lollipop plot showing distribution, functional types and counts of SNPs.

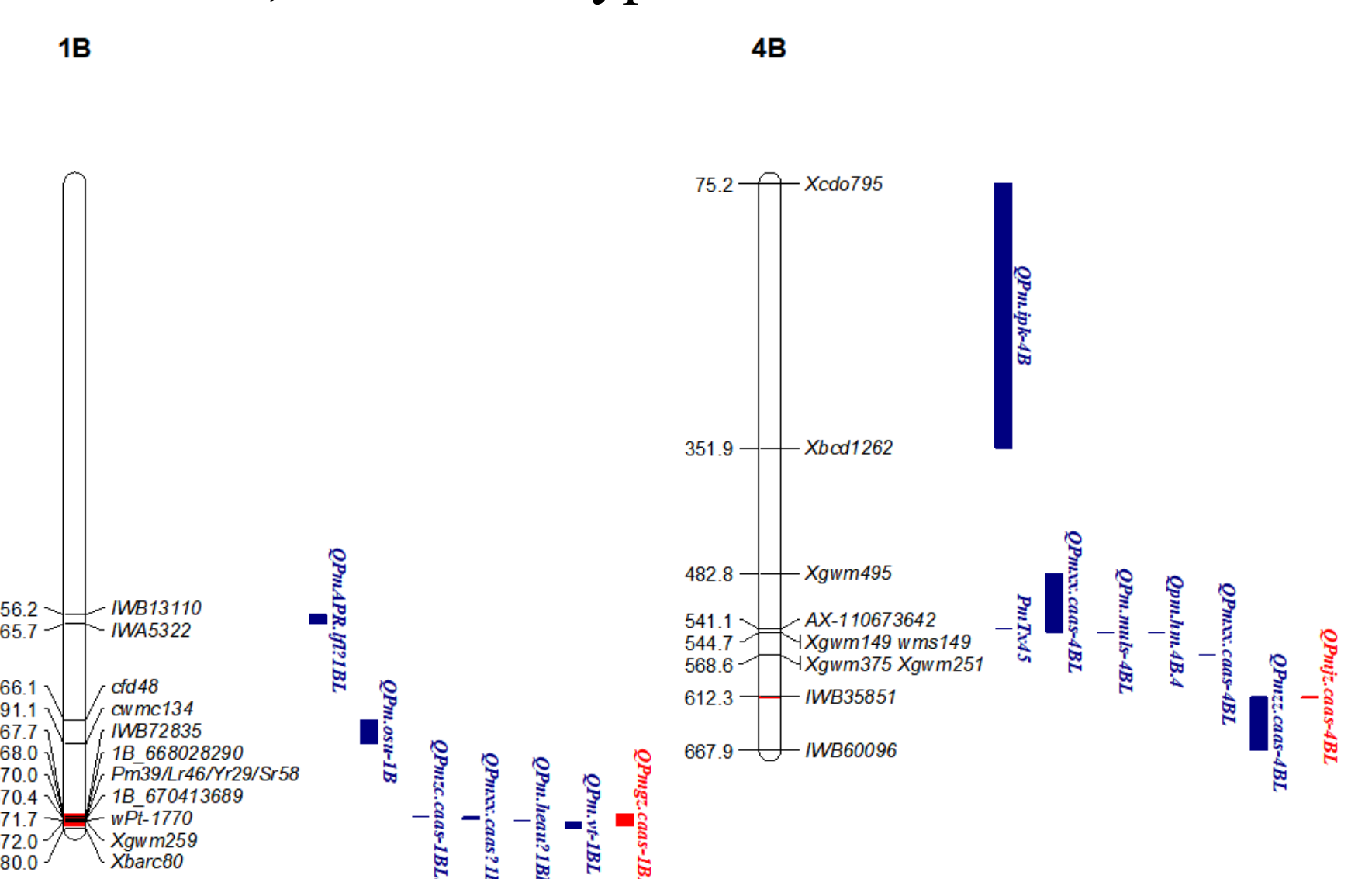


Fig. 4 Comparison of physical intervals between the previously reported powdery mildew resistance loci and the two QTL *QPmz.caas-1BL* and *QPmz.caas-4BL* identified in this study. Blue bars indicate the intervals of published resistance loci, while red bars represent the target regions of *QPmz.caas-1BL* and *QPmz.caas-4BL*, respectively.

CONCLUSION

A stable major adult-plant resistance QTL, *QPmz.caas-4BL* (*PmZM30*), was consistently identified on chromosome 4BL in three RIL populations, together with two minor loci on 1BL (corresponding to *Pm39/Yr29/Lr46/Sr58*) and 5BL. The 4BL locus was fine-mapped to a 0.99-Mb interval harboring 14 high-confidence candidate genes. Diagnostic KASP markers were developed and validated in a 343-cultivar panel, where the favorable ZM30 haplotype showed low frequency (9.3%) and thus great breeding potential. *PmZM30* represents a valuable new resource for durable powdery mildew resistance in wheat breeding.

FUNDING

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Session 5

AI-Accelerated Precision Plant Breeding

Day IV: Thursday, 24 September 2026

Keynote Lecture 13

AI-Accelerated Data-Driven Breeding: Integrating Genomics, Phenomics, and Optimization

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Abstract

Plant breeding has long been regarded as an art, relying on the experience and intuition of skilled breeders. Today, however, breeding objectives are becoming increasingly diverse and complex, while advances in genomics, high-throughput phenotyping, and artificial intelligence (AI) are rapidly expanding what can be measured, predicted, and ultimately designed. In this talk, I will discuss how these advances can be integrated into a data-driven framework for predictive breeding. AI can contribute at multiple stages of the breeding process. Image-based deep learning can transform subjective visual assessments by breeders into objective quantitative phenotypes, while representation learning can extract useful information from high-dimensional genomic and phenomic data. Integration of genomic, metabolomic, microbiome, and environmental information further provides opportunities to model complex biological interactions underlying plant performance. Prediction, however, is not the ultimate goal of breeding. What matters is how predictions are translated into better decisions. Using examples from medicinal perilla and crop mixtures, I will show how genomic prediction can be extended from predicting individual performance to predicting the potential of crosses and genotype combinations. Breeding simulation and optimization can further support decisions on mating and resource allocation across generations. When the number of possible combinations becomes too large for exhaustive field testing, Bayesian optimization provides a framework for using both predicted performance and uncertainty to determine what should be tested next. Together, these approaches extend the role of AI from phenotype prediction toward decision-making and optimization. By closing the loop between data collection, prediction, decision, field experimentation, and learning, AI-accelerated data-driven breeding may help breeders explore genetic and biological diversity more efficiently and design crops and cropping systems for increasingly complex agricultural challenges.

