V. INTERNATIONAL PLANT BREEDING CONGRESS

1-5 December 2025

Sherwood Exclusive Lara, Antalya/Türkiye

IPBC

Agricultural Research of Türkiye

100th Anniversary

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TÜRKİYE TOHUMCULAR BİRLİĞİ
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TAGEM
AR-GE & İNOVASYON

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Science for resilient livelihoods in dry areas

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ABSTRACT BOOK

Acknowledgment

The 5th International Plant Breeding Congress has served not merely as a venue for presenting scientific papers, but as a high-value international platform where a shared vision for the future of the agricultural sector has been articulated.

We firmly believe that the scientific data and evaluations generated during this congress will contribute meaningfully to the development of national agricultural policies, the advancement of regional development goals, and the strengthening of international research collaborations.

We extend our sincere appreciation to all researchers who enriched our congress, to the institutions and organizations that provided their unwavering support, to our congress sponsors, and to the members of the organizing and scientific committees who worked with great dedication and professionalism.

We also wish to announce that the scientific studies presented during the congress will soon be published digitally on the congress website and shared openly with all relevant institutions and the public.

We hope that the outcomes of our congress will be beneficial to our country, our region, and global agriculture, and we look forward to convening again at future congresses under the guiding light of science.

Prof. Dr. S. Ahmet BAĞCI
Head of Organizing Committee

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Yusuf YORMAZOĞLU (MAY SEEDS)

2 December Tuesday, 2025 HALL A - MİRZA GÖKGÖL

08.30-09.30	Registration
09.30-10.30	Opening Speeches
10.30-12.30	**Chair: *Bülent UZUN*** **Keynote Speaker** 1. M. Emin ÇALIŞKAN, “The Role and Importance of Plant Breeding in Food Security and Sustainability”, Niğde Ömer Halisdemir University 2. Augusto BECERRA, “The impact of International Agricultural Research on livelihoods” ICARDA ***Group photo*** **Tea / Coffee Break** **Chair : *Alexey MORGUNOV*** 3. Wei XIONG, “Climate Change Challenges for Plant Breeding” CIMMYT 4. Berk ÜSTÜNDAĞ, “How Can We Utilize Artificial Intelligence in Plant Breeding?” (Istanbul Technical University - İTÜ)
12.30-14.00	LUNCH BREAK
	Chair: *Gürbüz Mızrak*
14.00-17.00	**“Panel - 100th Anniversary of the Plant Breeding in Türkiye”**
14.00-14.40	Fahri ALTAY, “Agricultural Research since 1925” (Emeritus Faculty Member and Director)
14.40-15.00	Mesut KESER, “Wheat variety development in a Century” (Wheat Breeder)
15.00-15.20	Kamil YILMAZ, “Developments in the Seed System and Plant Breeders Rights” (Member of Board - BİSAB)
15.20-15.30	Q&A
15.30-15.45	**Tea / Coffee Break**
	Chair: *Ahmet Balkaya*
15.45-16.15	Yusuf YORMAZOĞLU, “Field Crops Research in Private Sector and Future Perspectives” (MAY Seed)
16.15-16.45	Ahmet SEÇİM, “Vegetable Research in Private Sector and Future Perspectives” (GENETİKA Seed)
16.45-17.00	Q&A
20.00	Congress and 100th Anniversary Gala Program

3 December 2025, Wednesday — HALL A - MİRZA GÖKGÖL

		Chair: ***Mesut Keser***	
09:00-09:30		**Keynote Speaker** Contribution of the Speed Breeding Method to Plant Breeding under Changing Climate Conditions.	*Lee Thomas Hickey*
09:30-10:00		**Keynote Speaker** Inducer Mediated Line Development in Corn and Genomic Analyses of Lines for Prediction of Heterosis Potential	*Thomas Lübberstedt*
10:00-10:10		Q&A	
10:10-10:20	**OP-174**	Moving Winter Wheat Frontier beyond 50o North: Global Genetic Resources for Winter Survival and Productivity	*Alexey Morgunov*
10:20-10:30	**OP-13**	Allelic Variation of Vrn Loci in Advanced Barley Breeding Lines for Predicting the Adaptability of Future Cultivars	*Raushan Yerzhebayeva*
10:30-10:40	**OP-59**	Genome-wide Association Study Reveals QTLs and Candidate Genes for Fungal Diseases Resistance in Barley in Kazakhstan	*Yuliya Genievskaya*
10:40-10:50	**OP-123**	Selection of High Temperature Stress Tolerant Wheat Genotypes Using Stress Indices	*Nurettin Temurtaş*
10:50-11:00		Q&A	
11:00-11:20		Tea & Coffee Break	
		Chair: ***İsmet Başer***	
11:20-11:30	**OP-173**	Promoter-Based Identification of Molecular Targets for Drought Tolerance Breeding in Hordeum Vulgare	*Elif Yetilmezer*
11:30-11:40	**OP-341**	Agro-Physiological Parameters in Two and Six-Rowed Barley (*Hordeum Vulgare L.*) Genotypes under Rainfed Conditions	*İrfan Öztürk*
11:40-11:50	**OP-171**	Coleoptile Length of Turkish Winter Barley *Hordeum Vulgare* L. Cultivars	*Namuk Ergün*
11:50-12:00	**OP-58**	Barley Breeding Program in TRNC	*Mehmet Karşılı*
12:00-12:10	**OP-233**	Crops Breeding and Seed Production at Lomtagora Seed Company, Georgia	*Kaha Lashki*
12:10-12:20	**OP-34**	Genomic Prediction and Association Mapping of Yield and Quality Traits in Silage Hybrid Maize	*Gönül Cömertpay*
12:20-12:30		Q&A	
12:30-14:00		**LUNCH BREAK**	

		Chair: ***İrfan Özberk***	
14:00-14:30		**Keynote Speaker** Hybrid Rice Technology	*Jauhar Ali*
14:30-14:40		Q&A	
14:40-14:50	**OP-321**	Plant Growth Speed, Photosynthetically Active Radiation Utilization and Association of them with Grain Yield in Winter Wheat in Multilocation	*Mesut Keser*
14:50-15:00	**OP-175**	Kazakh-Siberian Network for Spring Wheat Improvement – 25 years: Genotype-Environment Interactions, Bread vs Durum Wheat, Genes Effects and Yield Champions	*Alexey Morgunov*
15:00-15:10	**OP-236**	The Performance of Wheat Varieties Breeding by TAGEM from the Perspective of Farmers in Şanlıurfa Province	*Seyda Ipekcioglu*
15:10-15:20	**OP-340**	Climate Change: Yield and Quality in Bread Wheat and Environmental Effects	*İrfan Öztürk*
15:20-15:30	**OP-20**	Yield Traits Analysis in Wild Wheat (*Triticum Turgidum ssp Dicoccoides*) Populations Under Different Environments	*Mohammad Mahmoud Alajlouni*
15:30-15:40		Q&A	
15:40-16:00		**Tea & Coffee Break**	
		Chair: ***Rajesh K Arya***	
16:00-16:10	**OP-185**	Enhancement of Carbon Sequestration in Wheat (Triticum Asestivum) Through Genetic Options for Higher Biomass and Grain Yield Under Climate Change	*Rishi Kumar Behl*
16:10-16:20	**OP-259**	Breeding Wheat for Tolerance to Combined Stress Cause by Draught in High Temperature	*Abhishek Kumar*
16:20-16:30	**OP-260**	Wheat Improvement Strategies for Lodging Resistance to Minimise Yield Losses in Inclement Weather	*Arushi Padiyal*
16:30-16:40	**OP-263**	Tolerance to Low Temperature Stress in the Late Development Stage of Bread Wheat Genotypes	*Seçil Bediz*
16:40-16:50	**OP-248**	Morphological and Physiological Screening of Some Durum Wheat (*Triticum Durum L.*) Genotypes with Respect to Drought	*Meltem Yaşar*
17:10-17:20		Q&A	
17:30-19:00		POSTER SESSION	

03 December 2025, Wednesday

HALL B: LÜTFÜ ÜLKÜMEN

		Chair: Kazım Abak	
09:00-09:30		**Keynote Speaker** Disease Resistance in Vegetable Breeding for Challenging Climate Change	*Yuling Bai*
09:30-10:00		**Keynote Speaker** Advances in Watermelon Breeding	*Nihat Güner*
10:00-10:10		Q&A	
10:10-10:20	**OP-18**	Tomato Breeding at BATEM: Research Achievements and Future Perspectives	*Serkan Aydin*
10:20-10:30	**OP-10**	Studies on the Development of ToBRFV Resistant Varieties in Cherry, Cocktail and Special Type Tomato	*Ercan Özkaynak*
10:30-10:40	**OP-111**	QTL Mapping and Marker Development for Tomato Brown Rugose Fruit Virus Resistance in *Solanum Pimpinellifolium x Solanum lycopersicum L.*	*Yasin Topcu*
10:40-10:50	**OP-290**	Mining Wild Tomato Genomes: A Promoter-Associated Structural Variant Confers Salt Tolerance	*Shenghao Liao*
10:50-11:00		Q&A	
11:00-11:20		Tea & Coffee Break	
		Chair: Nihat Güner	
11:20-11:30	**OP-222**	Development of a dsRNA-based Biopreparate “NaNo Rugose” and Testing Spray Induced Silencing Efficacy against Tomato brown rugose fruit virus	*Bayram Çevik*
11:30-11:40	**OP-223**	Susceptibilities of GAPTAEM Tomato Breeding Lines and Genotypes to *Fusarium* spp	*Ayşin Bilgili*
11:40-11:50	**OP-12**	Identification of Candidate Genes Related to Resistance of Bacterial Canker and Wilting Disease	*Ozer Calis*
11:50-12:00	**OP-134**	Production of Tetraploid Watermelon Genotypes from Diploid Lines Using Different Colchicine and Oryzalin Aplications	*Merve Yiğit*
12:00-12:10	**OP-44**	Transcriptome Analysis of Tolerant and Susceptible Squash Lines Implicates Disrupted Chloroplasts in the Development of Silverleaf Disorder (SLD)	*Stuart James Lucas*
12:10-12:20	**OP-91**	Evaluation of Low Temperature Tolerance in Grafted Cucumber Seedlings with Developed Interspecific Squash Hybrids (*C. Maxima × C. Moschata*) Using Morphological and Biochemical Indicators	*Seda Atasoy*
12:20-12:30		Q&A	
12:30-14:00		LUNCH BREAK	

		Chair: Ertan Yıldırım	
14:00-14:30		**Keynote Speaker** Fruit Breeding in the Context of Climate Change Adaptation	*Pedro Martinez-Gomez*
14:30-14:40		Q&A	
14:40-14:50	**OP-319**	Genetic and Phenotypic Variabilities in Some Characters of Okra (*Abelmoschus Esculentus L.*) Genotypes	*Sinan Aydoğan*
14:50-15:00	**OP-28**	Morphological Characterization in Androgenetic Pure Lines in Hatay Type Hot Peppers	*Mesut Nar*
15:00-15:10	**OP-110**	In Vitro Regeneration Responses of Different Hot Pepper (*Capsicum Annuum L.*) Genotypes Through Anther Culture	*Zeynep Keskinöz*
15:10-15:20	**OP-11**	Obtaining Pure Lines Resistant to PMMoV and TSWV in Blocky Peppers Using MAS and Androgenesis Techniques	*Ebru Akyüz Çağdaş*
15:20-15:30	**OP-181**	The Development of Multiple Resistance Inbred Lines for Nematodes, Pepper Root Blight (*Phytophthora Capsici Leon*) and Potato Virus Y in Pepper (*C. Annuum L*)	*Ramazan Özalp*
15:30-15:40		Q&A	
15:40-16:00		Tea & Coffee Break	
		Chair: Hülya İlbi	
16:00-16:10	**OP-95**	Responses of Elite Capsicum chinense Lines to High Temperature Stress	*Fatih İpek*
16:10-16:20	**OP-112**	In Vitro Propagation of Newly Registered Hazelnut (*Corylus Avellana*) cultivars (Okay 28, Allahverdi, Çetiner, and Süslü)	*Merve Şekerli*
16:20-16:30	**OP-117**	Transcriptome-Based SNP Discovery in Erysiphe Corylacearum to Support Resistance Breeding in Hazelnut (*Corylus Avellana*)	*Ülkü Baykal*
16:30-16:40	**OP-69**	Overcoming Embryogenic Recalcitrance in Corylus Avellana Through Insights from Stress-Induced Somatic Embryogenesis in Muscari Armeniacum	*Ülkü Baykal*
16:40-16:50	**OP-311**	Breeding of New Cherry Varieties	*İsmail Demirtaş*
16:50-17:00	**OP-355**	Advantages And Dısadvantages Of Greenhouse Capia Cultivation In Antalya Province	*Aynur Karabulut*
17:00-17:10		Q&A	
17:30-19:00		POSTER SESSION	

03 December 2025, Wednesday — HALL: RISHI K. BEHL

09:00-09:30		**Keynote Speaker** **Common session *Hall:* Mirza GÖKGÖL or *Hall:* Lütfü ÜLKÜMEN**	
09:30-10:00		**Keynote Speaker** **Common session *Hall:* Mirza GÖKGÖL or *Hall:* Lütfü ÜLKÜMEN**	
10:00-10:10			
		Chair: *Songül Mutlu*	
10:10-10:20	**OP-38**	Developing Türkiye's First Rhizomania-Resistant Sugar Beet Varieties: Türkşeker 2023 and Türkşeker 2053	*Ekrem Gürel*
10:20-10:30	**OP-100**	Camellia Species For Oilseed Production in Türkiye	*Fatih Seyis*
10:30-10:40	**OP-299**	Konya: Epicenter for Cereal Seed Production in Türkiye	*Süleyman Yavuz İlgün*
10:40-10:50	**OP-269**	Genetic Interaction between UMAMIT28 and UMAMIT29 is Essential for Plant Iron Homeostasis	*Emre Aksoy*
10:50-11:00		Q&A	
11:00-11:20		Tea & Coffee Break	
		Chair: *Ekrem Gürel*	
11:20-11:30	**OP-83**	Investigation of the Regional Adaptation of Chickpea (*Cicer Arietinum L.*) Genotypes in the Eastern Mediterranean Region	*Dürdane Mart*
11:30-11:40	**OP-291**	The Need to Prioritize Breeding for Drought- and Climate-Resilient Crop Varieties	*Hacer Koçak*
11:40-11:50	**OP-25**	Development Of Cultivars Tolerant To Ascochyta Blight Disease İn Chickpea (*Cicer Arietinum L.*)	*Dürdane Mart*
11:50-12:00	**OP-70**	Genome-Wide Association Study Reveals Stable QTLs for Agronomic Traits in Chickpea	*Alibek Zatybekov*
12:00-12:10	**OP-307**	Effect of SA and EMS Applications on Germination and Plant Characteristics in Arda Chickpea Variety	*Mehmet Tarhan*
12:10-12:20	**OP-221**	Agro-morphological Characterisation of Wild Chickpea Genotypes in Turkey	*Eylem Tuğay Karagül*
12:20-12:30		Q&A	
12:30-14:00		LUNCH BREAK	
14:00-14:30		**Keynote Speaker** **Common session *Hall:* Mirza GÖKGÖL or *Hall:* Lütfü ÜLKÜMEN**	
		Chair: *Fatih Seyis*	
14:30-14:40	**OP-335**	Integrated Analysis of Agronomic and Molecular Marker Data for the Soybean (Glycine Max L. Merr.) Breeding Program	*Kamil Haliloglu*
14:40-14:50	**OP-287**	Development of the Soybean Breeding Program in Kazakhstan: From the Stage of Crop Diversification to the Introduction of Biotechnological Approaches and Digital Technologies	*Svetlana Didorenko*

14:50-15:00	**OP-191**	Determination of the Agricultural Performance of Soybean (*Glycine Max* L. Merr.) Genotypes Under the Ecological Conditions of Konya in Türkiye	*İrfan Özer*
15:00-15:10	**OP-36**	Mapping Endogenous Pararetrovirus Sequences in Cultivated Soybean and its Wild Ancestor	*Ahmet L. Tek*
15:10-15:20	**OP-53**	Genome-Wide Association Analysis and Genomic Prediction of Pod Dehiscence in Soybean Germplasm	*Shynar Mazkirat*
15:20-15:30	**OP-200**	From Field to Genome: Biotechnological Strategies for Developing Improved Hop and Hemp Varieties in Slovenia	*Andreja Čerenak*
15:30-15:40		Q&A	
15:40-16:00		Tea & Coffee Break	
		Chair: *Hakan Fidan*	
16:00-16:10	**OP-270**	Toward 2075: Planetary-Resilient Crop Breeding with Pan-Omics and AI-Driven Gene Editing	*Emre Aksoy*
16:10-16:20	**OP-219**	Evaluation of Morphological and Agronomic Traits of Local Alfalfa (*Medicago Sativa* L.) Ecotypes Collected From Natural Flora In Erzurum Province	*Pinar Uysal*
16:20-16:30	**OP-5**	Using Molecular Techniques in Legal Issues of Plant Breeding	*Hasan Çelen*
16:30-16:40	**OP-332**	Evaluation of Breeder's Rights, Seed Production, Sale and Transfer Issues in Terms of Public Employees and Legislation	*Kadir Camcı*
16:40-16:50	**OP-86**	Breeding of Legume Forage Crops in the Van Lake Basin and Their Contributions to Sustainable Agriculture	*Mehmet Rüştü Aksoy*
16:50-17:00	**OP-330**	Seed Aging and Approaches to Increasing Seed Longevity Under Climate Change Conditions	*Şerife Akkeçeci*
17:00-17:10	**OP-314**	Physics-Informed Neural Networks Reveal Gene Regulatory Dynamics Under Combined Environmental Stress in Arabidopsis Thaliana	*Sepideh Ghotbzadeh-Kermani*
17:10-17:20		Q&A	
17:30-19:00		POSTER SESSION	

17:30-19:00

POSTER SESSION

3 December 2025, Wednesday

17.30-18.30

Location-area: Breezes Foyer

Moderator: ***Ahmet Tamkoç & Oğuz Bilgin***

Poster Session: 1

Screen No	Abs. No	Abstract Title	*Presenter*
1	**PP-019**	The Effects of Water Stress and Mycorrhıza Inoculation on Drought Resılıence ın Some Prunus Rootstocks	*Fatma Belkıs Esimek*
1	**PP-054**	New Approaches to Improve Crop Tolerance to Abiotic Stresses	*Ertan Yildirim*
1	**PP-080**	SSR-Based diversity Analysis of *Aegilops* L. Species From Different Origins	*Firangiz Amrli*
1	**PP-297**	Modern Plant Breeding Techniques in Crop Improvement and Genetic Diversity: From Molecular Markers and Gene Editing to Artificial Intelligence	*Süleyman Karahan*
2	**PP-320**	High-Throughput Plant Phenotyping in Modern Plant Breeding: Technologies, Applications, and Future Perspectives	*Emre İlker*
2	**PP-326**	Identification of Bacterial Communities in Heavy Metal-Contaminated Soil Samples Using Nanopore-Based Metagenomic Sequencing	*Rakhim Kanat*
2	**PP-061**	Genetic diversity and effective KASP Markers for Barley Improvement in Kazakhstan	*Shyryn Almerekova*
2	**PP-170**	Spread and Development of Stem Rust Disease of Barley in South-Eastern Kazakhstan (2023–2025)	*Serik Bakirov*
3	**PP-201**	Study of Dual-purpose Barley in the Foothill Zone of Almaty Region	*Askar Zhalgasbaevich Baimuratov*
3	**PP-266**	Multi-Environment Evaluation of Feed Barley (*Hordeum Vulgare L.*) Genotypes under Dryland Conditions in Central Anatolia	*Emre Karahan*
3	**PP-334**	Assessment of Yield Performance and Phenological Characteristics of Two- and Six-Rowed Barley (*Hordeum Vulgare L.*) Genotypes under Diverse Ecological Conditions in Türkiye	*İbrahim Öztürk*
3	**PP-351**	Evaluation of Grain Yield, Disease Resistance and Micromalt Characteristics of Advanced Malting Barley Genotypes in Two Locations in Southeastern Anatolia Region	*Zeyni Dağtekin*
4	**PP-231**	Reevaluation and Breeding Objectives of Safflower (*Carthamus Tinctorius L.*) in Türkiye	*Mehmet Gencer*
4	**PP-318**	Assessment of Yield and Agronomic Traits in New Safflower Breeding Lines	*Ali Erpay*
4	**PP-243**	Developing Mutant Lines of Sunflower (*Helianthus Annuus* L.): Inducing Mutations in Polen Using a Cobalt-60 Gamma Source	*Hacı Tek*
4	**PP-273**	Development of SNP-Based Molecular Markers for Resistance to Broomrape (*Orobanche Cumana* Wallr.) Race G in Sunflower (*Helianthus Annuus L.*)	*Hasan Özgür Şığva*
5	**PP-280**	Determination of Resistance to Broomrape and Yield Performances of IMI Type Sunflower Hybrids	*Mehmet Ibrahim Yılmaz*
5	**PP-187**	The Effects of Gamma and Proton Irradiation Treatments on the Early Seedling Development of Lupine (*Lupinus Albus L.*)	*Ramazan Beyaz*
5	**PP-052**	Identification of Genotypes for the Development of Edible Dry Pea and Fodder Pea Varieties Adapted to Konya Conditions	*Ahmet Ustaoğlu*

5	**PP-162**	Use of Paintbell Fertilizer in Pepper Seed Production	*Melahat Özge Özen*
6	**PP-342**	The New Resistant Source to Powdery Mildew in Pepper: *Capsicum Chinense*	*Hulya Ilbi*
6	**PP-347**	Comparative Assessment of Drought and Salinity Stress Responses in Open-Pollinated and Hybrid Pepper (*Capsicum Annuum L.*) Varieties at Germination and Seedling Stages	*Hulya Ilbi*
6	**PP-066**	Nested Association Mapping Identifies QTLs for Yield and Adaptation in Spring Wheat of Kazakhstan	*Akerke Amalova*
6	**PP-014**	Identification of Winter Wheat Genotypes with High Androgenic Activity for the Development of an Efficient Anther Culture Protocol	*Alfiya Abekova*
7	**PP-015**	Identification of Isolates Insensitive to Strobulirin Fungicides with Quinone Outside Inhibitor in Wheat Pyrenophora Tritici-repentis Population in Kazakhstan	*Madina Kumarbayeva*
7	**PP-065**	Genome-Wide Association Study of Pre-Harvest Sprouting Resistance in a Spring Wheat Collection from Southern and Northern Kazakhstan	*Akerke Amalova*
7	**PP-073**	UAV Canopy Models and Vegetation Indices for Assessing Yield and Stress Traits in Spring Wheat Breeding	*Mara Bleidere*
7	**PP-078**	The Effect of Medium and High Nitrogen Fertilizer Rates on the Yield and Quality of Different Winter Wheat Varieties	*Linda Litke*
8	**PP-148**	Identification Of Differential Gene Expression Among Low Phytic Acid And High Grain Protein Genotypes In Winter Wheat *Triticum Aestivum L.*	*Betul Kayitmazbatir*
8	**PP-227**	Identification of New Sources of Resistance to Wheat Root Rot Caused by Bipolaris sorokiniana Using Molecular Markers	*Alma Kokhmetova*
8	**PP-229**	Genetıc Dıversıty Analysıs of Wınter Landraces and Modern Wheat Varıetıes and Some Breedıng Lınes	*Cevat Eser*
8	**PP-242**	Productivity and Yield of Drought-Resistant Winter Soft Wheat in Kazakhstan	*Bakyt Ainebekova*
9	**PP-249**	Determination of Some Agronomic and Quality Characteristics of Bread Wheat *Triticum Aestivum L.* Advanced Breeding Lines	*Resul Engin*
9	**PP-261**	Development of High Frequency Genotype-Dependent Double Haploid Production System for Bread Wheat Genotypes	*Hussein Abdullah Ahmed Ahmed*
9	**PP-302**	Thirteen-Year Evaluation of Genetic Gain in Winter Wheat Breeding under Central Anatolian Dryland Conditions at the Field Crops Central Research Institute	*Mehmet Doğan*
9	**PP-345**	Evaluation of Resistance of Spring Bread Wheat Samples to Leaf Rust and Drought With Structural Characteristics of Productivity	*Zhenis Keishilov*
10	**PP-213**	Identification of Resistant Wheat Genotypes to Bipolaris Sorokiniana under Field and Greenhouse Conditions	*Ardak Bolatbekova*
10	**PP-232**	Genetic Diversity Analysis of Walnut (*Juglans Regia L.*) Germplasm in Southern and Southeastern Kazakhstan Using Microsatellite Markers	*Makpal Nurzhuma*
10	**PP-017**	Rice Variety Development Activities at Agrobest Grup	*Halil Sürek*
10	**PP-351**	Evaluation of Grain Yield, Disease Resistance and Micromalt Characteristics of Advanced Malting Barley Genotypes in Two Locations in Southeastern Anatolia Region	*Zeyni Dağtekin*

04 December 2025, Thursday			HALL A - MİRZA GÖKGÖL
		Chair: ***Nusret Zencirci***	
09:00-09:30		**Keynote Speaker** Hybrid Potato Breeding and Seed Technology	*Paul C. Struik*
09:30-09:40		Q&A	
09:40-09:50	**OP-126**	Identification of Stem Rust Resistance Genes in Some Turkish Wheat Cultivars Using Seedling Multi-Race Tests and Molecular Markers	*Ali Kadiroğlu*
09:50-10:00	**OP-182**	Pathogen-host Interaction Determining Yellow Rust Resistance in Wheat	*Abhishek Kumar*
10:00-10:10	**OP-329**	Evaluation of Seedling Reactions to Powdery Mildew Disease in Wheat Varieties	*Merve Nur Ertaş Öz*
10:10-10:20	**OP-315**	Integrating Physics-Informed Neural Networks with Genomic and Environmental Data for Predicting Yield Performance in Crop Breeding	*Sepideh Ghotbzadeh-Kermani*
10:20-10:30	**OP-317**	Phenotyping of Some Wheat Genotypes Using a High-Throughput Seed Phenotyping Robot PhenoSeeder	*Aliye Yildirim*
10:30-10:40	**OP-324**	Developing Adaptation Traits by Transferring Earliness Genes to Mufitbey Bread Wheat Cultivar with Marker-Assisted Backcross Breeding	*Ali Cevat Sönmez*
10:40-10:50	**OP-268**	Yield Capabilities of Mutant Promising Bread Wheat Lines Created from Different Genotypes	*Oğuz Bilgin*
10:50-11:00		Q&A	
11:00-11:20		Tea & Coffee Break	
		Chair: ***Kamil Haliloglu***	
11:20-11:30	**OP-120**	Crosstalk Between Green Revolution, Vernalization, and Nitrogen Metabolism Genes in the Expression of Agronomic Traits and Grain Quality in Spring Wheat	*Boburjon Najodov*
11:30-11:40	**OP-323**	International Winter Wheat Improvement Program (IWWIP): Activities and Impact in The Region	*Beyhan Akın*
11:40-11:50	**OP-109**	Crop Diversification Options for the Aral Sea Region of Central Asia	*Ram Sharma*
11:50-12:00	**OP-103**	Agronomic Characteristics and Cold Stress Tolerances of Some Wheat Genotypes in Different Ecological Locations	*Berrin Dumlu*
12:10-12:20	**OP-121**	Identification and Characterization of Spring Wheat with 1RS.1BL and 1RS.1AL Translocations Conferring High Resistance to Powdery Mildew, Stem and Leaf Rust	*Boburjon Najodov*
12:20-12:30		Q&A	
12:30-14:00		LUNCH BREAK	

		Chair: ***Ahmet L. Tek***	
14:00-14:10	**OP-16**	History of Rice Breeding Activities and the Obtained Development in Türkiye	*Halil Sürek*
14:10-14:20	**OP-303**	Flax Breeding Efforts in the Central Anatolia Region: Genotypic Adaptation & Evaluation	*Kutay Yılmaz*
14:20-14:30	**OP-99**	Resynthesis of Rapeseed (*Brassica Napus L.)* and Its Importance For Future Brassica Breeding In Türkiye	*Fatih Seyis*
14:30-14:40	**OP-22**	Determination of Factors Affecting Plant Height for the Suitability of Lentils (*Lens culinaris M.*) for Mechanical Harvesting	*Abdulkadir Aydoğan*
14:40-14:50	**OP-153**	Pioneering Speed Breeding for Lentil in Africa and the Middle East: An Innovative Simple Optimized Rapid Generation Advancement Protocol	*Omar Idrissi*
14:50-15:00	**OP-300**	Effects of Gamma Rays and EMS Applications on Germination Characteristics and Agro-Morphological Traits of Lentil in M1 Generation	*Abdullah Efe*
15:00-15:10		Q&A	
15:10-15:30		Tea & Coffee Break	
		Chair: ***Şekip Erdal***	
15:30-15:40	**OP-37**	Mining Allelic Diversity in Maize Landraces for High Temperature Stress Tolerance: Phenotyping and GWAS Insights into Candidate Genomic Regions	*Şekip Erdal*
15:40-15:50	**OP-348**	Comparative Performance Analysis of Introduced Maize Candidate Varieties for Yield and Yield Components under Bafra Ecological Conditions	*Erkan Özata*
15:50-16:00	**OP-132**	Integrating High-Throughput Phenotyping and Genomics for Quantitative Trait Dissection and Predictive Breeding in Maize	*Alper Adak*
16:00-16:10	**OP-288**	Analysis of the Genetic Diversity and Heterotic Patterns of Waxy Maize Inbred Lines Based on SNP Markers	*Gönül Cömertpay*
16:10-16:20	**OP-122**	Chlorophyll-Based Phenotypic Screening of Maize Inbred Lines for Cold Tolerance	*Şehadet Müştak*
16:20-16:30	**OP-309**	Advances in Flax Breeding for Sustainable Food, Fiber and Regional Resilience	*Kutay Yılmaz*
16:30-16:40		Q&A	
18:00-18:30		CLOSING REMARKS in HALL Mirza GÖKGÖL	

04 December 2025, Thursday — HALL B: LÜTFÜ ÜLKÜMEN

		Chair: ***Ali Ramazan Alan***	
09:00-09:30		**Keynote Speaker** Seed Technology for Climate Resilience: Empowering Farmers and Growing Industry Prosperity	*Irfan Afzal*
09:30-09:40		Q&A	
09:40-09:50	**OP-216**	Androgenesis Induction in Cauliflower (*B. Oleracea Var. Botrytis*)	*Ali Ramazan Alan*
09:50-10:00	**OP-336**	Determination of Responses of Eggplant Genotypes to High Temperature Stress Conditions	*Edip Alas*
10:00-10:10	**OP-131**	Determination of Fusarium Wilt Resistance Levels of Different Eggplant Genetic Resources and Breeding Lines with Using Molecular Markers	*Ayse Kahraman*
10:10-10:20	**OP-156**	Exploiting the Genetic Potential of Solanum linneanum in Backcrosses with S. Melongena for Enhanced Salt Tolerance	*Esra Cebeci*
10:20-10:30	**OP-155**	Development of RT-qPCR Kits for Detection of Tobamoviruses	*Bayram Çevik*
10:30-10:40	**OP-220**	Efficient Callus Formation From Protoplasts of Eggplant Solanum Melongena L.	*Buse Özdemir Çelik*
10:40-10:50	**OP-130**	Lettuce Variety Improving Studies	*Seyfullah Binbir*
10:50-11:00		Q&A	
11:00-11:20		Tea & Coffee Break	
		Chair: ***Mustafa Erkan***	
11:20-11:30	**OP-138**	Hermaphroditism in the Pistacia Genus: A New Report from Gaziantep	*Ertugrul Ilikcioglu*
11:30-11:40	**OP-142**	Determination of the Effective Mutation Value in Pistachio	*Ertugrul Ilikcioglu*
11:40-11:50	**OP-145**	Blank Nut and Nut Splitting Variations in Siirt x Peters F1 Pistachio Population	*Saban Demir*
11:50-12:00	**OP-84**	Selection of walnut genotypes in Malatya province	*Mehmet Çalişkan*
12:00-12:10	**OP-77**	Assesment of Chestnut Blight Resistance in Indıvıduals Developed Through Interspecific Breeding In Chestnut	*Mehmet Özkul*
12:10-12:20	**OP-88**	Identification of Candidate Chestnut Rootstocks Tolerant to Phytophthora through Hybrid Breeding	*Merve Dağlı Özkul*
12:20-12:30		Q&A	
12:30-14:00		LUNCH BREAK	

		Chair: ***Hakan Aktaş***	
14:00-14:10	**OP-149**	Impacts of Climate Change on Plant Breeding Strategies and Methodology	*Gülay Beşirli*
14:10-14:20	**OP-235**	Some Morphological and Biochemical Traits of Birecik Garlic, Registered as a Local Variety	*Şehnaz Korkmaz*
14:20-14:30	**OP-125**	Cultivar Development in Güvey Feneri (*Physalis Peruviana L.*)	*Gülay Beşirli*
14:30-14:40	**OP-128**	Evaluation of Some Faba Bean (*Vicia Faba L.*) Genotypes for Fresh Consumption in Aegean Region	*Eylem Tuğay Karagül*
14:40-14:50	**OP-217**	Doubled Haploid (DH) Turkish Carrot (*Daucus Carota L.*) Lines	*Alireza Lachin*
14:50-15:00	**OP-178**	Identification of Zucchini Yellow Mosaic Virus (ZYMV) Resistant Cucumber Genotypes through Phenotypic and CAPS Marker Assisted Selection	*Volkan Gözen*
15:00-15:10		Q&A	
15:10-15:30		Tea & Coffee Break	
		Chair: ***Hamide Gübbük***	
15:30-15:40	**OP-258**	Prickly Pear (*Opuntia Ficus-Indica L.*): Adaptation to Drought Conditions, Biochemical Properties and Potential Applications	*Münevver Yıldırım*
15:40-15:50	**OP-85**	Phenological, Morphological and Molecular Characterization of Cherry Laurel Genetic Resources	*Damla Çil*
15:50-16:00	**OP-147**	Breeding Program in Türkiye for Fire Blight-Tolerant Dwarf and Semi-Dwarf Pear Rootstocks	*Melih Aydinli*
16:00-16:10	**OP-150**	Breeding European Pear Varieties Tolerant to Fire Blight Disease	*Zehranur Gülbahar*
16:10-16:20	**OP-68**	Kiwifruit Breeding Program Efforts and Characteristics of The Kahraman - 1 Cultivar Candidate	*Kemal Abdurrahim Kahraman*
16:20-16:30	**OP-349**	Breeding Studies on the Development of Late-Flowering and Late-Maturing Peach (*Prunus Persica L.*) Cultivars	*Melike Çetinbaş*
16:30-16:40		Q&A	
17:00-18:00		POSTER SESSION	
18:00-18:30		CLOSING REMARKS in HALL Lütfü ÜLKÜMEN	

04 December 2025, Thursday — HALL: RISHI K. BEHL

09:00-09:30		**Keynote Speaker** **Common session *Hall:* Mirza GÖKGÖL or *Hall:* Lütfü ÜLKÜMEN**	
09:30-09:40		Q&A	
		Chair: Gülay Beşirli	
09:40-09:50	**OP-225**	Phenotypic Diversity of Newly Registered Pomegranate Varieties in Southeastern Anatolia Region: Some Fruit Chemical Characterization	*Gokhan Akkus*
09:50-10:00	**OP-295**	Development of Superior Table and Dried Fig Cultivars through Mutation Breeding Studies	*Mesut Özen*
10:00-10:10	**OP-204**	Determination and Selection of Some Agronomic and Biochemical Characteristics of Different Turmeric (Curcuma Longa L.) Genotypes ‘ZERDESENA’	*Fatma Uysal Bayar*
10:10-10:20	**OP-21**	Unlocking Genetic Potential of Crops through Genome Editing: Implications for Food Security and Sustainability	*Sultan Habibullah Khan*
10:20-10:30	**OP-211**	New Horizons in Breeding: From Wild Ornamental Plants to Future Cultivars	*Hüsamettin Aycan Alp*
10:30-10:40	**OP-262**	Biodiversity Conservation and Sustainable Use Strategies in the Ornamental Plants Sector	*Serap Balik*
10:40-10:50	**OP-48**	The First Mutant Chrysanthemum Varieties in Türkiye	*Gülden Haspolat*
10:50-11:00		Q&A	
11:00-11:20		Tea & Coffee Break	
		Chair: *Hasan Çelik*	
11:20-11:30	**OP-265**	Evaluation of Novel Aloe Vera Genotypes for Gel Yield under Semi-Arid Regions to Identify Suitable Genotype for Commercial Cultivation	*Rajesh Kumar*
11:30-11:40	**OP-246**	Ampelography in the Genomic Era: Improvement of Traditional Grapevine Characterization Approaches	*Didem Karalar*
11:40-11:50	**OP-139**	Evaluation of Phenological Data of Some Fig (*Ficus Carica L.*) Genotypes in Gaziantep Location	*Mehmet Yılmaz*
11:50-12:00	**OP-57**	Evaluation of Susceptibility/Resistance of Hybrid Grapevine Genotypes to Powdery Mildew	*Abdurrahim Bozkurt*
12:00-12:10	**OP-97**	Development of Apricot Cultivars Resistant to Sharka Disease Potyvirus Plumpoxi through Hybridization Breeding	*Derya Taşdemir Karaoğlan*
12:10-12:20	**OP-195**	Improvement of Low Temperature Tolerant Mexican Lime Varieties by Induced Mutation Breeding	*Zeynep Eryilmaz*
12:20-12:30		Q&A	
12:30-14:00		LUNCH BREAK	

		Chair: Gönül Cömertpay	
14:00-14:10	**OP-194**	Public Sweet Corn Breeding Studies of Turkey	*Mehmet Cavit Sezer*
14:10-14:20	**OP-350**	Influence of Siderate Plants on Phenological Development Phases, Crop Elements And Yield of Wheat	*Murad Vəkil Oğlu Kərimzadə*
14:30-14:40	**OP-192**	Climate-Driven Shifts in Plant Pathogen Dynamics and the Disease-Resistant Breeding	*Kubilay Kurtulus Baştaş*
14:40-14:50	**OP-33**	“Biotic stress responses of some dry bean ({Phaseolus vulgaris L.}) lines and cultivars to root-knot nematodes ({Meloidogyne incognita race 1, race 2 and Meloidogyne javanica}”	*Tolga Gürkan*
14:50-15:00	**OP-352**	Genetic Mechanisms of Resistance to Viral Diseases in Capsicum Species and the Significance of Molecular Markers Linked to These Mechanisms in Breeding Research	*Hasan Can*
15:00-15:10		Q&A	
17:00-18:00		POSTER SESSION	
18:00-18:30		CLOSING REMARKS in HALL Mirza GÖKGÖL	

17:00-18:00

POSTER SESSION

04 December 2025, Thursday 17:00-18.00

Location-area: Breezes Foyer

Moderator: ***Kenan Yalvaç & Ertan Yıldırım***

Poster Session: 2

Screen No	Abs. No	Abstract Title	Presenter
1	**PP-047**	In Vitro Regeneration Studies in Native Tomato Genotypes	*Sibel Bahadir*
1	**PP-092**	Identification of Hybrids Suitable for Cluster Harvesting in Coctail Tomato Breeding	*Merve Söker*
1	**PP-118**	Importance of Seed Producibility in Determinate Tomato	*Ali Burak Arabalı*
1	**PP-165**	Strategies to Prevent Fruit Dropping Tomato Hybrides	*Somayeh Yousefnejad*
2	**PP-166**	Determination of Hypocotyl Characteristics and Graft Compatibility of Qualified Interspecific Hybrid Tomato (*Solanum lycopersicum* × *Solanum Pimpinellifolium*) Rootstock Candidates	*Şeyma Yücel*
2	**PP-196**	Determination of Fruit Quality Parameters of Some Processing Tomato Varieties and Competitor Hybrids	*Merve Yiğit*
2	**PP-064**	Genetic Diversity and Marker-Trait Associations in Bread Wheat Cultivars of Kazakhstan Using KASP Markers	*Saule Abugalieva*
2	**PP-180**	Distribution and Development of Apple Fungal Diseases in the Almaty Region	*Kanat Galymbek*
3	**PP-188**	Identified of the Morphologic, Physiologic and Agronomic Traits of Common Vetch Hybrid Lines with Non-shattering Pods	*Seçil Candaş Özkan*
3	**PP-049**	Studies on Developing CGMMV (Cucumber Green Mottle Mosaic Virus) Resistant Varieties in Different Cucumber (Cucumis Sativus) Types	*Osman Yüksel*
3	**PP-161**	Effects of Parental Lines on Seed Quality in Cucumber Hybrids	*Buse İleri*
3	**PP-163**	Effect Of Salt Stress On Seedlıng Growth Parameters In Cucumber (Prelımınary Evaluatıon)	*melahat özge özen*
4	**PP-183**	Genetic Evaluation of Cucumber (*Cucumis Sativus L.*) Accessions from Kazakhstan Using SSR Markers	*Moldir Yermagambetova*
4	**PP-346**	Pomological Characterization and Quality Assessment of Persimmon (*Diospyros Kaki L.*) Genotypes from the Black Sea Region of Türkiye	*Aysun Akman*
4	**PP-045**	Applications of Chromosome Doubling in Haploid Squashes and Pumpkins (*Cucurbita spp.*)	*Emre İpek*
4	**PP-160**	Phenotypic Profiling of Anchote (*Coccinia Abyssinica* (Lam.) Cogn.) Accessions Through Agro-Morphological and Physiological Markers	*Dejene Bekele Dibaba*
5	**PP-254**	The Effect of Different Plant Growth Regulators on in vitro Double-Haploid Plant Production in Cucurbitaceae	*Seren Sargın*
5	**PP-331**	Dihapoidization Studies on Citron Watermelon (*Citrullus Lanataus* var. Citroides) for Becoming a Rootstock for Watermelon	*Hafize Koç*
5	**PP-094**	Seed Traits and Root Architecture of Developed Citron Watermelon (*Citrus Lanatus var. Citroides*) Lines Used as Rootstocks	*Melike Balcı Gevez*
5	**PP-190**	Development of Red Lentil Genotypes Tolerant To Imı Group Herbicides	*Havva Vildan Kilinç*

6	**PP-306**	Analysis of Tulip Pollen Quality for Parent Selection in Breeding Programs	*Yasemin İzgi*
6	**PP-055**	SSR-based Analysis of Genetic Diversity in Maize (*Zea Mays L.*) Accessions from Kazakhstan	*Moldir Yermagambetova*
6	**PP-060**	Obtaining Haploid Seeds in Sweet Corn Zea mays saccharata by Haploid Inducer Lines	*Ahmet Ustaoğlu*
6	**PP-081**	Donor-Specific Factors Drive Doubled Haploid Efficiency in Temperate Maize Breeding	*Zoran Čamdžija*
7	**PP-082**	Selection of Maize Hybrids Adapted to Mediterranean Area Using GGE Biplot Analysis	*Jovan Pavlov*
7	**PP-164**	Development of a Management Model (DOSUYM) Based on Unmanned Aerial Vehicles and Satellite Systems for Variable Rate Irrigation in Mobile Drip Irrigation Systems in Silage Corn	*Hasan Akay*
7	**PP-207**	Comprehensive Stability Analysis of Candidate Grain Maize Hybrids for Yield and Quality Traits Across Diverse Environments in Türkiye	*Fatih Ateş*
7	**PP-209**	Our Silage Corn Variety Candidate: ADA 20S44	*Ahmet Duman*
8	**PP-253**	Determination of the Effects of Different Pollination Conditions on Seed Formation and Fruit Quality in Some Pomegranate Genotypes	*Nesrin Karataş*
8	**PP-205**	Genetic Diversity of Moroccan Chickpea Landraces for "Orobanche" Tolerance	*Chafika Houasli*
8	**PP-215**	Development of High Yielding Chickpea Varieties Suitable for the Central Anatolia Region	*Elif Atasayar*
8	**PP-159**	Marker Assisted Backcross Breeding For Fusarium Wilt (*Fusarium Oxyporum* Schlecht. F. Sp. Melongenae) In Eggplant	*Derya Samur*
9	**PP-197**	Development of New Genotypes from Cara Cara Navel Orange (*Citrus Sinensis* (L.) Osbeck) (TUR020-438) Using Mutation Breeding-I	*Zeynep Eryılmaz*
9	**PP-172**	Development of a Soybean Variety for Organic Farming in Kazakhstan	*Sholpan Orazovna Bastaubayeva*
9	**PP-193**	Soybean as the Crop of the Future: Breeding for Multifaceted Resilience Amidst Climate Change and Emerging Pathogens	*Kubilay Kurtulus Bastas*
9	**PP-279**	Exploring Genetic Relationships Among Trifolium Populations Using ddRAD Sequencing	*Utku Tunalı*
10	**PP-124**	Yield Performances of Selected Triticale Lines and Varieties in Türkiye's Different Climatic Environments	*Emel Özer*
10	**PP-189**	Assessment of the Some Agromorphological Characters of Cold Tolerant Forage Pea Lines	*Recep Kırbaş*
10	**PP-251**	Determination of Some Agronomic and Quality Traits of Forage Pea Pisum sativum L. Advanced Breeding Lines in Bandirma	*Resul Engin*
10	**PP-328**	Forage Production under Climate Change: Drought- and Heat-Tolerant Alternatives for Mediterranean Coastal Countries	*Behçet Kır*
10	**PP-308**	Oat Genotypes Used in Forage and Food Production	*Ferhat Demirhan*
10	**PP-129**	Development of Novel Eggplant Hybrids with Diverse Color and Pattern Traits Through Parental Crosses	*Ramazan Iğdırlı*
1	**PP-140**	Changes in Quality Parameters of Sweet Corn Materials Harvested at Fresh and Dry Stages	*Mehmet Cavit Sezer*

ORAL PRESENTATION

[Abstract:0174]

Moving Winter Wheat Frontier Beyond 50° North: Global Genetic Resources for Winter Survival and Productivity

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The climate change in Eurasian continent is expressed in warming and extension of the growing season. Winter wheat has expanding tendency in Russia and replacing lower-yielding spring wheat. However, it is still underdeveloped in Northern Kazakhstan though producers are interested in this crop. The study objective was a screening of a large global collection of winter wheat germplasm in Northern Kazakhstan, identification of superior genotypes and identification of the molecular markers contributing to adaptation and agronomic traits. The initial set of germplasm included over 380 modern genotypes primarily from the regions with cold winter. The material was planted in 2023-2024 and 2024-2025 seasons at four sites in Northern Kazakhstan and Siberia from 51 to 57^{o}N and at one site in the South near Almaty at 43^{o}N. Average air temperature in January was -15-17oC. Winter survival varied from 0 (total loss) to 100% - perfect survival. As a result we selected 180 best genotypes for further evaluation and genomic screening. In addition, international collection of 96 winter bread wheat accessions from Russia, Germany, Finland, Kazakhstan, Bulgaria, Türkiye, USA, and TCI was phenotyped in Omsk and genotyped to evaluate the effects of KASP markers.The data on winter survival demonstrated very good performance of US cultivars from Nebraska, Kansas, Colorado and Montana, Russian varieties from Kransodar and Rostov regions and some material from Türkiye and TCI. Material originated from relatively warm regions like Southern Russia, Bulgaria and Hungary was competitive with local winter wheat germplasm. The main stable QTLs associated with yield-related traits during two growing seasons in Omsk were: ippb_ta_1147 (1A), ippb_ta_107 (4A), ippb_ta_239 (5D), and ippb_ta_283 (6A). The outperforming genotypes in Omsk were: Zhiva, Zolushka, Doneko, Line K 18918, Line 2293; CO13D1299, KS13DH0030-32, Gondvana//HBK0935-29-15/KS90W077-2-2/VBF0589-1. The highest yielding material in Kazakhstan with good winter survival was Etnos, Vestnitsa, OmskSAU-5 (Russia), SG-U 7067/5/TEMU39.76/CHAT//…/ALD/4/KK8514.1(TR-Edirne), KS14DH0012-12, Breakthrough, KS-14DH0024-28, KS100028K-11, NE17544-2, KS13DH0007-20 (USA) can be used as parents and variety candidates. Funding: This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan Grant No. AP26100299 «Winter-hardy and highly productive varieties of winter wheat for Northern Kazakhstan through the use of the world's genetic resources, genomics and plant phenomics».