Keywords: Artificial intelligence, Genomic prediction, Phenomics, Bayesian optimization, Predictive breeding.

Keynote Lecture 14

From Data to Seeds: Digital Technologies Driving Innovation in Plant Breeding and Farming

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Abstract

Digital technologies are increasingly reshaping plant breeding as it enables it for more precise, data-driven, and sustainable decision-making processes. The recent advancements in digital tools, either in high-throughput phenotyping, genomic selection platforms, artificial intelligence, and integrated data management systems, are impacting modern breeding programs beyond human response capacity. Exploring data allows to expand our capacity to address complex agricultural challenges by integrating and harmonize diverse datasets, including genomic, environmental, phenotypic, and agronomic information. Expectations include accelerating crop genetic gains while optimizing the resources use. At the farm level, both demographic and socio-political factors have a word in decision making, with clear distinctions between economic priorities and environmental or animal welfare concerns, underscoring the need for tailored agricultural policies and practices. Currently, the traditional role of the farmer is evolving toward that of a technology-enabled operator, involving data interpretation and the calibration of digital systems. In this manner, farmers are increasingly engaging with data generated by agricultural platforms connect to outputs derived from plant breeding programs. To ensure meaningful outcomes, it is essential to establish an effective translation of complex, large-scale datasets originated from plant breeding and molecular science programs into actionable insights. Supporting sustainability goals, including enhanced crop resilience, reduced environmental impact, and improved food security, innovative approaches moving towards data integration, interoperability, and decision-support systems will enable breeders to optimize selection strategies. Evidence shows that digital breeding pipelines not only streamline operations, but also foster collaboration, and improve predictive accuracy in the breeding programs results. Identifying clearly the key barriers to farmer adoption such as data standardization, infrastructure constraints, and capacity building, realistic strategies will allow bridge the gap between technological potential and practical implementation. Ultimately, adoption of digital technologies in plant breeding provides a pathway toward more efficient, transparent, and sustainability-oriented agricultural systems.

Keywords: Digital plant breeding, Genomic selection, Artificial intelligence, Data integration, Decision-support systems, Sustainable farming.

Keynote Lecture 15

Genomic AI Prediction Framework Assisted by Proximal and Remote Sensing Data: Examples and Methods

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Abstract

The development of improved cultivars requires screening large numbers of candidate genotypes in multiple environments to identify stability and/or provide recommendations for local adaptation. However, the evaluation of genotypes in fields is expensive and time consuming. Genomic Selection GS by Genomic Prediction utilizes DNA information from the candidate genotypes as proxy providing surrogates of phenotypes to aid the selection process. It requires an initial data set comprised of genomic markers and phenotypes for model training. Hence, it is possible to select genotypes skipping their evaluation in fields. On the other hand, modern and automated systems have been developed to record large amounts of information occurring in fields such as weather stations and/or proximal and remote sensing. These technologies help to better characterize the development of the genotypes in fields and to understand the relationship between genotypes and environmental conditions through sensors. The increasing availability of other omics of information is also increasing our expectations to improve the effectiveness of the selection process based on predictions. However, at the same time these larger data sets also present challenges to handle and leverage their information in the prediction context. New statistical and AI developments have been proposed to deal with the increasing nature of the data. During my talk I will provide some examples of methods and cases of study where multi-omic integration has been successfully implemented using real data. Also, I will discuss some of the challenges that we face during their implementation as well as recommendations about the research path to follow.

Keywords: Genomic Selection, Genomic Prediction, Artificial Intelligence, Multi-Omic Integration, Predictive Ability, and Plant Breeding.

Session 6

Gene Editing for Crop Improvement

Day V: Friday, 25 September 2026

Keynote Lecture 16

CRISPR-based Genome Editing for Climate-smart Agriculture

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Abstract

Recent advances in plant biotechnology are providing powerful and innovative solutions to address global challenges related to food security, malnutrition, climate change, and environmental sustainability. Emerging tools, such as advanced genomics, genetic engineering, and genome editing, are enabling precise improvement of crop traits. Genome editing permits accelerated improvement of traits such as multiple stress tolerance, resource-use efficiency, and climate resilience and extends beyond the traditional focus of crop breeding, which is mostly on yield enhancement and disease resistance. CRISPR-based genome editing has emerged as a transformative tool for crop improvement, offering unprecedented precision in modifying target genes. It holds significant promise for advancing climate-smart agriculture by simultaneously enhancing productivity, strengthening resilience to biotic and abiotic stresses, and reducing greenhouse gas emissions. Through targeted manipulation of genes associated with key agronomic traits, CRISPR enables rapid development of improved crop varieties tailored to changing environmental conditions. However, the identification of suitable target genes and beneficial alleles remains a critical bottleneck. To address this challenge, there is an urgent need to enhance the use of crop germplasm resources, including landraces and wild relatives conserved in global gene banks. These resources harbor extensive and largely untapped genetic diversity that can be leveraged for discovering novel genes linked to climate resilience and sustainability related traits. Integrating pangenome and super-pangenome sequences derived from large-scale sequencing of diverse germplasm collections with editing of the identified target genes offers a strategic pathway for improving traits associated with climate smart agriculture, such as water- and nitrogen-use efficiency, carbon sequestration capacity, and overall climate adaptability. This presentation will highlight the pivotal role of genome editing in harnessing genetic diversity to develop sustainable, resilient, and climate-smart agricultural systems.