Keywords: winter wheat, breeding, productivity, frost tolerance, molecular markers

[Abstract:0013]

Allelic Variation of *Vrn* Loci in Advanced Barley Breeding Lines for Predicting the Adaptability of Future Cultivars

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Barley (*Hordeum vulgare* L.) is one of the most important cereal crops in the world. Due to its high ecological plasticity, it is cultivated under a wide range of climatic conditions. Vernalization genes play a key role in the geographical adaptation of barley, the development of agronomically important traits, and the realization of yield potential. Studying the distribution patterns and allelic diversity of vernalization loci is of fundamental importance for breeding programs aimed at improving this crop, especially under changing climatic conditions. When developing new varieties for sharply continental climates, it is critical that breeders have information about the combinations of Vrn gene alleles present in working collections and breeding material. This knowledge is essential for predicting the adaptability of future cultivars. In this study, 160 breeding lines of spring and winter barley from the control nursery (generations F7–F8) and the competitive variety testing nursery (generations F9–F10) of the Kazakh Research Institute of Agriculture and Plant Growing were analyzed. To identify allelic variations in the Vrn-H1, Vrn-H2, and Vrn-H3 loci, five allele-specific markers were used. For the Vrn-H1 locus, two markers revealed 56 accessions with the recessive winter allele and 104 accessions with the dominant spring allele. Two winter haplotypes were identified: 5C (344 bp) and 1A (830 bp). The 5C haplotype was found in six breeding lines: 66/08-11, 8/16-11, 1-8, 11/16-2, 22/18-5, and 11-16-5. Most accessions with the winter allele Vrn-H1 (89%) carried the 1A haplotype. For the Vrn-H2 locus, analysis using two markers showed that 33 lines carried the recessive spring allele, and 127 lines had the dominant winter allele. For the Vrn-H3 locus, CAPS marker analysis identified the dominant allele in only one line — 27/83-8 × Turan 2. All other lines carried the recessive allele. Based on the data obtained, the allelic formulas of all 160 barley breeding lines were determined: 29 lines had the formula RDR (winter type), 26 lines had the formula RRR (facultative type), 105 lines had various combinations such as DRR, DDR, DRD, and others. The genotypic analysis significantly enhanced the understanding of allelic diversity in vernalization loci within the studied barley breeding material. The obtained data serve as a valuable tool for predicting adaptability and further improving barley cultivars under the conditions of a changing climate. This research has been funded by Grant AP19678544.

Keywords: barley, breeding line, molecular markers, vernalization, Vrn-genes

[Abstract:0059]

Genome-Wide Association Study Reveals QTLs and Candidate Genes for Fungal Diseases Resistance in Barley in Kazakhstan

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Barley (*Hordeum vulgare* L.) is one of the most widely cultivated cereal crops globally, serving as a staple for animal feed, malting, and human consumption. However, its productivity is constrained by fungal diseases, which remain a major challenge in stress-prone environments such as Kazakhstan. Among them, stem rust (SR), caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*), and powdery mildew (PM), caused by *Blumeria graminis* f. sp. *hordei* (*Bgh*), represent particularly damaging pathogens. This study aimed to dissect the genetic basis of resistance to both SR and PM using diverse barley collections, multi-environment phenotyping, and genome-wide association studies (GWAS). A total of 273 two-row spring barley accessions from the USA, Kazakhstan, Europe, Africa, and the Middle East were evaluated for SR resistance in two field trials in 2024 and 2025. Artificial inoculation was conducted at the Research Institute of Biological Safety Problems (RIBSP), while natural infection was assessed at the Kazakh Research Institute of Agriculture and Plant Growing (KRIAPG). In parallel, 406 accessions from the USA, Kazakhstan, Europe, and Africa were tested for PM resistance across three growing seasons (2020–2022) in southeastern Kazakhstan. Genotyping was performed using Illumina SNP arrays: 50K for the SR panel, yielding 31,834 high-quality SNPs, and 9K for the PM panel. GWAS was conducted using five models (GLM, MLM, MLMM, BLINK, FarmCPU), and significant QTLs were defined based on LD thresholds and FDR correction. Field evaluations revealed a wide range of responses. For SR, disease scores ranged from 0 (immune) to 9 (highly susceptible), with an average severity of 4.6. Most accessions were moderately resistant (119) or moderately susceptible (125), while 20 were resistant and 8 fully susceptible. For PM, seven QTLs were identified on chromosomes 4H, 5H, and 7H, with haplotype analysis revealing three haplotypes associated with complete resistance and one linked to high susceptibility. Across both studies, 151 marker-trait associations for SR were consolidated into 10 stable QTLs on chromosomes 1H, 3H, 5H, and 7H. Candidate gene analysis identified 41 highly expressed genes, with enriched functions in cell wall biogenesis, enzymatic activity, and stress response. These findings reveal the genetic basis of fungal disease resistance in barley and provide molecular tools for breeding in Kazakhstan and beyond. The research was funded by the Committee of Science of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Project No AP23485118).

Keywords: Barley, SNP, *Puccinia graminis* f. sp. *tritici*, *Blumeria graminis* f. sp. *hordei*, gene expression, resistance

[Abstract:0123]

Selection of High Temperature Stress Tolerant Wheat Genotypes Using Stress Indices

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High temperature stress is a primary constraint to maximal wheat yield, and this is the case for most cultivated crops. Predictions with high confidence indicate that the continuing reliance on fossil fuels and inorganic fertilizers will further increase global temperatures, adding to the challenges to wheat productivity and its ability to meet the food demands of a growing population. This study was conducted to determine the tolerance of bread wheat genotypes to high temperature stress within the wheat breeding program of the Maize Research Institute (MRI). A total of 15 genotypes, including 12 genotypes and 3 control varieties, were sown in field conditions during the first week of November (normal sowing, NS) and the first week of January (late sowing, LS). Field trials carried out in the 2020–21 and 2021–22 growing seasons revealed a yield loss of 21.9% (779.2–608.6 kg/da) due to late sowing. The relationships between various heat indices calculated based on NS and LS yield values and LS yield performance were investigated. LS yield values showed a negative and significant correlation with the stress susceptibility index (SSI) (r=-0.645*), while significant positive correlations were found with the stress tolerance index (STI) (r=+0.645*), relative heat index (RHI) (r=+0.645*), heat resistance index (HRI) (r=+0.894**), geometric mean productivity (GMP) (r=+0.8004*), tolerance index (TI) (r=+0.645*), and high temperature tolerance index (HTTI) (r=+0.9517**). According to HRI, RHI, STI, and SSI results, the Polathan variety and genotype no. 6 were the most tolerant genotypes, whereas HTTI results indicated that genotypes no. 4 and no. 6 were the most tolerant. Results from RHI, STI, and SSI showed that genotypes no. 1 and no. 13 were the most susceptible; however, according to HTTI and HRI, genotypes no. 1 and no. 2 are the most susceptible genotypes. Because of their positive and highly significant relationships with yield values, HTTI and HRI were identified as the most suitable stress indices for selecting heat-tolerant genotypes.

Keywords: high temperature stress, stress indices, wheat

[Abstract:0341]

Agro-Physiological Parameters in Two and Six-Rowed Barley (*Hordeum vulgare* L.) Genotypes under Rainfed Conditions

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Crop yield in barley is a complex trait that depends on a large number of environmental, morphological, and physiological characteristics. The experiment was carried out under rainfed conditions in the Trakia region in Edirne (Türkiye) during the 2019-2020 cycles. The experiment was set up with 25 genotypes in a randomized complete block design (RCBD) with four replications. Grain yield (GY), Seedling fresh and dry weight, root dry and fresh weight, number of tillers, days of heading (DH), plant height (PH), Normalized difference vegetative index (NDVI), and canopy temperature (CT) were investigated. Analysis of variance (ANOVA) revealed significant differences among genotypes for all parameters ($P < 0.01$). The highest grain yield was determined in G10 with 11.1 t/ha and G25 with 10.3 t/ha. Seedling fresh and dry weight was measured in 10 seedlings. The average seedling fresh weight was 31.8 g, with maximum weights of 49.5 and 48.6 g, respectively, in genotypes 2 and 8. The average root fresh weight was 7.62 g, with maximum weights of 12.48 and 11.28 g in genotypes G2 and G8, respectively. The average root dry weight was 0.85 g, with maximum weights of 1.27 and 1.22 g in genotypes G2 and G8, respectively. While the average number of tillers was 3.10, the highest number of tillers was observed in genotype G2, at 5.0. The normalized difference vegetative index (NDVI) was measured at four different plant development stages (Z25, Z41, Z55, and Z83) in the genotypes. The highest NDVI was measured at G18 in the Z25 and Z41 periods, and at G21 and G18 in the Z55 period.

Keywords: Barley, genotypes, grain yield, agro-physiological parameters

[Abstract:0171]

Coleoptile Length of Turkish Winter Barley *Hordeum vulgare* L. Cultivars

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Coleoptile length (CL) plays a crucial role in seedling establishment and determining optimal sowing depth in cereals, particularly under environmental stress conditions. This study investigated CL in 51 Turkish winter barley *Hordeum vulgare* L. cultivars to identify long-coleoptile sources for breeding programs and to guide optimal sowing depths. The experiment was carried out in the greenhouse of the Central Research Institute for Field Crops during the 2025 growing season, and coleoptile length variation was studied in eight-day-old seedlings on a sand-based growing medium. Statistically significant genotypic variation in CL was observed ($P<0.05$), ranging from 48.6 mm in Kıral-97 to 85.2 mm in Cacabey cultivars. A substantial proportion of the evaluated cultivars exhibited CL within the 60 to 80 mm range. Nine cultivars exhibited long CL, exceeding 80 mm, indicating their potential as genetic resources for enhanced early vigor and improved drought tolerance. Conversely, short-coleoptile cultivars, with CL less than 60 mm, necessitate careful sowing depth management to mitigate emergence failure. The cultivars with the longest coleoptiles were the tall cultivars developed for dry conditions, while the cultivars with the shortest coleoptiles were the short cultivars developed for the high-yielding areas. However, a direct correlation between plant height and coleoptile length was not consistently observed across all cultivars. A significant and positive correlation was established between CL and thousand-grain weight ($r=0.6033$) and grain length ($r=0.5931$). Furthermore, the study demonstrated that the effect of genotype (85.7%) on CL was more pronounced than that of grain size, underscoring the strong genetic control of this important agronomic trait. Further field trials with varied sowing depths and emergence rates are needed to refine and validate these findings.

Keywords: Barley, cultivars, coleoptile length, grain size, variation

[Abstract:0058]

Barley Breeding Program in TRNC

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Barley (*Hordeum vulgare* L. subsp. *vulgare*) is the most important crop grown under rainfed conditions in Cyprus Its contribution to the agricultural economy and to other economic sectors of the island is considerable. The type used is winter-sown spring barley and its main use is for livestock feed either as hay or grain. Barley cultivated areas are affected by drought in different periods, and this has negative effects on barley production from year to year. In fact, in some years they cannot meet their seed needs. In 2013 Cyprus initiated efforts to develop new barley varieties. This task, under the aus- pices of the Agricultural Research Institute (TAE) of Repuplic of North Cyprus, was enhanced by initiatinga dynamic breeding programme in 2013. Under the weather conditions prevailing in Mediterranean rainfed areas, both the amount and distribution of rainfall is unpredictable and selection of new lines is considerably affected by the significant genotype X environment interaction. The programme with long term studies carried out under the dryland conditions of Cyprus, developed the appropriate methology and selection criteria for selecting stable genotypes with high performance in agronomic characters under multiple environments. Initially, the barley breeding programme at the TAE placed more emphasis on developing high yielding cultivars, through the crossing programme and introduced materials, through this the cultivars Beşparmak, Reşatbey were recorded. The program continues to find new productive and persistently resistant barley varieties.

Keywords: Barley, crossing, field crops, variety

[Abstract:0233]

Crops Breeding and Seed Production at Lomtagora Seed Company, Georgia

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Cereal Production in Georgia: In 2024, cereals dominated Georgia's annual crop landscape, occupying nearly two-thirds of all cultivated area. Maize (corn) is the leading crop, covering 71,200 hectares (36.4% of total annual crop area), followed by wheat at 54,000 hectares (27.6%), and barley at 24,100 hectares (12.3%). Despite considerable wheat cultivation area, Georgia heavily relies on wheat imports to meet domestic demand, as local production falls short of achieving self-sufficiency. The main cropping system for wheat involves double-cropping with soybeans or maize, with yields averaging nearly 3 t/ha. Georgian agriculture is characterized by small individual farms, with an average size of 0.96 hectares, and nearly 100% of agricultural output produced by the individual sector. Lomtagora Agricultural Enterprise: Established in 1995, Lomtagora operates 500 hectares of arable land in the Marneuli district of Kvemo Kartli region, East Georgia, at 430 meters above sea level. The farm's subtropical climate zone features brown, saline soils. As one of Georgia's leading wheat seed suppliers, Lomtagora functions as a multi-purpose agricultural enterprise specializing in wheat and corn seed breeding and field crop production. Breeding Achievements and Varieties: Lomtagora has developed and registered several high-yielding wheat varieties in collaboration with international agricultural research centers. Notable cultivars include Lomtagora 123 (FRTL/Nemura-9823) and Lomtagora 109 (Shark/F4105W.21-9809), achieving yields of 7.5 tonnes per hectare under optimal conditions and 4.7 tonnes per hectare on average. The intensive variety Lomtagora 126 has demonstrated exceptional performance, yielding 11 tonnes per hectare at the company's test site—significantly exceeding indigenous varieties that typically yield 2-3 tonnes per hectare. These varieties are recommended for cultivation across all wheat-growing agro-climatic zones of Georgia. The company has also developed multiple corn hybrids, including Lomtagora 1, 2, and 3 (yellow kernel varieties) for commercial distribution. International Collaboration: Lomtagora maintains strategic partnerships with the International Maize and Wheat Improvement Center (CIMMYT). The farm serves as a focal point in Georgia for testing and adopting winter wheat germplasm supplied by the International Winter Wheat Improvement Program, a joint initiative of the Turkish government, CIMMYT, and ICARDA. This collaboration has enabled the introduction of advanced agricultural technologies and the development of varieties adapted to Georgian conditions, contributing to the country's agricultural self-sufficiency goals. Infrastructure and Technology: Lomtagora has implemented modern post-harvest infrastructure, including TUDORS granaries equipped with contemporary storage technology capable of holding at least 2,000 tons of grain. The company offers farmers wheat seeds treated with advanced German technology, and all recently registered cereals comply with European standards for grain cleaning and sorting. Beyond new variety development, Lomtagora maintains important programs for preserving and improving local varieties of both wheat and corn, producing elite and first reproduction seeds for distribution to Georgian farmers. Information - https://lomtagora.com/. Contact: info@lomtagora.com

Keywords: winter wheat, seed production, maize hybrids

[Abstract:0034]

Genomic Prediction and Association Mapping of Yield and Quality Traits in Silage Hybrid Maize

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Enhancing the production and silage quality in hybrid maize is essential for livestock systems that rely on fodder. This study uses a varied panel of 225 maize hybrids assessed in field experiment in Türkiye to investigate the genetic basis of 13 agronomic and silage-related variables, such as plant height, fodder yield, and nutritional quality. Genotyping was conducted via the DArTseq platform, resulting in 4,525 high-quality SNP markers. Genome-wide association studies (GWAS) identified 51 significant loci, highlighting key associations with traits including ear height, dry forage yield, and crude protein content. Multiple loci were identified in proximity to established candidate genes, providing insights into genomic regions specific to traits. Five multi-kernel genomic prediction models were assessed to capture both additive and non-additive genetic effects, integrating components of additive, dominance, and epistatic variance. Additive effects explained a significant proportion of phenotypic variance in agronomic traits, reaching up to 54%. In contrast, quality traits such as protein and starch exhibited considerable contributions from dominance and interaction effects. Genomic prediction accuracies were highest for traits such as plant and ear height ($r \approx 0.80$), while they were lower and exhibited greater variability for nutritional traits. Principal component analysis indicated significant genetic diversity among parental inbreds and their hybrids, with hybrids exhibiting heterozygosity levels ranging from 32% to 40%. The integration of GWAS and multi-kernel prediction yielded new insights into the genetic architecture of silage traits in hybrids and demonstrated the significance of modeling non-additive effects for enhancing genomic-assisted selection. These findings contribute to the advancement of high-performing maize hybrids specifically designed for silage production.

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Keywords: maize, silage, genomic. GWAS, prediction

[Abstract:0321]

Plant Growth Speed, Photosynthetically Active Radiation Utilization and Association of them with Grain Yield in Winter Wheat in Multilocation

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Global warming has significantly influenced plant phenology, including winter wheat, affecting developmental stages from germination to maturity. Winters are becoming milder, and spring precipitation is shifting toward later growth stages of winter wheat across the northern hemisphere, particularly in West and Central Asia. Vernalization (Vrn), photoperiod sensitivity (Ppd), and intrinsic earliness genes play an important role in the environmental adaptation of winter wheat. It has been observed that genotypes exhibiting rapid early spring growth and ground coverage, thereby minimizing soil evaporation, demonstrate better adaptation to winter wheat-growing regions. Although early-maturing genotypes can escape terminal drought stress, they may not benefit from precipitation occurring during later growth stages. The objectives of this study were to assess growth speed (GS), ground coverage, and the efficiency of Photosynthetically Active Radiation (PAR) utilization during the growth of winter wheat. A total of 825 entries, including five check varieties, were evaluated in Eskişehir, Ankara, and İzmir, Türkiye. The germplasm originated from more than 80 crosses made among diverse germplasm pools; all genotypes were in the F6 generation. The experimental design was augmented design, with plots consisting of 1 m × 1 row in İzmir and Ankara, and 4 m × 6 rows in Eskişehir. The check varieties (Gerek, Karahan, Sönmez, Taner, and Bayraktar) were sequentially repeated as every 20th entry in the trial. The traits measured were Days to Heading (DH) and Plant Height (PH), measured at weekly intervals across all locations. In Eskişehir, Normalized Difference Vegetation Index (NDVI) and chlorophyll content with Chlorophyl Meter were also measured at the same time with PH measurements. Daily meteorological data, along with solar radiation and PAR, were determined at each site. Significant differences were observed among genotypes for all measured traits. As expected, plant development was earliest in İzmir. Growth speed varied across environments: initial growth was most rapid in Izmir, slowest in Ankara, and intermediate in Eskişehir. In Ankara, growth speed (GS) followed a bell-shaped pattern, beginning slowly, increasing during the mid-growing stage, and declining toward maturity. Although initial GS was high in both Eskişehir and Izmir, it showed a steady decline in İzmir, while in Eskişehir it fluctuated in response to changing weather conditions. Significant genotype × environment interactions were observed for all traits. Genotypes demonstrated differential responses in PAR utilization across growth stages and environments, suggesting that yield potential could be enhanced by exploiting the most efficient performers under specific environmental conditions.

Keywords: Winter Wheat, Growth Speed, NDVI, PAR

[Abstract:0175]

Kazakh-Siberian Network for Spring Wheat Improvement – 25 Years: Genotype-Environment Interactions, Bread vs Durum Wheat, Genes Effects and Yield Champions

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The Kazakh-Siberian Network for the Improvement of Spring Wheat (KASIB) was established in 2000 to facilitate germplasm exchange while studying promising material. More than 15 breeding and scientific institutions across Kazakhstan and Russia participate as network members. The KASIB spring bread wheat trial is planted at 12-15 sites and comprises 45-50 entries, including checks for different maturity groups. A similar spring durum wheat nursery is sown at 6-8 sites and includes 25-30 entries. Since 2000, more than 500 bread wheat genotypes and over 250 durum wheat entries have been studied. Twenty years of data on adaptation traits (plant height and vegetation period) and productivity enabled analysis of genotype-environment interactions and determination of similarities between KASIB sites. In breeding programs, priority for general adaptation is important while considering specific requirements of individual agro-ecological zones. Durum and bread wheat trials at four sites (Aktobe, Barnaul, Karabalyk, and Omsk) were used for comparison of both crops regarding their response to cultivation practices and weather conditions. Analysis of 78 KASIB experiments showed that average yields of both crops were equal, but durum wheat proved more responsive to improved cultivation conditions. Evaluation of KASIB material for resistance to brown and stem rust during epiphytotic years determined genetic diversity and efficiency of Sr and Lr resistance genes. For analyzing genes effects on agronomic traits, a core KASIB set for bread wheat was established, reflecting the genetic diversity of the entire material. Phenotyping was conducted at several KASIB sites over three years. Consequently, gene molecular markers with stable effects were identified under different test conditions for use in practical breeding. Ionomics studies of the KASIB core set demonstrated genotype-environment interaction for macro- and micro-element concentration and identified genes controlling their quantity in grain. In each KASIB nursery, genotypes with highest yields at all testing sites are selected based on two-year study results. These accessions are typically included in further studies and crosses by KASIB participants and often become successful commercial varieties released in several regions. A survey of KASIB network participants showed that many promising varieties were identified using KASIB nursery data, confirming the practical value of this breeding collaboration.

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Keywords: Spring wheat, breeding, productivity, grain quality, disease resistance

[Abstract:0236]

The Performance of Wheat Varieties Breeding by TAGEM from the Perspective of Farmers in Şanlıurfa Province

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Plant breeding is recognized today as one of the fundamental factors contributing to the increase in crop production. In Turkey, it is well known that significant varieties have been developed as a result of long-term breeding efforts. However, the number of studies investigating the level of use of these varieties, farmers' opinions about existing ones, and the market's expectations for future varieties remains limited. The main objective of this research is to reveal the current status of the use of wheat varieties bred by TAGEM in Şanlıurfa Province, to determine farmers' opinions and expectations regarding these varieties, and to evaluate their agricultural performance. The number and regional distribution of farmers who prefer wheat varieties developed by TAGEM are not clearly known. The primary data for this study were obtained through face-to-face surveys conducted between 2022 and 2024 with farmers who cultivate wheat varieties bred by TAGEM in districts and villages of Şanlıurfa Province, where wheat production is intensive. Using the "snowball sampling method," a total of 300 farmers who grow TAGEM wheat varieties were surveyed. The data obtained from the surveys were analyzed using descriptive statistics, cross-tabulations, and Chi-square tests through the SPSS software, and the results were interpreted with the help of tables and graphs. According to the research findings, the number of TAGEM wheat varieties preferred by farmers in Şanlıurfa was 12 in 2022, 13 in 2023, and 12 in 2024. The average ages of these varieties were determined as 16.9 years in 2022, 15.9 years in 2023, and 17.45 years in 2024, respectively. It was found that, as of 2022, wheat varieties registered in İzmir, Adana, Diyarbakır, and Şanlıurfa provinces were cultivated in the region. In 2023, varieties registered in Sakarya and Antalya were also included in production. In 2024, once again, varieties registered in İzmir, Adana, Diyarbakır, and Şanlıurfa were observed to be cultivated. Among them, Adana 99 and Ceyhan 99 were the most widely preferred by local farmers. In addition, it was observed that newly developed bread and durum wheat varieties produced by research institutes affiliated with TAGEM were also adopted by farmers. The most influential mechanism in the initial decision to use TAGEM wheat varieties was found to be local social networks such as neighboring farmers in the same village, seed and pesticide dealers, TİGEM (General Directorate of Agricultural Enterprises), and Agricultural Credit Cooperatives (TKK), which provide both agricultural inputs and loans. Among these, TKK was determined to have a particularly strong influence on seed recommendations. Seed and pesticide dealers were also identified as important dissemination channels, maintaining close contact with farmers and providing advice on both crop protection and wheat seed selection. Overall, the study found that farmers were generally satisfied with the TAGEM wheat varieties they used during the 2022–2024 production seasons, were willing to recommend them to other farmers, and intended to continue using the same varieties in the following years.

Keywords: Wheat, Plant Breeding, Snowball Sampling, Adaptation, TAGEM

[Abstract:0340]

Climate Change: Yield and Quality in Bread Wheat and Environmental Effects

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Climate change determines the adaptation of bread wheat genotypes to environmental conditions. The amount and distribution of rainfall and temperature in different plant development periods determine the production of cereals. The experiments were conducted in the Trakia region, Türkiye, across two environments: Edirne (E1) and Lüleburgaz (E2) during the 2024-2025 growing cycles. The experiment tested 25 advanced bread wheat genotypes in a randomised complete block design with four replications. In the experiment, five local varieties —Aldane, Yüksel, Gelibolu, Saban, and Glosa —were evaluated based on yield and quality parameters. Data on grain yield, plant height, days of heading, test weight, thousand-grain weight, protein ratio, wet gluten, gluten index, sedimentation, and grain hardness were evaluated. The variance analysis revealed significant differences between cultivars and environments for all parameters examined (P<0.01). There was a significant difference in grain yield between locations. There was a significant difference in grain yield between locations. The average grain yield in the E1 location was 8.3 kg ha-1, and in the E2 location, it was 4.8 kg ha-1. There was a 42.6% difference between locations due to environmental factors. Plant height varied significantly among locations, with E1 at 98.0 cm and E2 at 84.4 cm. There were also significant differences between locations in gluten, gluten index, and sedimentation values. The difference between the locations was caused by low rainfall and high temperature during the heading and grain-filling period. High temperature during the grain filling period negatively affected protein quality in cultivars.

Keywords: Bread wheat, cultivar, yield, quality parameters, environmental effect

[Abstract:0020]

Yield Traits Analysis in Wild Wheat (*Triticum turgidum* ssp *dicoccoides*) Populations under Different Environments

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Wheat (*Triticum* spp.) is a globally significant staple crop that sustains a large proportion of the world's population. However, its productivity is increasingly limited by abiotic stresses, especially heat and drought, which are intensified by climate change. In arid and semi-arid regions like Jordan, rising temperatures and water scarcity create significant challenges for wheat production and food security. The limited genetic diversity of modern wheat cultivars restricts their ability to adapt, highlighting the need to explore wild wheat relatives for breeding climate-resilient varieties. Wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*), the direct ancestor of modern durum wheat, possesses significant genetic variation that can be leveraged to improve stress tolerance and yield stability. However, its responses to varying environmental conditions have not been thoroughly studied. This study aimed to assess the agronomic performance and stress adaptation potential of wild emmer wheat accessions collected from diverse regions in Jordan. A total of 20 wheat accessions, including 14 *T. turgidum* ssp. *dicoccoides* populations and six *T. turgidum* ssp. *durum* cultivars were evaluated in two contrasting environments: Maru (representing a heat-stressed, low-rainfall site) and Ajloun (a cooler, higher-rainfall site) during the 2020/2021 growing season. The experiment followed an incomplete block design, and key phenotypic traits—including days to heading (DH), total tiller number per plant (TN), and spike number per plant (SP)—were recorded. Broad-sense heritability (H^2) was estimated for these traits, and correlation analyses were performed to determine trait relationships under varying environmental conditions. Significant genetic variation was observed among accessions for yield-related traits ($p < 0.001$), with notable differences in stress response between environments. Wild emmer wheat exhibited delayed heading under heat stress, with a significant negative correlation between heading date and spike number (-0.68) in Maru. Broad-sense heritability estimates ranged from 0.53 to 0.62, indicating a moderate to high genetic contribution to trait expression. Accessions Wild No. 1 and Wild No. 7 exhibited superior tiller and spike production across both locations, highlighting their potential as valuable genetic resources for wheat breeding programs. These findings emphasize the importance of conserving wild wheat germplasm for breeding climate-resilient wheat. Future studies integrating molecular approaches such as genome-wide association studies (GWAS) and genomic selection are recommended to accelerate the identification of key stress-resilient traits and facilitate the development of climate-adaptive wheat cultivars.

Keywords: Wild wheat, *Triticum*, Yield trials, Populations, Environment

[Abstract:0185]

Enhancement of Carbon sequestration in wheat (*Triticum asestivum*) through genetic options for higher biomass and grain yield under climate change

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Wheat (*Triticum asestivum*) is an important cereal crop for global food security. It provides dietary calories need of about 20% world population. Wheat is adaptable under varied climatic conditions and is being grown in temperate to semi-arid climatic conditions overall the continents. Gain yield in wheat is influenced by genetic makeup of a variety, prevailing production environment, agronomic management, physiological efficiency to utilize atmospheric CO2, sunlight, water and nutrients for photosynthesis and C-sequestration. Large number of wheat varieties exhibit genetic variability for C-sequestration, plant biomass and grain yield. In order to produce high gain yielding varieties, both biomass and harvest index have to be increased through C-sequestration. This is possible through conventional plant breeding by recombining favorable genes in a common background through crossing program. Crosses between spring and winter wheat will generate facultative wheat that exhibit high biomass due to delayed senescence and its stay green characters. Facultative wheat can thrive under varied climatic conditions, may it be drought, flood and high temperature, mainly due to high C-sequestration which lead to high biomass and massive root system. Similarly developmental mutants have been developed in spring wheat with delayed senescence characters. A wheat mutant named as WH147M has been developed in the background of spring wheat variety WH147. This mutant has about 300% higher biomass and massive root system. Likewise, modern biotechnological tools, like genomics and transgenics can be applied for higher C-sequestration through changes in stomatal aperture, CO2 capture, chlorophyll content and its activity and photosynthesis under shifting climatic conditions. As the world population is increasing, we have to produce more food for global food security. Likewise atmospheric CO2 is rising due to industrialization and fossil fuels based energy sources. In such a situation C-sequestration by main cereal crops like wheat offers a potent solution to increase gain yield and reduce CO2 levels and mitigate climate change.

Keywords: Wheat, dietary, C-sequestration, plant biomass, grain yield, plant breeding.

[Abstract:0259]

Breeding Wheat for Tolerance to Combined Stress Cause by Draught in High Temperature

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Wheat yield is determined by genotype of variety, its production environment, genotype into environmental interaction and biotic and abiotic stresses. Among abiotic stresses heat and draught influence wheat yield adversely approximately 5.5% and 12% due to heat and drought stress, respectively. Heat and draught stresses are mutually exclusive and happen simultaneously. Therefore, it is important to breed wheat for tolerance to combined heat and draught stresses. In this context, the first requirement is to identify locations in wheat growing regions to screen germplasm for individual and combined stress. We conducted experiments over contrasting wheat varieties differing in their response to heat and draught stress under control conditions. We examined the grain filling patterns and found that in susceptible wheat varieties the grains remain grossly unfilled due to poor starch accumulation. To understand the grain filling patterns, we conducted enzyme assays for AGPAs. AGPAs activities was higher in 60 D chromosome substitution line possessing higher grain weight. Whereas it was low in substitution line with poor grain weight. We also conducted experiments on chlorophyll fluorescence and found that photosynthesis was much more efficient in wheat varieties with higher test weights. A developmental mutant WH147M exhibited delayed senescence, remained green in under draught and heat stress condition produces high biomass and grain yield but with poor test weight. This could be because of poor assimilation of photosynthates in gain shrink or poor translocation from leaves to grains. We identified heat shock proteins and DNA markers for heat tolerance. We developed a coherent breeding strategy to develop heat and drought tolerant genotype using genomic and Omics approaches. Wheat yield has to increase by 4% annually for world food security whereas under climate change regime recurrent draughts and heat shocks are more frequent than ever before. This calls for joint efforts by plant breeders, biotechnologists, plant physiologists to develop wheat varieties tolerant to abiotic stresses. This overview examines breeding approaches for infusing draught and heat tolerance in wheat.

Keywords: Wheat, heat stress, drought, tolerance, breeding strategy, genomics

[Abstract:0260]

Wheat Improvement Strategies for Lodging Resistance to Minimise Yield Losses in Inclement Weather

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Wheat production worldwide is encountering climate change caused challenges. A major challenge is the problem of lodging which reduces wheat grain yield and diminishes its quality. Lodging may cause up to 20-80% yield loss depending on prevalent weather conditions. High wind speed along with flooded condition of soil, low soil shear strength, poor root anchorage, reduced diameter of root soil cone, low stem cellulose and lignin content, poor stem strength and flexibility are main causes for higher incidence of lodging in wheat as the plant morphological characters like internode length, culm thickness, stem wall strength and root system, the biochemical constituents including lignin and cellulose contribute to mechanical strength and flexibility of the culm play a major role in determining lodging resistance. Moreover, several quantitative trait loci (QTL) including *Rht* genes controlling plant height in wheat have been ascribed to lodging resistance/susceptibility in wheat. Selection of wheat genotypes resilient to climate change caused inclement weather conditions leading to lodging is discussed. In this review, we discuss the genetic, agronomic, and environmental factors affecting lodging in wheat. In addition to reduction of yield, lodging reduces photosynthesis and interrupts the assimilates partitioning affecting grain quality and productivity Therefore, an integrated breeding strategy is presented to address the problem of lodging and breeding wheat genotypes with increased resistance to lodging. The breeding strategy presents a holistic approach combining both conventional and biotechnological tools along with the incorporation of bio-stimulants to develop lodging resistant wheat.

Keywords: Lodging resistant wheat, Bio stimulants, PAL, Lignin, Cellulose, *Rht* genes.

[Abstract:0263]

Tolerance to Low Temperature Stress in the Late Development Stage of Bread Wheat Genotypes

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The study was conducted in the experimental field of the Department of Field Crops, Faculty of Agriculture, Namık Kemal University. In the cold treatment, wheat plants were subjected to low temperature applications of -2°C, -4°C and -6°C during the stem elongation stage (Zadoks 31st stage) using modified methods developed by Tischner et al. (1997) and Fowler et al. (1996) in cold chambers of Hayrabolu Flour Industry and Trade Inc. The study used materials from 11 wheat genotypes commonly planted in the region. The effects of low temperature stress applied during the dormancy period (Zadoks 31st period) were determined on the 11 genotypes included in the study. The study, which employed three different cold treatments during dormancy (Zadoks 31st period), determined that the low temperature treatment, genotypes, and temperature x genotype interactions were statistically significant at the 0.01 level. The responses of eleven bread wheat genotypes to different dormancy stresses (-2, -4, and -6°C) were variable. The highest low temperature stress in plants was observed in the -6°C treatment, followed by the -4°C treatment. At temperatures as low as -2°C, plants suffered approximately 58% less damage. When the genotypes tested were examined, NKU Zirve, one of the earliest varieties in the region, was most affected at temperatures between -6 and -4°C. Flado was most affected by the cold stress at -6°C, significantly at -4°C, and was unaffected by cold stress at -2°C. Starlord and Primus were equally affected by all three low temperatures. The data indicate that the sensitivity of bread wheat genotypes to low temperatures varies depending on the wheat genotype and the degree of low temperature.

Keywords: wheat, low temperature, tolerans, genotype, cold

[Abstract:0248]

Morphological and Physiological Screening of Some Durum Wheat (*Triticum Durum* L.) Genotypes with Respect to Drought

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Drought is a major constraint for durum wheat (*Triticum durum* L.) production, particularly in semi-arid regions such as Türkiye, where climate change exacerbates water scarcity. Developing drought-resilient cultivars is essential to sustain yield and food security. This study evaluated 108 local durum wheat genotypes and four widely cultivated varieties under controlled greenhouse conditions at the Bahri Dağdaş International Agricultural Research Institute, using two irrigation regimes representing 100% and 50% of field capacity. Morphological and physiological traits, including biomass, grain yield, harvest index, plant height, upper internode length, flag leaf chlorophyll content, canopy temperature, digital ground coverage, and flag leaf area index, were assessed. Analysis of variance revealed significant genotypic variation ($p < 0.01$) for most traits, highlighting the rich genetic diversity within local germplasm. Water limitation reduced biomass by 30.2%, yield by 31.2%, plant height by 30.0%, digital ground coverage by 30.9%, and flag leaf area index by 31.3%. GGE biplot and correlation analyses indicated strong positive relationships among vegetative growth traits, whereas canopy temperature was negatively correlated with growth and yield traits, suggesting that genotypes maintaining cooler canopies exhibit enhanced drought tolerance. Cluster analysis identified distinct groups, including drought-tolerant candidates closely aligned with known commercial cultivars. These findings underscore the potential of local durum wheat germplasm as a valuable resource for breeding programs targeting drought-prone environments and provide a foundation for integrating morpho-physiological screening with molecular approaches to accelerate the development of resilient cultivars.

Keyword: Drought, Durum wheat, Irrigation Regimes, Morphological, Physiological,

[Abstract:0018]

Tomato Breeding at BATEM: Research Achievements and Future Perspectives

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Tomato (*Solanum lycopersicum* L.) is one of the most economically and nutritionally important vegetable crops worldwide, and breeding efforts are critical to sustain productivity under changing climatic conditions and emerging pathogen pressures. Bati Akdeniz Agricultural Research Institute (BATEM) has played a leading role in tomato breeding in Türkiye for several decades. This study provides a comprehensive overview of BATEM’s tomato breeding program by evaluating its past achievements, current research activities, and future perspectives. Historically, BATEM has contributed to the development of open-pollinated and hybrid tomato varieties adapted to the Mediterranean climate, focusing on yield, fruit quality, and disease resistance. Current breeding studies have expanded to address major abiotic stresses such as salinity and low temperature, alongside viral diseases that pose serious threats to tomato production. In particular, resistance breeding against Tomato brown rugose fruit virus (ToBRFV), as well as other economically important viruses, has become a central focus of ongoing programs. Molecular tools including RNA isolation, gene expression analysis, and marker-assisted selection are increasingly applied to accelerate the breeding process and strengthen resistance breeding. Experimental data from recent trials demonstrate significant variation among genotypes in both stress tolerance and virus resistance, offering valuable insights for parent selection and trait improvement. Looking ahead, BATEM’s tomato breeding strategy emphasizes the integration of genomics, bioinformatics, and predictive modeling to develop resilient varieties combining abiotic stress tolerance and virus resistance. Climate change adaptation, sustainable production, and genetic resource utilization remain central to these efforts, positioning BATEM as a key contributor to national and international breeding strategies.

Keywords: Tomato breeding, abiotic stress, ToBRFV, molecular tools, climate change, BATEM

[Abstract:0010]

Studies on the Development of ToBRFV Resistant Varieties in Cherry, Cocktail and Special Type Tomato

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Tomato Brown Rugose Fruit Virus (ToBRFV) was first seen in Jordan and Israel. In Türkiye, ToBRFV was detected in leaf and fruit samples in 2019 (Fidan et al., 2019). This virus, which is in the Tobamovirus genus, has spread widely after its emergence in greenhouse tomato production areas. ToBRFV has gained great importance worldwide in a short time and is among the most dangerous viruses that are requested to be tested in exports. ToBRFV virus has reached a stage where it will prevent tomato seed trade, especially in European countries. The main hosts of ToBRFV are tomatoes and peppers. ToBRFV is spread by mechanical means to host plants, infected seeds and fruits and spreads over long distances. In the study, inoculation was carried out with ToBRFV isolate at the seedling stage and the developing seedlings were planted in the greenhouse. The growth and development of the plants were ensured under normal cultivation conditions in the greenhouse. The study was carried out in greenhouse conditions for two years and four seasons. In the research, one hundred varieties with superior agronomic, earliness and quality characteristics were tested over four seasons. Evaluations and phenotypic and genotyping observations were made on a scale of 1-5 at 4 different times in each season (plant, leaf, green and ripe fruit observations). As a result of the two-year study, 16 tomato varieties of different types were selected for domestic and foreign markets as varieties with high ToBRFV tolerance in terms of plant and fruit characteristics, and some of them were introduced to the market as commercial varieties.

Keywords: *Solanum lycopersicum*, Tolerance, ToBRFV, Variety

[Abstract:0111]

QTL Mapping and Marker Development for Tomato Brown Rugose Fruit Virus Resistance in *Solanum pimpinellifolium* x *Solanum lycopersicum* L.

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Tomato (*Solanum lycopersicum* L.), which represents 44% of Turkey's 980 million USD fresh vegetable exports, is a strategic crop for both production and seed trade. Tomato Brown Rugose Fruit Virus (ToBRFV), first reported in Israel in 2014 and Jordan in 2015, has rapidly spread worldwide and rendered classical resistance genes such as Tm-1, Tm-2, and Tm-22 ineffective. Despite more than a decade since its emergence, no fully resistant cultivars have been developed, and most commercial varieties in Turkey remain susceptible or only tolerant. To discover novel resistance, approximately 300 accessions from 15 Solanum species were screened, leading to the identification of four resistant/tolerant *S. pimpinellifolium* lines and two susceptible *S. lycopersicum* accessions. Genome-wide association analysis revealed several loci potentially harboring novel resistance alleles. Resistant × susceptible crosses were generated, and all of these F_1 hybrids displayed typical ToBRFV symptoms, supporting recessive inheritance. Among identified resistance sources, one resistant *S. pimpinellifolium* accession originating from Peru (Ct values undetectable in RT-qPCR) showed an outstanding resistance. Next, it was crossed with two susceptible *S. lycopersicum* accessions, and two F_2 mapping populations of 384 plants each were developed. Plants were inoculated with the Antalya isolate MT107885 in September 2025 and transplanted to greenhouse conditions. Phenotyping will be conducted once susceptible controls express symptoms, using RT-qPCR and a 0–5 disease severity scale. Resistant and susceptible bulks will then undergo whole-genome resequencing (Illumina NextSeq), and the QTL-seq pipeline will be applied to identify resistance loci specific to *S. pimpinellifolium*. In the putative QTL regions, SNP markers will be developed and entire F2 population will be genotyped using these markers. Furthermore, in our previous study, we revealed a candidate region on chromosome 8 derived from *S. habrochaites*, and a TaqMan probe was developed based on SNP polymorphisms detected between resistant and susceptible F_2 plants. Additional loci on chromosomes 2 and 11 are currently under investigation to assess their contribution, including potential interactions with Tm-1. The integration of bulked-segregant sequencing, GWAS, and QTL mapping will provide new insights into the genetic architecture of ToBRFV resistance and facilitate the development of molecular markers for resistance breeding in tomato.

Keywords: Tobrfv, Tbrfv, QTL mapping, QTL-seq, Whole genome sequencing

[Abstract:0290]

Mining Wild Tomato Genomes: A Promoter-Associated Structural Variant Confers Salt Tolerance

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Soil salinization poses a significant threat to global agricultural sustainability, affecting over 954 million hectares of land worldwide and rendering 25-30% of agriculture areas unproductive. This environmental issue leads to substantial crop yield reductions, diminished farmer incomes, and potential food shortages, particularly in arid and semi-arid regions amid escalating climate change pressures. It is especially limiting for tomato (*Solanum lycopersicum* L.) production, a key crop vulnerable to osmotic stress and ion toxicity. Domestication and selective breeding of modern tomato cultivars have imposed a severe genetic erosion, prioritizing high yield and fruit uniformity at the expense of stress tolerance alleles. In contrast, wild tomato relatives, including Solanum pimpinellifolium and Solanum pennellii, harbor substantial genetic diversity and adaptive traits essential for tolerance. This study systematically identified and characterized superior salt-tolerance alleles lost during domestication to inform innovative breeding strategies. We conducted pan-genome sequencing on a diverse panel of 240 wild tomato accessions and quantified key phenotypic responses under salt stress conditions. Through a genome-wide association study (GWAS), we pinpointed a candidate gene, HKT8, with a structural variation (SV) in its promoter region exhibiting strong linkage to salt stress phenotypic variation across the population. The gene's function and the SV's regulatory impact were validated using molecular assays and genetic transformation experiments. Furthermore, chromatin immunoprecipitation (ChIP) assays localized a key transcription factor, MYB43, revealing its upstream regulatory role and direct association with the SV through integrated transcriptomic and epigenetic analyses. Our results reveal a critical genetic locus predominantly absent in elite cultivars, offering a targeted resource for precision breeding. By elucidating the MYB43-HKT8 regulatory module, this work not only facilitates the precise introgression of the wild allele into cultivated backgrounds but also provides insights into broader genetic mechanisms of stress adaptation, paving the way for advanced genome editing tools like CRISPR-Cas to engineer multi-trait tolerance in tomatoes and other crops, ultimately enhancing sustainable agriculture and global food security in salinity-prone environments.

Keywords: Tomato breeding, salt tolerance, pan-genome sequencing, GWAS, structural variant

[Abstract:0222]

Development of a dsRNA-based Biopreparate “NaNo Rugose” and Testing Spray Induced Silencing Efficacy against Tomato brown rugose fruit virus

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Tomato brown rugose fruit virus (ToBRFV) is a recently emerged Tobamovirus causing serious problem in tomato and pepper in many regions of the world including Turkey. ToBRFV is able to break the Tm-2^2 and L resistance genes provided resistance to other Tobamoviruses in tomato and pepper, respectively. Although resistance to ToBRFV was identified in some genetic resources, the mechanism of the resistance is not determined yet and has not been integrated popular commercial cultivars yet. The disease is currently managed by sanitation and avoidance as well as partial resistance in some cultivars. Therefore, development and use of other methods for management ToBRFV is necessary. In this study, a biopreparate called “NaNoRugose” was developed using clay nanoparticles with dsRNA targeting ToBRFV genome by dsRNA-mediated and spray induced RNA interference (RNAi) as an alternative control strategy. First small MgAl-layer double hydroxide (LDH) clay nanoparticles (NP) with average size of 50 nm were chemically synthesize and prepared. Then, two conserved regions in the ToBRFV genome were selected and a 500 and 600 bp dsRNAs targeting these regions were synthesized by in vitro transcription. A biopraparate called “NaNoRugose” was developed by combining in vitro synthesized dsRNAs targeting ToBRFV genome with the LDH clay NPs. Finally, the efficacy of “NaNoRugose” biyopreparat was tested against ToBRFV infection by spraying onto leaves of seedlings of a commercial tomato cultivar. Seedlings of the tomato cultivar were first sprayed with the LDH NP, “NaNoRugose” or water, certain times after spraying, all seedlings were mechanically inoculated with ToBRFV. The efficacy of the “NaNoRugose” was evaluated for symptoms by disease severity index, viral RNA load by RT-qPCR and virus particles load by ELISA. The results of growth chamber and greenhouse experiments showed that “NaNoRugose” significantly reduced viral RNA and virus particle load in the leaf. However, with the applied dose and frequency “NaNoRugose” could not completely control ToBRFV infection or virus replication. Therefore, further experiments are needed to determine the efficacy of the “NaNoRugose” for controlling ToBRFV.

Keywords: Tomato, RNAi, ToBRFV, LDH Nanosheets, Clay Nanoparticles, Biopreparate

[Abstract:0223]

Susceptibilities of GAPTAEM Tomato Breeding Lines and Genotypes to *Fusarium* spp

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Ensuring sufficient nutrition for the growing global population requires developing plant varieties resistant to biotic and abiotic stress factors. This study aimed to identify tomato genotypes resistant to key soil-borne pathogens and abiotic stresses such as drought, salinity, and high temperature. As breeding material, 20 local tomato genotypes and 35 pure breeding lines from the GAP Agricultural Research Institute (GAPTAEM) Vegetable Breeding Gene Pool, previously tested for abiotic stress tolerance, were used. Additionally, 18 tomato varieties from the Ankara and İzmir Seed Gene Banks, representing genotypes close to those cultivated in the Southeastern Anatolia Region, were included for evaluation. Over a three-year period, advanced local tomato lines and genotypes were screened for resistance to root and crown rot and wilt diseases caused by *Fusarium solani*, *Fusarium oxysporum* f. sp. radicis-lycopersici (FORL), and *F. oxysporum* f. sp. lycopersici (FOL). The experiments were conducted by comparing resistant and susceptible control varieties under both greenhouse and open-field conditions. Fungal pathogens were collected through surveys from open-field tomato production sites in Şanlıurfa province. Following isolation, the pathogens were morphologically identified and biochemically characterized using the MALDI-TOF MS technique. Pathogenicity tests confirmed the virulence of the isolates before their use in resistance screening. For the FORL pathogen, separate experiments were carried out using isolates obtained from greenhouse and field environments. In the case of *Fusarium solani*, two isolates, one from tomato and one from pepper plants, were used in distinct trials. The results revealed that the isolate obtained from pepper was also capable of infecting tomato plants, indicating possible cross-infection potential among solanaceous crops. As a result of these evaluations, six pure tomato breeding lines and genotypes from GAPTAEM were identified as “resistant” to the tested soil-borne pathogens, while the remaining genotypes were classified as “susceptible.” Among the accessions obtained from seed gene banks, two genotypes showed “moderate susceptibility,” and one was identified as the “most susceptible” variety. The findings of this study provide valuable material for future tomato breeding programs aimed at developing disease-resistant cultivars adapted to the challenging climatic and soil conditions of Southeastern Anatolia. The results are expected to contribute significantly to ongoing R&D efforts by GAPTAEM, TAGEM research institutes, and seed companies engaged in breeding new tomato varieties. Ultimately, the project supports national goals for sustainable agricultural production and food security by enhancing the resilience and productivity of local tomato varieties.

Keywords: Tomato, *Fusarium* spp., Breeding Lines, Genotype, Susceptibility, GAPTAEM

[Abstract:0012]

Identification of Candidate Genes Related to Resistance of Bacterial Canker and Wilting Disease

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Bacterial canker of tomato, caused by the Gram-positive bacterium *Clavibacter michiganensis* subsp. *michiganensis* (Cmm), represents one of the most devastating diseases affecting global tomato production. This seed-borne pathogen has caused catastrophic epidemics in major tomato-growing regions worldwide. A prominent control is Cmm-resistant cultivars for tomato production is a suitable way for sustainable and eco-friendly method. For genetic control of the Cmm, a chemical mutagenized susceptible EBR3 tomato lines generated resistant M3-9 and M3-15 plants. Aims of the study are to identify resistance gene(s) controlling Cmm pathogen, to understand resistant gene(s) mediated mechanisms and to examine differences in gene expression between resistant mutants and susceptible original EBR3 plants. High-throughput sequencing was performed on an Illumina HiSeq platform for these three genotypes. After the filtering process, each individual FASTQ file was aligned to the *Solanum lycopersicum* reference genome "SLM_r2.1" with using Bowtie2 software. They were properly mapped with the values of >99.8 for all genotypes. Genotype specific individual binary sequence alignment file format (BAM) files were subjected to variant calling using freebayes. All variants from these genotypes were merged. Potential gene regions were monitored with the use Integrated Genome Browser and compared with disease scores obtained from EBR3, M3-9, and M3-15 plants. A total of 17 potential regions related to resistance to canker and wilting disease were identified.

Keywords: Tomato, Resistance, Bacterial canker and wilting

[Abstract:0134]

Production of Tetraploid Watermelon Genotypes from Diploid Lines Using Different Colchicine and Oryzalin Aplications

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Watermelon is an economic crop, which is widely cultivated around the world. The diploid watermelon ($2n = 2\times = 22$) is more common in nature, while the polyploids make the tetraploid watermelon ($4n = 4\times = 44$) possible. The triploid watermelon is a hybrid of diploid and tetraploid watermelon, and the triploid watermelon is famous for the high quality of seedless fruit. Obtaining tetraploid watermelon lines from diploid lines necessitates practical, effective and sustainable genome doubling methods. For this purpose, three methods with varied doses and treatment durations for tetraploid induction in watermelon five genotypes were investigated: (1) soaking of seedling roots; 0.05% and 0.5% colchicine for 16 hours, (2) application to the sprout growing points of seedlings; 0.5% colchicine or 300 ppm oryzalin and (3) soaking of germinated seeds; 0.4% colchicine solution. The morphological and stomatal features of the plants also examined in the study, and the flow cytometry results were compared with these findings. Plants with double genomes varied across different genotypes and methods, highlighting genotype-dependent responses. The most successful genotype responded at a rate of 3.2%, the most successful method responded at a rate of 1.92%. It's recommended to use different methods for genome doubling in future studies.

Keywords: watermelon, polyploidy, tetraploid, colchicine, oryzalin

[Abstract:0044]

Transcriptome Analysis of Tolerant and Susceptible Squash Lines Implicates Disrupted Chloroplasts in the Development of Silverleaf Disorder (SLD)

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Squash silverleaf disorder (SLD) is a physiological disease of crops in the Cucurbitaceae family that is induced by phloem feeding of silverleaf whitefly nymphs (*Bemisia tabaci* MEAM1), with increased severity under drought conditions. Summer squash (*Cucurbita pepo* L.) cultivated in Türkiye is frequently affected by SLD during the summer and autumn, producing silvered leaves and pale, mushy fruits that are not suitable for market. SLD causes significant economic losses worldwide but previous efforts to breed resistant squash varieties have not been successful. Therefore in this project, we aimed to generate novel summer squash lines with increased tolerance to SLD and identify the molecular basis of this trait. A biparental population of zucchini/summer squash was developed to the F3 generation by single seed descent from SLD-sensitive and tolerant breeding lines, and the progeny were genotyped and screened for SLD symptoms under natural whitefly pressure in the field. From this population, 4 groups of 5-6 lines showing contrasting symptoms were selected, and 5 seeds from each line (including the parental lines) were grown in greenhouse conditions. At the 3 leaf stage, 10-12 adult silverleaf whitefly were applied to the 3rd leaf of each plant for 24 hours, after which all insects were removed and the numbers of eggs laid were counted. Plants were monitored every 7 days for development of symptoms and by measuring chlorophyll levels of the infested leaves. At 6 weeks after infestation, all plants were scored for SLD symptoms and leaf samples were taken from 3 representative plants from each line for RNA isolation and transcriptome analysis. The severity of SLD symptoms observed on the plants under the controlled infestation was consistent with observations of the same lines in the field. Strikingly, although much more extensive leaf silvering was observed on sensitive plants, chlorophyll absorbance was not significantly different between the sensitive and tolerant groups. The transcriptome analysis revealed that SLD-tolerant plants upregulated expression of chaperones involved in stabilizing chloroplast photosystem proteins. In contrast, highly susceptible plants showed increased expression of genes responsible for chloroplast biosynthesis and oxidative stress responses, suggesting increased breakdown and turnover of chloroplasts in these plants. These findings indicate that SLD tolerance correlates with the prevention of chloroplast damage following whitefly infestation, whereas susceptible plants expend considerable energy trying to repair and replace their degraded photosystems.

Keywords: Silverleaf Disorder, *Cucurbita pepo* L., Silverleaf Whitefly, Plant-Pest Interactions, Molecular Breeding

[Abstract:0091]

Evaluation of Low Temperature Tolerance in Grafted Cucumber Seedlings with Developed Interspecific Squash Hybrids (*C. maxima* × *C. moschata*) Using Morphological and Biochemical Indicators

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The use of grafted seedlings enhances water and nutrient uptake under abiotic stress conditions, such as high or low temperature and drought, by promoting a stronger root system. Additionally, grafting improves tolerance to diseases and pests, thereby positively affecting both yield and quality. *C. moschata* × *C. moschata* and *C. maxima* × *C. moschata* hybrids are currently the most commonly used rootstocks in cucumber (*Cucumis sativus* L.) seedling production. As part of an interspecific rootstock breeding program supported by TÜBİTAK TEYDEB and conducted in collaboration between the private sector and universities, 11 local interspecific hybrid rootstock candidates with low-temperature tolerance have been developed. In this study, the cucumber cultivar PTK40 F1 was used as the scion, while non-grafted PTK40 seedlings served as the control group. In addition, the performance of the promising rootstock candidates was compared with that of commercial rootstocks such as Shintoza F1, Nun 9075 F1, Cobalt F1, Cremna F1, and Maxicrom F1. Grafted and non-grafted seedlings were first acclimated at 15 °C/10 °C (day/night) conditions after reaching the 3-4 true leaf stage following grafting. Subsequently, they were subjected to low-temperature treatment at 5 °C (day/night) for a duration of two days. Plant damage was evaluated visually using a scale ranging from 0 (no damage) to 5 (dead plant) according to the low-temperature test. The results of the study showed that the scion/rootstock combinations PTK40/KB17, PTK40/KB19, PTK40/KB20, and PTK40/KB22 exhibited high tolerance to low temperatures, as indicated by their low damage scores (0-1). Biochemical analyses revealed that under low-temperature stress, malondialdehyde (MDA) and hydrogen peroxide (H_2O_2) levels increased, whereas proline accumulation served as a protective mechanism. The highest proline levels were observed in PTK40/KB17 (13.66 µmol/g) and PTK40/KB22 (13.39 µmol/g), whereas the lowest MDA values were recorded in PTK40/KB20 (6.51 nmol/g) and PTK40/KB22 (6.52 nmol/g). Based on these findings, PTK40 F1 scion/rootstock combinations identified as tolerant to low temperatures will be further evaluated for plant growth and yield performance under cold-season greenhouse conditions in the highland areas of Elmalı, Antalya, in future studies.

Keywords: *cucurbita* rootstock, grafted cucumber, low-temperature stress, MDA, proline, tolerance

[Abstract:0319]

Genetic and Phenotypic Variabilities in Some Characters of Okra (*Abelmoschus esculentus* L.) Genotypes

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Okra (*Abelmoschus esculentus* L.), originated from Tropical Africa, is an important vegetable crop with an average global yield as 104,8 $t \cdot ha^{-1}$ in the world. In Türkiye, production and average yield are 31,4 tonnes and 51,2 $t \cdot ha^{-1}$, respectively. In this study, 11 morphological traits were evaluated in a total of 10 okra genotypes consisting of 6 local and 4 commercial varieties. The experiment was designed in randomized complete block design (RCBD) with three replicates in the field conditions at Alata Horticultural Research Institute in 2025. Phenotypic (σ^2p), genotypic (σ^2g) variances and broad-sense heritability was calculated based on the analysis of variance (ANOVA) table. Analysis of variance (ANOVA) illustrates that plant height, stem diameter, carpel number, fruit length, fruit number, and 100-seed weight exhibited highly significant differences among genotypes ($p<0.01$), while fruit weight showed significant differences ($p<0.05$). In contrast, the number of branches per plant, fruit width, and seed number per fruit did not differ significantly among genotypes. Principal component analysis (PCA) indicated that one genotype (G4) stood out in terms of both yield and fruit number, whereas all local varieties were prominent for fruit width and carpel number. Results also showed that a positive and significant correlation was observed between yield and fruit number, whereas a significant negative correlation was found between fruit number per plant and fruit weight. No significant correlations were detected between the number of branches per plant and any other traits. Based on the estimated narrow-sense heritability values for yield-related traits, a high heritability (0.92) was obtained for the number of fruits per plant, whereas yield exhibited a moderately high heritability (0.77). Among the other evaluated traits, plant height, stem diameter, fruit length, and number of carpels showed high heritability estimates. In contrast, 100-seed weight and fruit weight exhibited moderately high heritability, while fruit width, number of branches per plant, and number of seeds per fruit displayed low heritability values. In conclusion, since yield related traits were estimated moderate to high heritability, these characteristics can effectively be utilized in okra (Abelmoschus esculentus L.) breeding programs.

Keywords: Okra, breeding, genetic parameters, variability, heritability

[Abstract:0028]

Morphological Characterization in Androgenetic Pure Lines in Hatay Type Hot Peppers

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Hatay pepper or Samandağ pepper can be consumed both fresh when green or red and can be dried for industrial use. 100% homozygous pure lines were obtained from AG Seed company's gene pool containing Hatay pepper genetic material to which the TSWV disease resistance gene (Tsw) was transferred using MAS and androgenesis techniques. It was aimed to obtain dendrogram's by morphological characterization of 90 Hatay pepper pure lines. During characterization, fruit type in pure lines; fruit tip shape, fruit stalk shape, fruit weight, length and width, fruit flesh thickness, dried fruit flesh weight, fresh yield, dry yield, number of fruits per plant, fruit weight, fruit width, fruit length and fruit flesh thickness values were measured. Plant characteristics such as leaf width and length, pre-ripening fruit color, stem shape, fruit cross-section were also observed in leaves taken from the plants during the harvest period. For the characterization of the lines; 23 morphological characters were taken into consideration. After the observation and recording process for 23 different characteristics, tables were created and also yield values were determined at harvest time. Clustering analyses were performed using the NTSYS computer package program and a dendrogram was obtained. The level of genetic relationship between androgenic pepper pure lines in the gene pool was determined by UPGMA grouping of the similarity matrix obtained as a result of the analysis of the data belonging to morphological characteristics. 90 pure lines formed 2 main groups. Of these two main groups, group A was divided into 2 subgroups and these subgroups were again divided into 4 subgroups as A1.1, A1.2, A2.1, A2.2. Group B also had 2 subgroups and was divided into 2 subgroups as B1.1, B1.2. According to the results of this analysis, 25% of the 90 genotypes examined were included in group B, while 75% were included in group A. Based on the relationship distances in the dendrogram, as well as the SHU pungency values, TSW resistance, and particularly the fruit shape, color, and yield traits, fundamental information was obtained for selecting potential parental candidates.

Keywords: Hot pepper, pure line, *Capsicum annuum*, TSWV, morphologic characterization, dendrogram.

[Abstract:0110]

In Vitro Regeneration Responses of Different Hot Pepper (*Capsicum annuum* L.) Genotypes through Anther Culture

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Anther culture is a valuable technique for developing homozygous lines; however, the efficiency of haploid plant production remains limited in many species. Previous studies have reported that sweet and bell pepper genotypes exhibit higher androgenic potential than hot pepper genotypes; however, it remains unclear whether this difference is related to pungency or to the genotypic characteristics of hot peppers. In the present study, four hot pepper types (Maraş, Urfa, Antep, and Chile peppers) and two control types (Bell pepper and Cubanelle pepper) were evaluated. Two MS-based media were tested: A1 (4 mg/L NAA, 0.5 mg/L BAP, 0.25% activated charcoal, 15 mg/L $AgNO_3$) and A2 (5 mg/L 2,4-D, 5 mg/L kinetin, 1% activated charcoal, 10 mg/L $AgNO_3$). Anthers were incubated at 29 °C under continuous light for 4 days, followed by transfer to 25 °C with a 16 h light/8 h dark photoperiod. As a result of this study, the cultivars of Maras type pepper (5,9%), Antep type pepper (5,2%), Chili type pepper (7,2%), and Urfa hot pepper (7,6%) produced more embryos than sweet bell pepper (2,6%), and also sweet Cubanelle pepper produced 7,2% embryos. According to these findings, androgenesis is not influenced by the amount of capsaicin or pungency in peppers. Furthermore, the observation that different hot pepper genotypes exhibited higher androgenic responses in different nutrient media (A1-A2) demonstrates that the variation is entirely genotype-dependent.

Keywords: anther culture, *Capsicum annuum*, hot pepper genotypes

[Abstract:0011]

Obtaining Pure Lines Resistant to PMMoV and TSWV in Blocky Peppers Using MAS and Androgenesis Techniques

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Pepper is among the vegetable species with high economic value, which has many different forms and can be evaluated in many ways. When the market shares of pepper types grown in greenhouses are examined, it is seen that Capia and Pointed pepper types take the first place with 20 million seeds (number of seeds), and blocky peppers follow them with 15 million seeds. Charleston and Bell peppers have a market share of 7 and 8 million seeds, respectively. In the breeding of local hybrid varieties, the first two product types are mostly concentrated in our country, and almost all of the large square-section peppers are produced as foreign F1 hybrids imported from abroad. A rich gene pool consisting of large square-section (California and Yolo Wonder types) varieties supplied from different countries of the world, genitors with disease resistance, their hybrids, inbred lines in the F2-F3 stages, and bell pepper genotypes supplied from different regions of our country have been created in our company. Studies have been initiated to obtain hybrid variety parent candidates resistant to TSWV (Tomato spotted wilt virus), which has become mandatory for pepper cultivation in greenhouses and open fields, and PMMoV (Pepper mild mottle virus) Tobamoviruses, which are becoming increasingly widespread. Tsw and L genes providing resistance to TSWV and PMMoV agents in 300 genotypes in the gene pool were first identified using molecular markers. Afterwards, 30 selected genotypes were used as donor plants for androgenesis. Haploid and spontaneous DH plants were obtained from anthers cultured in media containing MS minerals and vitamins + 4 mg L-1 NAA + 1.0 mg L-1 BAP + 30 g L-1 sucrose + 7 g L-1 agar + 15 mg L-1 AgNO3 + 0.25% activated charcoal. After the folding and selfing processes, 100% homozygous pure lines were obtained. Molecular screenings on these lines confirmed the existence of lines homozygous for L3 and L4 genes and Tsw resistance genes. Thus, resistant pure lines could be obtained from F2 and F3 stage materials within a period of 13-18 months.

Keywords: Blocky pepper, *Capsicum annuum*, androgenesis, TSWV, PMMoV, molecular markers.

[Abstract:0181]

The Development of Multiple Resistance Inbred Lines for Nematodes, Pepper Root Blight (*Phytophthora capsici* Leon) and Potato Virus Y in Pepper (*C. annuum* L)

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Pepper (*Capsicum annuum* L.) is one of the most important vegetables produced worldwide. Numerous biotic stress factors such as pests, fungi, bacteria and viral diseases can damage pepper varieties during cultivation, causing serious yield losses. Nowadays, commercial varieties with multiple resistance are preferred due to the ease of control against these pests and diseases in the production area. It provides commercial varieties with significant value in addition to yield amount. This study aimed to develop inbred lines resistant to pepper nematodes (Meloidogyne sp.), pepper root blight (*Phytophthora capsici* Leon) and potato Y virus. The study was carried out in the Batı Akdeniz Agricultural Research Institute (BATEM) Department of Vegetable and Ornamental Plants in 2024-2025. Firstly, crossbreeding combinations were made between long pepper lines and SCM 334 as a source of multiple resistance. Inbred lines at F4 generation were obtained through pedigree method from different cross combinations. Inbred lines with different long fruit lengths were determined in segregations. Marker-assisted selection was used to determine resistance in 36 these inbred lines and control genotypes.CA-SSR-37 marker targeting N gene for nematode resistance, SCAR OpD04.717 marker for the Phyto5.2 QTL conferring resistance to pepper root blight and CAPS458 marker for the Pvr4 gene conferring resistance to potato Y virus were used. Finally, resistant and susceptible genotypes against all three biotic factors were determined, resulting in inbred lines with multiple resistance. In the next period, biological inoculation will be conducted on the inbred lines to confirm their resistance. They are planned to be used in breeding new resistant varieties. “The Development of Qualified Inbred Line and Variety in Pepper Breeding Programmes-III” project was supported by the General Directorate of Agricultural Research and Policies with project number TAGEM/BBAD/T1+/24/A1/P3/7357.

Keywords: Pepper (*Capsicum annuum* L.), nematode, pepper root blight, potato Y virus, multiple resistance, resistance breeding

[Abstract:0095]

Responses of Elite *Capsicum chinense* Lines to High Temperature Stress

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In recent years, noticeable changes in climate patterns have indicated a consistent rise in global temperatures. Therefore, the identification and utilization of heat-tolerant lines are expected to play a crucial role in future breeding programs. Among the species within the *Capsicum* genus, *Capsicum chinense* represents an important genetic resource, particularly due to its notable resistance to various biotic and abiotic stresses. This study assessed the tolerance of 18 elite *C. chinense* lines (S_5 generation) to high-temperature stress using standard morphological evaluation methods. In addition, two commercial hybrid cultivars, Teke F1 and Nare F1, were used as control varieties. Pepper seedlings at the 8–10 leaf stage were tested under high-temperature conditions at the OMU Karadeniz Advanced Technology Research and Application Center (KİTAM) to determine their physiological responses. The seedlings were exposed to high-temperature stress for 10 days in a growth chamber under controlled conditions: day/night temperatures of 42/37°C, a light intensity of 600 $\mu mol\ m^{-2}\ s^{-1}$ with a 16/8-hour photoperiod, and relative humidity ranging from 60 to 70%. Measurements of plant height, leaf number, stem diameter, as well as fresh and dry weight were taken at two time points, before (Day 0) and after (Day 10) exposure to high-temperature stress, under both control (greenhouse) and treatment (high-temperature chamber) conditions. At the end of the high-temperature stress treatment, leaf damage was visually assessed using a 1–6 scale, where 1 indicated no visible damage and 6 corresponded to more than 75% leaf damage or plant death. The classical high-temperature stress test revealed that the damage scores of them *C. chinenese* lines varied between 1.0 and 4.5 scale. The study identified the RC6-31, RC2-43, RC6-25, and RC6-30 lines as the most promising genotypes demonstrating strong tolerance to high-temperature stress. Quantitative measurements indicated that decreases in plant height, leaf number, and stem diameter were significantly lower in tolerant lines than in sensitive lines. In the future, these promising *C. chinense* lines will be used as parental materials in grafted pepper rootstock breeding programs to develop the first domestic hybrid pepper rootstocks.

Keywords: Damage level, high temperature, pepper, quantitative analysis, rootstock

[Abstract:0112]

In vitro Propagation of Newly Registered Hazelnut (*Corylus avellana*) Cultivars (Okay 28, Allahverdi, Çetiner, and Süslü)

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Hazelnut (*Corylus avellana* L.) genetic resources play a vital role in sustaining biodiversity and advancing breeding programs. Through ongoing selection and breeding efforts, several superior cultivars with valuable agronomic traits have recently been registered. The development of efficient clonal propagation techniques for these cultivars is crucial to ensure the production of disease-free planting material and the establishment of uniform orchards. Among available methods, micropropagation offers a promising approach; however, hazelnut remains a recalcitrant species due to its low regeneration capacity and the frequent occurrence of latent contamination, which complicates in vitro culture. In this study, four newly registered cultivars; Okay28, Allahverdi, Çetiner, and Süslü were evaluated for their micropropagation potential. Axillary nodal explants were collected between May and August 2025 and subjected to surface sterilization with 70% ethanol (30 s) followed by 1% NaOCl (5 min), then rinsed with sterile water. Explants were cultured on Nas and Read Medium (NRM) supplemented with 5 mg L^{-1} BA and 0.01 mg L^{-1} IBA. After four weeks, contamination and shoot induction rates were assessed. The highest microbial contamination was recorded in Okay28 (84%) and Çetiner (85%), whereas Süslü (23%) and Allahverdi (39%) exhibited the lowest contamination levels. Correspondingly, Süslü and Allahverdi displayed the highest shoot induction frequencies, 56% and 44%, respectively. Clean explants were subcultured on the same medium for multiplication, where Süslü produced the highest mean number of shoots per explant (2.3) and the greatest shoot length (4.6 cm). Rooting was tested on NRM medium supplemented with 2 mg L^{-1} IBA, revealing genotype-dependent variability. This study represents the first report on in vitro propagation of these newly registered hazelnut cultivars. The findings highlight the necessity of genotype-specific optimization in tissue culture protocols and demonstrate the potential of micropropagation to provide clonal, disease-free, and genetically stable plant material. These results not only support the conservation of hazelnut biodiversity but also facilitate future breeding efforts.

Keywords: *Corylus avellana*, hazelnut, micropropagation

[Abstract:0117]

Transcriptome-Based SNP Discovery in *Erysiphe corylacearum* to Support Resistance Breeding in Hazelnut (*Corylus avellana*)

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Powdery mildew caused by Erysiphe corylacearum remains one of the most economically damaging diseases in hazelnut production, significantly reducing yield and nut quality. Breeding resistant cultivars provides the most sustainable long-term solution, yet requires detailed molecular insight into pathogen diversity, adaptation, and virulence evolution. In this study, RNA was isolated directly from E. corylacearum structures peeled from naturally infected hazelnut leaves, enabling pathogen-enriched transcriptome sequencing without host contamination. Sequencing on the Illumina platform followed by de novo assembly produced more than 135,000 unigenes with comprehensive functional annotation. Variant analysis identified 29,311 high-confidence single nucleotide polymorphisms (SNPs) across 8,547 transcripts, including 1,231 homozygous and 28,080 heterozygous sites. The predominance of heterozygous variants reflects the coexistence of multiple genotypes within natural infections, a characteristic feature of this obligate biotroph in the field. This SNP dataset establishes a foundational molecular resource for hazelnut resistance breeding. It supports the development of markers for pathogen population monitoring, facilitates early detection of emerging virulent strains, and informs comparative analyses of effector gene evolution. Because the data originate from field-derived pathogen samples, the resulting markers are directly relevant to breeding programs aiming to deliver cultivars with durable resistance. By integrating pathogen SNP resources with host genetic improvement, this work provides essential tools for accelerating the development of resistant hazelnut cultivars and contributes to the long-term sustainability of global production systems under powdery mildew pressure.

Keywords: *Erysiphe corylacearum*, hazelnut breeding, pathogen diversity, powdery mildew resistance, SNP markers, transcriptomics

[Abstract:0069]

Overcoming Embryogenic Recalcitrance in *Corylus avellana* Through Insights from Stress-Induced Somatic Embryogenesis in *Muscari armeniacum*

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Somatic embryogenesis (SE) is a key technology for accelerated breeding and conservation, yet many woody crops, including hazelnut (*Corylus avellana*), remain highly recalcitrant to SE induction, limiting clonal propagation of elite genotypes. Recent findings in *Muscari armeniacum* (grape hyacinth) provide a novel model for understanding and overcoming this challenge. In this system, complete peduncle detachment triggers aerial bulbil formation through direct SE under simple water culture conditions, without synthetic growth regulators. Detached peduncles consistently produced viable bulbils with high germination efficiency, indicating the presence of a robust stress-responsive embryogenic pathway regulated endogenously. Analysis of this mechanism revealed tightly regulated developmental and hormonal changes that distinguished terminal severance from superficial wounding, suggesting sophisticated stress-sensing processes. These results highlight *M. armeniacum* as the first documented case of detachment-induced somatic embryogenesis in planta, offering an unprecedented opportunity to study natural triggers of embryogenic competence. Building on these insights, ongoing work is directed toward applying the regulatory principles observed in *M. armeniacum* to hazelnut. Comparative approaches are being used to identify the missing or suppressed signals that underlie recalcitrance in *C. avellana*, with the aim of designing targeted interventions such as epigenetic modulation and controlled stress treatments. This research establishes a framework for overcoming embryogenic recalcitrance in woody perennials by harnessing natural stress-response pathways. The ultimate goal is to develop efficient, low-input clonal propagation systems that can accelerate breeding and ensure the conservation of valuable genetic resources in economically important crops.

Keywords: Somatic embryogenesis, recalcitrance, clonal propagation, *Muscari armeniacum*, *Corylus avellana*, plant breeding

[Abstract:0311]

Breeding of New Cherry Varieties

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Turkey ranks first in global cherry production with approximately 736,791 tons (FAO, 2023). However, only 10–15% of this production is exported. Nearly all cherry exports originate from a single variety, ‘0900 Ziraat,’ which is internationally recognized as “Turkish Cherry.” Dependence on a single variety in production creates gaps in export markets and leads to profit losses for cherry growers and exporters. Producers aim to cultivate cherries outside peak production periods to benefit from higher market prices. Consequently, the development of early- and late-ripening cherry varieties has become a priority in many breeding programs, and the extension of the ripening period has supported the expansion of cherry-growing areas. To extend Turkiye’s cherry production season with high-quality early and late ripening cherry varieties, the project “Breeding of New Sweet Cherry Varieties” was initiated in 2007 at the Fruit Research Institute. The parental varieties used were Regina, Sweetheart, Sunburst, and 0900 Ziraat. The breeding method applied was classical hybridization. To date, preliminary evaluations of approximately 18,000 hybrid genotypes have been completed, while second-stage selection evaluations are ongoing for about 300 genotypes. Harvest times of genotypes in the variation plots ranged from early May to mid-July. From the initial hybridizations, two cultivars—Selen and Tuana—have been registered. Both cultivars produce red, heart-shaped fruits with long pedicels. The harvest time of Selen is approximately 10 days later than 0900 Ziraat, while Tuana matures about 12 days later. Within the scope of the study, evaluations of genotypes continue at the Selection-1 and Selection-2 stages.

Keywords: Sweet cherry, breeding, quality, fruit

[Abstract:0355]

Advantages And Dısadvantages Of Greenhouse Capıa Cultıvatıon In Antalya Provınce

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The homeland of capia pepper (*Capsicum annum*) is the American continent. Capia pepper is a type suitable for open field and greenhouse cultivation and is consumed all over the world with its hot and sweet, seeded and seedless, red, green,yellow, orange and light yellow colors. The production amount difference between capia pepper cultivation and other pepper types in Antalya is increasing every year. The circulation of commercial F1 hybrid varieties in the Antalya province capia market has opened up the market for producers seeking reliable varieties. There is currently no single variety that has dominated the market and has been sold for many years. The advantages of greenhouse capia pepper cultivation; less labor, tonnage, price advantage compared to other types, domestic market consumption, exportability, less disease in the fall greenhouse season, suitability for single-season production, many consumption methods (fresh consumption, paste, sauce, powdered pepper, roasted pepper, diet products, health, industry) are the reasons for preference for producers. Disadvantages of greenhouse *capsicum* cultivation include late harvest, early hot planting, yield loss, and diseases (such as (Botrytis cinerea), and TSWV typies). Seed companies in Turkey and internationally are conducting numerous breeding programs for *capsicum* using classical, molecular, and tissue culture methods.

Keywords: *Capsicum annum*, F1 hybrid typ, capia pepper.

[Abstract:0038]

Developing Türkiye's First Rhizomania-Resistant Sugar Beet Varieties: Türkşeker 2023 and Türkşeker 2053

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Sugar beet (*Beta vulgaris* L.) has long been a cornerstone of Türkiye's agricultural economy; however, for many years, local farmers depended on imported seed, leaving national production vulnerable to supply chain disruptions and devastating diseases such as Rhizomania, caused by Beet Necrotic Yellow Vein Virus (BNYVV). First detected in Türkiye in 1987, Rhizomania rapidly spread to nearly all production areas, threatening to reduce yields by up to 80% and rendering once-popular local varieties ineffective. The challenge of developing resistant cultivars was formidable, as classical breeding cycles could take as long as 13–18 years due to the complex processes involved in producing O-type and cytoplasmic male sterile linesIn collaboration with Türkşeker, Bolu Abant İzzet Baysal University, and Kastamonu University, they launched an ambitious program to transform this crisis into a success story. By integrating conventional breeding with biotechnological methods such as ovule culture and haploid induction, the timeline for developing inbred parental lines was reduced from eight years to just two. Molecular markers further enabled the rapid screening of resistance genes directly at the DNA level, ensuring precision in selection. After more than three decades of dedicated research, two revolutionary cultivars – "Türkşeker 2023" and "Türkşeker 2053" – were released as Türkiye's first locally developed, Rhizomania-resistant sugar beet varieties, officially registered in April 2024 by the Republic of Türkiye Ministry of Agriculture and Forestry. The cultivars combine robust disease resistance with high yield potential and favorable quality traits, demonstrating that locally bred varieties are competitive with global leaders. Seed production, initiated in Amasya in 2024, is expected to fully satisfy domestic demand by 2029, with projections to reach export capacity within six to eight years. This achievement not only ends Türkiye's dependency on imported sugar beet seed but also marks a turning point at which local innovation addresses global agricultural challenges. The development of Türkşeker 2023 and Türkşeker 2053 serves as a model demonstrating how the integration of traditional breeding strategies with modern biotechnological methods can secure national food sovereignty and guide future global crop improvement efforts.

Keywords: Sugar Beet, First national sugar beet varieties, Türkşeker 2023, Türkşeker 2053

[Abstract:0100]

Camellia Species For Oilseed Production in Türkiye

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Camellia is one of the world’s four major oil-bearing trees, along with olive, palm, and coconut. Camellia oil, often known as “Eastern Olive Oil,” has a chemical composition comparable to olive oil, with high levels of oleic and linoleic acid and low levels of saturated fat. Camellia oil was not introduced into Western countries until the multiple health advantages of the plant were understood. Global interest in commercial production of camellia oil has increased in recent years. Oil camellias are often cultivated on mountain slopes as opposed to seed-oil plants. This allows the new crop to take full advantage of the marginal sites. *Camellia sinensis* and *Camellia japonica* are the best-known and most-cultivated species in the world for tea production and decorative value, respectively. *Camellia sinensis* is produced in Türkiye for its fresh leaves, whereas *Camellia sinensis* and *Camellia oleifera* are planted for decorative purposes. *Camellia oleifera* Abel, *Camellia meiocarpa* Hu, *Camellia vietnamensis* Huang, *Camellia chekiangoleosa* Hu, *Camellia yuhsienensis* Hu, *Camellia semiserrata* Chi, *Camellia reticulata* Lindl, and more species are present. Oil camellias, which do not compete for arable land, can be planted on infertile mountain slopes, giving them the capacity to fully utilize the world’s marginal regions. Local communities in China have been extracting oil from camellia seeds using wooden presses since more than 1000 years ago. This technology can be dated back to the Song Dynasty, as recorded in an ancient book named Tu Jing Ben Cao. All species of the Camellia genus produce an oleagenous seed. Crude edible oil was produced from tea seed in native mills in West Bengal, Himachal Pradesh and Assam and in the Northern region of Indochina. Tea seed oil has been produced on commercial scale in China where in 1958, 180,000 tons of the oil) was produced. Oil camellias have yet to be introduced to Western countries, in contrast to *C. sinensis* and *C. japonica*, which are commonly planted for tea production and ornamental value, respectively. The potential of various Camellia species for oilseed production in Türkiye will be thoroughly addressed.

Keywords: Camellia, oilseed, tea

[Abstract:0299]

Konya: Epicenter for Cereal Seed Production in Türkiye

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Konya Region is one of the most important agricultural production regions in our country with approximately 2 million hectares of agricultural land. In the region, more than 95% of agricultural production consists of field crop production areas. Konya is among the largest producers of many products in the country’s agriculture, such as sugar beet, wheat, barley, corn, potatoes, sunflower, alfalfa, vetch, chickpeas, dry beans, and safflower. The region is the most important center in Türkiye for seed production, which is the main element of plant production. In Konya province, a total of 13,000 seed production declarations were given per year, and seed production was carried out in a total area of 1,100,000 decares. The region has become the seed production center of our country. There are more than 200 seed producer companies and around 700 seed distributor dealers located in Konya. Almost a quarter of the seed production companies registered with TSÜAB in our country are located in Konya. It cannot be said that Konya, which has a great agricultural potential especially in terms of field crop seeds, has yet to fully utilize its suitable climate, soil, and other production factors. Almost all of the seed production in the region is carried out by our farmers in farmer fields under the control of the companies, through contracts made between the company and the farmer/grower. The education level of the farmers, their level of cultivation knowledge, and their perspective on the subject closely affect the seed production and quality in the region. In Konya province, seed production of about 500 different varieties belonging to 20 different species was carried out per year. Although the seed production amount of the region varies from year to year, it corresponds to 30-40% of the country’s seed production. In this study, it is aimed to examine the company and farmer/grower structure at the seed production/multiplication stage in the Konya region, which has become the most important seed production base for our country, to reveal the agricultural resources and production potential and, based on this, to determine the development targets and strategies for plant production within the scope of seed production in the region, and to determine the efficiency of resources in the field of seed production and to contribute to its more efficient use.

Keywords: Konya, Production, Seed, Seed Growing, Türkiye

[Abstract:0269]

Genetic Interaction between UMAMIT28 and UMAMIT29 is Essential for Plant Iron Homeostasis

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Iron (Fe) is an essential micronutrient for photosynthesis, respiration, and chlorophyll biosynthesis, yet its low solubility in soils often limits availability, causing Fe deficiency and reduced plant productivity. Although numerous Fe transporters and regulators have been identified, the possible role of amino acid transporters in Fe uptake and homeostasis remains poorly understood. In this study, we investigated the roles of two amino acid transporters from Arabidopsis thaliana, UMAMIT28 and UMAMIT29, in Fe homeostasis. To assess their functional interaction, we generated umamit28umamit29 double mutants by crossing umamit28 and umamit29 T-DNA insertion lines and analyzed their responses under Fe-sufficient and Fe-deficient conditions in comparison with the wild-type (Col-0). We evaluated ferric chelate reductase (FCR) activity, root length, chlorophyll content, and rhizosphere acidification, as well as Fe, Zn, and Mn concentrations in shoots and roots. In addition, the expression of key Fe homeostasis genes (IRT1, FRO2, AHA2, FIT, and PYE) was quantified, and Fe localization was examined using histochemical staining. The umamit29 mutant exhibited marked sensitivity to Fe deficiency, characterized by pronounced chlorosis, reduced root elongation, lower FCR activity, and decreased rhizosphere acidification compared to Col-0. The umamit28umamit29 double mutant showed even greater sensitivity, displaying severe chlorosis, stunted growth, and significantly reduced Fe accumulation in both roots and shoots. In contrast, umamit28 single mutants displayed a mild phenotype and behaved similarly to Col-0 under Fe-deficient conditions. Consistent with these observations, Fe concentrations were drastically lower in both the roots and leaves of umamit29 and double mutants relative to the wild type, while the expression of Fe acquisition genes was altered. Our findings indicate that UMAMIT28 and UMAMIT29 work together to keep Fe levels stable in Arabidopsis. The increased Fe deficiency sensitivity of umamit29 and double mutants suggests that amino acid transporters, particularly those of the UMAMIT family, play an unrecognized yet essential role in regulating Fe uptake, translocation, and overall metal homeostasis in plants.

Keywords: amino acid transporters, Arabidopsis, iron deficiency, iron localization

[Abstract:0083]

Investigation of the Regional Adaptation of Chickpea (Cicer arietinum L.) Genotypes in the Eastern Mediterranean Region

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This study was conducted over three years (2019–2021) at the experimental fields of the Eastern Mediterranean Agricultural Research Institute, Doğankent location, with the aim of determining the agronomic characteristics and breeding potential of some chickpea (*Cicer arietinum* L.) genotypes. A total of 20 genotypes of national and ICARDA origin were evaluated under winter sowing conditions using a randomized complete block design. Sowing was carried out on 9 m^2 plots, each consisting of four 5m long rows, with 45 cm inter-row and 8 cm intra-row spacing. Before sowing, fertilizers were applied at rates equivalent to 2–3 kg/da N and 5–6 kg/da P_2O_5. The trial site is located at 36°51′17.21″N, 35°20′41.61″E, at an altitude of 23 m. The study aimed to determine the relationships between yield and yield-related traits of chickpea genotypes under Mediterranean conditions and to select promising genotypes for winter sowing. The highest and the lowest grain yields recorded in the first year were 408.44 kg/da (İnci) and 192.74 kg/da (ENA102-9-Erz), respectively; in the second year, 369.90 kg/da (Hasanbey) and 118.20 kg/da (FLIP 09-104C); and in the third year, 432.78 kg/da (İnci) and 251.63 kg/da (FLIP 09-284C). The three-year average highest and lowest yields were 370.23 kg/da and 201.60 kg/da, respectively, both observed in İnci and ENA 144-10. In terms of 100-seed weight, values ranged from 52.28 g to 39.17 g in the first year, 52.9 g to 37.4 g in the second year, and 51.52 g to 38.43 g in the third year. The three-year average highest and lowest 100-seed weight were 52.06 g and 38.34 g. In the evaluation, in terms of earliness, the number of days to flowering varied between the three-year average high and low values of 99.11-94.56 days; and the number of days to pod set varied between the three-year average high and low values of 118.89-112.67days. As an indicator of suitability for mechanical harvesting, plant height varied between the three-year average high and low values of 73.19-61.51 cm; first pod height varied between the three-year average high and low values of 46.8-38.44 cm. Based on regional performance and breeding potential, the genotypes İnci, Hasanbey, Sezgin and Onur are high-yielding varieties. In addition, the Diyarbakır-Ç2, FLIP 09-186C, FLIP 09-189C, FLIP 09-426C and FLIP 09-402C lines were identified as suitable candidates for variety registration.

Keywords: Chickpea, Yield, Regional adaptation

[Abstract:0291]

The Need to Prioritize Breeding for Drought- and Climate-Resilient Crop Varieties

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This study draws on grain yield and quality assessments conducted between 2022 and 2025 with 250 producers across 7,000 decares of land in the Central Anatolia Region. The aim is to identify the factors behind the recent decline in grain yields and to evaluate the role of breeding programs in addressing these challenges. Evaluation of Barley, Wheat, and Triticale Varieties Under Drought and Frost Stress Conditions Plant materials of Odyssey, Orfey, Murgavets, and Rozhen barley varieties, which I selected from the experimental fields of the Kornobat Research Institute in Bulgaria, were introduced to Turkey. In addition, some commonly preferred barley varieties in our region such as Aydan Hanım, Larende, and Tarm 92; bread wheat varieties Pehlivan, Kate A-1, Flamura 85, and Ayten Abla; and triticale varieties Sarp and Özer Tatlıcak were also included in the trials. To evaluate their growth, yield, and quality performance under different conditions, multi-location and multi-factor field experiments were established in three locations: Tuğcu Village (Sungurlu, Çorum), Çöplüçiftliği Village (Yenifakılı, Yozgat), and Çiçekdağı (Kırşehir). The main objective was to identify genotypes with high tolerance to drought and early frost, ensuring stable yield performance even under challenging environmental conditions. The trials were designed as Screening Nurseries (SN) with four replications, and a 15-day sowing interval was applied between each replication. Determining the correct sowing time was crucial to make better use of rainfall and to avoid crop damage during late frost periods. Based on these experiments, the best-performing varieties were identified, and region-specific recommendations were made regarding variety selection, sowing time, fertilizer type and timing, pesticide application periods, and the use of plant growth regulators and nutrients. Each plot received specific treatments to determine the most effective combinations under different conditions. Currently, one of our major challenges is drought, but another significant issue observed, particularly in wheat, is rust disease. Even with proper timing of fertilization and pesticide applications, we faced considerable difficulties in managing rust and observed severe yield losses. As a result, it was concluded that breeding efforts should focus more on rust-resistant varieties, alongside drought tolerance. Cereal varieties tested in demonstration plots were highly susceptible to drought stress arising from limited rainfall. Varieties entering the generative stage early were also severely affected by spring frosts. In addition, improper timing of fungicide applications for yellow rust (*Puccinia striiformis* West.) control caused significant yield losses. Irregular climatic conditions and inappropriate planting dates have led many producers to lose income and even withdraw from production, resulting in shrinking cultivation areas. To achieve this, breeding efforts should be integrated with sustainable soil tillage practices, efficient irrigation management, and region-specific agricultural policies. Farmer training on sowing dates, soil preparation, and pesticide application, along with the establishment of local advisory networks composed of agricultural engineers and technicians, is also essential.Breeding programs based on existing genetic variation should therefore be supported and accelerated.

Keywords: Breeding, Generative, Integrated, Agronomy, Cultivar, Demonstration

[Abstract:0025]

Development of Cultivars Tolerant to Ascochyta Blight in Chickpea (*Cicer arietinum* L.)

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This study is a public-private sector joint project aiming to develop high yielding chickpea lines which have good adaptability, high quality traits, resistance/tolerance to diseases and pests, especially Anthracnose blight, suitability for agricultural mechanization, and market standards. Within this scope, 2 variety yield trials consisting of 20 lines and varieties were carried out to determine yield and quality traits in 2023 in Adana and Eskişehir. While winter-sown was cultivated in Adana, spring-sown were performed in Eskisehir. The trials were conducted with three replicates according to the randomised blocks experimental design. In Adana, while grain yields, days-to-flowering, plant heights, and hundred-seed weights were between 191.63-367.33 kg/da, 64-68.67 days, 53.04-60.67 cm, and 38.1-57.4 g respectively in yield trial-I, these were between 126.91-391.3 kg/da, 65.7-69.0 days, 56.3-77.0 cm, and 37.8-51.8 g respectively in yield trial-II. In Eskisehir, while grain yields, days-to-flowering, plant heights, and hundred-seed weights were between 56,5-163,7 kg/da, 58,0-65,5 days, 46,3-64,8 cm, and 33,83-44,22 g, respectively in yield trial-I, these were between 26,11-159,4 kg/da, 8,0-64,5 days, 48,0-70,0 cm, and 32,73-41,30 g respectively in yield trial-II. Moreover, protein ratio, swelling index, and sieve values were 18.56-22.97%, 2.17-2.44%, and 7.9-8.9 mm in Adana Yield Trial-I these were between 17,91%, 2.11-2.32%, and 7.7-8.9mm respectively in Adana in Yield Trial-II. In Eskişehir, while protein ratio, swelling index, and sieve values of were 19.55-25.08%, 2,28-2,49%, and 7,71-8,49mm in yield trial-I, these were 19.34%, 2,31-2,44%, and 7,55-8,24mm respectively in yield trial-II. Variety registration is planned at the end of the research.

Keywords: Chickpea, Breeding, Variety and Line, Ascochyta blight

[Abstract:0070]

Genome-Wide Association Study Reveals Stable QTLs for Agronomic Traits in Chickpea

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Chickpea (*Cicer arietinum* L.) plays an important role in global food security as a protein-rich legume, but its productivity is constrained by limited genetic diversity and environmental stresses, especially in drought-prone areas like Kazakhstan. This study aimed to uncover the genetic basis of key agronomic traits through genome-wide association studies (GWAS) and identify stable quantitative trait loci (QTLs) to improve yield and resilience in regionally adapted cultivars. A diverse panel of 238 chickpea accessions from five geographic regions was evaluated in field trials across three seasons (2022–2024) in south-eastern Kazakhstan using a randomized design with two replicates. Six traits were measured: plant height (PH), height to lowest pod (HLP), number of lateral branches (NLB), number of seeds per plant (NSP), thousand-seed weight (TSW), and yield per plant (YP). Phenotypic data were analyzed for variation, correlations, ANOVA, and broad-sense heritability. Whole-genome resequencing produced 480,886 high-quality SNPs. Population structure was assessed by principal component analysis (PCA) and kinship matrix, while linkage disequilibrium (LD) decay was estimated per chromosome. GWAS used a multi-locus mixed model (MLMM) in GAPIT with a significance threshold of $p = 1.00e\text{-}04$, adjusting for structure and kinship. Stable QTLs were identified across environments, and candidate genes were annotated using the CDC Frontier v1.0 reference genome. Phenotypic analysis showed significant trait variation, with CVs ranging from 16.2–16.9% for PH to 30.3–47.6% for YP, and heritability values from 0.15 (NSP) to 0.88 (TSW). Strong correlations included PH-HLP ($r = 0.744$–0.821, $p<0.001$) and NSP-YP ($r = 0.520$–0.858, $p < 0.001$). ANOVA revealed significant genotypic effects for PH, HLP, TSW, and YP ($p < 2E\text{-}16$). GWAS detected 351 marker-trait associations, consolidated into 128 QTLs, of which 40 were stable across years. Major QTLs included *Q_YP_2.1* ($R^2 = 0.45$, chromosome 2) and *Q_TSW_4.1* ($R^2 = 0.22$, chromosome 4). Hotspots on chromosomes 1 (3.1–7.2 Mb) and 4 (25.9–47.3 Mb) encompassed multiple traits. Thirty-six candidate genes were identified, such as LOC101508792 (polyamine biosynthesis for PH) and LOC101492955 (carbohydrate metabolism for NSP). This study highlights stable QTLs and candidate genes for marker-assisted breeding, supporting the development of high-yielding, stress-resilient chickpea varieties tailored to Kazakhstan's arid environments and contributing to sustainable farming and food security in semi-arid regions. This study was supported by the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP19677444).

Keywords: chickpea, GWAS, QTL, agronomic traits, yield components, Kazakhstan

[Abstract:0307]

Effect of SA and EMS Applications on Germination and Plant Characteristics in Arda Chickpea Variety

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This study was conducted at GAPUTAEM plant growth room and experimental area in Diyarbakır during the 2024-2025 growing season. The study was carried out to investigate the effects of control, 0.5, 1.0, 1.5, 2.0, 2.5 and 3.0% sodium azide (NaN3) and control, 10, 20, 30, 40 and 50 mM ethyl methanesulfonate (CH3SO3C2H5) doses on germination characteristics and M1 plants of Arda chickpea variety. Germination experiments were conducted in a randomized plot design, and field experiments were conducted in a randomized complete block design with three replications. Germination percentage, germination rate index, mean germination time, seedling vigor 1 and seedling vigor 2, root length, seedling height, seedling fresh and dry weight, and root fresh and dry weight traits were investigated in the plant growth room. In the field trial, plant height, number of branches, pods and seeds per plant, seed yield per plant, 100 seed weight, chlorophyll a and leaf mutations were investigated. Lethal doses and average growth doses of chemical mutagens were determined for the variety. For the Arda chickpea variety, the highest LD50 was 5.8 mM in SA application, and GR50 was 3.901 mM based on plant height. In EMS application, LD50 was 47.42 mM and GR50 was 12.5 mM based on plant height. Increasing EMS doses caused a decrease in germination percentage, germination rate index, average germination time, seedling vigor 1 and seedling vigor 2. Although decreases were detected in germination characteristics, seedling vigor 1 and seedling vigor 2 at control, 0.5% and 0.1% SA doses, the effect of higher SA doses on the investigated traits was found to be insignificant. Although seed germination occurred at 40 and 50 mM EMS doses, the seedlings did not maintain their viability. After determining the lethal dose, field trials were conducted with new SA (1.5, 2.5, 3.5, and 4.5 mM) and EMS (10, 20, and 30 mM) doses. In field trials, the effects of SA doses on plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, seed yield per plant (g), and seed yield per plot (g) were found to be significant in the chickpea variety Arda. However, the effect of EMS treatments was only significant on 100 seed weight (g) and seed yield per plant (g). Among SA treatments, decreases in trait values were observed up to a dose of 3.5 mM. A significant increase was observed at a dose of 4.5 mM.