Keywords: CRISPR genome editing, Climate-smart agriculture, Germplasm diversity, and Pangenomics

Keynote Lecture 17

Functional Validation of the *MYB4-12* Homolog to Modulate *PAL2*-Mediated Phenylpropanoid Flux Toward Capsaicin Biosynthesis in *Capsicum annuum* L.

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Abstract

Capsaicin is the major pungent compound in chili pepper and contributes not only to flavour but also to plant defence and several pharmacological applications, including analgesic and anti-inflammatory activities. Enhancing capsaicin accumulation in *Capsicum annuum* therefore represents an attractive target for both crop improvement and industrial utilization particularly for medical application. Recent studies identified *CcMYB4-12*, an *R2R3-MYB* transcription factor from *Capsicum chinense*, as a transcriptional regulator of *PAL2*, a key entry-point enzyme of the phenylpropanoid pathway. Through repression of *PAL2*, *CcMYB4-12* appears to influence carbon partitioning between lignin and capsaicinoid biosynthesis, suggesting a potential regulatory role in capsaicin accumulation. The aim of this study is to identify and functionally characterize the corresponding *MYB4-12* homolog in *C. annuum* and to investigate its interaction with *PAL2* as a target for metabolic engineering of capsaicinoid biosynthesis. In parallel, a microspore-derived haploid plants system is being established as a platform for genome editing and the rapid generation of doubled-haploid edited lines. The current work combines regulatory gene validation with targeted mutagenesis of the phenylpropanoid pathway to better understand the *MYB4-12/PAL2* regulatory mechanism and its contribution to capsaicin biosynthesis. The resulting gene-edited resources are expected to provide valuable insights into capsaicinoid metabolism and establish a foundation for the development of high-yield pepper cultivars with enhanced capsaicin content and improved medicinal and industrial value.

Key words: *C. annuum*, Capsaicin, Genome editing, and microspore culture

Keynote Lecture 18

New Breeding Tools to Enhance Crop Quality and Sustainability

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Abstract

Rapid global population growth, which inherently drives an ever-increasing demand for food, is placing growing pressure on global food systems. While increasing crop yield remains a central objective of breeding programs, current priorities increasingly extend beyond productivity to encompass both nutritional quality and environmental sustainability. This shift reflects the need to develop staple crops capable of providing essential nutrients and bioactive compounds while simultaneously reducing the ecological impact of agricultural systems. Enhancing these traits through breeding therefore contributes not only to improved human health but also to more sustainable and resource-efficient food production. Despite its global importance, wheat has historically lagged behind other major cereals in terms of genomic resources and efficient transformation systems. Its polyploid nature poses significant challenges for functional genomics and for the improvement of complex traits through conventional breeding. Traditional breeding approaches are indeed often labor-intensive and time-consuming. In contrast, recent advances in genome editing (GE) technologies offer powerful, time-efficient, and cost-effective alternatives. These recent technological breakthroughs now allow the precise editing of one, two, or all three homoeologous gene copies, providing unprecedented opportunities to dissect gene function and to modify agronomically important traits. GE tools have already been widely applied to modulate the content of health-relevant compounds, enabling the development of crops with enhanced nutritional profiles. CRISPR–Cas systems are routinely used for gene knockouts, while more advanced and precise platforms—such as cytidine base editors, adenosine base editors, and prime editing—have recently been deployed in wheat. Together, these new breeding tools have the potential to accelerate the development of wheat varieties with superior nutritional quality, improved resilience, and greater sustainability, addressing both current and future challenges in global food security.

Keywords: CRISPR/Cas9, crop breeding, food, genome editing, and nutritional quality.

Keynote Lecture 19

Precision Plant Editing: From Barley to Amaranth with CRISPR in Hand

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Abstract

Targeted mutagenesis and gene editing with programmable nucleases, particularly CRISPR/Cas systems, have become central tools for functional genomics and precision crop improvement. These technologies have been widely adopted in major crops such as barley, yet remain underutilised in so-called orphan crops, including amaranth, despite their agronomic potential and nutritional value. Barley benefits from well-established transformation pipelines and genome-editing workflows, whereas comparable platforms for amaranth are only beginning to emerge. This presentation will compare the current state of precision genome editing in barley and amaranth, highlighting methodological advances, technical bottlenecks, and strategies for transferring optimised protocols across species. Case studies will illustrate the targeted modification of genes controlling plant architecture, stress resilience, and pigment biosynthesis, demonstrating how CRISPR-based approaches can accelerate trait discovery and crop diversification. By bridging model and underrepresented crops, precision plant editing offers a powerful framework for expanding breeding targets and enhancing sustainable agricultural production.

Keywords: mutagenesis, CRISPR/Cas systems, barley, stress resilience, and breeding.

Poster Presentation 7

See poster on the next page

Novel Mitochondrial Genome Editing Reveals Cytoplasmic Male Sterility in Tobacco and Seedless Fruit Traits in Tomato

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Abstract

Using tobacco as our initial species, we employed a novel genome-editing technology targeting the mitochondrial genome. After eliminating the mitochondrial *atp1* gene (an essential energy gene) via meganuclease knockout, the gene was repurposed to function as a nuclear gene through synthetic design and insertion using *Agrobacterium Tumefaciens*. These edits were verified by PCR and PacBio sequencing of the mitochondrial genome. The nuclear *ATP1* gene was under the control of the widely used *CaMV 35S* promoter. We discovered two novel traits of interest: (1) a pollen sterility phenotype; and (2) a seedless fruit phenotype. Both traits have tremendous agronomic potential. The pollen sterility trait is inherited maternally because the *atp1* perturbation resides in the mitochondria and thus falls under the class of traits referred to as cytoplasmic male sterility (CMS). CMS traits are vital in producing high-yielding hybrid seeds. Our novel system could be applied to crop species for which viable CMS-based hybrid seed production systems aren't widely deployed (rice, wheat, etc.). The seedless fruit trait observed is akin to that found in seedless watermelons (small, soft, underdeveloped seeds). It has the potential to develop seedless varieties of fruit species for which seedless options are currently limited or unavailable, such as blackberries and muscadine grapes. Our initial results were published in 2023 (<https://doi.org/10.3389/fpls.2023.1253640>). Because tobacco and tomato are closely related and no changes to the meganuclease or *ATP1* gene were needed, we applied our system to tomato. We showed that the abortive seed development trait was similarly manifest in this crop species. Aside from their seedless phenotype, these tomatoes were otherwise normal in size, color, and form. We are currently working on developing a seedless Sugar Baby watermelon. Regarding the CMS and hybrid breeding aspects of the project, our current focus is on developing strategies based on RNAi and CRISPR-TSKO technologies (ongoing work) to create male-sterile plants that retain their seed production capacity. The RNAi and CRISPR-TSKO work will be published in 2027.