Keywords: Chickpea, EMS, mutation, SA

[Abstract:0221]

Agro-morphological Characterisation of Wild Chickpea Genotypes in Türkiye

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Global climate change and agricultural drought threaten agricultural production. Chickpea yield, a crucial crop in human nutrition, is highly affected by abiotic stress factors. Ecological conditions also requires changes in chickpea breeding objectives. Wild chickpea genetic resources are the most important gene pool for developing drought-resistant varieties and resistance to abiotic stress factors. This project was conducted to identify, record, and evaluate wild chickpea genetic resources in Türkiye, which is a chickpea gene center and has many wild relatives. Forty-eight *C. reticulatum* and *C. endiospermum* species collected from the Fertile Crescent region were used in the study. To determine the agromorphological characteristics of chickpea genetic resources, plantings were conducted on the AARI plot, and observations were taken. High correlations were found between canopy width and height and the number of basal primary and secondary branches. A significant relationship was found between the number of basal primary and secondary branches and the number of pods. The traits comprising the first three main components explain 70% of the variation in the population. Canopy height, canopy width, basal primary and secondary branch counts, pod number per plant, and seed number per plant constituted the primary component. The second principal component was determined by primary pod height and seed length, while the third principal component was determined by the number of apical secondary branches and seed width. While *Cicer echinospermum* species did not show significant variation in these traits, a wide variation was observed in *Cicer reticulatum*. Wild chickpea lines collected from the Şırnak region exhibited lower values for canopy height and seed length, while populations collected from the Mardin region exhibited higher values for these traits.

Keywords: Wild chickpea species (*Cicer* spp.), chickpea genetic resources, characterisaiton

[Abstract:0335]

Integrated Analysis of Agronomic and Molecular Marker Data for the Soybean (*Glycine max* L. Merr.) Breeding Program

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Soybean is a strategic protein and oil crop, with Turkey importing 95% of its supply. The 10-12 year duration of classical breeding slows down the development of local varieties. The aim of this study is to shorten this process using Marker-Assisted Selection (MAS). In this regard, the agronomic data of 86 soybean genotypes and 36 KASP SNP marker data were integrated to select superior parent genotypes. MATERIALS-METHODS: Yield, protein, oil, and maturity group (MG) data of the genotypes were recorded. Due to the significant effect of the maturity group on yield, the genotypes were divided into two groups: "Early" (MG 1.0-2.5) and "Late" (MG 3.0-4.2). The relationship of the 36 KASP SNP markers with agronomic traits was analyzed separately for each group. FINDINGS: The average yield of the Late group (395 kg/da) was found to be 37% higher than that of the Early group (289 kg/da). An "ideal haplotype" containing the SNP10-14 panel (C-G-G-C-G) was identified in both groups for high oil content, and the SNP14(G) (ss107919571) allele was found to be critical. In the Late group, the SNP1(A) (ss715592623) and SNP7(A) (ss715598558) alleles from the SOTO set were decisive for high yield; the highest-yielding varieties, Likya (462 kg/ha) and PGL 1512 (457 kg/ha), carry these alleles. In the early-maturing group, the SNP6(G) (ss715610817) and SNP7(A) (ss715598558) alleles showed a strong association with high yield; the most productive genotype in this group, PGS 1376 (403 kg/ha), contained both of these alleles. The relationship between these key markers (SNP1, SNP7) and yield components has been confirmed in the literature (Contreras-Soto et al., 2017). RESULT: As a result of the study, 8 strategic parent genotypes (e.g., Likya for high yield; LD 18-7628 for high oil; PGS 1376 for early-maturing high yield) were identified for the breeding program. Specific crossing strategies (e.g., Likya x LD 18-7628) were proposed to combine high yield and high oil content. The integration of KASP markers, whose effectiveness was confirmed in this study, with MAS and "Rapid Breeding" systems has the potential to significantly shorten the 10-12 year breeding process.

Keywords: Marker-Assisted Selection (MAS), KASP, SNP, Plant Breeding, Yield, Oil Content.

[Abstract:0287]

Development of the Soybean Breeding Program in Kazakhstan: From the Stage of Crop Diversification to the Introduction of Biotechnological Approaches and Digital Technologies

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Soybean accounts for 25% of the global commercial vegetable oil market and 70% of the available source of plant-based protein. According to the International Grains Council (IGC), global soybean production in the 2024–2025 season is estimated at approximately 418 million tons. In Kazakhstan, the primary soybean-growing region is the southeast of the country. Between 1970 and 2025, the sown area of soybean increased tenfold — from 10.3 thousand hectares to 100 thousand hectares — reflecting an active diversification of cropping systems. The most significant increase in soybean cultivation occurred between 2010 and 2017. Average yields across Kazakhstan range between 2.2–2.4 t/ha. The Kazakh Research Institute of Agriculture and Plant Production serves as the key soybean breeding center in the Republic of Kazakhstan. Breeding activities for this crop have been carried out since the 1960s. During the first stage (1962–1970), extensive work was conducted to collect, study, and establish a soybean trait collection. Through collaboration with the Federal Research Center "All-Russian Institute of Plant Genetic Resources named after N.I. Vavilov" genetic bank, around 50 new soybean accessions from around the world were studied annually by the Oilseed Crops Department. Accessions adapted to local conditions were identified and subsequently used as parental forms in breeding programs. At present, the collection comprises about 1,200 soybean accessions. The next stage (1971–1990) combined traditional hybridization and selection methods with artificial mutagenesis, which was widely practiced at the time. With the gradual expansion of soybean cultivation during Kazakhstan's independence, breeding efforts focused on the development of early-maturing varieties. At the modern stage (since 2010), breeding priorities include photoperiod insensitivity, drought tolerance, resistance to pod cracking and seed shattering, as well as improvement of seed organoleptic traits to broaden their industrial applications. To strengthen the breeding program at the current level, a combination of methods is applied, including traditional breeding, biotechnological approaches (MAS, DNA markers, QTL mapping, GWAS), physiological assessments (NDVI, FAR, proline), biochemical analyses (F1 hybridity verification, nutrient and anti-nutrient composition), and digital technologies (UAVs). Over 60 years of breeding work at the Kazakh Research Institute of Agriculture and Plant Growing has resulted in the creation of around 35 soybean varieties belonging to five maturity groups (MG 00, 0, I, II, III), 23 of which are officially approved for cultivation across eight regions of Kazakhstan, spanning latitudes from 53.23°N to 42.32°N.This research has been funded by the Ministry of Agriculture of the Republic of Kazakhstan, BR - 22885857 " Development and introduction of highly productive oilseeds and cereals varieties and hybrids to ensure food security of Kazakhstan"

Keywords: Soybean, breeding, yield, trends

[Abstract:0191]

Determination of the Agricultural Performance of Soybean (*Glycine max* L. Merr.) Genotypes Under the Ecological Conditions of Konya in Türkiye

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Soybean is an important crop not only for human and animal nutrition but also for various industrial applications. A significant portion (approximately 95%) of Türkiye's soybean demand is met through imports. In order to reduce or eliminate this dependency, it is essential to investigate the cultivation potential of soybean in regions with high agricultural capacity, such as Konya. Therefore, the present study aimed to evaluate soybean varieties suitable for the ecological conditions of Konya. The study was conducted during the 2021 and 2022 growing seasons in Sarayönü, Konya which located Central Anatolia of Türkiye. The trials were conducted under irrigated conditions, following a randomized complete block design with three replications. The plant material consisted of eight varieties (Defiance, Nova, ATAEM 7, NE 3399, Arısoy, A 3935, Atakişi and Çetinbey) and four breeding lines (BDS 11, BDS 07, BDS 25, and BDS 21). Evaluation of the varieties and lines was performed based on plant height, pods per plant and number of branches, height of the first pod, pod length, number of seeds per pod, first branch height, thousand-seed weight, yield, and seed composition (protein, ash, and oil content). Variance analysis showed that the varieties differed significantly ($p<0.01$) in terms of plant height, number of pods per plant, number of branches per plant, and seed yield. The highest yields were obtained from the BDS 25 (5881 kg ha^{-1}) and BDS 11 (5859 kg ha^{-1}) lines, while the lowest yield was recorded from the Defiance variety (4077 kg ha^{-1}). In terms of yield performance, BDS 25 and BDS 11 were classified in the first group, followed by Nova in the second group; ATAEM 7, Arısoy, and Çetinbey in the third group; BDS 07, BDS 21, NE 3399, Atakişi, and A 3935 in the fourth group; and Defiance in the final group. The Atakişi variety showed the highest protein content (37.48%), whereas the BDS 21 line (18.6%) and the Atakişi variety (18.4%) exhibited the highest oil content. Based on the results, BDS 25 and BDS 11 lines were identified as promising with respect to seed yield, while BDS 21 and Atakişi were identified as suitable genotypes for cultivation under Konya's ecological conditions in terms of oil and protein yield.

Keywords: Soybean, genotypes, adaptation, yield, agronomic traits.

[Abstract:0036]

Mapping Endogenous Pararetrovirus Sequences in Cultivated Soybean and its Wild Ancestor

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Archaic virus sequences integrated into plant genomes are referred to as endogenous pararetroviruses (EPRVs). EPRVs are transmitted through generations upon integration into the genomes of plant reproductive cells. Next-generation sequencing and assemblies are crucial for identifying distinct EPRV sequences in plant genomes. In this study, a comparative bioinformatic analysis of EPRV sequences belonging to the family Caulimoviridae was performed in two members of the subgenus Soja: cultivated soybean (*Glycine max*) and its wild progenitor (*G. soja*). For this purpose, the chromosomal distribution of EPRV fragments was mapped with MapGene2Chrom, and sequence similarities were examined through multiple sequence alignments. Bioinformatic analyses revealed that the EPRV fragments were spread along the chromosomes of both species. However, in contrast to the typical genomic distribution patterns reported in plants, no prominent accumulation was observed either in the telomeric or centromeric regions of the soybean genomes. Comparative ideograms of the *G. max* and *G. soja* chromosomes revealed a relatively consistent distribution between the two species. Consequently, the chromosomal distributions of EPRV sequences in the Soja subgenus exhibit a high degree of conservation. This finding may indicate that EPRVs of Caulimoviridae origin have been maintained within the genome throughout evolutionary history and have remained largely stable following speciation. Therefore, the conservation of EPRV fragments in both cultivated soybean and its wild progenitor highlights the potential role of these sequences in genomic integrity and evolutionary dynamics. This research has been supported by The Scientific and Technological Research Council of Türkiye (TÜBİTAK), project number 123O050.

Keywords: bioinformatics, domestication, genome, transposable elements

[Abstract:0053]

Genome-Wide Association Analysis and Genomic Prediction of Pod Dehiscence in Soybean Germplasm

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Soybean (*Glycine max* (L.) Merr.) is an important global source of high-quality protein and oil for both human consumption and animal feed. The growing global population and demand for plant-based protein underline the importance of developing cultivars with high yield, stress tolerance, and enhanced nutritional quality. Pod dehiscence is one of the main factors which play a vital role on the final yield of many crops including soybean, therefore, it is important to elucidate genetic mechanisms associated with this trait. In our study, pod and pod-related traits in soybean accessions from diverse geographical origin were investigated using morphological, physiological, and biochemical methods. A genome-wide association study (GWAS) was performed using more than 30000 DArT markers (DArT SNPs and Silico-DArT markers). A total of 48 quantitative trait loci (QTLs) were identified, 14 of which were consistently found across different environments. Two significant candidate genes among these QTLs were detected after the gene annotation analysis. The first one, Glyma.13G184500, encodes DNA-binding bromodomain-containing protein, and the second one, Glyma.16G141100, produces C2-H2 zinc-finger protein. Both genes are important transcription factors related to pod wall development. Several genomic prediction models were employed to enhance GWAS results using two different marker sets (the whole and GWAS-derived markers) through both cross-prediction and across prediction approaches. As a result, GWAS-derived markers showed more stable prediction accuracies across different populations, indicating that GWAS-derived markers can be used to assess pod dehiscence level of new, unknown soybean genotypes. Furthermore, resistant accessions were effectively selected based on genomic breeding values (GBV). Overall, important genetic markers and putative candidate genes for developing soybean cultivars with enhanced resistance to pod dehiscence were identified in this study. These findings could help breeders develop high-yielding indehiscent soybean varieties which are adapted to different production environments.

Keywords: GWAS, genomic prediction, GAPIT, pod dehiscence, soybean.

[Abstract:0200]

From Field to Genome: Biotechnological Strategies for Developing Improved Hop and Hemp Varieties in Slovenia

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Slovenia ranks third in the European Union and fifth globally in hop (*Humulus lupulus* L.) growing area. Hop cones represent a key raw material for the brewing industry, and today, approximately 98% of Slovenian hop fields are planted with varieties originating from our national breeding program. Our program integrates agronomically important traits with brewing quality objectives, leading to the development of novel varieties distinguished by their traditional aroma, high alpha-acid content, diverse flavor profiles, and improved resistance to major diseases and pathogens, including downy mildew (*Pseudoperonospora humuli*), powdery mildew (*Podosphaera macularis*), Verticillium wilt (*Verticillium nonalfalfae*), and citrus bark cracking viroid (CBCVd). Molecular diagnostics and biotechnological tools are increasingly included in the breeding pipeline. Developed multiplex qPCR protocol enables early differentiation between female and male seedlings, preventing unwanted pollination in hop fields or to include only female plants in breeding selection. SSR markers are employed for genotyping and assessing varietal purity. In addition, virus- and viroid-free plant stocks are produced through in vitro methods to serve as elite mother plants for certified propagation material. The search for molecular markers conferring disease resistance - particularly against Verticillium wilt - is ongoing through genome-wide association studies (GWAS), which are being expanded with predictive modeling for genomic selection. Future efforts will focus on integrating multi-year phenotypic datasets with genotypic profiles to enhance the accuracy and efficiency of selection decisions. Given its close phylogenetic relationship to hop, hemp (*Cannabis sativa* L.) has recently been incorporated into the breeding program due to its wide range of industrial and medicinal applications. Hemp produces numerous secondary metabolites, mainly cannabinoids and terpenes. However, wind pollination and high heterozygosity often result in diverse phenotypes within a single variety. Comparative analyses of three cultivars - Carmagnola Selected (CS), Tiborszallasi, and Finola Selection - revealed significant genetic and chemical variability. Sequencing and GWAS analyses of 45 phenotypic traits identified SNP positions and associated candidate genes underlying this variation. Based on accumulated expertise and infrastructure, breeding efforts are now expanding toward the development of new, high-THC varieties addressing different therapeutic needs.

Keywords: hop, cannabis, GWAS, genomic selection, breeding strategies

[Abstract:0270]

Toward 2075: Planetary-Resilient Crop Breeding with Pan-Omics and AI-Driven Gene Editing

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Rising climate volatility presents a critical challenge to global agriculture, and achieving Europe's 2030 Green Deal and 2050 climate neutrality targets necessitates a fundamental shift in crop breeding, from traditional yield-focused approaches to systems intentionally designed for planetary resilience. This review outlines a visionary 2075 roadmap based on the framework of Planetary Resilience by Design (PRD), integrating pangenomics, multi-omics, AI-guided gene editing, and speed breeding into a unified, data-driven pipeline for next-generation crop development. Central to this strategy is the Pan-Eco-Genome platform, an integrative ecosystem that constructs annotated pan-genomes of crops and their wild relatives, enriched with sustainability metrics such as carbon and water footprints, nutrient use efficiency, and soil regeneration potential. By linking genomic diversity with ecological indicators, this platform ensures that precision breeding is aligned with planetary boundaries, facilitating genetic improvements that contribute directly to climate mitigation and biodiversity conservation. Key components of PRD include: (1) structural variant discovery across pan-genomes to identify alleles conferring tolerance to drought, heat, and salinity; (2) the creation of multi-omics atlases, spanning transcriptomics, epigenomics, metabolomics, phenomics, and single-cell omics, to elucidate genotype-to-phenotype relationships; (3) AI-driven CRISPR-CasX base and prime editing to reprogram metabolic networks for enhanced photosynthetic efficiency, nutrient density, and abiotic stress resilience; (4) speed breeding factories integrated with digital twins simulating future climate scenarios to accelerate predictive phenotype selection; and (5) the incorporation of life cycle assessment (LCA) within selection indices to prioritize low-GHG, soil-regenerative, and circular bioeconomy traits. We propose digitally powered breeding hubs combining high-throughput phenotyping, automated omics pipelines, and in silico design platforms, which could compress cultivar development cycles from decades to under five years. Case studies, including perennial wheat for carbon retention and nitrogen-efficient barley, demonstrate the operational feasibility of PRD-guided approaches. Enabling EU regulatory frameworks, such as the Revised GMO and NGT Policy, provide a transparent and ethically guided environment for genome editing. Finally, we outline a policy–science co-development roadmap: development of omics and data infrastructure nodes (2025–2040), establishment of integrated breeding hubs (2040–2060), and monitored field deployment of resilient cultivars (2060–2075). Together, these strategies provide a comprehensive pathway toward climate-smart, equitable, and sustainable agriculture, harmonizing technological innovation with environmental stewardship and global food security.

Keywords: artificial intelligence, gene editing, life cycle analysis, pangenomics, pan-eco-genome platform, speed breeding

[Abstract:0219]

Evaluation of Morphological and Agronomic Traits of Local Alfalfa (*Medicago Sativa* L.) Ecotypes Collected From Natural Flora In Erzurum Province

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The diversity of genetic resources is fundamental to plant breeding, a process that plays a significant role in increasing agricultural production. The wild plant forms and local populations found in a country constitute the gene pools necessary for developing new varieties. Environmental issues experienced in the last century have made the conservation of plant genetic resources a major global concern. These materials are fully adapted to the ecological conditions of their regions and are therefore of great importance for current and future breeding efforts. Transferring existing plant diversity from the present to the future is possible through surveying, collecting, preserving and evaluating said plant diversity. Alfalfa is the most widely cultivated leguminous forage plant worldwide due to its adaptability, longevity, and the high quality and yield of its forage. This study was conducted to determine the morphological and agronomic characteristics of 14 local alfalfa (*Medicago sativa* L.) ecotypes obtained from seeds collected from the natural flora of various districts in Erzurum Province. The seeds were germinated in a greenhouse and then transplanted into the field at a spacing of one plant per square metre. Over a two-year period, observations were made on ten plants from each ecotype, evaluating traits such as days to flowering, main stem length and thickness, number of stems and lateral branches, flower colour, thousand-seed weight, days to seed maturity, lodging resistance, number of cuts and thinning rate. The results showed that days to flowering ranged from 170.0 to 178.1, main stem length from 45.6 to 90.7 cm, stem thickness from 2.32 to 6.14 mm, number of stems from 7.7 to 37.2 and number of lateral branches from 12.1 to 19.2. These traits showed statistically highly significant differences among ecotypes ($p < 0.01$). In contrast, thousand-seed weight (0.95–2.35 g), days to seed maturity (240.0–249.0 days) and lodging score (2–5) showed no statistically significant differences between ecotypes ($p > 0.05$). The findings revealed that certain ecotypes exhibited superior traits, indicating their potential value for use in breeding programmes.

Keywords: *Medicago sativa*, ecotype, morphological traits, agronomic performance, Erzurum

[Abstract:0005]

Using Molecular Techniques in Legal Issues of Plant Breeding

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Protecting the rights of breeders and varieties developed through plant breeding is at least as important as plant breeding itself. Breeders should prioritize the use of new breeding technologies to protect their rights in their own breeding activities. This study lists the potential legal issues of plant breeding and variety commercialization, how molecular techniques can be used in these issues, and the benefits they will provide breeders. Furthermore, it compiles different legal and technical perspectives on the application of new molecular techniques in various plant breeding legal processes. Examples of various cases from different countries around the world, including in Türkiye, are presented along with the critical points of the cases, possible and implemented measures, and benefits of the breeders achieved by these measures. It demonstrates that molecular techniques are a very useful, quick and efficient method for protecting breeders' rights, but breeders need to establish a centralized and impartial molecular database and work on variety identification protocols at various stages, from seed to product. The lack of a technical standard regarding the extent to which molecular similarities are considered the same variety is a major obstacle using molecular techniques in variety identification and legal proceedings. It was recommended that technically accepted variety identification protocols be published by breeders, a molecular databases be established, studies be conducted to determine the level of similarity above which similarities are considered the same variety across species or product groups, and that legal collaboration be undertaken from the start of breeding programs to the commercialization of varieties and monitoring of industry. It was emphasized that the most important step for development of legal precedents is breeders should to develop a common technical opinion on the use of molecular techniques in variety identification.

Keywords: Plant breeding, legal issues, molecular techniques

[Abstract:0332]

Evaluation of Breeder’s Rights, Seed Production, Sale and Transfer Issues in Terms of Public Employees and Legislation

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Plant breeding is a fundamental element of agricultural sustainability in the face of global challenges such as population growth, climate change, and food security. Breeding activities conducted in public research institutions are of strategic importance both in generating societal benefits and strengthening scientific innovation capacity. However, legal and ethical issues arise in protecting the rights of public sector breeders regarding the new plant varieties they develop, in the sharing of income derived from these rights, and in the process of converting these rights into economic value. This study aims to evaluate the legal, ethical, and political aspects of breeder’s rights from the perspective of public employees, based on the provisions of the “Regulation on the Protection of Breeder’s Rights for New Plant Varieties,” the “Regulation on the Transfer of Plant Varieties, Variety Candidates, and Breeding Material to Seed Companies, Seed Production, and Sale of Marketing Rights,” and the “Directive on the Utilization of Breeder’s Rights by Personnel Working in Research Institutes and Stations of the General Directorate of Agricultural Research and Policies.”

The research utilized a legislative review method; the aforementioned legislation was examined article by article. In particular, Article 6, which defines the breeder’s exclusive right over the registered variety, and Article 11, which determines the scope of the transfer of rights, were evaluated from the perspective of public employees. Articles 5-9, which regulate the procedures and principles regarding the transfer of production and marketing rights for varieties developed in public research institutions, were analyzed in terms of public-private sector collaborations. The findings indicate that the legislation clearly defines breeder’s rights and generally. Despite being compliant with UPOV principles (Regulation on the Protection of Breeders’ Rights for New Plant Varieties, Article 3), the lack of uniformity in the application of income sharing (TAGEM Directive, Article 7) and rights transfer processes for public employees is evident. In conclusion, given the current structure where public interest is not adequately protected and ethical oversight in private sector contracts is weak, it is necessary to increase ethical awareness among public breeders, harmonize legislation, ensure transparency in revenue sharing, and develop collaboration models that prioritize the public interest. Effective implementation of legislation and protection of the rights of public breeders are of strategic importance for establishing a sustainable system and strengthening the national agricultural innovation capacity.

Keywords: : breeders rights, public employee, seed production, intellectual property, ethics, legislation.

[Abstract:0086]

Breeding of Legume Forage Crops in the Van Lake Basin and Their Contributions to Sustainable Agriculture

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The Eastern Anatolia Region of Türkiye, with its distinctive topography, harsh climate, and extensive rangeland resources, stands out as a major hub for livestock production. Within this region, the Van Lake Basin occupies a strategic position due to its ecological diversity and high forage production potential. However, forage production in the basin faces significant challenges caused by abiotic stress factors, including severe winters, short growing seasons, drought, salinity, and low temperatures, all of which limit the yield and quality of existing forage crop varieties. This situation underscores the importance of breeding region-specific legume forage crops to both close the forage deficit and enhance the quality of livestock production. This study evaluates the breeding potential of key legume forage crops—alfalfa *Medicago sativa*, sainfoin *Onobrychis viciifolia*, and vetch species *Vicia* spp. and their role in strengthening sustainable agriculture within the Van Lake Basin. Local populations were characterized in terms of morphological traits, yield parameters, and their adaptability to stress conditions. Statistical analyses based on Turkish Statistical Institute (TUIK) data indicated that alfalfa yields in the region remain significantly below the national average, while sainfoin and vetch yields are closer to average levels. Importantly, sainfoin and vetch populations demonstrated broad genetic variability, providing valuable material for breeding programs. The integration of conventional selection methods with molecular marker-assisted breeding and biotechnological tools presents promising opportunities for the development of new, stress-tolerant cultivars suited to the basin's ecological conditions. Beyond livestock feeding, legume forage crops contribute to sustainable agriculture through multiple ecosystem services. These include enhancing soil fertility via biological nitrogen fixation, reducing reliance on chemical fertilizers, preventing erosion, improving organic matter cycling, and supporting water conservation. Additionally, they play a crucial role in biodiversity maintenance, reducing feed costs for farmers, and fostering regional economic growth. In conclusion, the breeding of legume forage crops in the Van Lake Basin addresses not only the critical forage shortage for livestock production but also provides significant ecological and economic contributions. Such efforts strengthen the foundations of sustainable agriculture, promote environmental protection, and enhance long-term food security in the region.

Keywords: Van Lake Basin, legume forage crops, breeding, sustainable agriculture, genetic resources

[Abstract:0330]

Seed Ageing and Seed Life Span Increasing Approaches Under Climate Change Conditions

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The rapidly increasing impacts of global climate change are posing new and complex challenges in seed science and technology. Increasing temperatures, fluctuations in humidity levels, oxidative stress, and environmental uncertainties accelerate the aging process of seeds, negatively impacting their viability, germination potential, and genetic integrity. This poses a critical threat to the long-term conservation of genetic resources, the maintenance of biodiversity, and the adaptability of agricultural production to climate change. This study aims to comprehensively evaluate current physiological, biochemical, molecular, and technological strategies for extending seed longevity under changing climate conditions. The study first addresses the physiological and molecular basis of seed aging, and thoroughly discusses the roles of reactive oxygen species (ROS) accumulation, lipid peroxidation, protein and DNA damage, and antioxidant defense systems. Approaches aimed at enhancing the effectiveness of enzymatic defense mechanisms (e.g., superoxide dismutase, catalase, and peroxidase enzymes) during the aging process stand out as important factors supporting seed biological resilience. Additionally, the effects of low temperature and humidity combinations, as well as modern techniques such as controlled atmosphere storage (CAS), vacuum storage systems, and nanocoating, on seed longevity were emphasized. The literature has shown promising results in gene editing studies (e.g., the CRISPR/Cas9 system) and priming (osmotic, thermal, biopolymer) applications aimed at enhancing antioxidant enzyme activities at the molecular level. The development of artificial intelligence-assisted modeling and hyperspectral imaging (HSI) technologies in recent years has provided revolutionary advances in the early detection of seed aging processes and monitoring the storage process. Consequently, extending seed life in the face of the deepening impacts of climate change requires the holistic integration of not only genetic factors but also advanced storage technologies, biotechnological innovations, and data-based analysis systems. This study provides a comprehensive scientific framework for the sustainable management of seed banks and the development of adaptive strategies in agricultural production.

Keywords: seed aging, seed lifespan, climate change, priming, nanocoating, gene editing.

[Abstract:0314]

Physics-Informed Neural Networks Reveal Gene Regulatory Dynamics Under Combined Environmental Stress in Arabidopsis thaliana

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Plant responses to abiotic stress involve highly complex gene regulatory networks (GRNs) that orchestrate transcriptional reprogramming across multiple temporal and environmental scales. Understanding these dynamic interactions is fundamental to developing stress-resilient crops, yet modeling such systems remains challenging because of their nonlinear feedback loops, stochastic gene behavior, and limited availability of time-resolved expression data. Conventional statistical or correlation-based methods often fail to capture the mechanistic basis of these responses. To address these limitations, this study presents a physics-informed neural network (PINN) framework designed to reconstruct and interpret GRN dynamics in Arabidopsis thaliana exposed to combined salt and heat stress. Publicly available RNA-Seq data are utilized to quantify differential expression profiles under multiple stress combinations and recovery stages. Unlike purely data-driven neural models, the PINN explicitly incorporates biological prior knowledge in the form of ordinary differential equations (ODEs) that represent transcriptional activation and repression processes among core stress-responsive genes. The model simultaneously minimizes data-fitting loss and ODE-constrained residuals, thereby allowing the estimation of hidden regulatory parameters, inference of causal connections, and enhanced biological interpretability. Preliminary analyses indicate that the proposed model effectively reproduces time-dependent expression patterns, capturing both transient and steady-state dynamics observed under stress exposure. The PINN identifies several candidate regulators involved in abscisic acid (ABA)-mediated signaling and cross-talk between salt- and heat-responsive pathways. It is anticipated that continued optimization will further improve predictive accuracy and reveal previously unrecognized gene–gene interactions underlying complex stress adaptation mechanisms. The integration of artificial intelligence with mechanistic biology represents a powerful paradigm for decoding plant transcriptional regulation. The developed framework demonstrates how physics-informed learning can bridge the gap between data-driven inference and dynamic biological understanding. Ultimately, this approach is expected to guide marker-assisted and genomic selection by pinpointing master regulators that drive adaptive responses, thereby contributing to intelligent and climate-resilient breeding strategies in crop improvement programs.

Keywords: ABA signaling, intelligent plant breeding, stress tolerance, gene network dynamic

[Abstract:0126]

Identification of Stem Rust Resistance Genes in Some Turkish Wheat Cultivars Using Seedling Multi-Race Tests and Molecular Markers

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Stem rust (*Puccinia graminis* f. sp. tritici, Pgt) remains one of the most destructive diseases of wheat, necessitating continuous evaluation of resistance sources in both bread (*Triticum aestivum*) and durum (*T. durum*) wheat germplasm. Multi pathotypests and molecular analyses in this study were conducted in 2022 and 2023 at the Turkey-ICARDA Regional Cereal Rust Research Center, operating within the Aegean Agricultural Research Institute. In this study, 66 bread (*Triticum aestivum*) and 17 durum (*T. durum*) wheat cultivars released by Agricultural Research and Policies, and Commercial Companies in the National Varieties List between 1975 and 2021 were evaluated at the seedling stage against seven virulent Pgt races (TKKTF, TKSTF, TKTTF, THTTF, TTKTF, TTTTF, and TTKTT). Most commercial cultivars exhibited high infection across all races, indicating the absence of major differential-set resistance genes. However, a subset of genotypes, including bread wheat Poyraz and durum wheats Eminbey, Yaren, Alatay, and Artuklu, showed complete resistance, suggesting the presence of multiple Sr genes. Race-specific responses revealed that resistance in many cultivars was conferred by major genes outside the differential set. Multi pathotype analyses of seedling stage confirmed phenotypic structure, with durum wheats predominantly grouping in resistant clusters and bread wheats in susceptible ones. Molecular analysis using 15 SSR loci identified 10 polymorphic markers with moderate informativeness (mean PIC = 0.229; mean Shannon index = 0.525), while five loci were monomorphic and excluded. Sr2 was present in over 60% of bread wheat but absent in durum, whereas Sr21 and Sr28 were more frequent in durum. Other loci, including SR13 and SR25, showed no clear type association. These results demonstrate that the panel captures both phenotypic and genetic variation, highlighting the generally superior seedling resistance of durum wheats, the presence of race-specific and broad-spectrum resistance in selected genotypes, and type-associated allelic patterns at SSR loci. The findings provide a foundation for the deployment of durable Sr genes and for the strategic use of Turkish wheat germplasm in stem rust breeding programs.

Keywords: Pathotype diversity, *Puccinia graminis* f. sp. tritici, Multi-pathotype tests, Race-specific resistance, Resistance genes, SSR markers

[Abstract:0182]

Pathogen-Host Interaction Determining Yellow Rust Resistance in Wheat

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Wheat is considered a major crop among all the cereals for global food security. The grain yield in wheat is affected by various biotic and abiotic stresses. Yellow rust caused by the *Puccinia striiformis* is a dreadful pathogen, causing huge yield losses varying from 30% in normal conditions and up to 90% in epiphytotic conditions. This obligate pathogen has diverse pathotypes that have the capability to evade resistance offered by Yr genes of wheat. As per the gene-for-gene hypothesis, a mismatch has to be created between the virulence gene of the pathogen and a resistant gene of the host. Several techniques have been used to diagnose development of rust and resistance patterns of host for pustules size, type, and disease progression pattern of rust on wheat leaves. Moreover, spore germination, formation of haustoria, development of mycelia, and secondary sporulation are important to determine severity of the disease. Different wheat varieties react differently to different yellow rust pathotypes. A wheat breeder has to identify resistant gene(s) in the host that can confer resistance to prevailing pathotypes. The conventional approach of differential host technique is fraught with environmental fluctuation. This warrants for application of DNA-based markers for the identification of resistant genes in the host against known races of *Puccinia striiformis*. Among such markers, SSRs, SNPs have been used to identify QTLs and to establish ESTGs to create a back library. CRISPR-Cas has been used for genome editing to develop rust-resistant wheat varieties. Likewise, DNA Methylation technique is used for silencing rust susceptible genes so that virulence of pathogen is counteracted. Knockout mutants are also important to evade matching of virulence genes of pathogen and corresponding genes for resistance in host. Recently many biotechnological institutes and companies are using Omics including transcriptomics to genetically tailor resistance in wheat varieties. Transcriptomes with known resistance genes are developed and inserted in cellular system of a variety. Being self-replicating they express resistance against matching strains of virulence genes in pathogen. Thus, resistance breeding can be performed at industrial scale to cope up with monoculture of wheat cultivars over large area. This paper deals with such approaches.

Keywords: Wheat, *Puccinia striiformis*, pustule type, Disease Progression, DNA markers

[Abstract:0329]

Evaluation of Seedling Reactions to Powdery Mildew Disease in Wheat Varieties

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Wheat is one of the most consumed grain groups both globally and in Turkey, meeting 20% of daily calorie needs and 25% of protein needs, according to data (FAO 2025). However, there are many stress factors affecting both yield and quality in wheat production areas. Among the pathological factors, powdery mildew, seen in wheat fields, occurs almost every year in the Thrace, Eastern Marmara, and Black Sea regions. In the Aegean region, it is observed only during springs with high humidity and cool temperatures. In this study, seedling resistance was determined by screening bread and durum wheat varieties developed by TAGEM Institutes for powdery mildew. Experiments were conducted in the greenhouses of the Disease and Pest Resistance Unit of the Field Crops Central Research Institute. Powdery mildew samples obtained from the Yenimahalle field in Ankara were used as inoculum sources. A differential set was added to the genotypes planted in 55x35x7 cm pots to determine the race. The inoculum, obtained at a concentration of 1x106, was sprayed onto 7-day-old seedlings using a hand sprayer. Evaluations were made at the end of the 7th, 14th, and 21st days according to a 0-9 scale (0: immune, 1-3 (resistant): reaction type with necrosis and/or chlorosis areas with a small amount of mycelium, 4-6 (moderately resistant): reaction type with little chlorosis and a high density of mycelium, 7-9 (susceptible): reaction type with a high density of mycelium) (Leath and Heun 1990). The results shows that 18% of a total of 143 bread wheat varieties were identified as resistant and 52% as susceptible, while 24% of 41 durum wheat varieties showed resistant and 66% susceptible reactions.

Keywords: powdery mildew, resistance, bread wheat, durum wheat

[Abstract:0315]

Integrating Physics-Informed Neural Networks with Genomic and Environmental Data for Predicting Yield Performance in Crop Breeding

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Accurate prediction of crop yield under variable environmental conditions remains a major challenge in modern plant breeding. Conventional genomic selection (GS) methods often rely on purely statistical or black-box machine learning models that overlook the underlying physiological mechanisms driving genotype × environment (G×E) interactions. To address this gap, we propose a novel framework based on Physics-Informed Neural Networks (PINNs) that integrates genomic marker information and environmental variables within biologically meaningful constraints. This approach aims to enhance both predictive accuracy and interpretability in yield prediction models. Genotypic data were represented using single nucleotide polymorphism (SNP) markers derived from publicly available breeding datasets. Environmental variables—including temperature, precipitation, and soil moisture—were obtained from corresponding field trials and climate databases. The PINN model architecture was designed to jointly minimize two loss components: (1) the data-driven loss capturing the observed yield values, and (2) a physics-based loss derived from a simplified crop growth equation linking biomass accumulation and photosynthetic efficiency to temperature and water availability. The network was trained using TensorFlow with automatic differentiation to ensure adherence to both data and biophysical principles. Comparative analyses were performed against conventional deep neural networks (DNNs) and ridge regression best linear unbiased prediction (RR-BLUP). Preliminary experiments demonstrated that the proposed PINN achieved higher prediction accuracy (up to 15% improvement in RMSE reduction) compared to purely data-driven models across multiple environmental conditions. Furthermore, the inclusion of physiological constraints stabilized predictions under extreme climatic variability, reducing model overfitting. Feature attribution analysis indicated that specific SNPs within drought-response QTL regions and temperature-related variables contributed most strongly to yield variability. The physics-informed framework thus provided mechanistic insight into genotype–environment relationships beyond what standard machine learning approaches offer. Our results highlight the potential of integrating AI with domain-specific biological knowledge to create interpretable and robust prediction tools for crop breeding. The proposed PINN framework bridges the gap between statistical genomic selection and process-based crop modeling, offering a new direction for designing resilient crop ideotypes under climate change. Future work will expand the model to multi-trait prediction and integrate remote-sensing indices for enhanced environmental characterization.

Keywords: Physics-informed neural network, genomic selection, SNP markers, crop yield prediction.

[Abstract:0317]

Phenotyping of Some Wheat Genotypes Using a High-Throughput Seed Phenotyping Robot PhenoSeeder

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Quantification of seed morphology is crucial for selecting superior genotypes in both agricultural production and modern wheat breeding programs. Characteristics such as seed size, weight, and volume directly influence germination performance, seedling vigor, uniform emergence, and adaptability under stress conditions. In this study, five bread wheat (*Triticum aestivum* L.) genotypes (Efe, Egem, Zeybek, Ünsal35, and Kayra) were characterized using the *pheno*Seeder high-throughput robotic seed phenotyping system, which enables rapid, precise, and non-destructive measurement of individual seed traits. A total of 48 seeds per genotype were analyzed for length, width, projected area, weight, volume, and density. Statistical evaluation was performed using descriptive statistics (mean ± standard deviation), boxplots, and Pearson correlation analysis to assess relationships among traits. The results revealed clear morphological differences among wheat genotypes. Efe and Egem consistently exhibited the largest and heaviest seeds, with mean weights of 60.72 ± 8.61 mg and 61.58 ± 6.16 mg, and seed volumes of 45.62 ± 6.51 mm³ and 46.23 ± 4.96 mm³, respectively. In contrast, Kayra showed the smallest seed dimensions, with the lowest values for weight (45.62 ± 4.96 mg), volume (34.52 ± 3.57 mm³), and projected seed size (19.68 ± 1.48 mm²). These findings indicate substantial genotype-driven variation in seed morphology. Correlation analysis demonstrated strong positive associations among seed morphological traits, suggesting coordinated variation across genotypes. Seed size was strongly correlated with seed weight ($r \approx 0.90$) and seed volume ($r \approx 0.90$). In particular, the relationship between weight and volume was exceptionally high ($r \approx 0.98$), reflecting stable seed-filling patterns across genotypes. In addition, seed length and width showed moderate-to-strong correlations with seed size ($r \approx 0.78$ and $r \approx 0.79$, respectively). Meanwhile, seed density remained relatively stable across all genotypes (1.31–1.33 mg/mm³) and showed only weak relationships with other traits, indicating that density may represent an independent characteristic. Overall, this study demonstrates the value of high-throughput seed phenotyping for capturing genotypic variation in wheat seed traits and supporting early selection in breeding programs. This work was supported by the PHENOWEX project, funded under the Horizon Europe Framework Programme (Grant No. 101160158).

Keywords: automated phenotyping, high-throughput phenotyping, seed, seed morphology

[Abstract:0324]

Developing Adaptation Traits by Transferring Earliness Genes to Mufitbey Bread Wheat Cultivar with Marker-Assisted Backcross Breeding

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Bread wheat (*Triticum aestivum* L.) has been one of the most strategic crops worldwide since ancient times. Human population is growing at an unprecedented rate. In order to prevent potential food crises in the near future, both globally and locally, it is crucial that we swiftly develop high-yielding, and high-quality wheat varieties that can adapt to extreme conditions brought about by global climate change. Utilising proven bread wheat varieties as parents that have well adaptive capacity to various growing regions and desirable alles controlling high yield and quality is one of the most efficient perspective in wheat breeding programmes. In this study, the Müfitbey variety, which is well adapted to the high-altitude regions of Central Anatolia, was selected as the recurrent parent. The marker-assisted backcross breeding (MABB) method was chosen to transfer earliness allelles, which are controlled by a few genes, to new lines. The aim is to produce new varieties that flower 4–5 days earlier than the Müfitbey variety and carry its preferred characteristics. Initially, a bioinformatics analysis of the target QTLs was carried out. Suitable lines and varieties for use in the breeding studies were selected from the John Innes Centre Breeder Toolkit. These included 11 Watkins local lines, and Pfau and Weebill varieties. The selected donor parents were then crossed with Mufitbey to obtain F1 plants. The F1 plants and parents were germinated in Petri dishes, transplanted into trays, vernalised and grown. They were then backcrossed with Mufitbey to obtain Backcross 1 plants. To determine which Kompetitive Allele Specific PCR (KASP) markers to use in the study, leaves were harvested from the parents and the F1 plants at the three-leaf stage. Following DNA isolation from the leaves using the SDS method, the DNA was screened with the 55 selected KASP markers asssociated with early flowering. As a result, The lines and varieties carrying the QTL names Q7A-Mat, Q7A-TTA, Q7A-Hd, Q7A-BM, Q7A-GN, Q7A-CO, Q7A-SplN, Q7B-Ph, Q7B-BM, Q7B-Hd, Q7D-BM, Q7D-Boot and Q7D-Hd were selected as donor parents. A total of 41 KASP markers were found to be polymorphic on chromosomes 7A (17), 7B (13) and 7D (11), which can be used to screen these QTLs for the transfer of earliness alleles. A total of 702 Backcross1 seeds were obtained from 52 spikes belonging to 15 combinations in the backcrossing study conducted with Müfitbey, including nine local materials, two foreign materials, and four Turkish varieties.

* This research was conducted in the laboratories, glasshouses and growth chambers of the John Innes Centre in the UK. It was supported by the TÜBİTAK 2219 Overseas Postdoctoral Research Programme. I would like to thank Dr Simon Griffiths and members of his group for their invaluable support in carrying out this work.

Keywords: improving bread wheat adaptation, earliness QTLs, marker-assisted backcross breeding, KASP markers

[Abstract:0268]

Yield Capabilities of Mutant Promising Bread Wheat Lines Created from Different Genotypes

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Thirty-five mutant lines developed through breeding studies conducted by the Department of Field Crops at Tekirdağ Namık Kemal University, Faculty of Agriculture, Tekirdağ, were used as material. The six bread wheat varieties derived from these lines by mutagen application and eight bread wheat varieties commonly grown in the region were used for comparison. In the study, 49 genotypes were tested using a partially balanced lattice design at four different locations including central Tekirdağ, Hayrabolu, Edirne and Silivri. In the experiments, each genotype was sown in 5-square-meter plots with 15 cm row spacing and 5 meters row length, in three replicates. In the studies, 5 kg of pure nitrogen and phosphorus (20.20.0 fertilizer) was applied at sowing, 6.9 kg of pure urea at the tillering stage, 4.6 kg/da of pure nitrogen at the beginning of stem formation, and 3.9 kg/da of pure nitrogen before heading. According to the variance analysis performed on the obtained data, there were statistically significant differences in grain yield among the control varieties, mutant lines and commercial varieties. Grain yields for the genotypes ranged from 480.46 to 611.03 kg/da. The highest yield was in the NZFE 285 mutant lines with 596.19 kg/da. NZFE 285, NZFE 289, NZFE 249, NZFE 256, NZFE 242, NZFE 260, NZFE 284, NZFE 288, NZFE 287, NZFE 292, NZFE 239, NZFE 267, NZFE 245, NZFE 274, NZFE 269, NZFE 262 and NZFE 255 mutant lines were in the same statistical group with this mutant line. The lowest grain yield was in NKÜ Asiya variety with 480.46 kg/da, followed by NZFE 271with 481.46 kg/da, NZFE 277 with 500.66 kg/da. Three of the mutant lines obtained from the Sagittario variety, one of mutant lines obtained from the NKÜ Lider variety, two of the Tekirdağ variety, and two of mutant lines obtained from the NKÜ Asiya variety yielded grains superior to control varieties. The average grain yield of the eight ticari bread wheat varieties was 569.38 kg/da. The mutant lines NZFE 285, NZFE 289, NZFE 249, NZFE 256, NZFE 242, NZFE 260, NZFE 284 and NZFE 288, were given higher grain yields than the average of commercial varieties.

Keywords: Bread wheat, mutant line, grain yield, control, standard variety.

[Abstract:0120]

Crosstalk Between Green Revolution, Vernalization, and Nitrogen Metabolism Genes in the Expression of Agronomic Traits and Grain Quality in Spring Wheat

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Spring bread wheat (*Triticum aestivum* L.) is a fundamental staple crop in Russia, crucial for food security and agricultural sustainability. Major cultivation areas are concentrated predominantly in Western and Eastern Siberia and the Southern Urals. However, in the non-Chernozem zone of Russia, spring wheat is particularly valued for producing grain with superior baking qualities and is frequently employed for re-seeding failed winter wheat crops, ensuring consistent grain production and distributing harvesting activities across different periods. Despite these advantages, cultivating spring wheat in this region is challenging due to the area's unpredictable climatic conditions, characterizing it as a zone of risky farming practices. This study investigates a comprehensive collection of spring wheat varieties with a focus on uncovering relationships between key genetic markers and observed agronomic characteristics. Genotypic analysis was conducted using PCR-based molecular markers associated with critical genes controlling nitrogen metabolism (NRT-B1, PAMT-B2, BT2-3A, TAGS2-A1, NLP-3, GRF9), vernalization pathways (VRN-1), photoperiod sensitivity (PPD-1) and dwarfing genes (RHT-1, RHT-2). These findings underscore the importance of integrating genotypic data with phenotypic evaluations to optimize breeding strategies for the development of high-yielding, climate-resilient wheat varieties. The genetic diversity observed among the analyzed genotypes provides valuable resources for breeding programs targeting the risky farming zones of Central Russia and beyond. Each of these genetic pathways significantly influences crucial agronomic traits, including plant height, flowering time, nitrogen use efficiency, yield stability, and grain quality.

Financial support: The study was funded by the State Assignment FGUM-2025-0001

Keywords: spring wheat, vernalization, photoperiod, dwarfing genes, baking quality, agronomic traits

[Abstract:0323]

International Winter Wheat Improvement Program (IWWIP): Activities and Impact in the Region

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International winter wheat improvement program (IWWIP) (www.iwwip.org) is a partnership between Ministry of Agriculture and Forestry of Türkiye, CIMMYT and ICARDA to develop winter/facultative germplasm for the region of Western and Central Asia, facilitate global winter wheat germplasm exchange, and training wheat scientists. In total, there is about 15 mln ha of winter wheat in the main target area of IWWIP. The breeding programs in these countries cooperate closely with the program. The main breeding priorities are high yield, wide adaptation, rust resistance and grain quality. Annually 500-600 crosses are made which are subjected to conventional multi-locational breeding framework in Turkey. IWWIP's strategy in breeding is based on combining an effective traditional approach with application of genomic tools and molecular markers, speed breeding to accelerate genetic gains. After the opening of Speed Breeding Facility in Izmir, IWWIP has actively used and achieved three generations per year for winter wheat. This facility allows for greater genetic gain by increasing the number of generations per year and reducing the time required for the introduction of new traits into elite germplasm. The germplasm developed by program as well as the winter wheat cultivars and lines received from global cooperators are assembled and distributed into two types of international nurseries; for rainfed and irrigated/high rainfall conditions. These nurseries are offered annually to public and private breeding programs and distributed to more than 50 cooperators in all continents. IWWIP impact has primarily been with new winter wheat cultivars combining broad adaptation, high yield potential, drought tolerance and disease resistance. A total of 145 IWWIP originated cultivars have been released in 12 countries covering 2.5–3.0 Mha estimated.

Keywords: iwwip, winter wheat breeding, advanced techniques, regional impact

[Abstract:0109]

Crop Diversification Options for the Aral Sea Region of Central Asia

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Winter wheat and cotton have long been the dominant crops in the rotation in the Aral Sea Region of Central Asia. Since these two crops deplete soil nutrients, using them exclusively in the rotation would deteriorate the soil, resulting in land degradation over time. ICARDA, in collaboration with national partners in Uzbekistan, has been working on introducing diverse crop options in the Aral Sea Region, which could help improve soil health for sustainable food and fiber production and increase farm income. Multiple crops, not commonly grown in the Aral Sea Region, which were introduced for cultivation were short-duration mungbean varieties, chickpea, lentil, safflower, barley, triticale, and rye. Improved varieties of winter and spring wheat were also introduced for varietal diversity in the wheat landscape. Field Days were organized to provide the farmers with information about these introduced crops and offer them multiple options for diversifying the present wheat–cotton rotation. A detailed analysis of mungbean cultivation on soil health, farm income, and dietary consumption was conducted. All crops successfully grew under the environmental conditions in the Aral Sea Region of Uzbekistan, suggesting their suitability for diversifying the cropping systems. Among the crops evaluated, only a short-duration mungbean variety, 'Durdona', was suitable for cultivation in the prevalent wheat–cotton rotation. This variety of mungbean, maturing in 70 days, is suitable both as a spring and a summer crop. It was possible to grow 2 crops of mungbean in the same plot, May 1 to July 15, and July 16 to September 30. This option increases cropping intensity as well. Chickpea, lentil, and safflower were suitable as spring crops. Barley, rye, and triticale were suitable as winter crops. Barely could also be grown as a spring crop, while the cold-tolerant chickpea could be planted in autumn. Autumn-planted chickpea produces a higher yield than a spring crop. Inclusion of Durdona mungbean improved soil health by increasing soil organic matter and total nitrogen by 8% and 14%, respectively. This improvement in soil health resulted in a more vigorous cotton crop following mungbean cultivation. There was a 30% increase in the number of cotton bolls per plant due to improvement in soil health by growing mungbean. By cultivating Durdona mungbean, farmers were able to earn additional net income up to USD 1000 per hectare within a period of three months. The mungbean-producing farm families consumed more of this healthy food legume than the families buying mungbean exclusively from the market. On a family basis, mungbean producers consumed 25 to 53% higher mungbean grain than the non-producers. Crop diversification resulted in improved soil health, increased farm productivity and income, and higher consumption of nutritious food legumes. These positive results from crop diversification research are changing the mindset of farmers and policymakers for its adoption for a greater sustainability of crop production and food and nutritional security in the Aral Sea Region of Uzbekistan. The results have broad implications for improving cropping system diversity across the Aral Sea Region of Central Asia and beyond.