Keywords: genome editing, seedless fruits, cytoplasmic male sterility, hybrid breeding, mitochondrial genome, RNAi, CRISPR, meganucleases, *Agrobacterium*-mediated transformation, tobacco, tomato, watermelon

Novel Mitochondrial Genome Editing Reveals:

Cytoplasmic Male Sterility in Tobacco and Seedless Fruit Traits in Tomato

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We are using **mitochondrial genome editing** to investigate the consequences of eliminating the essential mitochondrial *atp1* gene after transferring its function to the nuclear genome. Applying this system in tobacco and tomato revealed two traits of potential agricultural value: **pollen sterility and seedless fruit**.

Because the *atp1* modification resides in the maternally inherited mitochondrial genome, the pollen sterility phenotype represents **cytoplasmic male sterility (CMS)**, an important tool for **hybrid seed production**. Using tobacco as a model, we combined mitochondrial genome editing with an RNAi-based strategy to overcome the defective seed phenotype associated with our original approach. This enabled the development of a complete three-line hybrid seed production system consisting of CMS, Maintainer, and Restorer lines. This strategy could provide new CMS systems for crops where effective systems are currently unavailable or limited. I am further optimizing through CRISPR-TSKO.

Mitochondrial *atp1* editing also produced fruit containing small, soft, underdeveloped seeds. This approach could potentially enable the development of **seedless varieties** in crops where seedless options are currently unavailable.

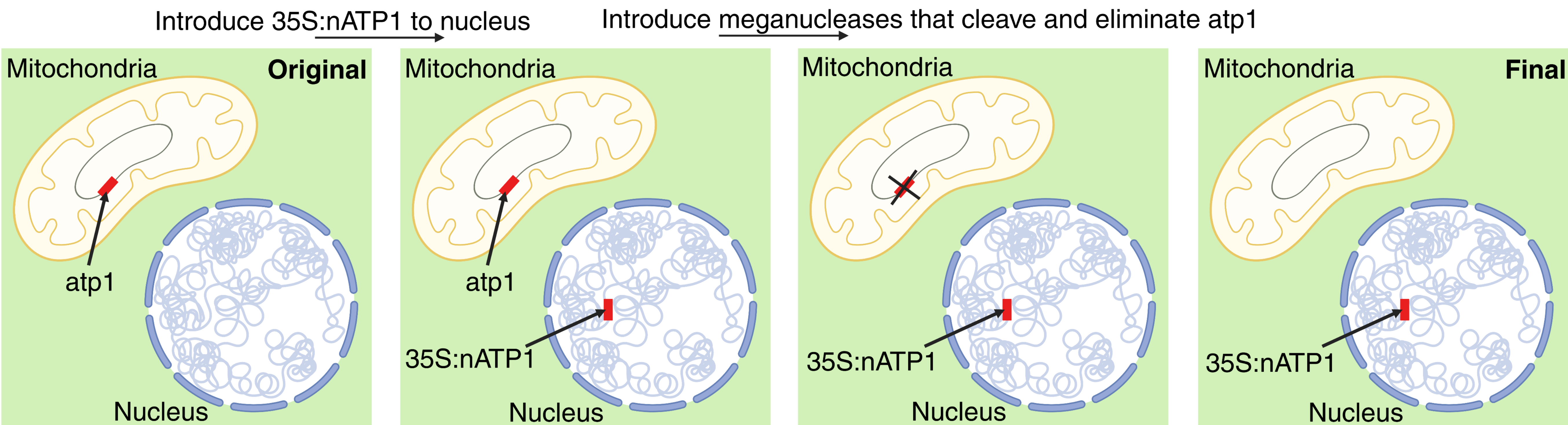


Figure 1. Summary of experimental approach: 35S:nATP1 is added to the nucleus followed by eliminating *atp1* from the mitochondria

Tobacco Results*:

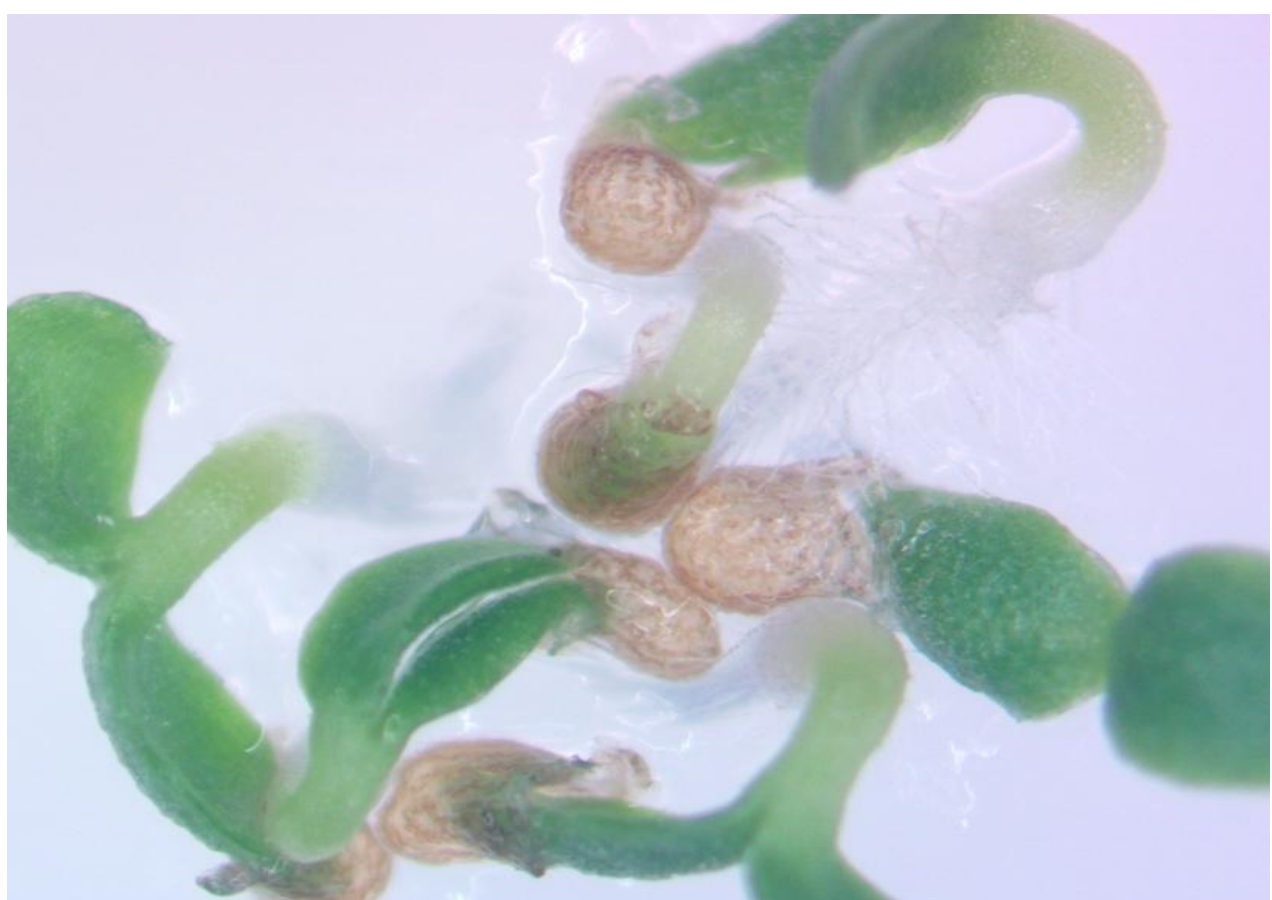
*Published work:



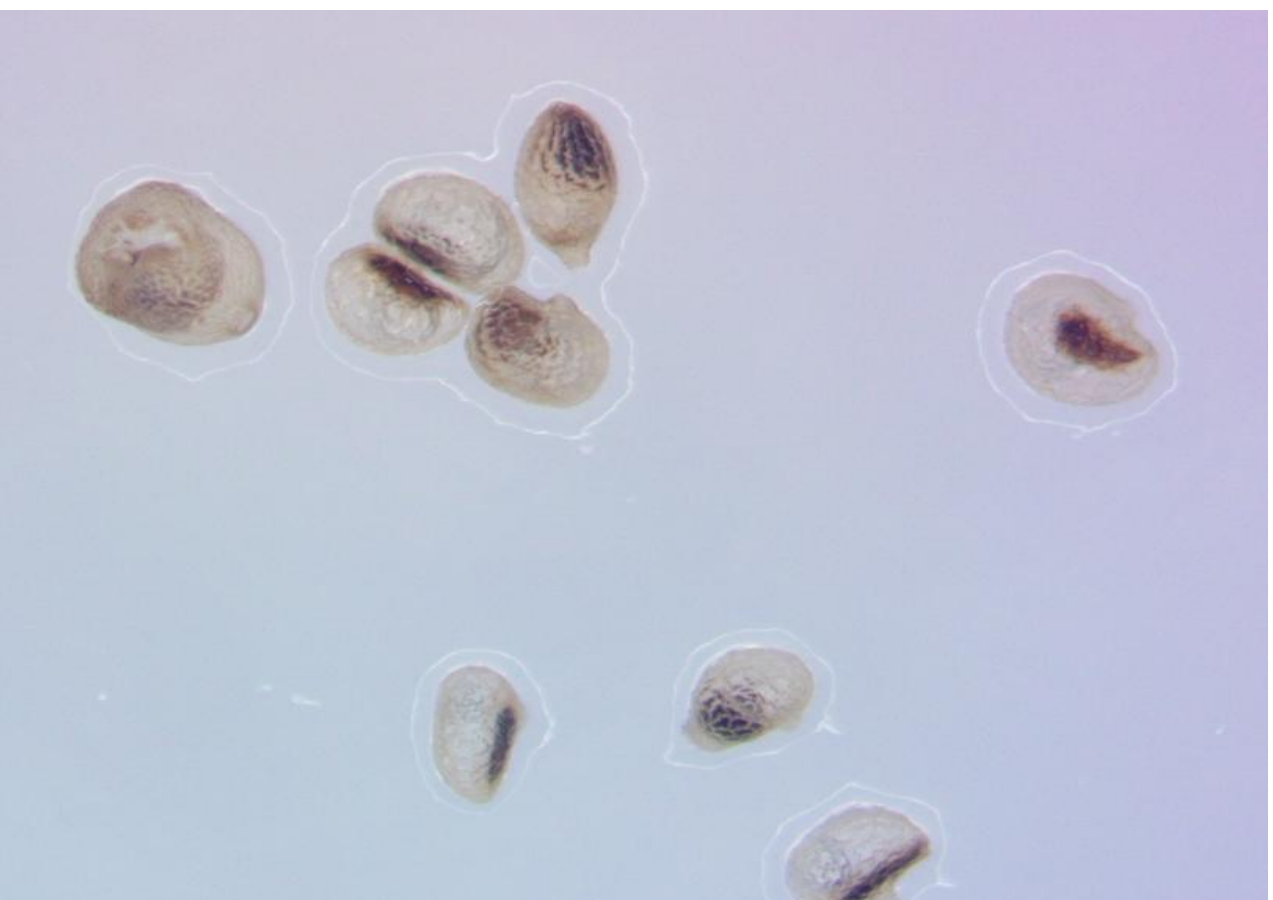
Wild Type



35S:nATP1/Δ*atp1*



Wild Type

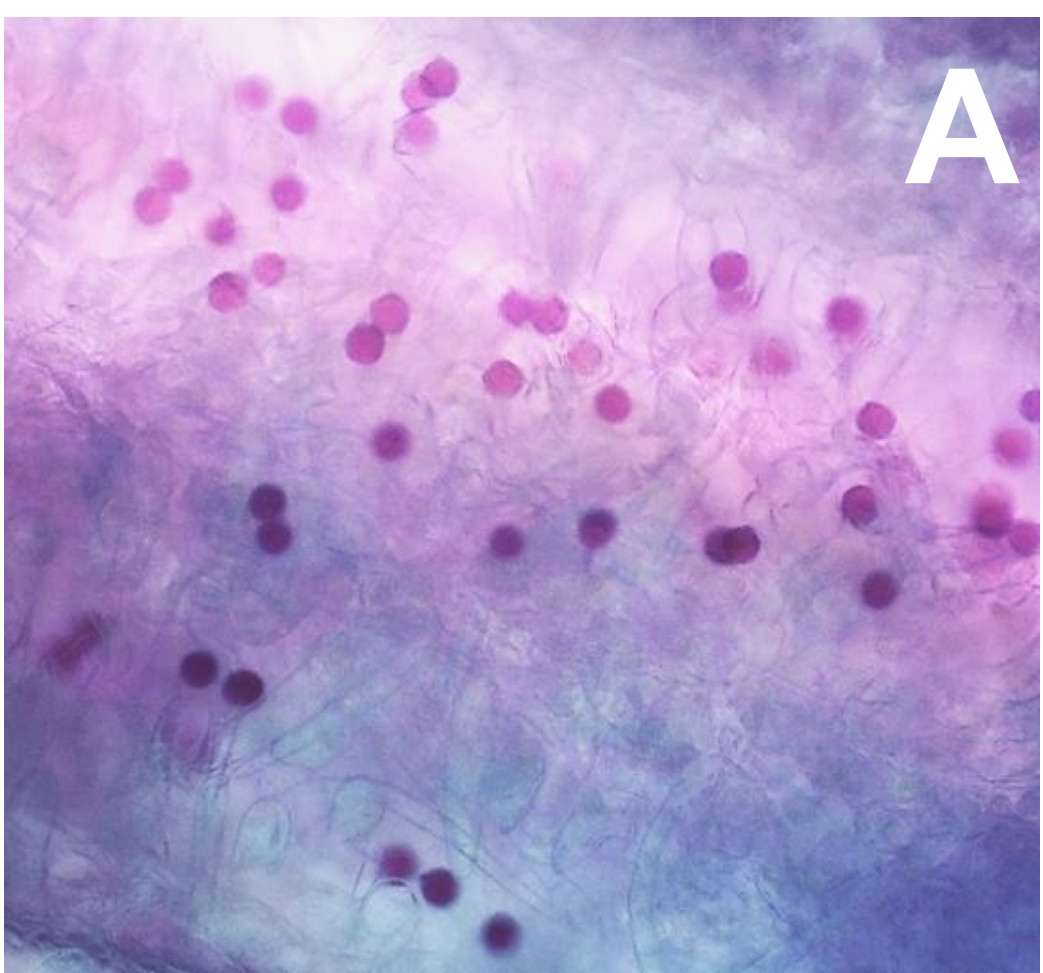


35S:nATP1/Δ*atp1*

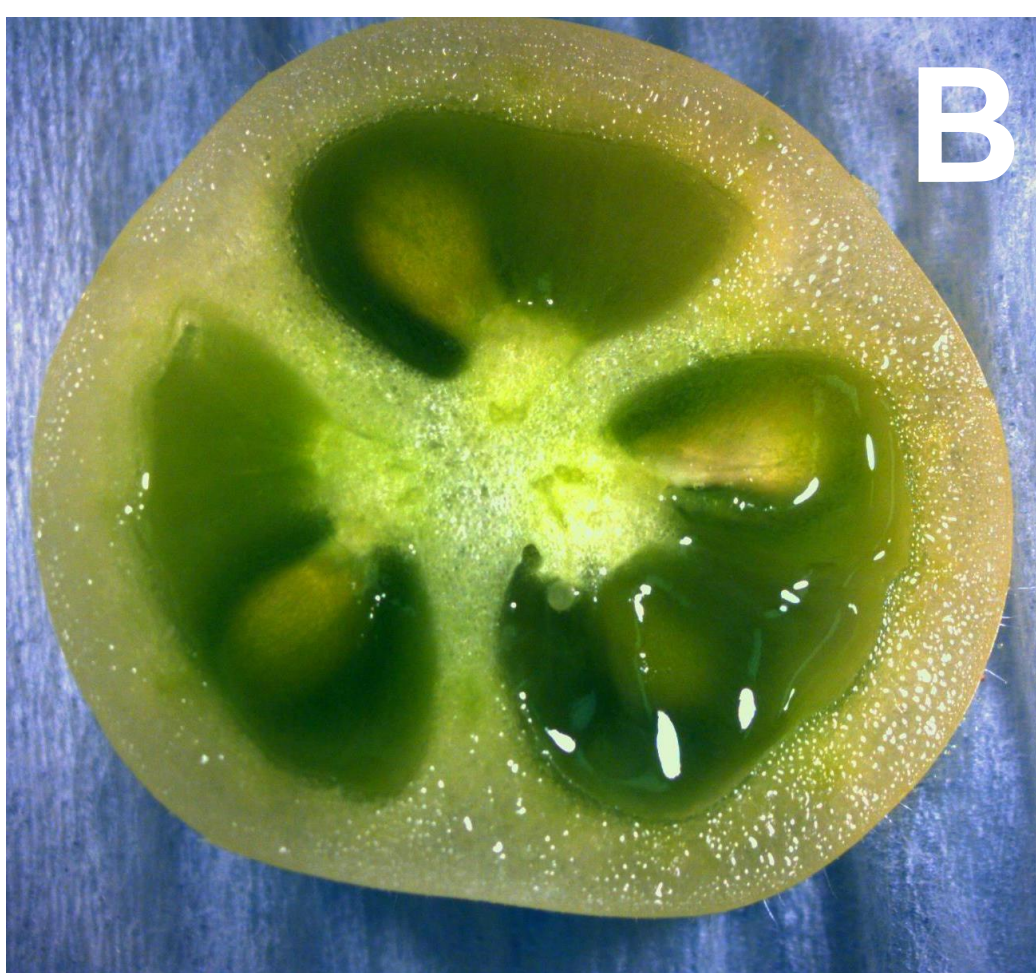
Tomato Results:

Wild-type (top):

- (A) anthers stained for pollen
- (B) immature fruit cross section
- (C) mature seeds
- (D) mature fruits



A



B



1mm



D

Mutant (bottom):

- (A) anthers stained for pollen
- (B) immature fruit cross section
- (C) underdeveloped seeds
- (D) mature fruits



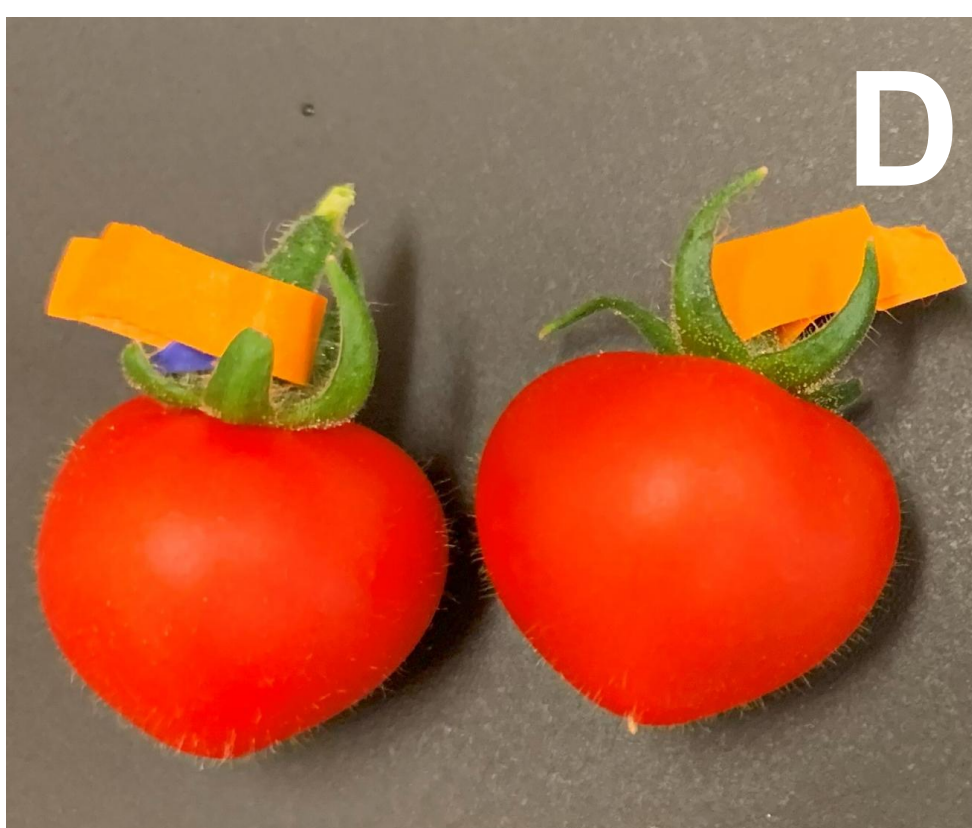
A



B

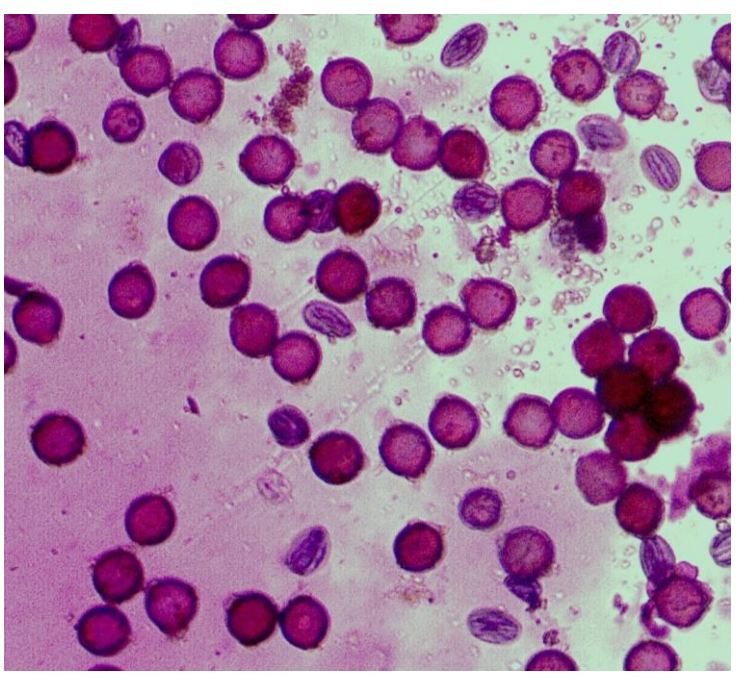


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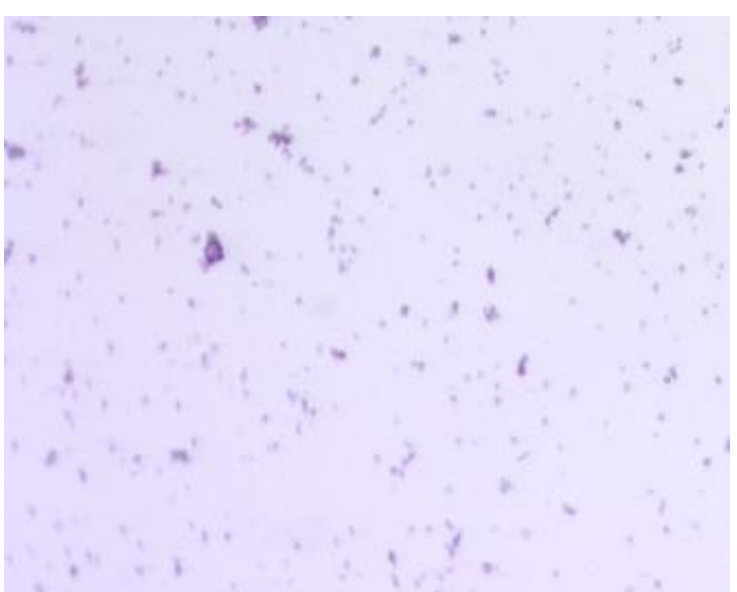


D

RNAi-based strategy: uncoupled the abortive seed trait from the CMS trait



Wild-Type stained pollen



RNAi Mutant stained nonviable pollen



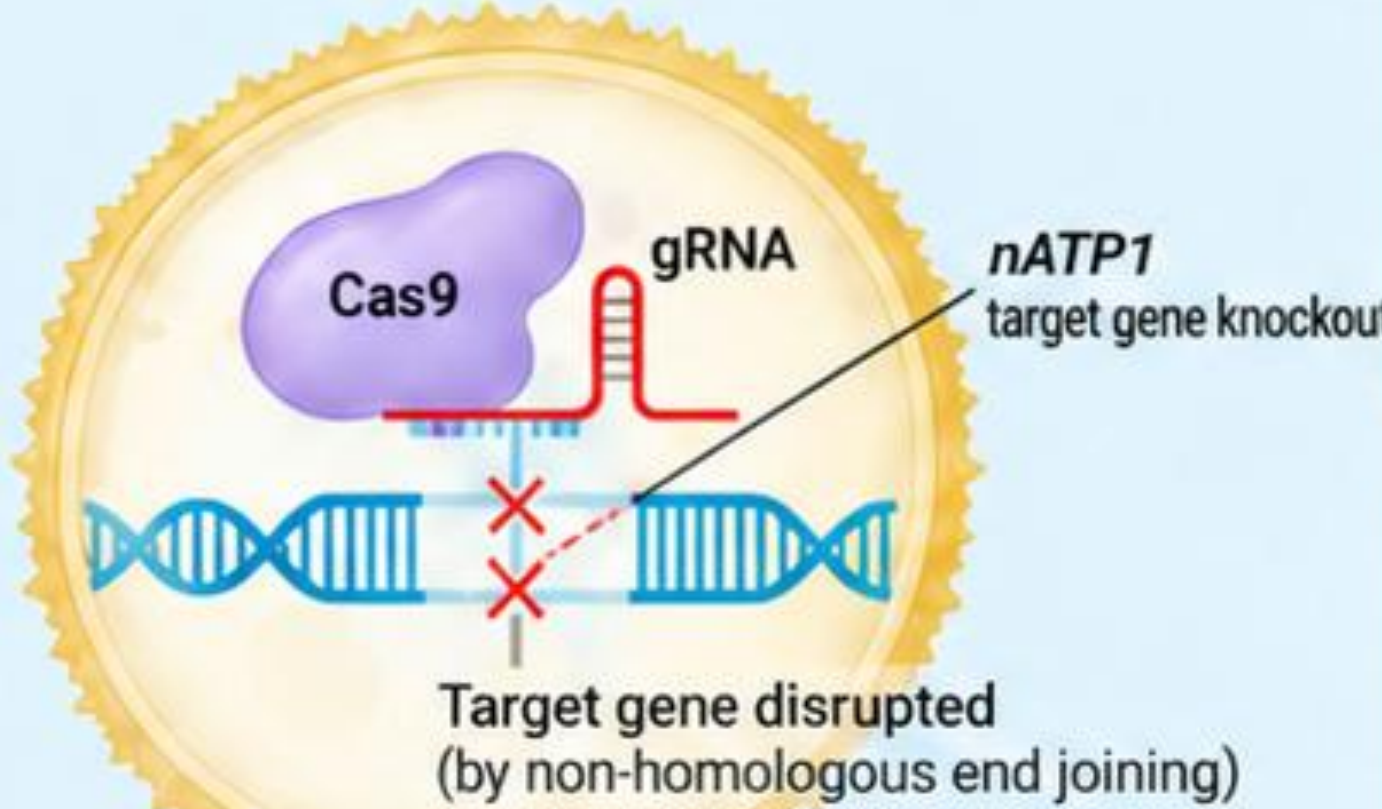
CMS Line

Restorer Line

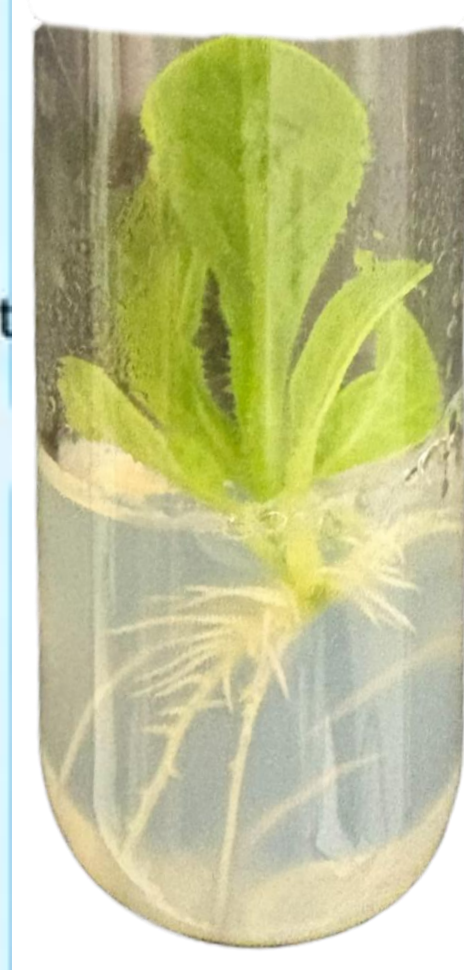
Maintainer Line

CRISPR – Tissue Specific Knock Out (Cas9)

Action in young anther cells (anther lineage only)



CRISPR-TSKO acts specifically in young anther cells



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