Keywords: Crop Diversification, Soil Health, Grain Legumes, Crop Rotation, Aral Sea Region, Mungbean

[Abstract:0103]

Agronomic Characteristics and Cold Stress Tolerances of Some Wheat Genotypes in Different Ecological Locations

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Bread wheat (*Triticum aestivum* L.) is one of the most widely cultivated cereal species worldwide and is crucial as a primary source of energy and protein in human nutrition. This plant, which accounts for a significant share of global grain production, is successfully cultivated in diverse regions thanks to its adaptability to a wide range of climatic and soil conditions. Within the scope of breeding efforts, agronomic and technological traits such as yield potential, hectolitre weight, 1000-grain weight, protein content, and gluten quality are prioritized. Furthermore, developing resistance to environmental stressors such as cold, drought, and disease is a critical strategy for increasing the resilience of new wheat varieties and reducing production risks. Understanding the responses of genotypes to environmental variables is essential for the success of breeding programs. Especially in regions with harsh climates, such as Eastern Anatolia, developing genotypes that can tolerate low temperatures is crucial for both maintaining yield consistency and achieving high-quality products. Therefore, developing high-yield, high-quality wheat varieties that are adaptable to regional conditions is crucial. This study was conducted during the 2023-2024 production season using 18 wheat genotypes in a randomized complete block design with three replications at four different locations (Aziziye, Pasinler, Erzincan, and Muş) to determine wheat adaptation to different agroecological conditions. Genotypes were examined for yield, yield components, and quality criteria, as well as for determining cold tolerance. The findings revealed statistically significant differences among genotypes, locations, and location × genotype interactions. When all locations were evaluated separately, highly significant differences were found among genotypes ($p<0.01$). This demonstrates the decisive influence of environmental factors on genotype performance and the need for region-specific adaptation studies. Cold tolerance tests revealed that certain genotypes exhibited high tolerance to low temperatures, while others stood out in terms of yield. These results suggest that these genotypes are promising candidates in terms of both their resistance to climatic stresses and their yield potential. In regions with harsh climates, such as Eastern Anatolia, incorporating lines with these traits into variety development programs is crucial for sustainable wheat production. The study results provide valuable information both for identifying genetic material that will contribute to breeding programs and for developing regional variety development strategies.

Keywords: Wheat, cold tolerance, yield

[Abstract:0121]

Identification and Characterization of Spring Wheat with 1RS.1BL and 1RS.1AL Translocations Conferring High Resistance to Powdery Mildew, Stem and Leaf Rust

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In modern wheat breeding programs, special attention is given to wheat-rye chromosomal translocations as a means of introducing resistance genes, which play a crucial role in enhancing plant productivity and adaptability. The targeted use of wheat-rye translocations in the wheat breeding process allows for the expansion of genetic diversity and the creation of new varieties. Translocation 1RS has gained widespread use due to its association with resistance genes such as Lr26, Lr45, Sr31, Sr50, Sr59, Yr9, Yr83, Pm8, and Pm17. The objective of this study was to evaluate the effectiveness of the 1RS.1BL translocation in conferring resistance to major fungal diseases in spring wheat varieties and lines. Field experiments were conducted over three consecutive growing seasons (2022–2024) at the Russian State Agrarian University – Moscow Timiryazev Agricultural Academy. The experimental design involved randomized $1 m^2$ plots with three replications per genotype. DNA was extracted from leaf tissue using standard protocols, and PCR with primers SCM9 was used to detect the presence of 1RS.1BL and 1RS.1BL translocations. Disease resistance was assessed weekly using a 9-point scale, where 1–3 indicated susceptibility, 5 moderate resistances, and 7–9 high resistance. Plants scoring between 7 and 9 points were considered resistant. A total of 50 wheat varieties and lines were evaluated. Among these, only one variety carried the 1RS.1AL translocation, while five synthetic lines carried the 1RS.1BL translocation, with two of them showing heterogeneity. Lines No. 35, 65, 67, 187, and 217 demonstrated strong resistance to leaf rust in 2022 and 2023 (rating 9). In 2024, lines No. 187 and 217 exhibited a moderate decline in resistance (rating 5), likely due to elevated disease pressure under exceptionally high infection conditions. The same season also witnessed the most severe outbreak of stem rust in nearly three decades; nevertheless, all 1RS.1BL lines retained high resistance to stem rust (rating 9), confirming the durability of 1RS.1BL-mediated protection. Resistance to powdery mildew was more variable and genotype-dependent. Lines No. 65 and 187 showed stable resistance across all years, while No. 35 and 217 improved notably by 2024. These findings underline the value of the 1RS.1BL translocation in delivering stable, broad-spectrum resistance to multiple fungal pathogens in synthetic hexaploid wheat (SHW). The study also highlights the potential utility of the 1RS.1AL translocation, albeit found in only one line. The identified genotypes represent promising breeding material for the introgression of resistance genes into other varieties and creation of new resistant varieties suitable for cultivation in regions susceptible to fungal plant diseases. This work was supported by the Ministry of Science and Higher Education of the Russian Federation (Federal Scientific and Technical Program for the Development of Genetic Technologies for 2019–2030, Agreement No. 075-15-2025-480 dated May 29, 2025).

Keywords: synthetic wheat, 1RS.1BL translocation, powdery mildew, stem, leaf rust, disease resistance

[Abstract:0016]

History of Rice Breeding Activities and the Obtained Development in Türkiye

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The history of rice breeding activities and the obtained development in Türkiye will be examined and evaluated in this paper. It is known that the history of rice cultivation in Türkiye goes back to Fatih period. Rice breeding activities started in the different countries of the world at the beginning of the 20th century. Rice variety development studies started in Tosya town of Kastamonu province in Türkiye in the1930s. Harun Aziz Bey, attending a six-month training course on rice cultivation in Italy in the 1930s, tested 44 rice varieties introduced from abroad for the first time. According to the results of the experiment, the varieties Kasımbeyaz, Karaköy Pirinci, Akçeltik, Maratelli, Sarıkılçık, Restono, Amerikano and Benlok were recommended for Tosya rice growing area. The Summer Crops Research Station established in Antalya in 1937, introduced the rice varieties from abroad and they tested them. Blue Rose and Caroline varieties were determined adaptable to the southern part of Türkiye. In the 1960s, rice variety development studies were carried out by Tarsus Irrigated Agricultural Research Institute and Yeşil Agricultural Research Institute. In these studies, it was determined that Blue Rose and IR-8 cultivars adapted well to the Mediterranean coastal areas and R. Bersani, Ribe, Maratelli, Sezia, Rialto, Roma, Arborio and Baldo varieties were adapted to the Thrace part of the Marmara region. After the establishment of Thrace Agricultural Research Institute in 1970, rice breeding activities were transferred to Edirne Agricultural Research Institute from Yeşilköy Agricultural Research Institute. The breeding activities conducted on a regional basis until 1982, and it was transferred into a national project in 1982. Some other research institutes in İzmir, Adana, Antalya, Diyarbakır, Ankara and Samsun took part in the project. As a result of these breeding efforts, 14 rice varieties were developed by the introduction method, 78 by the crossing-selection method and 3 by mutation method in the government institutes. The first rice varieties were registered in 1990 under the names of Trakya, İpsala, Meriç, Altınyazı, and Ergene. The most popular variety among the local developed varieties is Osmancık-97, it became a rice brand in Türkiye and provided important contributions to the rice sector. An annual 0,9% yield increase was achieved through breeding activities in Türkiye in the years between 1960 and 2000. As a result of variety development, the average rice yield increased to 8 tons per hectare in the 2000s from 5 tons per hectare in the 1990s. After 2014, the private company research institutes also started to develop rice varieties.

Keywords: rice, rice breeding, rice variety, rice yield

[Abstract:0303]

Flax Breeding Efforts in the Central Anatolia Region: Genotypic Adaptation & Evaluation

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Flax Linum usitatissimum L. is a multipurpose crop valued for its seed, oil, and fiber; however, optimizing genotypes for specific agro-ecological zones remains a major breeding challenge. Flax breeding research was initiated in 2023 to address this gap in the Central Anatolia Region (CAR). This study aimed to evaluate the agronomic performance of 97 flax genotypes under regional conditions and to identify promising candidates for oilseed and fiber flax improvement. The research was conducted over two consecutive years (2023–2024) at the İkizce Research and Demonstration Farm of the Central Research Institute for Field Crops, Ankara, using an augmented experimental design with three check cultivars (Karakız, Beyaz Gelin, and Sarı Dane). Agronomic traits including plant height, technical stem length, number of capsules per plant, thousand-seed weight, seed yield, and straw yield were recorded and analyzed. Oilseed flax genotypes performed well, exhibiting stable adaptation and high yield potential. Several entries exceeded both the trial and standard averages, showing promise for further yield and stress-tolerance breeding. Seed yield ranged between 18.26 and 87.88 kg/da in 2023 (trial average: 54.49 kg/da; standard average: 37.72 kg/da) and between 20.54 and 125.00 kg/da in 2024 (trial average: 50.69 kg/da; standard average: 45.44 kg/da). In contrast, fiber flax genotypes exhibited limited growth, with plant height ranging from 35.00–55.00 cm in 2023 and 39.50–55.20 cm in 2024. Technical stem length reached a maximum of 42.60 cm, remaining below the minimum threshold required for fiber processing. These findings indicate that the climatic and soil conditions of the CAR are suboptimal for fiber flax production. Overall, while environmental constraints limited fiber development, the region's conditions favored the selection of high-yielding and stable oilseed flax genotypes. The results clearly demonstrate that current oilseed flax cultivars are not fully adapted to CAR and highlight the need for continued breeding research. The identified superior genotypes provide valuable genetic resources for future breeding programs targeting yield stability and stress tolerance under semi-arid conditions.

Keywords: Central Anatolia Region, fiber flax, flax breeding, genotype evaluation, oilseed flax, yield performance

[Abstract:0099]

Resynthesis of Rapeseed (*Brassica napus* L.) and Its Importance for Future Brassica Breeding in Türkiye

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The Brassicaceae family is unique in its capability of interspecific hybridization, and many methods for such hybridization have already been discovered. This in turn facilitates the creation of synthetic complexes from different species as well as from their polyploids. As known, rapeseed (*Brassica napus* L.) is and amphidploid interspecific hybrid arising from the cross of *B. oleracea* and *B. rapa*. Rapeseed itself, is compared with other plants a very new plant in Turkish agriculture. Adaptation trials were performed beginning form the year 2000. Unfortunately only a few cultivars were released of Turkish origin. If you consider the genetic variability present in both diplod forms and the present variability in Turkish *Brassica* species there are possibilities to use this variation in developing genotypes adapted to ecological conditions of Türkiye. Interspecific hybridization of rapeseed can help to improve traits such as yield, resistance to pests and diseases and the fatty acid composition of seed oil, increasing the contents of oleic and linoleic acids and reducing the erucic acid content. Due to advancements in breeding and agronomical practice, genotypes developed from the genus *Brassica* have evolved globally to become the most important oil crops. Because of intensive breeding work beginning in the 1970s, genetic variation in rapeseed (*B. napus* L.) has become limited. If the desired variation is not present, species within related forms and species are used. To date, developed interspecific rapeseed (*B. napus* L.) forms have been characterized using morphological and molecular methods, and it has been determined that these forms represent a new gene pool. The determination of yellow flowered *B. oleracea* genotypes and the detection of *B. oleracea= forms displaying edible oil are interesting plant materails for Brassica breeding in Türkiye. They may be helpful in developing new rapeseed cultivars in Türkiye. Interspecific hybridization of rapeseed is an important way to innovate breeding resources. The possibility of developing new rapeseed cultivars will be discussed in detail.*

Keywords: *Brassica, interspecific hybrid, quality, breeding*

[Abstract:0022]

Factors Influencing Plant Height in Lentil (*Lens culinaris* M.) for Mechanical Harvesting

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The primary goal of agricultural activities is profitability as in every sector. A product that is economically unviable is not adopted by farmers. Profitable crop production is associated with yield and production costs. In legumes, the harvesting method plays a role in determining costs. Morphologically, lentil is relatively short and does not grow upright compared to other plants, especially cereals. This affects the harvesting method and can lead to additional and significant costs. Therefore, the suitability of the lentil plant for mechanical harvesting is more important than for other plants. When varieties unsuitable for mechanical harvesting due to their short height are grown, profitability decreases, and farmers abandon production.

The experimental trials were conducted at the İkizce Research and Application Station, affiliated with the Field Crops Research Institute, during the 2020/21 and 2021/22 growing seasons. Seven different varieties were used in the trials during each growing season. Experimental materials were planted as summer and autumn sowings in both years. This study aimed to determine the characteristic(s) that most affect the suitability of the lentil plant for mechanical harvesting and its height in terms of growing season. In the combined analysis, statistically significant differences in plant height were found between year, variety, growing season, year*growing season, and growing season*variety. Furthermore, plant height was correlated with days to 50% flowering, days to maturity, yield, and first pod height.

Keywords: *lentil, plant height, variety, growing season, autumn planting, summer planting*

[Abstract:0153]

Pioneering Speed Breeding for Lentil in Africa and the Middle East: An Innovative Simple Optimized Rapid Generation Advancement Protocol

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Lentil (*Lens culinaris* Medik.) breeding is traditionally constrained by long generation times, limiting the speed of genetic improvement and new performance varieties release. To address this challenge, we developed, optimized and implemented the first speed breeding (SB) protocol for lentil in Africa and the Middle East, based on extended photoperiod techniques (Idrissi 2020). By adjusting light intensity (Mitache et al., 2024 a), red-blue ratio (Mitache et al., 2024 b), and duration (Mitache et al., 2023), and optimizing plant growth conditions, we successfully advanced 14 intraspecific and interspecific lentil populations from F2 to F6 generation under controlled growth chamber conditions. This protocol enabled us to achieve six generations per year, with average generation cycle of about from 62 days, demonstrating the effectiveness of speed breeding in reducing generation time. In terms of effective implementation, over than 1500 F6-7 lentil homozygous advanced lines were produced and transferred in to field nurseries for seed multiplication and preliminary selection, previous to yield trials aimed at developing new improved varieties (Mitache et al., 2024 c). Beyond enhancing breeding efficiency, the SB protocol proved to be resource-efficient and easily adaptable to small- and medium-scale breeding programs. This work marks a pioneering achievement in lentil breeding pipeline for the region, demonstrating the strong potential of SB to accelerate varietal development and contribute to food security and agricultural sustainability. Idrissi, O. (2020). Application of extended photoperiod in lentil: Towards accelerated genetic gain in breeding for rapid improved variety development. Moroccan Journal of Agricultural Sciences 1:1. Mitache, M., Baidani, A., Houasli, C., Khouakhi, K., Bencharki, B., & Idrissi, O. (2023). Optimization of light/dark cycle in an extended photoperiod-based speed breeding protocol for grain legumes. Plant Breeding, 142(4), 463476. Mitache, M., Baidani, A., Bencharki, B., & Idrissi, O. (2024 a). Exploring the impact of light intensity under speed breeding conditions on the development and growth of lentil and chickpea. Plant Methods, 20(1), 30. https://doi.org/10.1186/s13007-024-01156-9 Mitache, M., Zeroual, A., Baidani, A., Bencharki, B., & Idrissi, O. (2024 b). Influence of red–blue light ratio on the phenology and morphology of different lentil (*Lens culinaris* Medik) and chickpea (Cicer arietinum) genotypes under a simple and resource-efficient in-house speed breeding method based on the application of extended photoperiod. Plant Breeding, 143(6), 773784. https://doi.org/10.1111/pbr.13206 Mitache, M., Baidani, A., Zeroual, A., Bencharki, B., & Idrissi, O. (2024 c). Rapid generation advancement through speed breeding in lentil (*Lens culinaris* Medik.). Crop Breeding and Applied Biotechnology, 24(3), e48632435.

Keywords: Lentil, speed breeding, extended photoperiod, homozygous advanced lines, genetic gain.

[Abstract:0300]

Effects of Gamma Rays and EMS Applications on Germination Characteristics and Agro-Morphological Traits of Lentil in M1 Generation

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This study was carried out in the GAPUTAEM plant growth room and trial area in Diyarbakır province during the 2023-2024. growing season. The study aimed to determine germination characteristics and some agro-morphological traits of lentil cultivars (Firat-87, Koc-21, Tigris, Şakar) under gamma irradiation (100, 200, 300 Gy) and EMS (20, 40, 60, 80, 100 mM) treatments. In the study, germination traits such as number of days to germination, seedling length, root length, seedling fresh and dry weights, root fresh and dry weights, 50% effective growth dose, germination rate, germination energy, germination rate index, number of leaves per plant and vigour index and agro-morphological traits such as number of plants at emergence, plant height, number of flowers per plant, number of pods, number of pods on the flower stalk, number of grains per plant and grain weight per plant were investigated. Germination experiments were conducted in randomized plots design, and field experiments were conducted in randomized block design with 3 replications. As a result, it was revealed that both mutagenic treatments had significant effects on the germination and agro-morphological characteristics of lentil cultivars. The highest GR50 value in gamma irradiation was obtained in Fırat-87 (337.3 Gy), followed by Tigris (314.4 Gy), Sakar (287.1 Gy) and Koc-21 (278.5 Gy). In the EMS application, GR50 values were determined as 86.029 mM for Fırat 87, 64.3 mM for Koc-21, 64.06 mM for Sakar and 49.03 mM for Tigris, respectively. The treatments created significant genetic variability in the cultivars. Among the varieties, Tigris variety was positively affected by both beam and EMS applications. High doses of applications reduced the number of pods and seeds per plant and plant seed weight. While the highest seed number per plant was obtained in Tigris variety (80 mM; 205.1) for EMS application, it was obtained in Koç-21 variety (100 Gy; 121.1) for gamma application. Grain weight in the plant increased especially in Fırat-87 (4.2 g) and Şakar (4.8 g) varieties in 100 Gy application. In Tigris variety, seed weight per plant increased in both gamma (100 Gy; 3.8 g) and EMS (100 mM; 6.9 g) applications compared to the control. The findings obtained in the study show that lentil varieties respond differently to mutagenic treatments and yield-enhancing mutations can be obtained. However, dose selection and application strategies must be carefully determined in order to optimize mutations.

Keywords: EMS, gama rays, *Lens culinaris*, lentil, mutation

[Abstract:0037]

Mining Allelic Diversity in Maize Landraces for High Temperature Stress Tolerance: Phenotyping and GWAS Insights into Candidate Genomic Regions

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Due to climate change, the development of climate-ready maize varieties is attracting increasing attention from breeders. Among abiotic stresses, high temperature stress (HTS) appears particularly difficult to manage in open fields compared to drought, making genetic tolerance one of the most promising solutions. The EU project MineLandDiv (Mining Allelic Diversity of Maize Landraces for Tolerance to Abiotic and Biotic Stresses) aims to explore maize landraces (LDs) as a reservoir of unique alleles for broadening the genetic base of modern breeding programs. In this study, a panel of 300 maize landraces originating from European and American sources was assembled from >1,200 accessions identified in previous EU initiatives. These landraces are being phenotyped under high temperature stress in field (Antalya), growth chamber (Sakarya), and controlled greenhouse (Antalya) trials conducted between 2024 and 2025. In parallel, the panel was genotyped with ~35,000 SNPs and subjected to genome-wide association study (GWAS). The analyses revealed two candidate regions on chromosomes 8 and 9, which showed strong association with tassel blast symptoms under HTS. These findings demonstrate that landraces could provide valuable allelic diversity for developing maize germplasm better adapted to climate change.

Keywords: Phenotyping, Genotyping, grain yield, tassel blast, climate resilience, breeding for heat tolerance

[Abstract:0348]

Comparative Performance Analysis of Introduced Maize Candidate Varieties for Yield and Yield Components under Bafra Ecological Conditions

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The aim of this study was to determine the performance of three introduced hybrid maize candidate varieties (HAV774, HAV911, and HAV923) in comparison with three standard varieties (P2088, DKC6980, and KALUMET) in terms of grain yield per decare and other important agronomic traits (Tassel Emergence Time (ÇGS), plant height, first ear height, harvest grain moisture, etc.) under Bafra ecological conditions. Furthermore, the study aimed to identify promising candidate varieties adapted to the region based on the obtained data. The trial was conducted with four replications during the 2020-2021 maize growing seasons. Analysis of variance showed a statistically significant difference at the 1% level among the genotypes for grain yield per decare. The highest yield was obtained from the standard variety P2088 with 14.247 ton/ha. Among the candidate varieties, HAV911 (13.013 ton/ha) and HAV774 (12.543 ton/ha) were found to be promising, surpassing the average of the standards (12.535 ton), with HAV911 being in the same statistical group (ab) as P2088. Morphologically, HAV923 stood out with the longest plant height (280.3 cm) and the highest first ear height (100.0 cm). Grain moisture content ranged between % 22.5 and %26.2. The results indicate that the HAV911 variety, which has high yield potential, should be evaluated as a candidate for regional adaptation and a new commercial variety.

Keywords: Grain Yield, Hybrid Cultivar,nAgronomic Performance, Adaptation

[Abstract:0132]

Integrating High-Throughput Phenotyping and Genomics for Quantitative Trait Dissection and Predictive Breeding in Maize

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High-throughput phenotyping (HTP) technologies, particularly those enabled by unoccupied aerial systems (UAS, UAVs, drones), are transforming modern plant breeding by providing scalable and precise data on dynamic traits that were traditionally labor-intensive to measure. Several case studies illustrate how the integration of HTP with quantitative genetics and genomic prediction can accelerate crop improvement. In the first case, convolutional neural networks (CNNs) were applied to RGB drone imagery for tassel detection in maize. By prioritizing simplicity in computational design while maintaining high accuracy (0.91–0.99 across multiple environments in Texas and Wisconsin), this approach demonstrated that relatively modest CNN architectures can replace subjective flowering observations, scaling trait evaluation to hundreds of hybrids and environments. A second case study focused on temporal plant height (TPHT) across 516 recombinant inbred lines (RILs) in three maize populations under irrigated and non-irrigated conditions. Using Weibull growth curve modeling, a novel Plant Height Growth Ratio (PHGR) was introduced, revealing genetic mechanisms distinct from TPHT alone. Notably, the flowering activator mads69 was discovered under stress conditions, while genomic prediction accuracies were more stable for PHGR than TPHT, underscoring the utility of growth-curve-based traits for quantitative genetic dissection and prediction. In a third example, temporal senescence was monitored through RGB imagery across 14 drone flights. Logistic growth modeling yielded biologically interpretable traits—Days to Senescence (DTSE) and Grain Filling Period (GFP)—which were integrated into genomic (M1) and genomic-phenomic (M2) prediction models. The inclusion of phenomic indices (NGRDI, ExR) substantially improved predictive ability, particularly under cross-validation schemes involving untested genotypes and time points, highlighting the importance of coupling growth modeling with machine learning in predictive breeding. Finally, a multi-omics case integrated phenomic, genomic, and enviromic data for grain yield prediction. Temporal vegetation index trajectories (NGRDI) were summarized using area-under-curve (CHIAUC) and functional PCA (CHIFPCA), achieving stronger genotype differentiation than yield alone across multi-environment trials. Genomic mapping identified key regulators (br2, mads69, phyC1, rap2, miR172, gl15), while multi-omics prediction improved yield prediction by ~18.5%, particularly for untested genotypes. Together, these case studies demonstrate that integrating HTP with statistical modeling, machine learning, and genomic data enables novel trait definitions, enhances genetic mapping resolution, and improves prediction accuracy. Such frameworks provide a scalable path toward modern predictive plant breeding and the development of climate-resilient maize germplasm.

Keywords: High-throughput phenotyping (HTP), Temporal plant height (TPHT), Senescence, Quantitative genetics, Machine learning / deep learning, Functional data analysis

[Abstract:0288]

Analysis of the Genetic Diversity and Heterotic Patterns of Waxy Maize Inbred Lines Based on SNP Markers

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Maize breeding programs necessitate information regarding the genetic diversity and genetic relationships among elite inbred lines in order to enhance the development of new cultivars. Waxy maize is a special corn type which grains are rich in amylopectin, have gained popularity as raw materials in the industrial and food sectors. The Manier Seed has a collection of homozygous elite waxy maize inbred lines from different sources and these sources can be used for improving new waxy maize hybrids for industrial and food purposes. In this study, a total of 20,459 SNP markers were used to analyze the genetic diversity and population structure of 469 waxy genotypes. Modified Roger (MR) genetic distance values were calculated for assessing kinship of waxy inbred lines. The highest MR distance coefficient between individuals was found to be 0.548 between lines MNwx168 and CM2_87, between MNwx20 and CM2_86, and again between MNwx_106 and CM2_86. The lowest MR distance coefficient was found to be 0.11 between line CM21 and CM25. Neighbor Joining (NJ) pedigrees were constructed based on the Modified Roger (MR) genetic distance values. Based on a population structure analysis, the 469 waxy maize inbred lines were divided into four population (K=4) corresponding to their heterotic groups: Stiff Satlk, Lancaster, Iodent, and miscellaneous. The results of this study demonstrated that the identification of heterotic groups is significantly influenced by the knowledge of genomic diversity. This knowledge will facilitate the effective and efficient management and utilization of the germplasm to create new waxy maize hybrids.

The authors express their gratitude to Scientific and Technological Research Council of Turkey (TÜBİTAK) for providing research grants for this study under the project no:TEYDEB1501 -3240501

Keywords: Waxy maize, inbred line, genetic diversity, structure, heterotic group, SNP

[Abstract:0122]

Chlorophyll-Based Phenotypic Screening of Maize Inbred Lines for Cold Tolerance

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Maize (*Zea mays* L.) is a globally significant crop that has evolved from a staple food and feed grain into a valuable industrial raw material supporting various sectors including food, feed, starch-based sweeteners, vegetable oil, biodiesel, cosmetics, and textiles. Due to its widespread applications, maize continues to hold a vital position in agricultural production and the economy. However, in recent decades, global climate change has negatively impacted maize production through drought and heat stress. In temperate regions such as Türkiye, early sowing is a strategy to escape summer drought and maximize the use of spring rainfall. Nevertheless, early planting exposes seedlings to cold stress during germination and early growth stages, making cold tolerance a crucial trait for sustainable maize cultivation.In this study, 50 inbred maize lines obtained from the Maize Genetics and Genomics Database (MaizeGDB) were evaluated under controlled conditions at the Maize Research Institute. The experiment was conducted in a factorial randomized complete block design with three replications. Seedlings were grown under optimal conditions until the two-leaf stage and then exposed to cold treatments at 4°C and 6°C, followed by recovery under optimal conditions. Chlorophyll content was measured at the 7th and 14th days using a chlorophyll meter (SPAD method), and data were subjected to statistical analysis.Results showed that cold stress significantly influenced chlorophyll content across maize lines. At 4°C, lines 47, 41, and 27 exhibited the highest chlorophyll levels on day 7, while at 6°C, lines 40, 18, and 3 were the most tolerant. On day 14, the most tolerant lines at 4°C were 10, 20, and 27, whereas at 6°C, lines 11, 7, and 1 performed best. Overall, chlorophyll-based phenotypic screening effectively distinguished tolerant and sensitive maize lines under cold stress. The results highlight the potential of chlorophyll content as a rapid, non-destructive indicator for identifying cold-tolerant genotypes, which could support breeding programs aimed at improving early-season adaptation and resilience to climate variability.

Keywords: *maize, cold tolerance, chlorophyll content, abiotic stress, phenotypic screening, inbred lines*

[Abstract:0309]

Advances in Flax Breeding for Sustainable Food, Fiber, and Regional Resilience

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Flax (*Linum usitatissimum* L.) is a versatile crop cultivated for both its high-quality fiber and oil rich in α-linolenic acid (omega-3). Its dual-purpose nature positions it as a promising species for sustainable agriculture and nutritional improvement. In light of climate change and the growing demand for functional foods, flax breeding has gained renewed global attention. Enhancing oil quality, fiber characteristics, seed traits, and disease resistance are now key breeding objectives supporting regional and global food security. This study highlights recent innovations in flax breeding worldwide and assesses Türkiye's position and potential within this research area. The main objectives include: (i) evaluating breeding strategies for oil, fiber, and seed quality improvement, (ii) emphasizing genetic resistance to *Fusarium oxysporum* (*Fusarium* wilt), and (iii) exploring the potential of perennial flax in sustainable production systems. Global flax research has advanced through genomic selection, transcriptomic profiling, and molecular marker-assisted breeding. Leading programs in Canada, China, Russia, France, Lithuania, and the United States (particularly in North Dakota, a major flax-producing state) have developed elite genotypes combining high oil content, improved fiber quality, disease resistance, and desirable seed traits. North Dakota's breeding efforts emphasize adaptability to diverse agro-ecological conditions, resistance to biotic stresses, and optimization of fatty acids composition for nutritional and industrial applications. In Türkiye, flax breeding remains limited but increasingly active, focusing on genotype adaptation, fatty acids composition, disease resistance, and yellow-seeded flax development. Yellow-seeded flax offers high potential for organic and bakery markets, while enriching omega-3 content and supporting human health. It is increasingly desired by European Union countries; however, the yellow seed coat trait is controlled by multiple genes, making breeding more challenging. Türkiye possesses several yellow-seeded flax genotypes that could meet this international demand, representing an important opportunity for national breeding programs. Integrating molecular tools with conventional selection can accelerate breeding progress. Research on perennial flax indicates potential benefits for soil health, carbon sequestration, and reduced input dependency. Strengthening national breeding capacity, expanding germplasm evaluation, and fostering international collaboration (including knowledge exchange with Canada and North Dakota flax breeding programs) will be essential for positioning Türkiye as a regional contributor to global flax innovation.

Keywords: Flax (*Linum usitatissimum* L.), flax breeding program, *Fusarium* wilt resistance, oil and flax quality, sustainable agriculture, yellow-seeded flax

[Abstract:0216]

Androgenesis Induction in Cauliflower (*B. oleracea* var. botrytis)

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Cauliflower (*Brassica oleracea* var. botrytis) is one of the important Brassica vegetable crops grown and consumed all around the world. It is more similar to broccoli. While broccoli head contain clusters of developed flower buds, cauliflower head consist of tightly packed, undifferentiated flower buds. The thick and fleshy flower curds (head) of cauliflower are used as vegetable. The consumed parts contain high levels of health promoting bioactive chemicals. In cauliflower breeding programs, main goals are the development of new varieties with high adaptability, tolerance to biotic and abiotic stresses, high yield, uniform and high head quality. Commercial cauliflower varieties are F1 hybrid varieties produced by crossing genetically pure lines for hybrid vigor and uniformity. The most important step in breeding high quality F1 hybrid varieties is the development of genetically stable inbred lines that can be used as parents. Although it has hermaphrodite flowers, they are protogynous and tend to be pollinated by insects. Development of inbred cauliflower lines with the conventional self-pollination via bud pollination is a difficult, expensive and lengthy process as it requires at least eight generations depending on the complexity of the traits of interest. In some brassica species, androgenesis-based gametic embryogenesis technology was shown to be provide high numbers of haploid and doubled haploid (DH) plants. DH lines are completely homozygous and can be used in breeding programs to replace conventionally produced inbreds. We are carrying out experiments to develop DH plants from two open pollinated (OP) standard lines (cvs. Erfurter and Snow ball). Culturing anthers containing late uni-nucleate and early bi-nucleate stage microspores in solid and liquid androgenesis induction media (NLN13) resulted in androgenic callus and embryo development. Androgenic plants developed were acclimatized to in vivo and grown in the greenhouse. Selfed seeds were obtained from one DH plant flowered in the summer of 2025. Other androgenic cauliflower plants will be acclimatized in the Fall of 2025 and characterized in the greenhouse in 2026. Doubled haploid (DH) plants were obtained from both donor OP cauliflower lines. Our results show that anther culture-based androgenesis technique can provide sufficient numbers of DH lines that can be used in cauliflower breeding programs.

Keywords: Androgenesis, Breeding, Cauliflower, Doubled Haploid

[Abstract:0336]

Determination of Responses of Eggplant Genotypes to High Temperature Stress Conditions

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In recent years, one consequence of the global climate problem has been the increasing prevalence of high-temperature stress, which threatens agricultural production today and is expected to be a key factor in the impending food crisis. This study aims to determine the various effects of high temperature stress on different eggplant genotypes. Twelve eggplant genotypes identified in previous studies as being either tolerant or sensitive to high temperatures were used in this study. To induce high temperature stress, the plants were grown in the R&D greenhouse during the summer, while the control group plants were grown in open vegetable production plots. The study involved establishing field and greenhouse trials for the 12 eggplant genotypes according to a randomised block design. To prevent plant death and the total loss of photosynthesis and enzyme function, the greenhouse temperature was lowered to 45°C with the help of fan-pads when it exceeded this temperature. The open field trial was used as the control, with eggplant seedlings planted according to climatic conditions. Care procedures such as watering, fertilisation and spraying were performed on eggplant plants grown in greenhouses and in the field. Pollen viability and germination tests, as well as measurements of plant height, number of fruits per plant, average fruit weight, fruit length, fruit setting rate, total yield, damage scale, and heat tolerance index, were performed on plants grown in both greenhouses and the open field during the eggplant genotypes' vegetation periods. The effect of high temperature varies according to genotypes and in parameters such as pollen testing, fruit set rate, number of fruits per plant and yield. Diyarbakır local eggplant lines numbered 23, 25 and 33, and genotype numbered 65 of the *S. aethiopicum* species stood out as genotypes tolerant to high temperature stress.

Keywords: *solanum melongena*, pollen viability, high temperature stress, STI.

[Abstract:0131]

Determination of Fusarium wilt resistance levels of different eggplant genetic resources and breeding lines with using molecular markers

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Eggplant (*Solanum melongena L.*) is a major vegetable crop with great potential for genetic improvement owing to its large and mostly untapped genetic diversity. Türkiye is the 4th country with the highest production amount among the world's eggplant producing countries. The most important factor limiting eggplant production is its susceptibility to soil-borne diseases such as Fusarium and Verticillium wilt. Fusarium wilt described for the first time in Japan. Soil pathogenic eggplant fungus *Fusarium oxysporum melongenae* causes vascular wilt disease in eggplant and generates serious yield losses, especially in Asian, European and Mediterranean countries. This disease is also commonly encountered in both greenhouse and open-field cultivations. Grafted seedlings are often used to avoid disease. However, this is costly. Therefore, using resistant varieties is important to avoid the use of chemical pesticides for disease control and to reduce input costs. Resistance to Fusarium wilt in eggplant is monogenic. In the Aegean Agricultural Research Institute, vegetable genetic resources are used extensively in both open-pollinated and hybrid variety breeding studies. In this study, our advanced eggplant breeding lines and germplasm in our gene pool were examined for Fusarium resistance with using molecular markers. In this study, 48 eggplant genotypes, including landraces, advanced inbred lines, and registered varieties, were screened for Fusarium wilt resistance using the SCAR426 molecular marker. The marker effectively distinguished resistant and susceptible genotypes, producing clear 426 bp bands in homozygous resistant lines and 800 bp bands in susceptible ones. Among the tested materials, only one inbred line ETA5 was found to carry the resistance allele.

Keywords: landraces, FOM, marker, variety

[Abstract:0156]

Exploiting the genetic potential of *Solanum linneanum* in backcrosses with *S. melongena* for enhanced salt tolerance

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Soil salinity is a major constraint on global agriculture, severely limiting crop productivity. Eggplant (*Solanum melongena* L.), an economically important vegetable, is particularly sensitive to salt stress. Wild relatives such as *Solanum linneanum* L. provide valuable genetic resources for improving stress tolerance. This study evaluated the salt tolerance potential of *S. linneanum* and its backcross progenies with cultivated eggplant, aiming to identify breeding materials for the development of resilient cultivars. Three backcross lines (Lin1, Lin2, Lin3), derived from *S. linneanum* and the open-pollinated cultivar 'Topan374', were tested alongside 'Topan374' (negative control) and *S. linneanum* (positive control). The experiment followed a completely randomized block design with three replications, each consisting of six plants. Plants were subjected to 150 mM NaCl, and tolerance levels were assessed through morphological parameters (plant height, stem diameter, leaf number, anthocyanin presence and prickliness) and physiological stress indicators, including malondialdehyde (MDA) and proline content. Salt stress significantly reduced growth traits across genotypes. The wild parent maintained superior tolerance under 150 mM NaCl, while the backcross progenies (Lin1, Lin2, Lin3) showed better morphological performance than the sensitive cultivar, retaining higher growth under salinity. In addition, they exhibited elevated MDA and proline levels, in some cases exceeding those of the positive control, indicating activation of protective stress mechanisms. These findings demonstrate that introgression from *S. linneanum* can enhance salt tolerance in cultivated eggplant. The promising performance of backcross lines highlights their potential as valuable genetic resources for breeding salt-resilient cultivars, supporting sustainable eggplant production in saline-prone environments.

Keywords: abiotic stress tolerance, climate-resilient breeding, genetic introgression, secondary gene pool, wild relatives utilization

[Abstract:0155]

Development of Real-Time RT-qPCR Kits for Detection and Identification of Tobamoviruses

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Tobamoviruses are economically important virus group which consist of more than 40 plant viruses infecting many plant families including the Solanaceae, and Cucurbitaceae. Tobamoviruses are easily transmitted mechanically from plant to plant and able spread rapidly in production areas, remain viable in plant debris in the soil for a long time. Moreover, Tobamoviruses can also be transmitted by seeds and transported to different countries and continents, through seed trade. Therefore, rapid and accurate, and economical detection and identification of Tobamoviruses is crucial for reducing damages caused by viruses, breeding for virus resistance, and monitoring viruses in seeds and agricultural crops. PCR-based methods have become standard for virus detection and are routinely used for the single and multiplex detection and quantification of plant viruses in various tissues and samples. Although many RT-PCR and real-time RT-PCR (RT-qPCR)-based methods have been developed for the diagnosis of Tobamoviruses, their commercialization into diagnostic kits has been very limited and to our knowledge there is no RT-qPCR kits for detection of Tobamoviruses. Therefore, degenerate/specific primers and probes were designed by comparing the complete genome sequences of all Tobamoviruses. One-step SYBR Green and TaqMan probe-based RT-qPCR methods were developed for detection of all or group of Tobamoviruses infecting crops in Solanaceae, and Cucurbitaceae using these primer and probe sets. These method was optimized and validated using number of Tobamoviruses and non Tobamoviruses. In addition, TaqMan probe-based RT-qPCR methods for simplex and multiplex detection of commonly tested economically important Tobamoviruses including Tobacco mosaic virus, Tomato mosaic virus, Tomato brown fruit rugose virus, Cucurbit green mottle mosaic virus and Pepper mild mottle mottle virus were developed and optimized. The primers and probes developed and methods optimized for detection of Tobamoviruses either individually or as a group were converted to commercial kits. The prototypes of the kits were produced and validated by two different laboratories in the public sector and available for trail and sale.

Keywords: Tobamoviruses, Detection Kits, Prototype, RT-qPCR, SYBR Green, TaqMan porbes

[Abstract:0220]

Efficient Callus Formation from Protoplasts of Eggplant *Solanum melongena* L

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Protoplast culture and callus formation from leaf-derived protoplasts were investigated in two different genotypes of eggplant (*Solanum melongena* L.) in order to evaluate genotype differences in response. Plants of eggplant were propagated under *in vitro* conditions and leaves were used as the source material for protoplast isolation. The protoplasts isolation were obtained through enzymatic digestion using 1.5% (w/v) Cellulase R-10 and 0.5% (w/v) Macerozyme R-10 for 16 hours at 25°C under dark conditions. After digestion, the released protoplasts were filtered, purified, and carefully collected to ensure high viability and uniformity of the culture material. Following isolation, protoplasts were cultured in KM8p medium supplemented with 0.2 mg/L 2,4-D, 0.5 mg/L zeatin, and 1 mg/L NAA. The culture medium was buffered with 0.05% (w/v) MES to maintain pH stability and support cell development. Cell division was observed during the early stages of culture, indicating successful protoplast viability and regeneration capacity. After approximately four weeks, a high frequency of visible callus formation was achieved from the cultured leaf-derived protoplasts. The same protocol was applied to both eggplant cultivars to ensure consistent comparison. The results demonstrated significant genotypic variation in callus induction efficiency, suggesting that genetic background plays an important role in protoplast regeneration and callus development in eggplant.

Keywords: Callus formation, eggplant, leaves protoplast, protoplast culture

[Abstract:0130]

Lettuce Variety Improving Studies

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Lettuce (*Lactuca sativa* L.) belongs to the *Asteraceae* family and it can be grown in fields and greenhouses throughout the year in Türkiye. Lettuce is a vegetable whose leaves are consumed fresh. Additionally, in China and Egypt, there are varieties of lettuce whose stems are consumed fresh, cooked, or pickled. While lettuce can generally be grown in home gardens in all regions of our country, commercial-scale production in the Aegean, Marmara, and Mediterranean regions is possible throughout the year, except for the months of June to August. In Türkiye, like all winter vegetables, the majority of the varieties used in lettuce cultivation consist of imported varieties and it is seen that lettuce breeding studies are very few. Lettuce breeding studies are economically important for our country and more lettuce varieties need to be developed. In this study, it was aimed to develop new qualified lettuce lines and varieties. The study was started with 36 parent varieties consisting of batavia, romaine, crisphead and lolo rosso types. A total of 208 hybrid combinations were obtained by crossbreeding between parents. Of these, 75 lettuce populations were in F1 and 133 were in F2 generation. Additionally 74 single plants were selected from lettuce populations in 7 different F2 stages. Studies are carried out according to the pedigree method.

Keywords: Lettuce breeding, variety development, pedigree method

[Abstract:0138]

Hermaphroditism in the Pistacia Genus: A New Report from Gaziantep

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The genus Pistacia (Anacardiaceae) consists of twelve species that high economic and cultural importance and mostly spreading in Mediterranean and Asian countries. All species in the genus are dioecious. Their flowers are unisexual, naked, and anemophilous. Both staminate (male) and pistillate (female) inflorescences are bearing several hundred individual flowers. Although species within the Pistacia genus are generally known to be dioecious, very few cases of exceptional sex types and flower distribution have been reported in some populations. These situations present opportunities for studying sexual differentiation and sex determination mechanisms in Pistacia species. The Pistachio Research Institute's Field Gene Bank contains 232 genotypes of the Pistacia genus. UCB1 (*P. atlantica* x *P. integerrima*) added in the Field Gene Bank in 1998. Phenological observations revealed that a genotype derived from UCB1 seeds illustrated hermaphroditic flowers after long juvenile time in 2022. The hermaphrodite tree has illustarted that the flowers on the inflorescences on all branches are hermaphroditic. These flowers demonstrate the capability of maturing pistils and stamens, self-pollinate, and fruit (seed) develop. The 1,000 seeds of the tree were planted. Over 50% of them were germinated in 2024. Following that, here were no problems in the development of the germinated seeds, and healthy seedlings were obtained. This newly identified genotype could result in: a) Breeding program could focus on transfering the hermaphroditic floral trait to new pistachio cultivars. The project involves a variety of breeding methods, including cross-hybridization, where pollen from a hermaphroditic genotype is used as a pollinator. b)The newly developed hermaphroditic cultivars would possess the ability to self-pollinate. This would eliminate the need for non-productive male trees in commercial plantations, thereby maximizing the usable land and increasing yield per unit area. c)The consistent and reliable pollination provided by hermaphroditic cultivars would significantly reduce the occurrence of "blank" nuts, which are typically caused by insufficient pollination. This would improve both the quality and quantity of the harvest. d)The hermaphroditic genotype itself would be an invaluable resource for genetic research, providing material to study the mechanisms underlying the hermaphroditic trait. Ultimately, introducing these new hermaphroditic cultivars into pistachio production would lead to a substantial increase in the quantity of product obtained per unit area. At the same time, new hermaphroditic cultivars would enhance the overall productivity and profitability of pistachio cultivation.

Keywords: *Pistacia*, *Pistacia vera*, hermaphrodite, dioecious

[Abstract:0142]

Determination of the Effective Mutation Value in Pistachio

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In pistachio breeding program, there are some main objectives to develop new pistachio cultivars that possess a complete set of superior fruit characteristics, such as high green kernel color, large fruit size, thin shell, high splitting rate, low shell-separation resistance, and high yield. Also, desirable plant characteristics like resistance to diseases and pests, low tendency for alternate bearing, trouble-free grafting, high yield, and suitability for mechanical harvesting could be significant purposes. In recent years, classical breeding methods is too limited. Working with mutation breeding, a method previously unexplored in the pistachio species, leads to increase the variation of pistachio germplasm. For this purpose, the accurate determination of the Effective Mutation Dose (EMD), which is the fundamental stage of mutation breeding, is critical for creating a population with wide desired variation. This study aimed to determine the EMD in pistachio. For this research, buds from the widely cultivated Turkish 'Uzun' pistachio cultivar were irradiated in a Co60 source within an Experimental Gamma Irradiation Unit. The plant material was sourced from the Pistachio Research Institute. For the dose determination studies, grafting scions were collected from healthy trees, totaling 700 buds. Following that, 700 buds separated into seven distinct dose groups, each containing 100 buds. The scions were then transported to the Nuclear Energy Research Institute (NERI), which is under the Turkish Energy, Nuclear and Mineral Research Agency (TENMRA). Then the scions were irradiated at doses of 0, 10, 20, 30, 40, 50, and 60 Gy. The irradiated scions were brought back to the Pistachio Research Institute and grafted onto tube-grown seedlings, which were obtained from 'Siirt' pistachio seeds. Following grafting, observations were recorded, and data on viability, shoot length, and shoot thickness were collected. Using this data, a linear regression analysis was performed, and the EMD value was determined to be 31.47 Gray. The determined EDM would be used to deliver superior mutant plants in terms of yield and quality to producers from the rich variation expected to be generated in radiated population.

Keywords: pistachio, variety, breeding, mutation, mutant

[Abstract:0145]

Blank Nut and Nut Splitting Variations in Siirt x Peters F1 Pistachio Population

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Pistachio (*Pistacia vera* L.) is one of economically significant species in Anacardiaceae family. Pistachio is one of the third most produced nuts following hazelnut and walnut in Türkiye. Pistachio has very long juvenile stage and therefore marker assisted selection can be very fruitful in this species. To develop markers associated with nut characteristics, we crossed Siirt (female) and Peters (male) cultivars in 2016 and planted about 700 F1 progenies at the end of 2017. A total of 198 progenies had the first bloom in 2023, and the nuts from 360 and 380 F1 progenies were harvested in 2024 and 2025, respectively. The nuts of cv. Siirt was also harvested as a control. In both years, the nuts of 280 F1 progenies were characterized based on their blank nut and split nut traits. In 2024, the rate of blank nut was between 3% and 78%, while the control had 7%. The nut splitting rate was changed from 0% to 100%, while the control had 92%. In 2025, the blank nut percentage was changed between 2% and 52% and the splitting rate was between 0% and 100%. The cv. Siirt had 7% blank nut and 93% split nut rates in 2025. In a conclusion, a wide variation was obtained for both characters in Siirt x Peters F1 population in the both years. To develop markers for these characters, genetic data is underway.

Keywords: *Pistacia vera*, pistachio, blank nut, split nut

[Abstract:0084]

Selection of Walnut Genotypes in Malatya Province

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Anadolu is the center of origin for walnuts (*Juglans regia* L.) and many other fruit species. Walnuts are dioecious and cross-pollinate, so each seed-propagated tree represents a unique genotype. Türkiye, one of the world's leading walnut-producing countries, has a wide variety of seed-derived genotypes in addition to standard varieties, providing valuable genetic resources for breeding programs. Malatya, a province in Eastern Anadolu with intensive fruit production, relies primarily on locally adapted walnut genotypes. This study, conducted from 2015 to 2024, aimed to identify superior genotypes among local populations. Seven promising genotypes were selected based on fruit quality and tree characteristics. The weight of the shelled nut ranged from 13.03 to 17.03 g (average 15.03 g), while the kernel weight ranged from 7.03 to 8.58 g (average 7.80 g). The kernel percentage ranged from 48.82% to 58.09% (average 53.45%). Fruit dimensions were: length 37.91–45.95 mm, width 32.62–42.14 mm, and height 32.15–38.90 mm. The average shell thickness was 1.10 mm. All genotypes were 100% sound and had a sound meat ratio. Shell separation was easy in six genotypes and moderate in one. Five genotypes had smooth shells, while six cracked easily. Protandry was observed in five genotypes, and two were protogynous. In the kernel color analysis, the L*, C*, and ho values ranged from 45.19 to 60.44, 27.04 to 33.38, and 75.54 to 82.75, respectively. The shell color values were L* 51.82–60.21, C* 19.21–31.19, and ho 66.71–69.99. The proximate composition of the kernels included moisture (2.49–5.17%), protein (11.99–14.43%), ash (1.52–1.97%), and fat (59.21–71.73%). These results demonstrate the high variability and potential of local walnut genotypes in Malatya for future breeding and cultivation improvements. Registration procedures for the specified genotypes will continue. The study was supported by the General Directorate of Agricultural Research and Policies (TAGEM).

Keywords: *Juglans regia* L., Walnut, Selection, Malatya

[Abstract:0077]

Assessment of Chestnut Blight Resistance in Individuals Developed Through Interspecific Breeding in Chestnut

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Chestnut blight (*Cryphonectria parasitica*) is one of the most significant threats to chestnut production in Turkey and worldwide. The development of resistant cultivars has become essential to ensure sustainable chestnut cultivation. In this study, interspecific hybridization was conducted using local *C. sativa* (European chestnut) genotypes, namely İbrahimbey Işıklar, Karasu, and EGK-1, crossed with *C. mollissima* and *C. crenata* genotypes known for their disease resistance, including the cultivars Marigoule, Maraval, Bouche de Betizac (hybrids), and Akyüz (a complex hybrid). A total of nine different hybrid combinations were evaluated to determine their tolerance levels against chestnut blight.

The hybrid individuals developed for this purpose were assessed under optimum conditions using the small stem assay method involving inoculation with *Cryphonectria parasitica*. Disease progression and plant responses were monitored on annual shoots over time, and lesion development was supported with measurements up to the 68th day. This approach enabled a detailed evaluation of disease progression and survival performance of the hybrid individuals.

The results revealed a wide range of tolerance among the hybrid genotypes against chestnut blight. Combinations such as EGK × MG-21 and KS × MR-22 demonstrated relatively lower lesion development and higher survival rates, whereas some combinations, such as İB × MG-22, exhibited high susceptibility.

The findings underscore the importance of incorporating genetic resistance into breeding programs for chestnut blight management. They also highlight the potential of developing improved *C. sativa* -based plant material through interspecific hybridization with resistant cultivars, contributing to the production of blight-tolerant chestnut genotypes.

Keywords: *Castanea sativa* Mill., variety, resistance, hybrid

[Abstract:0088]

Identification of Candidate Chestnut Rootstocks Tolerant to *Phytophthora* through Hybrid Breeding

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Chestnut (*Castanea sativa*) is one of the most important non-wood forest products in Turkey from both ecological and economic perspectives. According to 2024 data, Turkey ranks third in the world chestnut production with 74,300 tons. However, the sustainability of this production is at risk due to biotic and abiotic stress factors as well as the influence of climate change on the distribution of pathogens. Among the diseases that cause the greatest losses in chestnut cultivation, ink disease (root rot) caused by *Phytophthora* species is the most destructive. In Turkey, the two most widespread pathogens are *Phytophthora cinnamomi* and *Phytophthora cambivora*, both of which seriously threaten chestnut production. In this study, controlled hybridizations were performed between hybrid parents (*C. sativa* × *C. crenata*) known for their resistance and local *C. sativa* genotypes adapted to national conditions. In the first stage, local cultivars (İbrahimbey Işıklar, Karasu, EGK-1) were hybridized with tolerant hybrids (Maraval, Bouche de Betizac, Marigoule) to create hybrid populations. In the second stage, hybrid seedlings grown under greenhouse conditions were tested by selecting healthy individuals with a stem diameter ≥5 mm at 9–10 cm above the soil surface. For pathogen inoculations, *Phytophthora* isolates identified by isolating from soil or fine roots were used. To minimize the risk of pathogen spread to the external environment, the experiments were conducted in a controlled semi-shaded greenhouse where chestnuts are not cultivated, with regular temperature and humidity monitoring. Individuals were arranged in a randomized block design and identified with double labels/plot codes. At the inoculation stage, 85 hybrids were used for each of the two pathogens, and in addition, a control group consisting of 85 individuals was not inoculated but only subjected to stem wounding with a cork borer followed by insertion of sterile PDA plugs. As a result of the experiment, inoculations with *P. cinnamomi* resulted in 68.3% mortality, whereas inoculations with *P. cambivora* resulted in 17.4% mortality. In the control group, the mortality rate remained at the level of 5%. The obtained data revealed that *P. cinnamomi* is a more aggressive pathogen causing faster mortality. This study provides important findings for the development of resistance against pathogens that threaten the sustainability of chestnut cultivation in Turkey. Considering the high aggressiveness of *P. cinnamomi*, it was concluded that this pathogen should be the primary target in breeding programs. The individuals obtained from the hybrid populations constitute a valuable resource for the identification of tolerant genotypes. It was further concluded that future breeding programs supported by selection studies and clonal propagation techniques, through the in vitro propagation of tolerant rootstock candidates followed by repeated inoculations, and the subsequent introduction of confirmed tolerant rootstocks into chestnut cultivation, are of critical importance for ensuring the long-term sustainability of chestnut production in Turkey.

Keywords: Chestnut, *Castanea sativa*, *Phytophthora cinnamomi*, *Phytophthora cambivora*, hybridization, resistance

[Abstract:0149]

Impacts Of Climate Change On Plant Breeding Strategies And Methodology

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Climate change intensifies abiotic and biotic stresses such as rising temperatures, water deficit, salinity, frost damage and the emergence of new pests and diseases through extreme climatic events, thereby threatening agricultural production on a global scale. These conditions directly affect food security and sustainable production targets, while plant breeding plays a crucial role in ensuring crop productivity and sustainability under changing climate conditions. In particular, tolerance to drought and heat stress, resistance to salinity, and resilience against emerging pest–disease complexes are among the key objectives of contemporary breeding programs. Although traditional breeding methods remain the foundation of crop improvement, they are limited in responding to rapidly changing environmental conditions. In contrast, modern approaches such as molecular markers, genomic selection, high-throughput phenotyping, and gene-editing technologies like CRISPR/Cas9 accelerate the breeding process and, when integrated with conventional methods, offer significant opportunities for developing climate-resilient cultivars. Furthermore, high-throughput phenotyping technologies and remote sensing–based stress monitoring offer valuable opportunities for integrating physiological and genetic data into breeding programs. Therefore, the identification and conservation of genetic resources, along with the application of novel technologies in breeding programs, are of critical importance for climate-resilient agricultural production. Nevertheless, ensuring sustainability in agricultural production also requires careful consideration of socio-economic dimensions. In this context, the development of climate-resilient cultivars is closely linked with farmers' adaptation strategies, climate-friendly agroecological approaches, and supportive policy mechanisms. The escalating global population and rising temperatures associated with climate change, alongside phenomena like drought, floods, and sudden climatic events, significantly impact the yield, quality, and resilience of all plant species. High-temperature stress negatively affects flowering, fruit set, and quality in fruit species, while drought and salinity limit growth, nutrient accumulation, and yield in vegetables. Consequently, breeding programs are concentrating on developing varieties with enhanced stress tolerance, improved water and nutrient use efficiency, and resistance to both high and low temperatures. This article highlights the shifting breeding targets and methodologies shaped by climate change, emphasizing their critical roles in fostering resilient, sustainable, and climate-smart agricultural systems.

Keywords: Plant breeding, climate change, drought tolerance, genomic selection, sustainability

[Abstract:0235]

Some Morphological and Biochemical Traits of Birecik Garlic, Registered as a Local Variety

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According to 2024 data from the Turkish Statistical Institute (TÜİK), fresh garlic production in the Birecik district of Şanlıurfa province reached 1.013 tons from 450 decares of cultivated area, while dried garlic production reached 2.250 tons from 2.250 decares. The currently registered garlic variety, Kastamonu Taşköprü, is not widely cultivated in the Southeastern Anatolia region, which has dominated national garlic production over the past five years, according to TÜİK data. The low cost of imported garlic encourages consumer preference for foreign products, consequently diminishing the competitiveness of domestic producers. Furthermore, the use of imported garlic as seed material, in addition to its consumption in the domestic market, negatively affects garlic cultivation and threatens the biodiversity of local Turkish garlic varieties. Supporting domestic and national resources in production will not only contribute to the production of healthy products but also ensure that the value of agricultural production is preserved for future generations. Birecik garlic was registered as a local garlic variety by the Local Variety Evaluation Commission of TTSM on 16.12.2024, based on the application of GAP Agricultural Research Institute. In the characterization studies carried out for the registration stages of the local variety, plants with leaves exhibiting a low degree of waxiness were found to had ellipse-oval bulbs with an average weight of 42.65 g, bulb width of 50.81 mm and bulb height of 42.10 mm. Birecik garlic, which forms compact bulbs, had an average of 20-30 cloves per bulb, with each clove weight was 1.2 g. Biochemical analyses revealed that Birecik garlic was distinguished by its total amino acid content (14.154,74 mg/100 g) compared to Taşköprü garlic (14.070,40 mg/100 g). In addition, Birecik garlic was found to contain higher amounts of proline than Taşköprü garlic (1.082,95 mg/100 g and 297.85 mg/100 g, respectively). Proline is an important amino acid that plays a role in enhancing plant tolerance to environmental stresses. Similarly, serine, an amino acid that increases tolerance to environmental stress conditions such as drought, salinity, or low temperature, was also detected in Birecik garlic (630.49 mg/100 g), and it is significant for plant development. Furthermore, the content of branched-chain amino acids in Birecik garlic (742.18 mg/100 g) was considerably higher than in Taşköprü garlic (332.86 mg/100 g). These findings highlight the superiority of Birecik local garlic in terms of its morphological and biochemical characteristics and demonstrate that it is an important local variety for the region, both in terms of production and nutritional value.

Keywords: Garlic, local variety, biochemical characterization, morphological characterization

[Abstract:0125]

Cultivar Development in Güvey Feneri (*Physalis peruviana* L.)

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Güvey feneri (*Physalis peruviana* L), commonly known in Türkiye as “altın çilek-goldenberry,” is a member of the Solanaceae family. The initial studies on this species were carried out to determine its adaptation potential. Owing to its promising agronomic traits, a selection breeding program was initiated, and comprehensive studies covering introduction, adaptation, breeding, yield, and quality traits were conducted between 1995 and 2025 at the Atatürk Horticultural Central Research Institute and under grower conditions. The candidate cultivar exhibited upright growth, with anthocyanin pigmentation at the internodes of both main and lateral branches. Plant height ranged from 1.30 to 1.65 m under open-field conditions and up to 2.30 m under protected cultivation. Leaf length and width were measured as 9.28 cm and 6.64 cm, respectively. Flowering began 30 days after transplanting, while fruits reached harvest maturity 55–60 days after anthesis, with a total growing period of 150–180 days. Fruit characteristics with calyx included an average fruit weight of 4.29 g, diameter of 25.08 mm, height of 34.08 mm, and pedicel length of 14.05 mm. Without calyx, the average fruit weight was 4.07 g, diameter 18.56 mm, and height 19.30 mm. At edible maturity, fruits were yellow–orange in color and slightly oval in shape. Each fruit contained an average of 288.29 seeds, with a thousand-seed weight of 1.21 g and approximately 810.93 seeds per gram. The candidate cultivar combines favorable plant growth, earliness, and desirable fruit traits, indicating its potential for the development and expansion of goldenberry cultivation in Türkiye.

Keywords: Goldenberry, Inca berry, ground cherry, cape gooseberry cultivar development, breeding

[Abstract:0128]

Evaluation of some Faba bean (*Vicia faba* L.) Genotypes for Fresh Consumption in Aegean Region

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To conduct a preliminary evaluation of genotypes obtained by propagating single plants selected from local broad bean (*Vicia faba* L.) populations under isolated conditions, 32 genotypes were evaluated, and lines suitable for fresh consumption were identified. Lines found to be superior in terms of fresh broad bean yield were also evaluated in a randomized complete block design with three replications in two years. In the trial 12 lines and 3 varieties (Lara, Seher, Salkım) were evaluated. In the first year the yield of the lines and varieties ranged from 1.5 to 2.2 tons per decare. Four lines ETA2, ETA7, ETA3, and ETA8, along with Lara and Seher varieties, were grouped in the same group in terms of suitability for fresh broad bean consumption, with pod lengths ranging from 11.3 to 11.8 cm. ETA7, ETA3, and ETA8 also had the highest values in terms of number of seeds per pod and pod length ranging from 4 to 5 cm. These lines were similar in yield and pod type to Lara and Seher which are popular fresh broad beans in the market, and were suitable for use as fresh broad beans. In the second year average fresh broad bean yield was 1.7 tons per decare. Statistical differences were found among the genotypes in terms of yield, pod length, pod width, pod thickness, and number of seed per pod. The line ETA1 had the highest yield, followed by Lara (2 tons/da). Lara (11.08 cm) and Seher (10.86 cm) ranked first in pod length. Lara, along with ETA3 and ETA8, had the highest values in pod number per plant. The lines ETA3, ETA7, and ETA8 are in the same group as Lara and Seher in terms of pod width. These lines also yielded suitable values in terms of pod length, pod thickness, and seed number, and were suitable for fresh broad bean consumption. As a result, the ETA 7 line was proposed for registration and registered as Tugay in 2020 and the seeds of the variety are distributed to farmers in Aegean region.

Keywords: Faba bean, *Vicia faba* L., fresh consumption, landraces

[Abstract:0217]

Doubled Haploid (DH) Turkish Carrot (*Daucus carota* L.) Lines

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Many generations of self-pollination are required to develop genetically stable inbred lines for use in carrot (*Daucus carota* L.) variety development programs. It is almost impossible to produce fully homozygous lines via self-pollination due to severe inbreeding depression problems experienced. Androgenesis-based gametic embryogenesis, a technique allowing the production of plants with from microspore cells of donor plants, can be used in the production of plants with a haploid set of chromosomes. Chromosome doubling converts haploid plants into fully homozygous doubled haploid (DH) carrot plants. DH plant production can replace conventional inbred development process in carrot breeding programs. Successful application of this technology can help plant breeders accelerate the development of inbreds within one generation. In DH carrot lines important agronomic traits are stabilized due to full homozygosity. In carrot, androgenesis induction can be induced by culturing anthers containing microspores at late uni-nucleate and early bi-nucleate stages in B5- and NLN-based induction media containing high sucrose and plant growth regulators. We investigated the potential for androgenic plant production potential in orange- and purple-rooted carrot lines. Anthers isolated from surface disinfected immature flowers of donor lines were cultured in 65 x 15 mm Petri dishes, which were kept in a growth room at 25oC in dark for two months. Androgenic responses were observed in callus and embryo forms within three months of culture. Donor genotypes showed significant differences in their responses to gynogenesis induction media. Orange-rooted donor lines showed higher gynogenic plant yield than purple-rooted lines. Regenerants obtained were acclimatized and grown in the greenhouse for morphological evaluations. The majority of the androgenic regenerants were diploid, while others were haploid and tetraploid. Some androgenic carrot plants were placed under protected cages for selfed-seed production. The results of this study showed that genetically pure lines can be produced from Turkish carrot germplasm. These DH carrot lines are currently being evaluated for agronomic traits.

Keywords: Acclimatization, Androgenesis, Breeding, Carrot, Doubled Haploid

[Abstract:0178]

Identification of Zucchini yellow mosaic virus (ZYMV) Resistant Cucumber Genotypes through Phenotypic and CAPS Marker Assisted Selection

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Cucumber (*Cucumis sativus* L.) is a major greenhouse crop after tomato, grown for fresh and industrial markets. Viral diseases cause significant economic losses in vegetables, with zucchini yellow mosaic virus (ZYMV) being a particularly destructive pathogen for cucurbits, leading to severe yield and quality declines in cucumber. Identifying resistant genetic resources is essential for sustainable breeding. The objective of this study was to screen twenty cucumber genotypes from the Bati Akdeniz Agricultural Research Institute (BATEM) germplasm pool for ZYMV resistance using both phenotypic and molecular approaches. The screened set included thirteen Plant Introduction (PI) accessions obtained from the U.S. Department of Agriculture (USDA) cucumber germplasm collection and five breeding lines and two cultivars. The experiment was conducted using a randomized complete block design with four replications. The susceptible cultivar ‘Hızır’ and the resistant cultivar ‘Multistar’ were used as controls to verify the virulence of the ZYMV inoculum. Plants were mechanically inoculated with ZYMV and maintained under controlled greenhouse conditions. Disease symptoms were recorded weekly for four weeks using a 0–4 severity scale. The presence of ZYMV was verified by reverse transcription polymerase chain reaction (RT-PCR), while the zym resistance allele was identified using a tightly linked cleaved amplified polymorphic sequence (CAPS) marker. Accessions exhibited significant variation in response to ZYMV infection. While several genotypes were moderately to highly susceptible, three accessions (PI 511818, PI 511819, and PI 511820), two lines (TH179 and TH185), and one cultivar (Gözen F1) showed strong resistance, remaining symptomless or developing only mild mosaic symptoms throughout the four-week evaluation. CAPS marker analysis confirmed the presence of the resistant allele in these genotypes, consistent with phenotypic data. In contrast, susceptible genotypes displayed the restriction pattern associated with the recessive zym-susceptible allele. The strong concordance between phenotypic and molecular results validates the CAPS marker as a reliable tool for selecting ZYMV-resistant cucumbers in breeding programs. Overall, this study demonstrates that combining phenotypic screening with marker-assisted selection enables efficient identification and utilization of ZYMV resistance in cucumber breeding.

Keywords: Cucumber, ZYMV resistance, screening, CAPS marker, genetic resources, plant breeding

[Abstract:0258]

Prickly Pear (Opuntia ficus-indica L.): Adaptation to Drought Conditions, Biochemical Properties and Potential Applications

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Prickly pear (Opuntia ficus-indica L.) is a climate-resilient cactus species that has attracted growing scientific and commercial interest due to its exceptional adaptation to drought conditions, extreme temperatures, and nutrient-poor soils. In an era of climate change, water scarcity, and land degradation, this species presents a sustainable alternative for agricultural production in arid and semi-arid regions. Its crassulacean acid metabolism (CAM) enables efficient water use by opening stomata at night, reducing transpiration and enhancing biomass production under environmental stress. Morphological features such as thick cladodes, waxy cuticles, and extensive root systems further support drought tolerance. Beyond its ecological adaptation, O. ficus-indica possesses rich biochemical properties. The fruits and cladodes contain high levels of vitamins (C, E, and B-complex), minerals, amino acids, and dietary fibers. Additionally, they are abundant in bioactive compounds such as polyphenols, flavonoids, betalains, and carotenoids, which contribute to strong antioxidant, anti-inflammatory, antimicrobial, and metabolic regulatory effects. These bioactive properties support its use in functional foods, nutraceuticals, and pharmaceutical formulations. The plant also offers industrial and cosmetic applications, including natural colorants, moisturizing agents, and seed oil rich in unsaturated fatty acids. Furthermore, prickly pear plays a significant environmental role by stabilizing soil, preventing erosion, sequestering carbon, and restoring degraded lands. It supports rural livelihoods and promotes climate-smart agriculture with minimal input requirements. Despite its advantages, challenges remain in postharvest handling, standardization of bioactive components, and large-scale commercialization. To fully harness its potential, further research is needed on genetic improvement, processing technologies, and value-added product development. This review examines the drought adaptation strategies, biochemical composition, and potential applications of O. ficus-indica, emphasizing its importance as a strategic crop for sustainable agriculture, food security, and economic development in the face of global climate change.

Keywords: *Opuntia ficus-indica*, Drought Adaptation, Biochemical Properties, Functional Food, Climate-Smart Agriculture, Sustainable Use

[Abstract:0085]

Phenological, Morphological and Molecular Characterization of Cherry Laurel Genetic Resources

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This study was conducted within the scope of the ongoing Cherry Laurel *Prunus laurocerasus L.* Genetic Resources Project, which was initiated in 1997 by the Hazelnut Research Institute through the Black Sea Region Cherry Laurel Selection Project. Between 2021 and 2023, phenological and morphological data were collected, and genetic relationships among 86 individuals were evaluated. In the study, the dates of first bloom, full bloom, end of bloom and harvest of cherry laurel genotypes were determined. Genotype 52 K 18 was identified as the earliest flowering (15 March), whereas genotypes 53 K 02, 53 K 04, and 61 K 04 were the latest to flower (25 April). Genotypes 52 K 18 and 55 K 05 were harvested earliest (13 July), while genotypes 08 K 03 and 28 K 18 were harvested latest (25 August). Among the cherry laurel genotypes, the number of fruits per cluster ranged from 7 to 25, cluster weight from 18.5 to 107.44 g, cluster length from 4.33 to 11.66 cm, fruit width from 9.75 to 22.59 mm, fruit length from 9.7 to 21.16 mm, fruit weight from 0.97 to 6.82 g, seed weight from 0.24 to 0.63 g, and total soluble solids content (TSS) from 13% to 24.5%. Molecular analyses were performed using 50 SSR markers in 86 individuals. The results revealed genetic diversity within the population, ranging from 2% to 40%, with an average of 18%.

Keywords: cherry laurel, biodiversity, characterization, SSR

[Abstract:0147]

Breeding Program in Türkiye for Fire Blight-Tolerant Dwarf and Semi-Dwarf Pear Rootstocks

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Pear (*Pyrus* spp.) rootstock diversity is limited compared to other temperate fruit species. The currently available pear rootstocks are not satisfactory in terms of vigor, yield, and quality. Quince rootstocks, which are widely used in pear cultivation, restrict pear production due to graft incompatibility issues and their sensitivity to biotic and abiotic factors. Another important factor limiting the sustainability of pear cultivation is fire blight disease (*Erwinia amylovora* Burrill). In years of severe infection, the disease can cause tree mortality and significant economic losses. Moreover, the measures taken to suppress disease severity are not environmentally friendly approaches. The first step in combating this disease is the development of tolerant rootstocks and cultivars. In this context, the Fruit Research Institute launched a breeding program about a decade ago aimed at developing weakly vigorous and fire blight-tolerant rootstocks. Within the program, genotypes with promising rootstock characteristics, obtained from seeds of wild pear collected from nature and from open-pollinated seeds of tolerant genotypes, have been evaluated for their suitability as rootstocks. To date, sufficient numbers of plants have been obtained from 167 rootstock candidates, and 89 of them have been grafted with the 'Deveci' cultivar to establish a selection plot. Phenological observations of the rootstock candidates in the selection plot are being conducted, and their effects on juvenility period, yield, and fruit quality are under investigation. So far, the first fruits have been observed in the 'Deveci' cultivar grafted onto 26 different rootstock candidates. Studies on propagation through hardwood cuttings, seedling production, and determining the fire blight tolerance levels of new individuals are ongoing.

Keywords: *Pyrus*, rootstock, dwarf, fire blight

[Abstract:0150]

Breeding European Pear Varieties Tolerant to Fire Blight Disease

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Fire blight disease presents significant challenges and carries notable financial implications in its management and control. The disease agent causes noteworthy economic losses in some fruit species, particularly pears and apples. The limited availability of licensed pesticides complicates disease management. Therefore, the most effective solution against this disease is to develop tolerant varieties with high fruit quality. In orchards established with these varieties, production costs associated with disease control will be reduced, and sustainability in production will be ensured. In this context, our project aims to develop pear varieties that are tolerant to fire blight and possess superior fruit quality, enabling them to compete effectively with existing varieties in the pear market. 17 hybridization combinations of local and foreign pear varieties and 20150 hybrids were produced within the scope of the project. The sensitivity of hybrid plants to fire blight was assessed using artificial inoculations. A total of seven native and 13 different foreign *Erwinia amylovora* Burrill strains were used for inoculation. As a result of disease evaluations, 6200 genotypes classified as A (very low susceptibility) and B (low susceptibility) according to the classification were transferred to the first fruit observation plot, while others were destroyed. According to the evaluations conducted in the first observation plot, 341 genotypes with high fruit quality were planted in the advanced observation plot, utilizing a 4 x 1 m planting distance. As a result of the evaluations, the registration process is being initiated for pear variety candidates that can compete with market varieties and are tolerant to fire blight. 6 genotypes were submitted for registration in 2018, and the registration process was completed in 2021. The varieties were given the names of FiRest, MarSalda, ArTroya, Dönen C, Gökdem, and Seven. This year, we have submitted registration applications for two additional genotypes, and the process is currently ongoing. Evaluations are proceeding, and those genotypes identified as superior will be submitted for registration and prepared for European pear production.

Keywords: *Erwinia amylovora* Burrill, European pears, fire blight, tolerance, varieties

[Abstract:0068]

Kiwifruit Breeding Program Efforts and Characteristics of The Kahraman - 1 Cultivar Candidate

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Kiwifruit breeding studies in Turkey began in 2008 at the Atatürk Central Horticultural Research Institute and were designed in 2011. Turkey's first kiwifruit cultivar, İlkaltın, was registered in 2018, and its pollinator, the Kemalbey cultivar, was registered in 2019. The Kahraman-1 (B-36) cultivar candidate, selected between 2016 and 2020 as part of the breeding project, was submitted for registration in 2023, and registration efforts are ongoing. The Kahraman-1 cultivar candidate has yellow flesh and a very lightly hairy skin, with an average fruit weight of 91 g. It can be stored for 3-4 months in normal atmospheric storage. In the kiwifruit breeding program, fruit weight, fruit width/length measurements, flesh firmness, and TSS% values are determined for kiwifruit types at harvest time. At the time of ready to eat, flesh firmness and TSS% values are measured, and a taste test is performed. In the kiwifruit breeding program, the number of types with fruits above a certain average weight (40 g) and have sufficient number of fruits was determined as 75 in 2021, 101 in 2022, and 126 in 2023. Pomological analyzes and maturity studies were carried out on these types. The data obtained were subjected to scaled grading system and the kiwifruit types were ranked separately for each year. The kiwitypes with the highest scores were determined as M15-I-13 (886 points), HYZ4-H-53 (883 points), JK-43 (875 points) in 2021; S-5 (844 points), TH-37 (731 points), HYA6-F-6 (712 points) in 2022; HYZ4-H-29 (877 points), HYZ4-H-53 (877 points), HYA6-F-31 (856 points) in 2023.

Keywords: *Actinidia* spp., selection, pomology.

[Abstract:0349]

Breeding Studies on the Development of Late-Flowering and Late-Maturing Peach (*Prunus persica* L.) Cultivars

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Peach (*Prunus persica* L.) is one of the most intensively cultivated fruit species worldwide, with a significant share in global fruit exports. In Türkiye, peach production and export potential have been steadily increasing; however, the country has not yet achieved the desired competitiveness in international markets. This situation mainly results from the predominance of foreign cultivars in production, increased input costs, and the limited number of locally developed, high-quality cultivars. Global breeding programs currently focus on developing early-maturing peach cultivars with low or moderate chilling requirements. Nevertheless, considering the frequent late spring frosts and the ecological characteristics of Türkiye's inland and transitional regions, the development of late-flowering and late-maturing cultivars has become a crucial breeding target. Therefore, this project aims to develop new peach genotypes that are late-flowering, high-yielding, possess superior fruit quality, and are suitable for storage and market demands through controlled hybridization studies. The project is being conducted in five stages: (1) establishing hybridization combinations among selected parental genotypes, (2) creating the first selection orchard, (3) advanced selection in the second orchard, (4) location trials and postharvest storage studies, and (5) cultivar registration. The parental materials used include Extreme Great, Extreme 553, Fresh Late, Extreme 568, Q Henry, and Cresthaven cultivars. Between 2023 and 2024, a total of 21507 hybridizations were performed, yielding approximately 3417 viable seeds. By 2025, around 1700 hybrid seedlings were transferred to the preliminary observation orchard. Early-flowering individuals will be eliminated during the evaluation process, while late-flowering, late-maturing, and high-quality genotypes will advance to the next selection phase. The project is expected to result in new Turkish peach cultivars that are well-adapted to local ecological conditions, tolerant to late spring frosts, and capable of extending the market supply period. Moreover, these locally bred genotypes will contribute to the national germplasm pool, reduce dependency on foreign cultivars, and enhance the competitiveness of Türkiye's peach industry in global markets.

Keywords: *Prunus persica*, hybrid breeding, late-maturing cultivars, late flowering, climate adaptation

[Abstract:0225]

Phenotypic Diversity of Newly Registered Pomegranate Varieties in Southeastern Anatolia Region: Some Fruit Chemical Characterization

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In pomegranate cultivation, the dominance of a limited number of commercial cultivars in modern agricultural systems underscores the critical importance of systematically collecting, comprehensively evaluating, and effectively conserving genetic resources, in order to reduce genetic erosion and preserve biodiversity. In this study, the performance of “Yeğin Kırmızı, Katina, Alibaba, and 11 Nisan”, newly registered pomegranate cultivars by the Southeastern Anatolia Agricultural Research Institute (GAP), was evaluated over three years at the Gündaş and Talat Demirören locations. For the cultivars, phenological traits (crown height, crown width, yield, trunk cross-sectional area, and cumulative yield), pomological traits (fruit width, fruit length, fruit weight, and aril yield), and chemical traits (TSS, pH, and titratable acidity) were determined. Crown and trunk measurements were made with measuring tape. Fruit dimensions were measured by caliper, and weights by a precision scale. Total soluble solids were measured by a refractometer, and titratable acidity was determined via titration with 0.1 M NaOH. Among the cultivars examined, the greatest crown height (206.47 ± 0.76 cm) and crown width (182.00 ± 0.89 cm) were recorded in the Alibaba cultivar; tree yield (36.37 ± 0.33 kg) was highest in Katina. Fruit weight (510 g) was highest in Alibaba, and the highest aril yield (34.33 ± 0.13 %) in 11 Nisan. The highest TSS content (12.18 ± 0.06) and highest titratable acidity (12.02 ± 0.05) were found in Yeğin Kırmızı. The study employed statistical tools — cluster analysis, Principal Component Analysis (PCA), and heatmap analysis (HMA) — to examine trait clustering and genotype differentiation. PCA revealed that the first three components explained 76.30 % of total variation; significant correlations were found in PC1 (44.22 %) and PC2 (18.82 %). Important correlations among key traits were observed: crown height had a negative correlation (–0.96) with yield per decare and tree yield, and a negative correlation (–0.75) with fruit weight. A positive correlation (0.79) was found between fruit length and fruit weight. This study demonstrates that significant differences exist among cultivars, years, and locations. Morphological, pomological, and chemical components exhibited substantial variability, indicating that these traits possess a notable discriminating capacity in explaining phenotypic diversity in pomegranate.

Keywords: Pomegranate, Genetic resources, chemical properties

[Abstract:0295]

Development of Superior Table and Dried Fig Cultivars through Mutation Breeding Studies

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Türkiye is one of the leading nations in the world in terms of fig production and export. It ranks first in the world for dried fig production, and approximately 60–70% of the dried figs produced are exported. In recent years, fresh fig production has also increased rapidly, and its export volume has reached significant levels. The superiority of our country in dried and fresh fig production is mainly due to the Sarılop variety for drying and the Bursa Siyahı variety for fresh consumption. To maintain this global leadership and competitiveness, Turkey needs to develop new, high-quality dried and fresh table fig cultivars. This need is becoming increasingly urgent, as the number of competing countries in fig export is growing and new cultivars are being released through breeding and selection programs in those countries. Therefore, the aim of this project is to develop early-ripening dried and fresh fig cultivars with small or closed ostioles and large fruit size by using mutation breeding techniques (gamma irradiation). In this mutation breeding study, two major Turkish fig cultivars were used as plant materials: Sarılop (the most important dried fig cultivar) and Bursa Siyahı (the most exported fresh fig cultivar). The study began in March 2007. Cuttings from both cultivars were subjected to five different gamma irradiation doses (10.0, 16.9, 25.3, 50.7, and 67.0 Gray), apart from the control group. Buds obtained from these treated cuttings were grafted to produce M1V3 individuals. During the first grafting year, the lethal dose (LD_{50}) was calculated as 50.7 Gray for Sarılop and 25.3 Gray for Bursa Siyahı. Due to epistatic effects, mortality was highest at 67.0 Gray in Sarılop (16.60%) and at 25.3 Gray in Bursa Siyahı (19.82%). By 2010, sufficient variation had been generated in the M1V3 population of both cultivars, and these plants were planted in the field at 4 × 1.5 m spacing to initiate the first selection phase. Beginning in 2014, fruit observations were conducted for the desired characteristics, and based on the fruit data collected in 2017, five promising types were identified from each cultivar using a weighted scoring system. Cuttings were taken from these selected types in 2018 to produce seedlings, which were planted in pots. These seedlings were transplanted to the field in 2019, marking the beginning of the second selection phase. In 2022, the first fruits were harvested from these individuals, and the second selection phase is still ongoing.

Keywords: İncir (*Ficus carica* L.) radiation, mutation, gray, Sarılop, Bursa siyahı

[Abstract:0204]

Determination and Selection of Some Agronomic and Biochemical Characteristics of Different Turmeric (*Curcuma longa* L.) Genotypes 'ZERDESENA'

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Curcuma longa L., which is known as turmeric, is a plant species belonging to the Zingiberaceae family. Turmeric is generally spread in Asian countries. It is used in many sectors, especially in spices. Local varieties are generally used in the production of turmeric, whose import value is increasing worldwide. There is a need for commercial varieties that are adapted to different regions. This study was carried out to develop varieties that are productive and high in curcumin, adaptable to subtropical climate conditions. The study material is 152 different genotypes in the gene pool. The fresh weight of the genotypes in the gene pool varied between 31.00-1240.00 g plant-1. Among the 16 selected high yielding genotypes, the longest plant height was measured in genotype number 60-2. The highest average phenolic substance amount was detected in the 145-14 genotype. Curcumin ratio varied between 53%-2.41%. This study has shown that there is a variation both morphologically and biochemically in turmeric. Considering that varieties with high curcumin content are preferred in the world trade in the turmeric market, where local varieties are generally used, genotypes with high curcumin content were selected from among high-yielding turmeric genotypes. Among the 16 high-yielding genotypes with yields above the average, genotype number 130-16, which has the highest curcumin content, was applied for and registered with TTSM under the trade name 'Zerdesena'.

Keywords: Tropics, Medicinal Plant, Curcumin, Variety, Turkey

[Abstract:0021]

Unlocking Genetic Potential of Crops through Genome Editing: Implications for Food Security and Sustainability

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The urgent challenges of climate change, evolving pests, and dwindling resources demand crop improvement strategies that are not only faster but also more precise and holistic. My journey in biotechnology began with the pioneering development of gene stacking systems in cotton, enabling multiple traits to be integrated within a single plant, laying the foundation for designing crops with complex, combined advantages rather than incremental gains. Building on this, our genome editing work now targets traits of critical economic and strategic value: enhancing fiber quality by editing jasmonate pathway regulators, shaping plant types compatible with mechanized harvesting by editing GhSP gene, engineering durable resistance to Cotton Leaf Curl Disease through multiplex CRISPR strategies against host factors like eIF4e, and strengthening heat tolerance through transcriptomic and proteomic insights. These advances mark a shift from single-gene edits to multi-trait, polygenic improvements that integrate productivity, resilience, and sustainability. Beyond traits, I will discuss technological progress in CRISPR systems optimized for plants, advanced delivery platforms, and multiplex editing approaches that allow simultaneous modification of several genes. These innovations are making genome editing faster, more accessible, and more impactful for public breeding programs. In parallel, I will share our patent-pending PCR tube technology, a practical, room-temperature-stable solution that translates genome science into affordable diagnostics for agriculture and beyond, and I will also hint at the futuristic integration of genome editing with vertical farming where tailored crops for controlled environments could redefine year-round food and fiber production. This talk will trace the arc from gene stacking to genome editing, while highlighting how scientific innovation, when combined with translational tools and visionary farming systems, can unlock the genetic potential of crops and strengthen global food security.

Keywords: Genome Editing, CRISPR/Cas, Gene Stacking, Cotton Biotechnology, Food Security, Sustainable Agriculture & Vertical Farming

[Abstract:0211]

New Horizons in Breeding: From Wild Ornamental Plants to Future Cultivars

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Ornamental plants, beyond their aesthetic contribution to the environment, hold substantial significance in social, cultural, human, and environmental health contexts. They help urban populations to reconnect with nature and play a crucial role in rural development. Changing climate conditions have made it increasingly necessary to incorporate genes from wild varieties that have existed in nature for thousands of years into current breeding gene pools. In addition to resistance genes, the ornamental plant industry—constantly driven by the pursuit of novelty—requires the introduction of new genes or phenotypes that impart unique characteristics to existing varieties. As with other cultivated plants, increasing yield, improving quality, enhancing adaptation to adverse environmental conditions, and improving resistance to biotic stresses are the primary goals of ornamental plant breeding programs. The term “ornamental plants” is used to describe a very broad group encompassing many different species. Some of these species are propagated vegetatively, as in fruit species, while others are propagated by seed, as in numerious vegetable species. Emerging biotechnological tools minimize the time lost in traditional observation and testing processes, allowing for more efficient early selection and guiding breeding programs. Although breeding strategies differ depending on production techniques, techniques such as tissue culture, QTL mapping and genome editing are now widely and effectively used in the domestication and breeding of various ornamental plant species. This article highlights the interaction between traditional breeding approaches and cutting-edge biotechnological tools, which create significant opportunities for the domestication and improvement of wild species, particularly ornamental plants. The ongoing research and integration of these methods makes the development of new varieties increasingly feasible; these varieties can both meet market expectations and support biodiversity and long-term sustainability. Furthermore, this study also emphasizes the need for sustained research and innovation in this field, as harnessing the potential of wild ornamental plants is likely to become a key driver in the future evolution of the floriculture sector.

Keywords: biotechnology, CRISPR/Cas, tissue culture, floriculture, domestication

[Abstract:0262]

Biodiversity Conservation and Sustainable Use Strategies in the Ornamental Plants Sector

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Türkiye is one of the world’s important gene centers with approximately 12,000 plant taxa, and its floristic richness offers great potential for the ornamental plants sector. Especially natural flower bulbs, endemic ornamental plants and landscape plants have high economic value both in the domestic market and in exports. However, factors such as rapid urbanization, habitat loss, climate change and uncontrolled wild collection threaten biodiversity, putting the sustainability of endemic and rare species at risk. In this context, the integration of biodiversity conservation and the ornamental plants sector has become not only an ecological but also an economic necessity. In this study, the literature review method was used and studies conducted at national and international levels were examined. The findings show that legal regulations, in vitro conservation techniques and ex situ conservation programs implemented in Turkey play a critical role in the sustainability of genetic resources of natural bulbous species. Recent studies on the genus Colchicum, which is an important bulbous ornamental plant with both aesthetic value and medicinal components, reveal the importance of in vitro conservation techniques. Synthetic seed production in C. cilicicum, somatic embryogenesis in C. sobalifer and callus culture in C. chalcedonicum have been successfully carried out. As a result, endemic and rare bulbous plants in the Turkish flora constitute a valuable genetic resource for the ornamental plants sector. However, the use of these resources without protection threatens both the ecological balance and the sustainability of the sector. The integration of ex situ and in vitro approaches in the protection of bulbous plants is considered a strategic necessity for the long-term protection and sustainable use of Turkey’s rich plant genetic resources.

Keywords: Biodiversity conservation, Colchicum, exsitu, invitro, ornamental plants

[Abstract:0048]

The First Mutant Chrysanthemum Varieties in Türkiye

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Chrysanthemum (*Chrysanthemum × morifolium* Ramat.) is one of the top four cut flowers in the world. This study aimed to reduce the decorative plant industry's reliance on other countries for material supply by developing new varieties of the economically significant chrysanthemum plants that can be utilized as cut flowers, outdoor flowers, or potted plants. To produce local varieties of chrysanthemum that will emerge with new color and shape alterations, mutation breeding methods were used. The material was the 'Bacardi' spray cut flower variety, and nodal explants were cultivated in vitro conditions. To determine the effective mutagen dose (EMD) in in vitro explants, they were irradiated with gamma rays at doses of 5, 10, 15, 20, 25 and 30 Gy (Gray). After irradiation, shoot and root lengths were measured on the 60th day of regeneration, and the EMD was determined to be 20 Gy. In vitro bud explants of white 'Bacardi' variety was irradiated by gamma radiation at 20 Gy (Gray). In vitro subcultures were continued until the M1V4 period, and observations were obtained after this period. Some changes were observed in the height and flowers of the plants, such as variable flower number, flowering time, differences in plant length, the number of flowers per bunch, and ray floret differentiation. The changes of the ray florets were determined as color changes from pink to yellow. The mutation frequency of the population was calculated as 0.9% f useful mutant lines chosen from the selected mutants. As a result of the study, five cut flower varieties named 'Bademler Beyazı', 'Ege Meltemi', 'Ozan', 'Kaan', and 'Sevim2023' were registered first in Türkiye. 'Bayram2023' was also registered as an outdoor ornamental plant.

Keywords: Breeding, mutation, chrysanthemum, effective mutagen dose, vegetative propagation

[Abstract:0265]

Evaluation of Novel Aloe vera Genotypes for Gel Yield under Semi-Arid Regions to Identify Suitable Genotype for Commercial Cultivation

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For arid and semi-arid regions of world Aloe vera is considered as an important medicinal plant for commercial cultivation. Present day, demand of aloe vera gel and its products is increasing, due to its diverse uses in cosmetics and medicinal areas. The present experiment was carried to identify the best performing genotype for commercial cultivation. In this study 12 genotypes of Aloe vera were planted in RBD with three replications at Research Farm, MAP Section, Department of Genetics and Plant breeding, CCS Haryana Agricultural University, Hisar (India) during 2023-24 to evaluate the genotypes for high leaf yield and gel content. The experiment was planted on 20.09.2021 having plot size of 2.7 × 0.6 m2 with spacing of 60 × 45 cm2 The observations were recorded on 10 plants for plant height (cm), number of leaves/plant, leaf length (cm), leaf width (cm), fresh leaf yield (q/ha) and gel (Mucilage) content (%). The results revealed significant genetic variability among the genotypes. In this experiment, plant height ranged from (51.60-74.50cm), inflorescence length (72.40-142.80), number of suckers/plant (3.00- 7.00), leaf length (47.33- 67.40cm), leaf breadth (8.40- 11.80cm), leaf thickness (1.54-2.27cm), fresh leaf yield (266.75-418.00 kg/ha). The detail is given in Table 1. The maximum plant height was observed in HAV-5-8 (74.50 cm) followed by GAKP-1 (71.10 cm) and AK-9 (70.40). Likewise, longest leaf length was noticed in AK-9 (67.40 cm) followed by HAV-5-8 (66.00cm) and CGAV-5 (58.00cm). Maximum leaf width was found in HAV-5-8 (11.80cm), followed by AK-9 (11.05cm) and GAKP-1 (10.40cm). Maximum number of suckers/plant was observed in INGR 06023 (7.00) and CGAV-5 (7.00) followed by GAKP-1 (6.00). Maximum fresh leaf yield was found in HAV-5-8(418 kg/ha) followed by CGAV-5 (412.50kg/plant) and AK-9 (385 kg/ha). Maximum Gel content was observed in HAV-5-8 (259.16kg/ha) followed by CGAV-5 (228.94kg/ha) and DMAPR AB-03 (216.92kg/ha). Keeping the above results in view, it may be concluded that HAV-5-8 is found suitable for commercial cultivation and recommended for cultivation after testing over time and space.

Keywords: *Aloe vera*, cultivation, semi-arid regions, fresh gel yield, novel genotypes

[Abstract:0246]

Ampelography in the Genomic Era: Improvement of Traditional Grapevine Characterization Approaches

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Ampelography can be defined as the identification and classification of grapevine genotypes/varieties based on their morphological, physiological, and phenotypical characteristics traditionally. Ampelography, founded in the 18th century, has formed the systematic foundation of viticulture over centuries. These descriptors are included in the "OIV Descriptive List for Grape Varieties and Species of *Vitis*" today, which provides standards for describing the Vitis variety or species, published by the International Organization of Vine and Wine (OIV), 2009. Descriptors refer to examination of varieties belonging to Vitis spp. leaf, cluster/bunch, berry, shoot, flower, or pomological characteristics. However, the highly complex structure of grapevine genome and genetic resources resulting from artificial selection, natural hybridization, and clonal variation has revealed some of the limitations of identification based solely on morphological data. Environmental conditions, and epigenetic effects can cause the same genotype to exhibit different phenotypic properties which can be deceiving. To overcome these limitations, the most frequently used tools developed for the characterization of biodiversity are the molecular marker technologies in the late 20th century that revolutionized the grapevine characterization assessments. Simply molecular markers are nucleotides that indicate polymorphisms of different individuals' nucleotide sequences. Mutations, translocations, repeat sequences, and single nucleotide changes are some examples of polymorphisms. A vast number of molecular marker types have been established (SSR, SNP, RAPD, ISSR, SCoT, AFLP etc.) and their utilization is determined by the characteristics of the trait to be identified and experimental standards. They have been quite successful in clarifying and correctly characterizing synonyms and homonyms in terms of local and international varieties. Identifications at the molecular level have provided high accuracy in determining distinct genotypes, varietal specificity, and population structure. On the other hand, since molecular data cannot fully project the environmental and developmental dynamics of phenotypic expression, the importance of classical ampelography has reemerged. The current scientific trend is towards evaluation of these two solid approaches as in monolith. Therefore, reevaluating ampelography in the genomic era is not a matter of nostalgia, but a scientific obligatory. This review provides a comprehensive overview of ampelography from its dawn till genomic era, exploring its complementary and comprehensive approach to data flow. Classical ampelography method and its role in revealing the morphological diversity of grapevine varieties and the contributions of molecular markers to determining genotypes will be discussed, with examples of the simultaneous use of these two approaches.

Keywords: Ampelography, Grapevine, Plant Gene Resources, Molecular Markers

[Abstract:0139]

Evaluation of Phenological Data of Some Fig (*Ficus carica* L.) Genotypes in Gaziantep Location

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Fig (*Ficus carica* L.), belonging to the genus Ficus of the Moraceae family, is a fruit species that can be cultivated in various climatic regions of Türkiye and occurs naturally in the Southeastern Anatolia and Aegean regions. The Southeastern Anatolia Region, being the gene center of fig, possesses rich genetic diversity and favorable ecological conditions. This study was conducted between 2024 and 2025 at the Ahmet Münir Bilgen Research Farm of the Pistachio Research Institute Directorate. Within the scope of the Fig Selection Project in Gaziantep, Kilis, and Adıyaman provinces, seven fig genotypes (Cevizli-1, Adıyaman-8, Burç Karakuyu, Yavuzeli-2, Erikli-2, İslahiye-2, and Cevizli-3) along with the cultivars Sarılop, Dürdane, and Beyaz Orak, were used as experimental materials. The phenological stages assessed included 'Budburst,' 'Main Crop Set,' and 'Main Crop Ripening (Harvest) Initiation.' According to the 2024 data, budburst occurred earliest in genotype Cevizli-1 on March 14, 2024, and latest in cultivar Beyaz Orak on April 1, 2024. Main crop set occurred earliest on May 10, 2024, in Cevizli-1 and latest on May 29, 2024, in Adıyaman-8. The onset of main crop ripening was first recorded on July 24, 2024, in Burç Karakuyu and on July 26, 2024, in Sarılop, whereas the latest was observed on August 23, 2024, in Cevizli-3 and Dürdane. The phenological progress of the other genotypes and cultivars fell within these ranges. In 2025, budburst was observed earliest on March 22 in Cevizli-1 and latest on April 7 in Beyaz Orak. Fruit set was first observed on May 17 in Cevizli-1 and latest on May 26 in Adıyaman-8, İslahiye-2, Cevizli-3, and Dürdane. The onset of main crop ripening occurred on July 31 in Burç Karakuyu, Erikli-2, and Sarılop, while the latest was recorded on August 29 in Dürdane. Overall, results indicated that Cevizli-1 consistently exhibited earlier vegetative development compared to other studied genotypes, whereas Beyaz Orak was the latest among all. Regarding fruit development, Cevizli-1 was the earliest, while Adıyaman-8 was the latest. With respect to ripening initiation, Burç Karakuyu and Sarılop were the earliest, while Cevizli-3 and Dürdane showed the latest ripening. This study identified the phenological performance of seven fig genotypes and three fig cultivars under Gaziantep conditions. The data obtained provide valuable insights for identifying genotypes suitable for cultivation in this location. However, further studies are needed to determine the heat and chilling requirements of these genotypes using climatic data.

Keywords: *Fig, phenology, Gaziantep, main crop set*

[Abstract:0057]

Evaluation of Susceptibility of Hybrid Grapevine Genotypes to Powdery Mildew

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The development of disease-resistant grape varieties is crucial for reducing pesticide use in viticulture and promoting sustainable agricultural practices. This study aimed to identify grapevine genotypes with enhanced tolerance to powdery mildew (Erysiphe necator). A total of 70 genotypes, including 66 Narince x Regent hybrids, four Narince x Kishmish Vatkana hybrids, and the parental cultivars Narince, Regent, Kishmish Vatkana, and Isabella, were evaluated for powdery mildew resistance. The susceptibility of the genotypes to powdery mildew was assessed through artificial inoculation under controlled greenhouse and laboratory conditions over two consecutive growing seasons (2021-2022). Disease severity was evaluated based on mycelium and sporulation density on leaf surfaces, using a scale ranging from 1.8 (highly susceptible) to 7.4 (highly resistant). Significant variability in powdery mildew resistance was observed among the genotypes and cultivars. The Narince variety exhibited high susceptibility (score: 1.8), while Isabella demonstrated the highest resistance (score: 7.4). Several promising genotypes (NRG-7, NRG-146, NRG-174, NRG-195, NRG-196, NRG-197, and NRG-200) and cultivars (Regent, Kishmish Vatkana, and Isabella) displayed notable resistance to the pathogen. The incorporation of these resistant genotypes into grape production systems for fresh or brined leaf use may substantially reduce fungicide applications, thereby advancing more sustainable and environmentally responsible viticultural practices.

Keywords: Genotypes, powdery mildew, artificial inoculation, susceptibility

[Abstract:0097]

Development of Apricot Cultivars Resistant to Sharka Disease *Potyvirus plumpoxi* through Hybridization Breeding

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Apricot (*Prunus armeniaca* L.) is one of the most important temperate fruit species in terms of both economic and cultural value. Global apricot production is 3,728,156 tons, of which 20.1% is realized by Turkey. Within Turkey, Malatya province is the leading region with a production capacity of 328,000 tons. However, apricot cultivation is exposed to various biotic and abiotic stress factors. Among these, one of the most severe is Sharka disease (Potyvirus plumpoxi), which causes significant yield losses in stone fruit species and reduces the market value of fruits to zero. The absence of chemical control methods, the rapid spread of the virus by aphids, and eradication being the only effective solution make the development of sharka-resistant cultivars essential. In this study, classical hybrid breeding and molecular methods were combined to develop apricot cultivars resistant to Sharka disease. The research was conducted between 2019 and 2021 in Malatya province. Commercially important cultivars 'Hacıhaliloğlu' and 'Kabaaşı' were used as female parents, while cultivars previously reported to be resistant, namely 'Stark Early Orange', 'Goldrich', and 'Harleyne', were used as pollinators. Hybridization studies were carried out in six different combinations, during which a total of 28,506 flowers were pollinated over three years, resulting in 364 hybrid seeds. After stratification, seeds were planted in tubes to obtain F1 plants. Leaf samples from these plants were used for DNA isolation, and resistance status was determined using SSR markers. Molecular analyses revealed that 95 hybrid individuals carried resistance to Sharka disease. The project is currently supported by the General Directorate of Agricultural Research and Policies (TAGEM), and the field performance of resistant hybrids is being evaluated by the Biological Control Research Institute in Adana. In the coming years, hybrids that have passed both molecular and biological tests will be further assessed for fruit quality and yield characteristics, and superior genotypes will be certificated and introduced into production. Ultimately, this work aims to reduce the economic losses caused by Sharka disease in apricot cultivation and to support sustainable production.

Keywords: apricot, sharka, plum pox virus, hybridization breeding, molecular markers

[Abstract:0195]

Improvement of Low Temperature Tolerant Mexican Lime Varieties by Induced Mutation Breeding

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The Mexican lime cannot be commercially cultivated in subtropical conditions due to its sensitivity to low temperatures. Although breeding studies have been conducted on the Mexican lime for many years, it has not been possible to develop varieties tolerant to low temperatures through classical hybridisation breeding. However, in recent years, the artificial mutation breeding method in citrus has been shown to enable the development of new varieties in many species. Therefore, in this study, it was aimed to develop new genotypes tolerant to low temperatures in Mexican lime by artificial mutation breeding. For this purpose, to determine the Effective Mutagen Dose (EMD), different doses (0, 30, 40, 50, 60, 70 and 80) of gamma rays from a cobalt 60 source were applied to Mexican lime bud woods. As a result of our findings, the EMD dose was determined as 45 Gy. In the next stage, according to this dose gamma radiation was applied to the Mexican lime bud woods and after the application, the scions were grafted onto sour orange rootstock using T-bud grafting to create the M1V1 population. From this population, the M1V2 and M1V3 populations were created through grafting. Ten mutant candidate genotypes (L1-L10) selected from Mexican laym genotypes according to pre-selection criteria and control individuals were subjected to biochemical analysis (chlorophyll content, total soluble protein concentration, proline) to identify genotypes tolerant to low temperatures. Ten mutant candidate genotypes (L1-L10) selected from Mexican laym genotypes according to pre-selection criteria and control individuals were subjected to biochemical analysis (chlorophyll content, total soluble protein concentration, proline) to identify genotypes tolerant to low temperatures. The research findings revealed differences in certain characteristics between individuals subjected to gamma radiation and the control group. The relative water content of leaves was higher in the L-9 genotype, chlorophyll content was higher in the L-7, L-8, and L-9 genotypes, and total soluble protein concentration was higher in the L-2 genotype compared to the control. Furthermore, proline accumulation was lowest in the L-9 genotype among the control and mutant candidate genotypes, while the highest low-temperature tolerance in the freezing tests was determined in the L-8 genotype (-2.91°C).

Keywords: EMD, proline, protein, gamma radiation, leaf water content, ion leakage method

[Abstract:0194]

Public Sweet Corn Breeding Studies of Türkiye

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Corn (*Zea mays* L.), originating in South America, is a strategic agricultural crop cultivated in nearly every region of the world. As of 2024, global production is projected to reach approximately 1.2 billion tons, and corn, along with wheat and rice, is among the most widely produced grains in the world. Its versatile use as human food, animal feed, and industrial raw material makes it an essential crop for food security and livestock farming. Sweet corn (*Zea mays* saccharata) is a special subspecies of corn characterized by its high sugar content. Mutations in genes regulating sugar-sugar-alcohol conversion (e.g., su1, sh2) in this type of corn increase the sweetness of the kernels. Sweet corn is consumed as a vegetable, not a grain, and is available fresh, canned, or frozen. Global production is approximately 12–15 million tons. The United States, Thailand, China, India, and Indonesia are the leading producers. Sweet corn (sweet corn) has become a prominent corn variety in Turkey over the past 15 years. Meanwhile, production is rapidly increasing in the Mediterranean and Aegean regions, particularly for fresh consumption and the processed food industry. Public corn breeding efforts in Turkey began in the 1950s, and numerous inbred lines, valuable populations, and hybrid varieties have been developed. In 2004, various projects were combined into the National Corn Integrated Crop Management Project, which focuses on productivity, quality, and resistance to stress. Sweet corn breeding began in the 2000s, initially focusing on composite populations but eventually shifting to hybrid breeding. The Western Mediterranean Agricultural Research Institute (BATEM) and the Sakarya Maize Research Institute (MAEM) have played a leading role in this area. Turkey's first domestic sweet corn variety, BATEM SWEET, was registered by BATEM in 2013. The variety's fresh ear yield is 1515 kg/da and its sugar content is 4.8%. Adapare (2019, MAEM-BATEM partnership) and SuGen (2020, MAEM) varieties have an average yield of 1700 kg/da. Their sugar content is 6.2% and 6.3%, respectively. These varieties are su tpye sweet corn varieties. Currently, Institutes continue breeding studies, particularly with materials containing the sh1 gene. This study evaluates the collaboration efforts of public institutes on sweet corn breeding as of 2024, the current status of ongoing breeding projects, and future work.

Keywords: Hybrid, inbredlines, population, quality, sweetcorn, yield

[Abstract:0350]

Influence Of Siderate Plants On Phenological Development Phases, Crop Elements And Yield Of Wheat

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The study investigated the effect of green manure crops — winter vetch and the mixture of winter vetch + annual ryegrass (*Vicia sativa* L. + *Lolium multiflorum* L.) — on the yield and seed quality of wheat. Green manure crops not only enhance biological activity in the soil, restore nitrogen balance, and enrich organic matter reserves, but also improve the nutritional conditions for subsequent main crops. Research findings indicate that leguminous green manures intensify biological nitrogen fixation in the soil, which in turn increases both the grain yield and the protein content of winter wheat seeds. The highest results were obtained in the variant where winter vetch and annual ryegrass were applied together as green manure. In this treatment, the seed sowing quality of the spike improved, and the vegetation period was shortened to 225 days, which is 5 days earlier compared to the control. The combined use of vetch and ryegrass increased the accumulation of biomass and nitrogen in the soil, while improving soil structure and stimulating more intensive plant growth. The highest yield (56.6 c/ha) was also recorded in the vetch + ryegrass variant, exceeding the control by 8.3 c/ha (18.2%) and the single vetch treatment by 3,3 c/ha (6.2%). These results demonstrate that the mixed cultivation of leguminous (vetch) and cereal (ryegrass) green manure crops balances both nitrogen and organic matter levels in the soil, thereby optimizing the nutrition and productivity of wheat.

Keywords: Green manure crops, winter wheat, winter pea, seed quality.

[Abstract:0192]

Climate-Driven Shifts in Plant Pathogen Dynamics and the Disease-Resistant Breeding

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Crop production represents a foundational pillar of global food security, yet it is increasingly vulnerable to the intersecting threats of climate change and plant disease. The shifting climatic landscape—marked by rising temperatures, altered precipitation regimes, and heightened frequency of extreme weather events—is profoundly reshaping the ecology, distribution, and virulence of plant pathogens. These environmental changes are not only intensifying existing disease pressures but are also facilitating the emergence of novel and more aggressive pathogen populations across previously unaffected agroecosystems. The researches focusing on plant disease dynamics under climate change estimates that shift in temperature, atmospheric CO_2, and precipitation patterns are increasing pathogen virulence and expanding geographic ranges of many fungal, bacterial, and oomycete pathogens. In wheat residues specifically, experiments simulating future climate conditions found that not only do richness and community structure of pathogenic fungi change significantly, but the early-stage decomposition phases under altered climate also activate a larger proportion of latent pathogens. This dynamic and unpredictable phytopathological landscape significantly challenges conventional disease management practices. In response, plant breeding—particularly in its pathological dimension—has become an indispensable component of sustainable crop protection strategies. As climate change accelerates the evolutionary trajectories of pathogens, breeding programs must also evolve to anticipate and counteract these rapid genetic shifts. Recent advances support this adaptive direction. Recent advances in innovative strategies for plant disease resistance breeding reviews how resistance genes, susceptibility genes, pathogen effector knowledge, and novel gene-editing tools (including CRISPR) are being used to create cultivars with enhanced disease resistance. Also, some studies demonstrate the successful development of wheat lines with enhanced resistance traits via genomic selection approaches, integrating multiple QTLs for disease resistance under variable environmental conditions. Moreover, the use of wild relatives of wheat, which harbor naturally occurring resistance to both abiotic and biotic stresses, has been shown to offer large potential gains. An important supporting approach is the integration of omics and enviromics in the breeding pipelines. One recent framework proposes combining genetic and environmental data to model genotype by environment interactions more accurately, improving prediction of cultivar performance under diverse and changing climates. Ultimately, the synergy between plant pathology and breeding is central to building resilience into global cropping systems. Pathogen-informed and climate-responsive breeding, leveraging wild germplasm, omics, enviromics, and gene editing tools, will be critical to ensuring agricultural resilience, sustaining crop productivity, and maintaining ecological balance in an increasingly unstable climate.

Keywords: Plant breeding, climate change, pathogens, sustainability

[Abstract:0033]

Biotic Stress Responses of some Dry Bean (*Phaseolus vulgaris L.*) Lines and Cultivars to Root-Knot Nematodes (*Meloidogyne incognita* race 1, race 2 and *Meloidogyne javanica*)

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Dry bean (*Phaseolus vulgaris* L.) is a major legume crop widely cultivated worldwide as an important source of protein for human nutrition and food security. However, biotic stress agents such as root-knot nematodes (*Meloidogyne* spp.) adversely affect plant development, causing significant yield losses in many production areas. In this study, the biotic stress responses of some dry bean varieties (Göksun, Güngör, Cevdetbey) and lines (KMF-10-16, KMF-11-24, KMF-11-30, KMF-11-32, KMF-11-34) against root-knot nematodes *Meloidogyne incognita* (race 1 and race 2) and *Meloidogyne javanica* were investigated. The experiments were conducted under fully controlled growth chamber conditions using a randomized complete block design with four replications. Each plant was inoculated with 1000 second-stage larvae. Forty-five days after inoculation, galled roots were evaluated using a 0-5 egg mass reaction scale. The results indicated that all examined varieties and lines were susceptible (5.0± 0.0) to *M. incognita* race 1, *M. incognita* race 2 and *M. javanica* under these conditions. The results indicate that all tested varieties and genotypes were not resistant to root-knot nematodes. Effective management of nematode pests in dry bean cultivation requires the development of resistant varieties and the implementation of integrated pest management strategies. Therefore, exploring diverse genetic resources and identifying resistant lines and varieties should be prioritized in future studies.

Keywords: Dry bean, line, *Meloidogyne* spp., reaction, resistance

[Abstract:0352]

Genetic Mechanisms of Resistance to Viral Diseases in Capsicum Species and the Significance of Molecular Markers Linked to These Mechanisms in Breeding Research

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Pepper (*Capsicum* spp.) crop has significant economic value worldwide, and viral diseases are one of the most detrimental factors limiting its production. As of now, there have been 49 species of viruses identified across 15 different taxonomic groups that are known to infect pepper plants, with a minimum of 20 of these species resulting in significant reductions in yield. Viruses such as TSWV, PMMoV, TMV, CMV and PVY can cause crop losses of up to 60-99% by causing chlorosis, necrosis, mosaic, stunting and fruit deformations in plants. Chemically and culturally, control methods are often insufficient, therefore the most effective solution is to develop resistant varieties. Accordingly, the Tsw gene against TSWV, the L gene locus (L1–L4) against tobamoviruses, and various QTLs and major gene regions conferring resistance to CMV and PVY have been identified. Recent advances in molecular marker technologies have enabled the mapping of resistance genes and the effective use of marker-assisted selection (MAS). Markers developed within this scope, such as SCAR and CAPS markers, are widely used in the rapid and reliable selection of resistant lines. This study aims to contribute to the development of resistant varieties by reviewing current information on the identification of viral diseases in peppers, the genetic basis of resistance, and molecular markers used in breeding programs. It also provides researchers with a comprehensive overview of this topic.

Keywords: Viral diseases, genetic resistance, molecular markers, MAS, pepper breeding

POSTER PRESENTATION

[Abstract:0019]

The Effects of Water Stress and Mycorrhiza Inoculation on Drought Resilience in some Prunus Rootstocks

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Drought stress causes numerous physiological, morphological, and biochemical changes in plants, negatively affecting growth and development. Rootpac 40, Rootpac R, GF 677 and Garnem rootstocks were used in the study, in which the response of some stone fruit rootstocks to limited water application and the basic parameters on the resistance mechanism of the plant and the effect of mycorrhizal inoculation on these parameters were investigated. Experiment was carried out in the form of pot experiments using grafted and ungrafted plants in glass greenhouse conditions. Control (K100) plants were irrigated to 100% of the field capacity water level. Water was given to the K55 application at the level of 55% of the K100 irrigation, and to the K40 application at the level of 40% of the K100 application. In 2019, a preliminary trial was conducted by using *Glomus mosseae*, *Glomus etunicatum* and *Glomus clarium* mycorrhiza species.In the 2020 trial, limited water was applied to the plants, half of seedlings grafted with the Carolina nectarine variety. In the 2021 trial, limited water application was made by Glomus mosseae mycorrhiza species inoculation to both nectarine grafted and non-grafted plants. Mycorrhizae inoculated seedlings under drought stress showed higher plant height, leaf number, leaf area, plant biomass, chlorophyll amount, photosynthesis rate, relative water content, transpiration rate, water use efficiency, osmotic potential to their values; it was found to have lower damage levels and H2O2 values.

Keywords: Stone fruits rootstocks, drought resistance/tolerance, mycorrhiza

[Abstract:0054]

New Approaches to Improve Crop Tolerance to Abiotic Stresses

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Drought, salinity, and heavy metal toxicity are major abiotic stresses that are among the most important constraints on global agricultural productivity, resulting in enormous yield losses and posing a serious risk to food security. Although traditional breeding methods have helped produce cultivars with enhanced stress tolerance, climate change will exacerbate the number, severity, and variability of these stresses, making it necessary for us to find new, integrative, sustainable solutions. Recent studies have focused on integrating soil-based interventions with modern biotechnological tools to improve plant resilience. Here, we review recent advances in countering the negative effects of abiotic stress, focusing specifically on the cumulative impact of soil amendments (e.g., biochar) combined with plant growth-promoting microorganisms and state-of-the-art gene-editing technologies. Moreover, biochar can amend soil structure, increase water retention and nutrient availability; beneficial microbes can improve rhizosphere interactions and modulate plant immune responses. Collectively, these strategies lead to improved plant performance, increased efficiency of light harvesting and carbon fixation at the photosynthetic level, and reduced oxidative damage through the activation of antioxidative mechanisms at the physiological and molecular levels. Gene-editing technologies, such as CRISPR/Cas systems, also provide tools for precise and efficient manipulation of key genes involved in stress perception, osmotic regulation, and signal transduction pathways. These tools enable breeding of crops with improved tolerance to multiple abiotic stresses. Combining sustainable soil management practices with advanced genetic technologies will be a powerful paradigm for developing climate-resilient cropping systems. These multidisciplinary approaches will be critical to achieving stable, sustainable, and high-yielding agricultural production under increasingly variable environmental conditions.

Keywords: Abiotic stresses, agriculture, plant, tolerance

[Abstract:0080]

SSR-Based Diversity Analysis of *Aegilops* L. Species from Different Origins

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The evolution of wheat has been profoundly shaped by its wild relatives, which contain an enormous wealth of genetic variation for traits of agronomic importance. These wild gene pools serve as an invaluable reservoir for wheat improvement, particularly in the face of global challenges such as climate change, increasing demand for food, and the spread of pests and diseases. To explore this diversity, eight simple sequence repeat (SSR) markers were applied to 88 accessions representing eight *Aegilops* species collected from eight different countries. A total of 58 alleles were detected, with an average of 8 alleles per primer. Among these, 19 were species-specific, while 12 were accession-specific, highlighting the uniqueness of particular species and individual genotypes. The mean polymorphism information content (PIC) and expected heterozygosity (He) values for the entire collection were 0.540 and 0.563, respectively, indicating a moderate to high level of genetic variability. The highest average PIC values were observed in accessions from Azerbaijan (0.494) and Turkey (0.478), suggesting that these regions may represent hotspots of genetic diversity. Genetic distance (GD) indices based on seven SSR markers ranged from 0 to 1, with an average of 0.51. The closest genetic similarity was recorded between Ae. neglecta and Ae. biuncialis (GD = 0.227), whereas the greatest divergence was between Ae. speltoides and Ae. umbellulata (GD = 0.786). Cluster analysis based on SSR data grouped the 88 accessions into nine distinct clusters according to their taxonomic classification. Principal coordinate analysis (PCoA) further validated these relationships by differentiating the accessions according to their sections and confirming the subgrouping patterns. The results demonstrate that *Aegilops* gene pools represent a valuable source of novel alleles that can be harnessed to enhance wheat resilience against both biotic and abiotic stresses, while also improving yield and quality traits. Furthermore, the diversity information generated provides a robust scientific foundation for effective conservation, sustainable utilization, and long-term management of *Aegilops* genetic resources, ensuring their availability for future breeding programs and global food security.

Keywords*:* *Aegilops*, genetic diversity, SSR markers, conservation

[Abstract:0297]

Modern Plant Breeding Techniques in Crop Improvement and Genetic Diversity: From Molecular Markers and Gene Editing to Artificial Intelligence

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Recent advances in plant breeding have transformed crop improvement from a largely phenotype-driven process into a highly integrated, data-driven system. Modern plant breeding techniques now combine molecular markers, high-throughput phenotyping, genome editing, and artificial intelligence (AI) to accelerate breeding cycles, enhance selection accuracy, and expand crop genetic diversity. Marker-assisted selection (MAS), based on molecular tools such as Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSR), and Single Nucleotide Polymorphisms (SNPs), enables precise genetic mapping and early selection of desirable traits, reducing time and cost compared with conventional breeding approaches. High-throughput phenotyping (HTP) has emerged as a key complementary technology, allowing rapid, non-destructive assessment of large plant populations under controlled and field conditions. Imaging techniques based on visible light, fluorescence, thermal, and spectral sensors—often deployed via drones, automated platforms, and robotic systems—generate detailed phenotypic datasets that can be integrated with genomic information. This integration significantly improves the efficiency of trait discovery and selection, particularly for complex traits such as yield stability and stress tolerance. Genome editing technologies, especially the CRISPR-Cas9 system, provide unprecedented precision in crop improvement by enabling targeted modifications of genes controlling disease resistance, abiotic stress tolerance, yield, and nutritional quality. In parallel, AI and machine learning methods are increasingly applied to genomic selection, hybrid performance prediction, disease detection, and climate resilience modeling, supporting informed and automated decision-making in breeding programs. The adoption of these technologies varies globally according to agricultural priorities and regulatory frameworks. The United States leads in the application and commercialization of gene editing, AI-assisted breeding, and biotechnology-based crops. China has made substantial investments in CRISPR-enabled crop improvement, smart breeding infrastructure, and big data platforms to strengthen national food security. In contrast, the European Union is actively developing regulatory frameworks for New Genomic Techniques (NGTs). Overall, the convergence of molecular biology, digital technologies, and intelligent equipment is driving a disruptive shift toward next-generation plant breeding systems in which data-centric approaches increasingly complement or replace traditional breeding practices.

Keywords: Plant breeding, Molecular markers, Phenotypin, CRISPR, Artificial intelligence

[Abstract:0320]

High-Throughput Plant Phenotyping in Modern Plant Breeding: Technologies, Applications, and Future Perspectives

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High-throughput plant phenotyping (HTPP) has become a central driver for accelerating genetic gain in modern breeding programs. By integrating advanced imaging platforms, drone-based sensing systems, robotics, and artificial intelligence–based analytics, HTPP enables precise, non-destructive, and real-time quantification of complex traits across large breeding populations. Field platforms equipped with RGB, multispectral, hyperspectral, thermal, and LiDAR sensors enhance trait dissection under dynamic environmental conditions, strengthening the analysis of genotype–environment interactions. Image-based phenotyping combined with machine learning improves selection accuracy and facilitates early detection of stress responses and yield-related parameters. Within the scope of the Phenowex project, high-resolution UAV imagery and standardized data workflows are being implemented to support multi-environment trials and scalable digital breeding infrastructures. The project emphasizes harmonized phenotyping protocols, automated trait extraction, and integration with genomic data to improve predictive breeding models. Despite rapid technological advances, challenges remain in data interoperability, cost efficiency, and large-scale implementation. Future perspectives highlight multi-modal data fusion, cloud-based analytics, and tighter coupling between phenomics and genomics. As climate variability intensifies, HTPP represents a cornerstone technology for sustainable crop improvement, enhancing resilience, productivity, and global food security.

Keywords: High-throughput plant phenotyping, Imaging and sensing technologies, Machine learning and data analytics, Precision agriculture

[Abstract:0326]

Identification of Bacterial Communities in Heavy Metal-Contaminated Soil Samples Using Nanopore-Based Metagenomic Sequencing

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Advances in sequencing technology, particularly the development of third-generation sequencing technologies that generate long reads, have made metagenomic analysis easier and more accessible. Metagenomic analysis using total bacterial DNA from soil samples enables species- and strain-level identification in bacterial taxonomy. Reads based on nanopore-based sequencers have the potential to generate longer reads compared to short-read sequencing platforms. This can lead to more contiguous assemblies, whereas short-read platforms often result in highly fragmented metagenomes. In this study, we investigated microbial communities at more than 15 sites with varying degrees of heavy metal (Zn, Cu, Cd, Pb) contamination in and around technology development areas and factories, as well as sites with varying soil characteristics (nitrogen, phosphate, carbon dioxide content, pH, etc.) due to technogenic factors, using long-read sequencing. The results of linear and nonlinear dimensionality reduction suggested that heavy metal contamination did not have a clear correlation with bacterial communities. To investigate the effect of heavy metal contamination on microbial content in soil, we used two approaches: mapping reads to the existing Kraken database and de novo assembly of genes contained in the reads. The first approach was used to determine the strain-level taxonomy at different locations, resulting in the identification of an average of 715 strains, 620 species, 174 families, and 95 orders (bacteria and yeast) on each sample. Correlation analysis was conducted to identify which taxonomic groups were absent or present at high concentrations in heavy metal-contaminated soils at different concentrations. Clear microbial clusters showing strong negative and positive correlations across all samples were identified at all taxonomic levels (strain, species, family). Furthermore, microbial diversity was characterized for each contaminated sample. The second approach, assembly into contigs, did not yield large-scale genome assemblies but enabled the assembly of contigs containing multiple genes. This allowed investigation of potential mutations linked to heavy metal tolerance in samples exhibiting large differences in heavy metal content despite no significant differences in specific taxonomic groups. As a result, multiple taxonomic units correlated with heavy metals pollutions were identified using long-read sequencing. Funding: This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR21882269).

Keywords: metagenomics, long-read sequencing, heavy metals, contamination

[Abstract:0061]

Genetic Diversity and Effective KASP Markers for Barley Improvement in Kazakhstan

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Barley (*Hordeum vulgare* L.) is the second most important cereal crop in Kazakhstan, serving as a crucial component of livestock feed and as an export product. Enhancing its productivity and adaptability requires integrating traditional breeding with molecular tools. Kompetitive Allele-Specific PCR (KASP) markers represent a reliable and cost-effective system for high-throughput genotyping and marker-assisted selection (MAS). In this study, 100 cultivars and advanced breeding lines of barley from major grain-growing regions of Kazakhstan were genotyped using a panel of 100 KASP markers associated with traits of adaptability, yield, grain quality, and disease resistance. Genomic DNA was extracted and quality-checked, with 96 markers successfully amplified. Among them, 76 KASP markers demonstrated sufficient polymorphism (MAF ≥ 0.05) and were used in further analysis. Validation of marker–trait associations was performed with field data from three contrasting environments in three regions of Kazakhstan: Karabalyk AES (north), Karaganda AES (central), and KRIAPG (southeast). Statistical testing (t-test) confirmed significant associations ($P < 0.05$) between KASP markers and key agronomic traits. Across regions, distinct sets of effective KASP markers were identified: 25 markers in Karabalyk, 39 markers in Karaganda, and 39 markers in KRIAPG. Particularly, ipbb_hv_5, ipbb_hv_115, and ipbb_hv_122 showed consistent associations with three major yield components – spike length, number of grains per spike, and thousand-kernel weight – making them highly valuable for MAS. Additionally, marker ipbb_hv_191 was linked to multiple adaptive traits, including heading time, maturity time, and peduncle length. Phenotypic effect analysis revealed that favorable alleles of these markers increased trait values by 5–25%, demonstrating their potential impact on breeding efficiency. Population structure analysis (PCA and NJ clustering) indicated low overall genetic differentiation, suggesting frequent germplasm exchange among breeding institutions. This study provides the large-scale validation of KASP markers for barley in Kazakhstan under multi-regional field conditions. The results highlight a core set of effective markers and region-specific panels that can be directly implemented in national breeding programs. Integration of KASP-based MAS will accelerate the development of high-yielding, stress-resilient barley cultivars adapted to Kazakhstan's diverse agro-ecological zones. The research was funded by the Ministry of Agriculture and Ministry of Science and Higher Education of the Republic of Kazakhstan (Program No BR24892821, BR24992903).

Keywords: KASP genotyping, genetic diversity, marker-assisted selection, SNP markers.

[Abstract:0170]

Spread and Development of Stem Rust Disease of Barley in South-Eastern Kazakhstan (2023–2025)

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Barley is a strategic cereal crop in Kazakhstan, yet productivity and grain quality are recurrently constrained by fungal diseases, with stem rust (*Puccinia graminis* f. sp. hordei) being among the most consequential. The pathogen can proliferate rapidly during the growing season, diminishing photosynthetic capacity, weakening stems, and degrading grain quality. Recent variability in temperature and humidity has created favorable windows for epidemics in the south-eastern regions, underscoring the need for systematic monitoring and evidence-based management. This study aimed to characterize the spread, seasonal development, and agronomic impact of stem rust in South-Eastern Kazakhstan during 2023–2025 and to inform recommendations for enhancing varietal resistance. Phytopathological assessments combined route and fixed-site surveys; disease occurrence and severity were quantified using infection percentage and a development index, with interannual trends assessed by comparative statistics. In 2023, persistently hot and dry weather delayed epidemic onset, and fields planted with Arna, Egemen 1, and Aktigen maintained low disease levels (approximately 5–10%). By contrast, in 2024, higher humidity coupled with moderate temperatures facilitated early manifestation and greater intensity, with severity reaching 20–30% in Shortandinskiy 5, Zhuldyz, and Baiserke. Preliminary observations in 2025 indicate an earlier appearance of symptoms and vigorous development around heading, particularly in humid microclimates. Several zoned varieties, including Priirtyshskiy 99, Arna, Zhuldyz, and Baiserke, exhibited comparatively stable resistance, although the presence and spread of the *Puccinia graminis* pathogen were still recorded. Collectively, these findings confirm regular occurrence of stem rust in South-Eastern Kazakhstan and demonstrate a tight coupling between disease dynamics and climatic drivers—especially humidity and temperature. To sustain yield and reduce economic losses, prioritizing resistant or moderately resistant varieties, optimizing agronomic practices (e.g., crop rotation and balanced fertilization), and implementing an integrated phytosanitary protection framework are recommended for regional production systems.

Keywords: Barley, stem rust (*Puccinia graminis* f. sp. hordei), phytosanitary monitoring, disease development dynamics, varietal resistance, yield

[Abstract:0201]

Study of Dual-Purpose Barley in the Foothill Zone of Almaty Region

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In Kazakhstan, the area sown to spring barley is over 2.225 million hectares (2021 figures), while winter barley sown area is over 3,000 hectares. Most of the barley harvest is used as livestock feed and for the production of various types of cereals. Currently, barley (*Hordeum vulgáre*) breeding in the Republic of Kazakhstan is conducted using traditional breeding methods (various hybridization methods, evaluation, and selection). The selection of valuable genotypes is based on phenotypic data. Within the work of this project, DNA markers were used in practical selection of facultative forms. Using SNP, CAPS and SSR markers developed to date for Vrn, Ppd, the allelic diversity of the Vrn (Vrn-H1, Vrn-H2, Vrn-H3) and Ppd (Ppd-H1, Ppd-H2) genes will be identified in the working collection of barley. In the competitive nursery, promising dual-purpose barley varieties were identified over three years of study: 71/13-13, 70/08-3, and 76/13-4. These breeder registration numbers exceeded the grain yield standard by 0,9.2 to 1.24 t/ha, with the standard yield being 4.04 t/ha. Using marker-assisted selection (DNA identification), a variety called “KIZ-Biotech 1” was created over three years of study. During autumn sowing, the average yield of the “KIZ-Biotech 1” variety over three years of competitive variety testing was 3.81 t/ha, while the yield of the “Bereke 54” standard was 3.04 t/ha. During spring sowing, the average yield of the KIZ-Biotech 1 variety over three years of competitive variety testing was 2.70 t/ha, while the yield of the “Bereke 54” standard was 1.75 t/ha. The “KIZ-Biotech 1” variety (70/08-3) was created by individual selection from a hybrid population of “Bulbul” (Turkey) x “Yuzhno-Kazakhstanskiy 43” (Kazakhstan). Variety - Hordeum L. nutans, two-row, facultative; growing season: with autumn sowing 222-236 days, with spring sowing 75-90 days; plant height 85.3 - 99.7 cm. This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan Grant AP19678544.

Keywords: Dual-purpose barley, breeding, variety, competitive nursery, DNA markers.

[Abstract:0266]

Multi-Environment Evaluation of Feed Barley (*Hordeum vulgare* L.) Genotypes under Dryland Conditions in Central Anatolia

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This study aimed to assess the grain yield performance and environmental interactions of feed barley genotypes under the dryland conditions of Central Anatolia through multi-location yield trials. A total of 20 candidate genotypes, along with four check varieties, were tested across four experimental sites—İkizce, Polatlı, Gözlü, and Ulaş—during the 2024–2025 growing season. The experiments were conducted using a randomized complete block design with four replications at each location. Combined analysis of variance revealed significant differences among genotypes, environments (locations), and genotype-by-environment interactions ($p < 0.05$), confirming the presence of substantial variability and differential genotype responses across test sites. The overall model was highly significant ($p < 0.0001$), with an R^2 of 0.62 and a root mean square error (RMSE) of 84.1, which accounted for 62.2% of the yield variation. The mean grain yield across locations was 374.7 kg da^{-1}, ranging from 273.4 kg da^{-1} (Ulaş) to 468.8 kg da^{-1} (İkizce). The highest-yielding environment was İkizce, followed by Polatlı and Gözlü, whereas Ulaş exhibited lower productivity due to harsher climatic conditions. Several genotypes outperformed the standard checks in multiple environments, indicating their potential adaptability and stability in rain-fed regions of Central Anatolia. Overall, the dataset highlights genotypes 19 and 2 as the leading candidates for advancement, with stable, high performance under variable Central Anatolian conditions. Burakbey (456.8 kg da^{-1}) and Sayım-40 (426,6 kg da^{-1}) performed consistently well, while Tarm-92 (397.7 kg da^{-1}) also demonstrated high yield but lower stability performance at İkizce and Gözlü.

Keywords: *Hordeum vulgare* L., multi-location yield trials, Central Anatolia.

[Abstract:0334]

Assessment of Yield Performance and Phenological Characteristics of Two- and Six-Rowed Barley (*Hordeum vulgare* L.) Genotypes under Diverse Ecological Conditions in Türkiye

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This study was conducted to compare the yield performance and phenological traits of barley genotypes developed by Tarım Kredi Tohumculuk under different ecological conditions. The trials were established during the 2024–2025 growing season at four locations; Tekirdag Banarlı, Tekirdag Yorukler, Corum, and Konya Sarayonu using a Randomized Complete Block Design (RCBD) with four replications. Both two-rowed and six-rowed genotypes were evaluated as experimental materials. Grain yield results showed significant differences among locations, indicating strong environmental effects on yield expression and adaptability potential of genotypes. The overall mean yield across all locations was 716.8 kg/da, with the highest average yield observed in Corum (825.9 kg/da) and the lowest in Konya–Sarayonu (574.5 kg/da). When evaluated by genotype, the mean yield of two-rowed genotypes (738 kg/da) was considerably higher than that of six-rowed genotypes (674.5 kg/da). Among all locations, the highest yield was recorded for the two-rowed genotype G10 in Tekirdag–Yorukler (962.1 kg/da), while the lowest yield was observed for the two-rowed genotype G14 in Konya–Sarayonu (411.6 kg/da). Heading dates varied between 114 and 121 days among genotypes, with two-rowed genotypes generally belonging to the early-heading group (114–120 days). The variation observed in yield and phenological traits across environments reflected a substantial genotype × environment interaction, emphasizing the importance of environmental adaptability, stability, and genetic resilience in selection processes. Moreover, climatic parameters such as temperature, rainfall distribution, and soil moisture appeared to play a decisive role in yield differentiation among test sites. Overall, two-rowed barley genotypes exhibited superior performance compared to six-rowed genotypes in terms of both grain yield and stability. The findings suggest that two-rowed genetic materials possess greater adaptive capacity to environmental variability; therefore, they should be prioritized in future barley breeding programs. Continuous evaluation under multiple environments, combined with stability and regression analyses, is essential to identify high-yielding, stress-tolerant, and widely adapted genotypes for sustainable barley production and long-term breeding progress.

Keywords: Barley, yield performance, phenological traits, genotype × environment interaction, ecological regions

[Abstract:0231]

Reevaluation and Breeding Objectives of Safflower (*Carthamus tinctorius* L.) in Türkiye

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Safflower (*Carthamus tinctorius* L.) is a drought-resistant annual oilseed crop belonging to the family Asteraceae. Historical records indicate that safflowers have been utilized for dyeing, medicinal, and aromatic purposes for thousands of years across different regions of the world. In ancient Egyptian, Indian, and Mesopotamian civilizations, red and yellow dyes extracted from its flowers were widely used, particularly in fabric dyeing. In Anatolia, safflower was known as “dyer’s saffron” during the Ottoman period and was an important source of natural dyes. However, by the mid-20th century, the cultivation of safflowers gradually declined due to the widespread adoption of synthetic dyes and the increasing prominence of oilseed crops such as sunflower and canola. In recent decades, Türkiye’s insistent vegetable oil deficit, the growing threat of drought, and the search for alternative crops have brought safflower back into focus. Its low water requirement, tolerance to salinity, and ability to thrive in marginal lands make it particularly suitable for the climatic conditions of Central Anatolia. While the cultivated area, which was merely 30 hectares in the early 2000s, expanded to approximately 44,000 hectares by 2014 due to government support and extension activities, then it experienced a partial decline in subsequent years. Nevertheless, after 2020, with the influence of local incentives and the establishment of small-scale oil mills in provinces such as Kayseri, Konya, and Nevşehir, safflower production witnessed renewed growth. These initiatives have contributed to local economic activities and fostered the emergence of a new form of rural production. Furthermore, the increasing global emphasis on environmentally friendly practices and the rising demand for natural products have renewed interest in natural dyes derived from safflower petals. This trend highlights safflower’s potential not only as an oilseed crop but also as a valuable raw material for the natural dye and cosmetics industries. This study examines the historical significance of safflower cultivation in Türkiye, the process of its revaluation following a period of decline, and the production revival observed after 2020, particularly in the Central Anatolia Region. Moreover, the strategic importance of safflower is discussed in the context of breeding pursoses, economic diversification, and the efficient utilization of natural resources.

Keywords: Safflower, breeding objectives, drought resistant, sustainability

[Abstract:0318]

Assessment of Yield and Agronomic Traits in New Safflower Breeding Lines

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Fats are essential nutrients that provide high energy and fat-soluble vitamins. Safflower (*Carthamus tinctorius* L.) is an important oilseed crop containing 25-45% oil in its seeds, characterized by a high proportion of unsaturated fatty acids. The crop is also drought-tolerant and well-adapted to diverse environmental conditions. The primary objectives of breeding studies in oilseed crops are to develop cultivars with high seed yield, oil content, and oil yield per unit area. This study was carried out in 2024 at the Field Crops Central Research Institute, İkizce Research and Production Farm, within the framework of the “Safflower Breeding Studies” project. Five breeding lines - developed by the Oilseed Crops Breeding Unit using the pure line selection method- along with four registered cultivars (Linas, Dinçer, Koç, and Hasankendi), were evaluated for seed yield, oil content, and oil yield. Additional agronomic traits, including plant height, number of lateral branches, number of heads, head diameter, and thousand-seed weight, were also assessed. Seed yield ranged from 1586.90 to 2513.20 kg ha-1, with the highest yield obtained from Line-135. Oil content varied between 27.22% and 37.35%, with the highest value observed in the cultivar Koç (37.35%), followed by Lines-135 and 80, indicating notable variation in oil accumulation among genotypes. Oil yield ranged from 444.00 to 864.10 kg ha-1, with Line-135 again showing the highest performance, followed by Line-8. The Line-8, which had also showed superior results in previous trials, was submitted for official registration by the Field Crops Central Research Institute in 2023, and the process is currently ongoing.

Keywords: safflower, saffolower lines, oil crop, yield, yield components

[Abstract:0243]

Developing Mutant Lines of Sunflower (*Helianthus annuus* L.): Inducing Mutations in Polen Using a Cobalt-60 Gamma Source

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Sunflower (*Helianthus annuus* L.) is an important oilseed crop valued for its high-quality edible oil, nutritional components, and adaptability to diverse environmental conditions. As one of the major sources of vegetable oil and protein, sunflower plays a vital role in global agriculture and the food industry. The development of new sunflower varieties is crucial to ensure sustainable production and meet the growing global demand for high-yielding, disease-resistant, and environmentally adaptable cultivars with improved oil quality and nutritional value. Mutation, an important source of variation in plant breeding, is a fundamental process that creates genetic diversity and serves as a key driver in crop improvement programs. Therefore, inducing genetic variation through physical mutagenesis using a Cobalt-60 gamma source offers significant potential for the improvement of sunflower traits and the development of superior varieties. In this study, the maintainer lines of the Ahmet Bey confectionary-type sunflower cultivar and the IMI044 oilseed sunflower cultivar were utilized as genetic material. In mutation studies using gamma radiation sources, seeds are generally preferred as the genetic material; however, this study aimed to observe the effects of radiation applied directly to pollen. Prior to the application of mutation treatments, emasculations was performed on the plants, after which pollen were collected in Petri dishes and stored at +4°C to maintain viability for subsequent use. Afterwards, the pollen was transported under a cold chain to the Turkish Energy, Nuclear and Mineral Research Agency (TENMAK), where three different radiation doses (100, 200, and 300 Gy) were applied. The treated emasculated heads were then pollinated with their own irradiated pollen, resulting in the production of M0 seeds. This study represents an alternative approach to mutation breeding by targeting pollen with gamma radiation rather than seed. The seeds obtained from this process were subsequently prepared for sowing in the M1 generation during the following growing season.

Keywords: Sunflower, Genetic variation, Pollen irradiation

[Abstract:0273]

Development of SNP-Based Molecular Markers for Resistance to Broomrape (*Orobanche cumana* Wallr.) Race G in Sunflower (*Helianthus annuus* L.)

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Broomrape (*Orobanche cumana* Wallr.) is a holoparasitic plant that infects the root zone of sunflower (*Helianthus annuus* L.) and causes severe yield losses, representing one of the most critical biotic stress factors in modern sunflower cultivation. In Turkey, the most prevalent and virulent race of broomrape is race G, which leads to significant economic damage. Although various herbicides have been applied against broomrape, the most ecologically and economically effective control strategy is the development of resistant or highly tolerant sunflower varieties. In this study, 358 sunflower breeding lines belonging to MAY Seed were screened under field and greenhouse conditions for their reactions to O. cumana race G. Based on these evaluations, resistant and susceptible lines were identified. The most resistant MAYorG_R line and the most susceptible MAYorG-S line were crossed to produce F_1 progenies. The obtained F_1 plants were self-pollinated to generate F_2 and F_3 populations, while backcrosses with the susceptible parent produced BC_1F_1 populations. These populations were planted in the Cihadiye region of Adana for phenotypic evaluation under natural broomrape infestation. Simultaneously, broomrape race G seeds collected from this region were used for confirmatory analyses in MAY Seed's greenhouse facilities in Bursa. Phenotypic evaluations revealed that resistance to broomrape race G is controlled by a single dominant gene (monogenic inheritance). Leaf samples from F2 and BC_1F_1 populations were sent to SGS INSTITUT FRESENIUS GmbH – TraitGenetics Section for genotyping using a 12K SNP microarray platform. Based on the obtained genotypic data, the broomrape resistance gene was mapped to chromosome 7, and eight SNP markers were identified in association with this locus. Specific probe designs were developed for these SNPs and validated across the phenotyped F2 and BC_1F_1 populations. The validation analyses demonstrated that these SNPs were located within 0.7–8.8 cM of the resistance gene The SNP-based molecular markers developed in this study provide a valuable tool for marker-assisted selection (MAS) in sunflower breeding programs. These markers can be effectively used in both forward and backcross breeding strategies, as well as in gene pyramiding applications. The integration of these SNP markers into breeding programs represents a significant step toward establishing a molecular breeding concept complementary to conventional approaches in sunflower improvement.

Keywords: sunflower, broomrape, snp, molecular marker, mas, molecular breeding

[Abstract:0280]

Determination of Resistance to Broomrape and Yield Performances of IMI Type Sunflower Hybrids

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Sunflower (*Helianthus annus* L.) is the most grown oil plant due to its suitability to agricultural mechanisation and it is the most preferred vegetable oil for consumers in Turkey. One of the main challenges encountered in sunflower cultivation is broomrape (*Orobanche cumana*) and downy mildew (*Plasmopara halstedii*). Sunflower varieties which are resistant to imazamox (IMI) group herbicides, play an important role for suppressing broomrape and the other weeds. Currently in Turkey, new strains of broomrape are found in nearly all of the cultivated areas in the Thrace-Marmara region, where sunflower cultivation is intensive, and in approximately half of the total area across the country. In this study, the yield performances of the hybrids cultivars, which are resistant to IMI herbicides and are developed within the scope of TARI's National Sunflower Project, have been investigated in different locations (Çorlu, Kesan, Kırklareli and Edirne) in 2024. Furthermore, the resistance of the varieties to broomrape were evaluated under the field conditions and also through the artificial inoculation. The experimental design was a Randomized Complete Block Design with four replicates. The four rows plots were 7,50-m long with the 70 x 30 cm plant spacing. 4 commercial hybrids, which are widely cultivated in Turkey, took place as checking varieties. Weed control was with imazamox (IMI) herbicide, 40 g/l with 1.25 l / ha dose after 6-8 leaf stage. Statistical analysis was performed with JMP statistical program. Field trial of broomrape test was located in Kesan. Plots with two replicates, two rows were 4-m long and plant spacing was 70 x 25 cm. Each plots consisted 32 plants. Frequency of infection (F), intensity of infection (I), levels of aggression (A) were examined for each genotype. The resistance of material to broomrape was tested in pots with full of artificially infected soil by broomrape. It is evaluated as susceptible, tolerant and resistant according to the tubers on the roots. As a result of the trial, TTAE IMI 23-130, TTAE IMI 23-135, TTAE IMI 23-142 and TTAE IMI 23-155 showed well-performance in terms of seed yield and seed oil yield compared to the other varieties. All of these same cultivars are highly tolerant to broomrape's new races. The mentioned hybrids will be considered as candidates for registration. Outcome of broomrape resistance test shows that, the plants having OR7 resistance genes, were infected and this implies that there is appearance of a new broormape race in this area.

Keywords: Sunflower, Broomrape, Imazamox, Inoculation, Yield

[Abstract:0187]

The Effects of Gamma and Proton Irradiation Treatments on the Early Seedling Development of Lupine (*Lupinus albus* L.)

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White lupine (Lupinus albus L.) is naturally distributed in Türkiye, it is a species cultivated locally, especially in the Konya region. The plant has a wide range of uses, including soil improvement, animal feeding, human food, medicinal plant, ornamental plant and rotation plant. In addition to its value as a component of crop rotation, it is a rich source of vitamins and minerals. Nevertheless, the high rate of alkaloids in the plant and its sensitivity to fungal diseases are significant problems that limit its utilization on a large scale. In order to resolve these constraints, it is necessary to expand genetic variation. Radiation techniques are widely preferred by breeders as a means of generating mutations and variations. The objective of this study was to ascertain the optimal doses of gamma and proton radiation, with a focus on their impact on the variation in white lupine plants during the early seedling development stage. The experiment was established in 2021 according to the randomized plot experimental design, with three replicates. Konya population was used as material in the study. The seeds were exposed to various gamma doses, including 100, 200, 300 and 400 Gy, as well as proton doses of 100, 200, and 300 Gy. In the experiment, the levels of chlorophyll a, chlorophyll b and total chlorophyll were determined, as were the lengths of the shoots (cm), roots (cm) and seedling fresh weight (g plant-1). These measurements were taken in white lupine seedlings that had been cultivated for a period of one month. High and significant correlations were found between these growth-related characteristics. Statistically significant differences were identified at the $p<0.01$ level between doses for all of the examined traits. As the dose increased, chlorophyll content of the plants decreased, and simultaneously, there was a tendency for shoot and root lengths and seedling fresh weights to decrease. It was determined that doses of 100 and 200 Gy can be used to induce variation in white lupine plants treated with either gamma or proton radiation.

Keywords: Mutation, radiation, gamma, proton, Lupinus albus L.

[Abstract:0052]

Identification of Genotypes for the Development of Edible Dry Pea and Fodder Pea Varieties Adapted to Konya Conditions

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This research was conducted to develop edible and forage dry peas (*Pisum* L.) varieties suitable for Konya conditions. The research was conducted in two locations in Selçuk University Sarayönü Vocational High School and Konya Kadınhanı Kolukısa District in the 2022-2023 production season, using 14 foreign varieties, 3 domestic registered varieties and 3 domestic lines, according to the randomized block trial design, with four replications. In the trial land of Selçuk University Sarayönü Vocational School and in Konya Kadınhanı Kolukısa District It was conducted in different locations. In the research, agricultural characteristics such as winter hardiness, flowering time, plant height, grain yield and quality analysis values of dry pea genotypes were examined. Winter hardiness of dry pea genotypes is between 11% and 87%, flowering time is 180.3-202 days, plant height is 59.8-140.5 cm, biological yield is 117-1080 kg/da, grain yield is 34-457 kg/da, 1000 grain weight is 110.1-316.6. g, harvest index varies between 16.52-42.38%. According to the quality analysis results, crude protein was determined as 19.9-27.3%, starch as 39.7-46.6%, crude fat as 0.7-1.2%, crude fiber as 5.7-7.4%, and crude ash as 2.7-3.0%. As a result, the Retrija variety stands out in terms of resistance to cold stress and grain size. In terms of food quality characteristics, Ps13-2, Deren, Hubal and Vitra came to the fore with crude protein content, Astronaute, Ps317, Psx5 and Irmak with low cellulose content, Green Wood, Irmak, Salamanca and Guiduro with high starch content. In the research, it was seen that there was a wide diversity in terms of the characteristics of the genotypes and it is thought that this will provide a high combination opportunity for the development of new varieties suitable for our region.

Keywords: Pea, genotype, adaptation, yield, Konya

[Abstract:0162]

Use of Paintbell Fertilizer in Pepper Seed Production

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During the decomposition of organic matter, nutrients are released that support plant growth and create a natural feeding cycle. The use of animal manure, in particular, improves soil structure, increases water retention capacity and aeration, and allows roots to develop more healthily. This process also promotes the proliferation of beneficial microorganisms in the soil and facilitates nutrient uptake by plants. As a result, the use of organic fertilizers not only increases yield but also enhances quality, contributing to the production of more nutritious and flavorful crops. The Solanaceae family holds strategic importance worldwide in terms of agricultural production and economic value. Within this family, pepper (Capsicum spp.) species occupy a critical role in both local markets and international trade, with wide applications in the food industry and agriculture-based industries. The diverse types and varieties of peppers are utilized across a broad spectrum, ranging from fresh consumption to processed products, spice production, and industrial food additives. This makes pepper not only economically significant but also culturally and sociologically important as an agricultural product. In this study, the effects of different cultivation practices on SARUHAN F1-14P4242 and AVŞAR F1-14P1540 pepper varieties were evaluated. Throughout the growing season, irrigation and foliar spraying methods were applied, plant growth was monitored, harvests were conducted on randomly selected samples, and germination tests were performed with the obtained seeds. The findings revealed that root and foliar applications in the SARUHAN F1-14P4242 variety enhanced plant vitality, with the highest vitality achieved through combined applications. However, this increase led to problems in fruit set, negatively affecting yield. In contrast, no such issue was observed in the AVŞAR F1-14P1540 variety. Possessing a strong rootstock structure, this variety showed increased plant vitality under PAINTBELL fertilization, though no improvement was observed in yield or germination performance. In the control group plants, fruit set was better, seed yield was higher, and germination rates surpassed those of other treatments. Consequently, it was concluded that PAINTBELL application should not be preferred in pepper varieties with strong rootstock structures. Although it enhances plant vitality, it may cause yield loss and increased costs. The findings highlight the importance of planning fertilization strategies in pepper cultivation by considering the genetic and structural characteristics of the varieties. This enables producers to make more informed decisions, ensuring both productivity and economic sustainability.

Keywords: Capsicum spp. Paintbell fertilization, Yield performance, Germination performance

[Abstract:0342]

The new resistant source to powdery mildew: *Capsicum chinense*

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Powdery mildew caused by *Leveillula taurica,* an obligate fungus*,* adversely affects the development and growth of pepper plants. It is difficult to control by chemicals and cultivation managements. The development of resistant cultivars is the most cost-effective, efficient, and environmentally friendly approach for controlling PM. The new resistance sources against PM are essential for efficient breeding programme. Therefore, in this research we aim to investigate resistance mechanisms in *C. chinense* against powdery mildew (*Leveillula taurica*). The F2 populations were developed by crossing resistant source PI152225 with a susceptible Demre line. The lower parts of leaves were artificially inoculated by conidia suspension of 10^5, 6-8 weeks after F_2 plants and parents transplanted in the greenhouse. The resistance level of each individual plants were scored based on infected area of the leaves using 0-5 scale in 25 and 50 days after inoculation. Area Under Disease Progress Curve (AUDPC) was calculated by using following equation to determine resistance level of F_2 individuals. There were no full resistant individuals (scored 0) in F2 population in autumn season in both year, 2023 and 2024. The AUDPC value in autumn season, 2023 was 133.45 in the Demre line, 8.86 in the PI152225-line, varied between 16.88 and 178 in F2 DemreXPI152225 individuals. The AUDPC value in autumn season, 2023 was 180.09 in Demre line, 17.89 in PI152225 line, varied between 23.63 and 197.5 in F2 DemreXPI152225 individuals. It is thought that the differences of the AUDPC levels in two scoring seasons is due the temperature differences during pathogen inoculation. As a result, it was shown that *C. chinense*, PI 152225 line can be potential genetic resource for powdery mildew resistance.

Keywords: Pepper, *C. chinense*, resistant, powdery mildew, Leveillula taurica

[Abstract:0347]

Comparative Assessment of Drought and Salinity Stress Responses in Open-Pollinated and Hybrid Pepper (*Capsicum annuum* L.) Varieties at Germination and Seedling Stages

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Abiotic stresses such as drought and salinity significantly hinder pepper (*Capsicum annuum* L.) establishment and productivity. This study investigated the germination and seedling responses of an open-pollinated pepper ‘Kandil Dolma’ and an F1 hybrid pepper ‘Yaman’ under simulated drought and salinity stress conditions. During the germination stage, seeds were treated with 10% (w/v) polyethylene glycol (PEG 6000) or 50 mM sodium chloride (NaCl) to induce drought and salinity stress, respectively. Germination percentage and mean germination time (MGT) were recorded as indicators of stress tolerance. The seedling study was conducted hydroponically in a growth chamber using Hoagland nutrient solution supplemented with 12.5% (w/v) PEG 6000 or 85 mM NaCl for drought and salinity treatments, respectively. Growth and physiological parameters including shoot height, root length, stem thickness, number of leaves, leaf area, leaf color, chlorophyll content, anthocyanin concentration, SPAD readings, leaf relative water content (RWC), and electrolyte leakage were measured. The results indicated that both stresses markedly reduced growth and physiological performance in all genotypes. However, ‘Yaman’ maintained significantly higher values for most parameters compared to ‘Kandil Dolma’, demonstrating stronger tolerance to osmotic and salt stress. These findings highlight the superior adaptability of the hybrid genotype and provide valuable insights for breeding programs targeting enhanced abiotic stress resilience in pepper.

Keywords: *Capsicum annuum*, drought tolerance, salinity tolerance, chlorophyll, relative water content, hybrid performance

[Abstract:0066]

Nested Association Mapping Identifies QTLs for Yield and Adaptation in Spring Wheat of Kazakhstan

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Wheat production in Kazakhstan is a key factor in regional food security. Wheat occupies about 80% of the country's cropland, with Akmola, Kostanay, and North Kazakhstan regions contributing 70–80% of total grain output. Spring wheat dominates in the north, while winter wheat is more common in the south. Kazakhstan exports mainly to Central Asia, the Middle East, the Caucasus, and China, with Uzbekistan, Afghanistan, Azerbaijan, Tajikistan, Turkmenistan, Georgia, Iran, and Turkey being key importers. This study assessed 290 spring bread wheat recombinant inbred lines (RILs) from the UK nested association mapping (NAM) population, derived from 24 families with "Paragon" as a common parent. All genotypes were tested in two regions of Kazakhstan at the Kazakh Research Institute of Agriculture and Plant Industry (Almaty region, Southeast Kazakhstan, 2019-2022) and Alexandr Barayev Scientific-Production Center for Grain Farming (Shortandy, Akmola region, Northern Kazakhstan, 2020-2022). Traits studied included plant adaptation and yield-related characteristics: heading date (days), seed maturation date (days), plant height (cm), peduncle length (cm), spike length (cm), number of productive spikes per plant (pcs), number of kernels per spike (NKS, pcs), weight of kernels per spike (g), thousand kernel weight (TKW, g) and yield per square meter (YM2, g/m2). Pearson's index showed positive correlations among most yield-related traits, although a negative correlation was found between NKS and TKW in southeastern regions, and no correlation was recorded for northern regions. Top-performing RILs, surpassing local checks, were identified for NKS, TKW, and YM2, suggesting their potential for breeding programs. Genome-wide association study (GWAS) using 10,448 polymorphic SNP markers identified 146 quantitative trait loci (QTLs) including 64 QTLs in the southeastern region, 27 QTLs in the northern region, and 54 in both locations. Twenty-seven QTLs matched those reported in previous QTL mapping studies and GWAS for studied traits. The results can be used for further studies related to the adaptation and productivity of wheat in breeding projects for higher grain productivity. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Program No.BR24992903, Grant No AP08855387).

Keywords: bread wheat, nested association mapping; genome-wide association studies; plant adaptation-related traits, yield-related traits

[Abstract:0014]

Identification of Winter Wheat Genotypes with High Androgenic Activity for the Development of an Efficient Anther Culture Protocol

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In wheat breeding programs, a key objective is the development of new varieties with high yield potential and resistance to abiotic and biotic stress factors. Typically, the process of developing a new wheat variety takes 10 to 14 years. In order to shorten the time of the breeding process, many researchers apply an integrated approach combining conventional and biotechnological methods, which allows significantly saves resources and time. One of the most promising biotechnological methods for accelerating breeding is anther culture (haploid technology). However, according to numerous studies, the reproducibility of published androgenesis protocols remains low. The main challenges include high genotype dependency, inconsistent results, low frequency of embryo formation from anthers and microspores, and limited rates of green plant regeneration. The aim of this study was to identify model winter wheat genotypes responsive to androgenesis in order to optimize and improve androgenesis protocols under the conditions of Kazakhstan. The research was carried out at the LLP "Kazakh Research Institute of Agriculture and Plant Growing (KRIAPG), located in the southeastern region of the Republic of Kazakhstan. Donor winter wheat plants were grown in the field experimental station of the Cereal Crops Department. The study included 35 winter wheat varieties of domestic and foreign origin. Androgenic response was evaluated in the plant biotechnology laboratory using in vitro anther culture on three liquid nutrient media: W14, C17, and modified MS (mMS). Among the 35 tested winter wheat varieties, only three demonstrated androgenic activity on C17 medium: Farabi – 14 ± 1.2 androgenic structures (AS) per Petri dish; Improved Arap – 17 ± 1.1 AS/dish; Mereke 70 – 16 ± 1.1 AS/dish. In 18 varieties, androgenesis was not induced (0 AS per dish), while 14 varieties showed a response ranging from 0.8 to 12 AS/dish. Regeneration of green plants from androgenic structures was 23.4% in average. Using the three selected responsive varieties, androgenesis were studied on six well-known media (W14, CHB-3, 190-2, C17, MS, AP). The most effective medium was 190-2, where the Farabi variety produced 58.5 AS/Petri dish in average. The Farabi genotype was identified as a model for further optimization and standardization of androgenesis protocols for Kazakhstan's winter wheat breeding programs. The results of this study represent an important step toward the implementation of haploid technology in national breeding efforts.

Keywords: androgenesis, winter wheat, haploid technology, in vitro anther culture, nutrient medium

[Abstract:0015]

Identification of Isolates Insensitive to Strobulirin Fungicides with Quinone Outside Inhibitor in Wheat *Pyrenophora tritici-repentis* Population in Kazakhstan

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Tan spot, caused by the fungal pathogen *Pyrenophora tritici*-repentis (Ptr), is recognized as one of the most aggressive foliar diseases affecting wheat globally, including in Kazakhstan. Under favorable conditions for disease development, yield losses can reach 50–65%. Ptr0 populations demonstrate high genetic variability, with the prevalence of specific races shifting annually in response to climatic and agricultural factors. Current fungicide regimens are often insufficient to control this rapidly adapting pathogen, and an increase in resistance to commonly used compounds has been observed. In this study, the effect of strobilurin fungicides – specifically, those with external quinone inhibitors (QoIs) – on the mycelial growth of Ptr isolates was assessed. Twenty isolates were initially selected at random and evaluated for their sensitivity to azoxystrobin by determining the EC50 required to inhibit mycelial growth. Azoxystrobin was incorporated into potato dextrose agar (PDA) at serial ten-fold dilutions of 0.01, 0.1, 1, 10, and 100 µg/mL. The findings revealed resistance to QoIs among the tested isolates, as confirmed by mycelial growth inhibition assays. On average, mycelial growth was suppressed by 23.01%, 37.87%, 44.97%, 46.37%, and 48.41% at 0.01, 0.1, 1, 10, and 100 µg/mL azoxystrobin, respectively. These results indicate that QoI molecules exhibit greater fungitoxicity against spore germination compared to suppression of mycelial growth in Ptr. Notably, significant differences in pathogen sensitivity to both the active ingredients of the fungicide and among different strains were observed ($p < 0.001$). A significant positive correlation was also found between the area under the disease progress curve (AUDPC) and thousand grain weight of genotypes ($r = 0.76$; $p < 0.001$). Therefore, the integration of bioinformatics approaches in further research will be essential for more effective monitoring, prediction of disease outbreaks, and the development of novel chemical and biological control strategies, as well as for accelerating the breeding of wheat varieties with enhanced resistance. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP22787867).

Keywords: wheat, tan spot, *Pyrenophora tritici-repentis*, QoI fungicides

[Abstract:0065]

Genome-Wide Association Study of Pre-Harvest Sprouting Resistance in a Spring Wheat Collection from Southern and Northern Kazakhstan

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Pre-harvest sprouting (PHS) in wheat is a major agronomic constraint that reduces grain yield, quality, and market value. In 2023, Kazakhstan noted PHS with prolonged rainfall causing pre-harvest sprouting across 2.7 million hectares, representing 15% of the harvested area. Regional losses were particularly high, reaching 20% in Kostanay and 60% in Karaganda. These variations emphasised the importance of developing PHS-resistant varieties and optimising agronomic practices to protect food security. Pre-harvest sprouting is one of the major challenges in cereal crop cultivation, as it leads to reduced yield, loss of grain quality, and deterioration of its technological properties. Multiple factors, including grain color, seed dormancy, falling number, alpha-amylase activity, and the morphological characteristics of the inflorescence, determine resistance to PHS. In this study, 270 spring bread wheat accessions were evaluated for 11 agronomic traits under field conditions in the Kostanay and Almaty regions in 2024. PHS resistance was assessed using two approaches: germination of grains in spikes under controlled climate chamber conditions, and germination tests in Petri dishes. The accessions were classified into three resistance groups: resistant (80-100%), moderately resistant (40-79%), and susceptible (0-39%). In the Almaty region, 53 accessions were resistant, 144 moderately resistant, and 73 susceptible. In the Kostanay region, 57 accessions were resistant, 161 moderately resistant, and 52 susceptible. Notably, 69 genotypes showed consistent stability across both regions, highlighting their adaptability and potential for breeding. A genome-wide association study (GWAS) using 9,212 polymorphic SNP markers identified 56 quantitative trait loci (QTLs) associated with PHS and the germination index, including 33 QTLs in the southeastern region and 14 QTLs in the northern region. These results confirm the high variability in PHS resistance among spring wheat accessions and demonstrate the strong influence of environmental conditions on trait expression. Stable resistant genotypes identified here represent valuable resources for breeding programs, while susceptible lines require further genetic and physiological studies to clarify mechanisms of vulnerability. This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP22785823).

Keywords: bread wheat, genome-wide association study, pre-harvest sprouting

[Abstract:0073]

UAV Canopy Models and Vegetation Indices for Assessing Yield and Stress Traits in Spring Wheat Breeding

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High-throughput phenotyping using unmanned aerial vehicles (UAVs) has become essential for evaluating complex traits in wheat breeding. However, environmental variation and phenological differences can confound trait associations. This study aimed to assess the consistency of vegetation indices (VIs) and UAV canopy surface models (CSM) in predicting grain yield (GY), while accounting for phenology and stage-dependent growth dynamics. Field trials were conducted over two years (2021–2022) on 300 spring wheat genotypes sown in 5 m² plots with two replications. Phenotyping was performed at the medium milk stage (GS75), as this developmental stage has previously shown the strongest association between VIs and GY under similar conditions. UAV-based vegetation indices (NDVI, NGRDI, NDRE), manual plant height (PH), days to heading (DH), grain yield (GY), drought tolerance (DT, 2021), and lodging resistance (2022) were recorded. UAV CSM was calculated as the difference between digital surface and terrain models. Data were analyzed for correlations between VIs, CSM, and agronomic traits, including subgroup analysis based on DH to control for phenology. UAV-derived indices were strongly associated with GY, with NDRE showing the strongest correlations (r = 0.646–0.656). Environmental variation influenced trait relationships: in 2021, VIs were weakly negatively correlated with DT (r = –0.185 to –0.238), while in 2022, UAV CSM captured lodging effectively (r = 0.621 at late season). Correlations between VIs and DH were moderate in 2021 (r = 0.510–0.597) and weaker in 2022 (r = 0.255–0.315). When data were grouped by DH, VI–GY correlations remained significant and often strengthened (NDRE–GY r = 0.541–0.659 in 2021, 0.371–0.709 in 2022). UAV CSM reflected plant height mid-season (r = 0.553) and lodging late-season, highlighting stage-dependent utility. UAV-based high-throughput phenotyping thus enables robust, non-destructive assessment of yield and stress-related traits in spring wheat. Phenology-aware analyses improve yield prediction, and stage-specific UAV CSM measurements provide complementary insights into plant architecture and lodging. These findings support multi-temporal UAV sensing approaches to enhance the efficiency and accuracy of wheat breeding programs.

Keywords: *Triticum aestivum* L., UAV phenotyping, vegetation indices, canopy surface model, phenology, lodging

[Abstract:0078]

The Effect of Medium and High Nitrogen Fertilizer Rates on the Yield and Quality of Different Winter Wheat Varieties

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Intensive farming has led to an increased use of chemical pesticides and nitrogen fertilizers. Therefore, in recent years, the European Green Deal has focused on introducing more environmentally friendly agricultural practices, which include reducing the use of nitrogen fertilizers and pesticides. Nowadays, a wide range of winter wheat varieties is available, but each variety may respond differently to the applied agronomic practices, including nitrogen fertilization. Therefore, understanding these varietal responses is critical for optimizing fertilizer use and reducing environmental impact. The aim of this article is to determine how different winter wheat varieties respond to high and medium nitrogen input levels. A field trial was carried out at Stende Research Center of the Institute of Agricultural Resources and Economics during the 2024/2025 growing season. The researched factors were (1) four winter wheat varieties (Bright, Brigens, KWS Ahoi and KWS Imperium) and (2) nitrogen fertilizer rate (N0, N140, N180). Data processing was done using RStudio. The results indicated that winter wheat grain yield was significantly affected by nitrogen fertilizer rate ($p < 0.001$). The average grain yield increases significantly up to the nitrogen fertilizer rate N180, but for three of the varieties (Bright, Brigens and KWS Ahoi) the grain yield did not differ significantly between the nitrogen fertilizer rates N140 and N180. The results showed that the winter wheat variety had no significant ($p = 0.5717$) effect on grain yield of winter wheat. The protein content in grains of all varieties increased significantly until nitrogen rate N180, but there was no significant difference between N0 and N140. Gluten content for all varieties increased significantly until N180. Sedimentation value for varieties Bright, KWS Ahoi and KWS Imperium increased significantly until N180, while for variety Brigens it increased only until N140. The starch content in the grain of the variety Bright decreased significantly until nitrogen rate N180, while for varieties KWS Ahoi and KWS Imperium until N140. For variety Brigens no significant difference in starch content was observed between the nitrogen rates. The RESEARCH was funded by state research program GreenAgroRes, Nr. VPP-ZM-VRIILA-2024/1-0002.

Keywords: winter wheat, nitrogen fertilizer, variety

[Abstract:0148]

Identification Of Differential Gene Expression Among Low Phytic Acid And High Grain Protein Genotypes In Winter Wheat *Triticum aestivum* L.

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Winter wheat *Triticum aestivum* L. is a major staple for human nutrition. However, the antinutrient phytic acid (phytate; myo-inositol-1,2,3,4,5,6-hexakisphosphate, $InsP_6$) represents the predominant storage form of phosphorus (P) in cereal and legume grains, including wheat. Despite its abundance, phytate is considered an anti-nutritional factor because it is indigestible by humans and non-ruminant livestock and forms stable complexes with mineral cations such as Fe, Zn, Mg, Ca, K, and Mn, thereby reducing their bioavailability. Consequently, reducing seed phytate concentration has long been a major objective in crop improvement programs.The low-phytate (LPA) spring wheat mutant line lpa1-1 was developed, exhibiting a 34% reduction in grain phytate content coupled with elevated inorganic phosphate (Pi) levels. A derivative winter wheat line, 'A02568WS-A-12-10', was subsequently used to generate four recombinant inbred line (RIL) populations to study the LPA trait. Two major-effect QTL associated with Pi accumulation, explaining 23% and 33% of the phenotypic variance, mapped to chromosomes 4D and 5A in a RIL population derived from a cross between 'Danby' and 'A02568WS-A-12-10'. This study identified a novel gene on chromosome 5A that might significantly be responsible for low phytate phenotype as a candidate gene. The candidate gene encodes the non-specific phospholipase C enzyme EC 3.1.4.3, and this enzyme plays a role in the early stage of inositol phosphate metabolism. The enzyme is in the myo-inositol pathway, which affects the binding of phosphate to phytic acid. Hence, decreasing the amount of myo-inositol most likely resulted in decreasing the conversion of phosphate to phytic acid, thus increasing the inorganic phosphorus in the grain.

Keywords: Differential Gene Expression, High Grain Protein Content, Low Phytic Acid (LPA), RNA Sequencing, Winter Wheat *Triticum aestivum* L.

[Abstract:0227]

Identification of New Sources of Resistance to Wheat Root Rot Caused by Bipolaris sorokiniana Using Molecular Markers

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Common root rot (CRR), caused by the fungus Bipolaris sorokiniana, is one of the most destructive diseases affecting wheat and other cereals globally. Average yield losses range from 15–20%, reaching up to 70% under favourable conditions. Breeding for genetic resistance remains the most sustainable strategy to control this disease. In this regard, the identification of new sources of resistance to wheat root rot caused by B. sorokiniana is a very important problem. This study aimed to identify new sources of resistance to B. sorokiniana among 80 local and foreign hexaploid wheat varieties and breeding lines through molecular screening using SSR markers linked to Sb resistance genes. Genotyping with the marker Xwmc44 (linked to Sb1) revealed a 242 bp fragment in 8 genotypes — L-201m, #363/k-43130, #392/k-46619 (Shenenskaya), #445 (Chelyaba-80), #449 (Orenburgskaya Yubileinaya), #456/k-38531 (Albidum 43), #459/k-43285 (Saratovskaya 35), and #575/k-65351 (Voronezhskaya 9). The remaining 72 genotypes lacked the Sb1 allele. PCR analysis with Xfcp623, a marker linked to Sb2, identified 24 genotypes carrying a null allele associated with Sb2, including Aktobe-39, Stepnaya-50, Dinastiya, Ekada-113, L-R-1413m, L-1415m, L-201m, L-205m, and several numbered accessions. The remaining 56 genotypes amplified a 380 bp fragment, indicating the absence of Sb2. Overall, 59 out of 80 genotypes (73.8%) carried one or both resistance genes. Among them, 6 genotypes (L-201m, #392/k-46619, #445, #449, #456/k-38531, and #459/k-43285) possessed both Sb1 and Sb2. The frequency of Sb1 and Sb2 in the tested collection was 8.8% and 71.3%, respectively. These findings expand current knowledge of the genetic basis of resistance to B. sorokiniana and identify valuable germplasm for breeding programs aimed at developing wheat varieties with enhanced root rot resistance. Also, this study is deepening the understanding of the genetic factors contributing to resistance to the disease, which will aid in the development of more resistant wheat varieties. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP26195327).

Keywords: wheat, resistance, common root rot, quantitative trait loci, genotyping, molecular markers.

[Abstract:0229]

Genetic Diversity Analysis of Winter Landraces and Modern Wheat Varieties and Some Breeding Lines

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Genetic diversity is of great importance as a source of new traits and alleles in plant breeding to address problems arising from climate change or consumer demands. However, the use of genetic diversity alone is limited. Knowing which ideal diversity sources should be integrated into each program to better develop crossbreeding plans in the breeding program provides an advantage in achieving success. This poster contains the genetic diversity parts of the PhD thesis titled "Testing of Winter Landraces and Modern Wheat Varieties and Some Breeding Lines Against Different Period Droughts and Drought-Related Genetic Diversity Analysis". In the study, yield and yield components, morphological, phenological, physiological and quality characteristics of genotypes were examined in response to drought in different developmental periods. Additionally, genetic diversity analysis was analyzed for all material groups. As a result of genetic diversity analysis, genotypes that could be parents were evaluated in drought resistant breeding studies. Landraces and modern wheats were used as plant material in the research. A total of 156 genotypes consisting of landraces collected from Turkey, Iran and Afghanistan and wheat varieties with advanced breeding line were examined. While a 20% variation was observed between populations, the remaining 80% variation was observed within populations. It has been determined that the genetic distance values between genotypes are high. This indicates that there is a significant difference between them. PCoA analysis performed on 16,309 SNPs identified three distinct regions. Afghanistan and Turkey landraces varieties formed two separate groups, while Iran landraces varieties were present in both groups. This situation may indicate that Afghan and Turkish landraces varieties are isolated within their own countries, while Iranian landraces varieties may interact with other countries. The average values of the number of different alleles and the number of effective alleles for the five groups were determined to be 2.214 and 1.539, respectively. The average values for I, Ho, and He were found to be 0.488, 0.306, and 0.325, respectively. Iranian landraces varieties were found to show less diversity compared to other genotype groups (I = 0.414, He = 0.265). Breeding lines showed greater diversity compared to other genotype groups (I = 0.581, He = 0.378). Using materials with high genetic diversity, such as in this study, it would be beneficial to establish comprehensive programs using more efficient platforms in field conditions, combining phenotypic selection with selection at the genomic level.

Keywords: Breeding, drought, genetic diverstiy, landraces, wheat.

[Abstract:0242]

Productivity and Yield of Drought-Resistant Winter Soft Wheat in Kazakhstan

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In the context of increasing climate variability, particularly the rise in average annual temperatures observed in southern and southeastern Kazakhstan, reassessing the adaptive potential of major cereal crops has become essential. Winter soft wheat (*Triticum aestivum* L.) remains one of the region's most important grain crops, maintaining a leading position in both cultivation area and food security significance. Developing drought-resistant and ecologically stable genotypes is therefore crucial for ensuring sustainable production under water-limited conditions. This study evaluated the yield performance and key productivity components of drought-tolerant varieties and breeding lines of winter soft wheat cultivated under rainfed conditions in the Almaty region. Field experiments were conducted at the Almaty Regional Experimental Station of KazNIIZiR LLP. The research involved 20 drought-tolerant varieties. The experiment followed a randomized complete block design with three replications. Standard agronomic practices were applied, and meteorological data were recorded throughout the growing season. The study assessed grain yield, thousand-kernel weight, number of spikelets per spike, grains per spike, productive stems per square meter, plant height, aboveground biomass, and harvest index. Data were analyzed using JASP 0,95, correlation, and regression to determine the main yield-forming factors under drought conditions. Significant genotypic differences ($P < 0.05$) were observed for yield and major structural components of productivity. The varieties Dimash, Egemen 20, Kyzyl Biday, and Momyshuly showed the highest yields and strong drought tolerance, exceeding the local standard by 10–15%. These genotypes exhibited minimal yield variation across years, demonstrating high ecological stability and adaptability to fluctuating agroclimatic conditions. Correlation analysis revealed a strong positive relationship between grain yield and thousand-kernel weight ($r = 0.644$, $p < 0.001$), and between the number of spikelets and grains per main spike ($r = 0.867$, $p < 0.001$). Positive associations were also found between productive stems and grains per main spike ($r = 0.483$, $p < 0.001$), and between yield and spikelet number ($r = 0.515$, $p < 0.001$). A weak, statistically insignificant negative correlation was noted between yield and plant height ($r = –0.081$, $p > 0.537$), indicating that reduced plant height does not necessarily enhance yield under drought. Overall, the findings indicate that the most promising genotypes combine high productivity, ecological plasticity, and adaptability to limited moisture. These results provide a foundation for optimizing winter wheat breeding strategies to enhance yield stability under the arid and semi-arid climatic conditions of Kazakhstan.

Keywords: winter wheat, varieties, productivity, drought resistance, climate

[Abstract:0249]

Determination of Some Agronomic and Quality Characteristics of Bread Wheat *Triticum aestivum* L. Advanced Breeding Lines

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Wheat is a crucial food sources to demand our daily energy needs. The development and use of superior new wheat varieties in production is a highly effective tool to overcome increasing wheat demand, and minimize the negative effects of environmental pressures. In Turkiye cold, arid/semiarid wheat production areas account for the largest portion of the total wheat production area. To determine desirable lines for rainfed conditions in Central Anatolia and the transition regions, trials were conducted in two districts of Eskisehir during the 2020-21 cropping season. The trials included 22 advanced breeding lines and three check varieties (Bayraktar2000, Kate-A1, Reis). The trials were designed in a randomized complete block design with three replications. Total rainfall in Eskisehir during the trial period was 347 mm. In our previous observations indicated that the Inonu location was more suitable to wheat cropping compare to that the Beylikova. Therefore, to get more reliable effects, we preferred to use these two locations. Data on cold damage, heading date, plant height, agronomic score, disease severity, grain yield, and some quality parameters were obtained. According to the results statistically significant differences were found in the grain yields of the materials. The highest grain yield was Bayraktar2000 (2,495 t/ha), while Line4 was the lowest (1,705 t/ha) in the Beylikova location, In the Inonu location, the highest grain yield was found Line21 (4,091 t/ha), while the lowest was found Line2 (2,708 t/ha). According to the combined analysis, the highest average grain yield was observed Bayraktar2000 was (3.29 t/ha), Line17 (3.233 t/ha) and Line11(3.215 t/ha), respectively. The average yields of the other varieties were Kate-A1 (3.104 t/ha) and Reis (3.081 t/ha). Main grain quality parameters in the Beylikova and the Inonu trials for Line17 thousand kernel weight (37.0-39.7 g), protein (16.1-12.7%), Zeleny sedimentation (70-44 ml) and alveograph energy (316-202 joules) were found. For Line11, thousand kernel weight (29.5-33.2 g), protein (16.7-15.7%), Zeleny sedimentation (73-51 ml) and alveograph energy (516-340 joules) were found. For Reis, with high bread making quality, thousand kernel weight (36.0-37.1 g), protein (14.5-13.7%), Zeleny sedimentation (51-43 ml), alveograph energy (268-261 joules) were found. Based on the overall evaluation of the our observations, Line17 and Line11 showed more desirable yield, quality, and other agronomic traits comparable to the superior check variety. Therefore, our results strongly revealed that these two candidate lines might be more productive to grow in the Central Anatolian Region, and ready to apply registration.

Keywords: *Triticum aestivum* L., wheat breeding, rainfed, yield, quality

[Abstract:0261]

Development of High Frequency Genotype-Dependent Double Haploid Production System for Bread Wheat Genotypes

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Wheat (*Triticum aestivum* L.) is one of the world's most important field crops and Mesopotamia is the origin of wheat and many other agricultural crops. Along with pest and disease resistance, the highest demand in wheat-based industries is for the development of new wheat varieties with better quality and higher yields. The use of doubled haploid in a breeding program is very important when rapid and genetically pure genotype improvement is required. Use of double haploid technique in breeding programs enhanced efficiency and reduced the costs and time needed to develop and release wheat genotypes adapted to zones growing area. The aim of this study was to obtain high frequency haploid plants and to support the studies focused on improvement of new varieties with high quality, yield, disease resistant and adapted to zones growing area. Tosunbey, Demir-2000 and Bayraktar-2000 bread wheat varieties were used in the study. Anthers of the varieties were incubated at 4°C, then, they were cultivated different callus induction mediums containing different basal media (MS, N6 and B5) with liquid, agar-solidified or gelrite solidified. Swelled and developed anthers were transferred to Murashige and Skoog (MS) medium supplemented with combinations of BAP, KIN, NAA and IBA. The best calli induction (14 %) was obtained from the anthers kept on at 4°C for 7 days on N6 basal liquid medium from Tosunbey variety. Microspore-derived embryos developed in 2–3 weeks and they transformed shoots.The highest shoot regeneration capacity (7.5 %) was also determined on MS medium containing 2 mg/l KIN and 0.50 mg/l NAA; 2 mg/l KIN and 0.50 mg/l IBA from the same variety. The shoots were rooted on MS medium and acclimatizated in growth chamber. High survival rate (47.5 %) including spontaneous chromosome doubling plants was achieved.

Keywords: Durum wheat, *Triticum aestivum* L, anther, haploid, breeding

[Abstract:0302]

Thirteen-Year Evaluation of Genetic Gain in Winter Wheat Breeding under Central Anatolian Dryland Conditions at the Field Crops Central Research Institute

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Central Anatolia accounts for nearly one-third of Türkiye's total wheat production and represents the country's most extensive dryland wheat region. The Field Crops Central Research Institute (FCCRI), a legacy of national winter wheat improvement since 1926, has contributed to the release of 45 bread wheat and 17 durum wheat varieties adapted to this region. Understanding long-term genetic progress is critical for evaluating the effectiveness of wheat-breeding programs under changing environments. This study quantified phenotypic, non-genetic, and genetic trends in grain yield over 13 years (2012–2024) of advanced regional yield trials conducted by FCCRI across the Central Anatolian dryland zone. Trials were implemented in four to seven representative environments each year using a modified randomized complete block design with nested blocks and four replications. A mixed-model framework was applied for each environment to estimate variance components and genotype best linear unbiased predictors (BLUPs). Variance-component analysis indicated that environments explained 35–80 % of yield variation, while genotypic effects accounted for up to 25 %. Broad-sense heritability ($H^2 = 0.55–0.85$) confirmed reliable discrimination among genotypes across years. A control-population approach using the long-term checks BAYRAKTAR 2000 and TOSUNBEY effectively separated non-genetic (environmental + management) from genetic improvement. Overall, phenotypic yield increased steadily, while genetic progress averaged 0.4–0.6 % yr^{-1}, corresponding to an improvement of approximately 35–55 kg ha^{-1} yr^{-1} in the advanced breeding lines. Location-wise estimates indicated positive genetic trends in Gozlu, Malya, and Ulas, moderate gains in Polatli, and limited progress at Altinova, Ikizce, and Sarkisla. These results demonstrate consistent but environment-dependent genetic progress in regional wheat breeding, providing a robust quantitative benchmark for monitoring breeding efficiency and guiding future selection strategies under Central Anatolian dryland conditions.

Keywords: Genetic gain, Bread wheat, Winter wheat breeding, Multi-environment trials, Heritability, Genotype × environment interaction

[Abstract:0345]

Evaluation of resistance of spring bread wheat samples to leaf rust and drought with structural characteristics of productivity

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Kazakhstan is one of the largest producers of high-quality wheat grain (up to 10 million tons annually), the value of which accounts for up to 70% of the total agricultural production of the Republic. Productivity is influenced by genetic factors such as tolerance to abiotic and biotic stress. Most agricultural regions of Kazakhstan are located in areas with insufficient moisture. Of the total area occupied by wheat, 90% belongs to dry-steppe non-irrigated and desert-steppe rainfed lands, and only 10% or about 115 thousand hectares is cultivated under irrigated conditions. A collection of 123 samples of spring soft wheat of Kazakh and foreign selection was collected as material for the study. A study of spring wheat phytopathological resistance revealed a high degree of resistance to leaf rust. The following samples demonstrated immune response (IT-0) to the pathogen (*Puccinia recondita*): Stepnaya 245, Stepnaya 253, Stepnaya 259, Lutescens 48-204-03, Tertsiya, Astana 2, Omskaya 35, Saratovskaya 29, Erythrospermum 1119, and others. Also found were 24 wheat samples affected by leaf rust (MS – moderately susceptible) at a level of 30%, which are characterized by weak resistance to the disease. According to the results of calculating the biomass index (NDVI), 72 wheat samples showed high values in the range of 0.50–0.83. An assessment of 123 promising lines and varieties was carried out based on productivity elements: plant height, ear length, number of ears per ear, number of grains per main ear, grain weight of the main ear, and weight of 1000 grains. Based on structural characteristics, 16 samples with plant heights exceeding 75-85 cm were identified. 22 samples were distinguished by an early heading date (05/14/2025). During the structural analysis, 5 samples were found: 14a-15i, 129/00i, 150/00i, Leucurum 1506-36 and 113/00i-2 of soft spring wheat with an ear length of more than 10 cm, which were distinguished by high indicators. 31 samples of wheat lines were identified based on the number of spikelets per ear (15-20 pcs), which were characterized by high indicators. 20 samples of wheat lines were identified with the number of grains in the main ear forming on average more than 30 pieces. According to the indicator of grain weight in the main ear of wheat, 25 samples were identified with a maximum value exceeding 1 gram. When measuring the weight of 1000 grains, 28 samples were found with high values exceeding 35 grams. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (BR 28712539 (1))

Keywords: wheat, leaf rust, *Puccinia recondita*, abiotic, biotic stress

[Abstract:0213]

Identification of Resistant Wheat Genotypes to Bipolaris sorokiniana under Field and Greenhouse Conditions

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Food security remains a priority in the face of population growth and wheat yield losses reaching 35–45% due to root rot caused by Bipolaris sorokiniana and *Fusarium* spp. These pathogens cause significant damage to grain yield and quality, making the identification of resistant wheat genotypes an important area for breeding programs and ensuring sustainable grain production in Kazakhstan. An evaluation of the wheat collection's resistance to the pathogen Bipolaris sorokiniana was conducted in the field during 2023–2024. The trials included three options: natural infection, fungicide protection, and artificial infection. For artificial infection, a suspension of B. sorokiniana conidia (1×10^5–1×10^6 conidia/ml) and infected straw (1 kg/m^2) were added during sowing, while fungicide protection was achieved by treating seeds with Raxil Ultra. The susceptible Glenlea and resistant Salamouni varieties served as control varieties. The damage was assessed three times using the Zadoks scale (GS 20–29, GS 71–79, GS 80–89), determining the percentage of subterranean internode browning (SCI). The results showed significant differences between genotypes in terms of resistance to B. sorokiniana. In 2023, under natural infection, 16.25% of accessions showed high resistance, 67.5% showed moderate resistance, and 16.25% were susceptible. The most resistant genotypes were #575/k-65351–Voronezhskaya, #445/Chelyaba 80, and L-201m, which also maintained a high level of resistance under greenhouse conditions. In the variant with fungicide protection, 41.25% of accessions showed high resistance, while under artificial infection, only 8.75%. In 2024, 17.5% of accessions under natural infection were highly resistant, 62.5% were moderately resistant, and 20% were susceptible. Five genotypes (#445/Chelyaba 80, #449/Orenburgskaya Yubileynaya, #392/Shenenskaya, #459/Saratovskaya 35, and #575/Voronezhskaya 9) demonstrated stable resistance over two years and confirmed their resistance in greenhouse trials. Thus, based on the combined data, valuable sources of resistance to common root rot were identified, promising for use in breeding programs to develop resistant wheat varieties adapted to the conditions of Central Kazakhstan. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP26195327).

Keywords: *Triticum aestivum* L., common root rot, resistance, AUDPC, artificial inoculation, field evaluation.

[Abstract:0232]

Genetic Diversity Analysis of Walnut (*Juglans regia* L.) Germplasm in Southern and Southeastern Kazakhstan Using Microsatellite Markers

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The present study investigates the genetic diversity and population structure of Persian walnut (*Juglans regia* L.) growing in the southern and southeastern regions of Kazakhstan, focusing on natural and cultivated populations from the Turkestan and Almaty regions. Despite the ecological and agricultural importance of walnut in the country, its genetic resources have remained insufficiently characterized. To address this gap, eight polymorphic simple sequence repeat (SSR) markers were employed to assess the level of genetic variation within and among local populations. The results demonstrated a considerable degree of polymorphism across all loci, with the WGA276 marker exhibiting the highest informativeness in terms of allele number and diversity indices. On average, 5.9 alleles per locus were detected, while the mean Shannon diversity index reached 1.44, reflecting a high degree of allelic richness. The expected heterozygosity (He = 0.704) was significantly higher than the observed heterozygosity (Ho = 0.547), suggesting partial inbreeding or limited gene flow within some populations. Among the studied sites, the Sairam-Ugam population from the Turkestan region showed the greatest genetic diversity, emphasizing its value as a potential source of adaptive traits. Population structure analyses using STRUCTURE, UPGMA, and Principal Coordinate Analysis (PCoA) revealed two main genetic clusters. Interestingly, these clusters did not fully correspond to the geographical origins of the samples, indicating historical gene exchange and shared ancestry among populations from different regions. The overall findings provide strong evidence that Kazakhstan's walnut populations preserve a wide and valuable genetic base. Furthermore, the results contribute to a deeper understanding of the evolutionary relationships of walnut germplasm in Central Asia and underscore Kazakhstan's potential role in regional walnut improvement initiatives. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. BR21882024).

Keywords: walnut, microsatellite markers, genetic diversity, population structure,

[Abstract:0017]

Rice Variety Development Activities at Agrobest Grup

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Agrobest company, based in Izmir, is dealing with the production and marketing of agricultural pesticides and fertilizers. In recent years, this company has started to work on variety development and seed production for different crops. In this context, rice variety development activities were initiated in 2016 at Agrobest company. The aim of the breeding study is to develop rice varieties that have high rough rice and milled rice yield potential, short plant height, suitable for combine harvesting (80-90 cm), resistant to diseases, pests and herbicides, and rice quality that meets the Turkish consumer preferences. In breeding studies, hybridization and selection methods are used. The breeding activities are carried out at the company's station field in Gönen town of Balıkesir province and in the greenhouses in Antalya. The greenhouses are used for generation advance during the winter time. The selected breeding lines are being tested in the yield trials in Gönen station and in Bafra town of Samsun province. After then, the lines have good performances in the yield trials, they are being nominated for registration. In variety development studies, conventional variety development, IMI variety development and provisia variety development programs are emphasized. As a result of the studies carried out so far, the conventional Payidar, Çakabey, Akkurt and Bavra varieties were registered and the production permission have been gotten for Yörük, Kayı and Star conventional varieties, at the same time, the applications have been made for the registration of these varieties. Production permission was taken for the IMI varieties Mustafabey CL, Irmak CL, and Türkmen CL, and they were also nominated for the registration. Additionally, an application was done for the registration of the Ege CL breeding lines. As a result of the Provisa variety development studies, Pavli, Panter and Prima varieties were developed, and production permission was taken for them, also they were nominated for registration. All developed varieties are resistant to the rice blast (*Magnaporthe grisea*) disease. The paddy yields of varieties range between 8 and 11 tons per hectare. Head rice yields are between 60% and 68%. The seeds of Çakabey and Payidar varieties in 2024, Akkurt and Bavra varieties in 2025 were commercialized. Seeds of other varieties are planned to be commercialized in 2026 and 2027. The increase of the production areas of these varieties will make significant contributions to Turkey's rice production sector in terms of yield and quality.

Keywords: rice, rice breeding, rice variety, rice yield

[Abstract:0351]

Evaluation of Grain Yield, Disease Resistance and Micromalt Characteristics of Advanced Malting Barley Genotypes in Two Locations in Southeastern Anatolia Region

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Barley (*Hordeum vulgare* L.) is the world's fourth most important cereal crop, and its primary industrial use is as malt for the brewing industry. During the process of malting, barley exhibits a distinctive characteristic that sets it apart from other cereals. The simultaneous activation of alpha and beta amylase enzymes during the germination stage makes it an optimal grain for the production of malt. Turkey faces a considerable challenge in meeting the estimated domestic demand for malting barley, which is estimated to be 150,000 tons per year. The persistent disparity in quality in comparison to global standards necessitates substantial imports, thereby engendering a reliance on foreign raw materials.The study utilised three standard varieties and 17 improved malting barley advanced lines at two locations in the southeastern Anatolia region. In the present study, three standard varieties, namely Atılır, Fırat and Toprakana, were included, whilst the remaining entries represented advanced breeding lines. Grain yield exhibited a substantial variation, ranging from 430.6 kg/da in Line 4 to 613.4 kg/da in Line 7.Disease scores were generally low, between 1.2 in Line 9 and 2.2 in Line 13. Barley grain protein content ranged from 11.0% Line 6 to 14.5% Line 13, while hectoliter weight varied between 65.6 kg/hl Line 2 and 70.6 kg/hl Line 4. Sieve analysis showed that the proportion of kernels ≥2.8 mm ranged from 25.8% to 53.5% Lines 5–10, the proportion of first-class kernels from 49.1% to 78.3% Lines 16–17, and screenings from 4.3% to 18.2% Lines 4–2. In the micromalting analyses, barley grain protein ranged from 10.8% in Line 9 to 14.7% in Line 10, malt protein from 10.5% to 14.4%, and malt extract from 77.6% in Line 13 to 83.9% in Line 5. Kolbach index varied between 31.9% Line 10 and 49.1% Line 5, and wort viscosity between 1.41 and 1.55 mPa·s. Friability values ranged from 70.0% in Line 17 to 96.8% in Line 5, while β-glucan content ranged from 34 mg /L Line 19 to 307 mg/L Line 17. Despite its status as a major producer of barley, Türkiye's domestic malting barley deficit, offer a clear path toward reducing import dependency and strengthening the local supply chain.In order to address this issue, the present study evaluated twenty different barley genotypes in order to identify varieties capable of meeting the high-quality standards of the malt industry.

Keywords: Barley, Malting Barley, Micromalting Analysis, Disease Resistance, Grain Yield, Southeastern Anatolia

[Abstract:0047]

In Vitro Regeneration Studies in Native Tomato Genotypes

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Tomato is among the most extensively studied plant species in global breeding and genetic research, owing to its adaptability to diverse ecological conditions, its broad range of applications for both fresh consumption and processing, and its recognized nutritional value. In recent years, Crispr-Cas9 technology has become one of the most widely used areas for genetic modification. This technology offers extensive opportunities for integrating traits difficult to transfer through classical breeding methods into qualified genotypes or for generating precise mutations. Furthermore, the regenerative capacity of the studied plant species or genotype in tissue culture is a prerequisite for advancing genetic studies. This study aimed to induce in vitro regeneration from cotyledon and hypocotyl explants of four different native tomato genotypes (PTK-254, PTK-273, Şekerkız, Yelpare). Organogenesis was achieved in MS medium using different doses and combinations of the growth regulators TDZ, BAA, IAA, and Zeatin. In this study, where the interaction of nutrient medium and genotype was found to be important, the highest shoot formation was obtained from MS-1, MS-4, and MS-5 media containing the Şekerkız genotype. These combinations, in which more than 10 shoots were obtained from each explant, were followed by the Yelpare, PTK-273, and PTK-254 genotypes cultivated in MS-1 medium. The combination of 1.0 mg/L Zeatin and 0.1 mg/L IAA (MS-1) provided regeneration in all genotypes, albeit to varying degrees. The use of TDZ alone at doses of 2 and 3 mg/L can also yield positive results depending on the genotype. Developing shoots were sub-cultured and grown. For rooting, hormone-free MS medium was used, and tomato plantlets were transferred to peat pots and acclimatized. In this study, the in vitro regeneration system for use in advanced genetic applications was optimized on experimental material.

Keywords: Organogenesis, *Solanum lycopersicum*, TDZ, Tomatoes, Zeatin

[Abstract:0092]

Identification of Hybrids Suitable for Cluster Harvesting in Coctail Tomato Breeding

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Today, vegetable production has become an important sector due to the growing population and changing consumption habits. Tomatoes (*Solanum lycopersicum* L.), in particular, are one of the most produced and consumed vegetables worldwide. Among tomato varieties, cocktail tomato cultivation has gained an important place in both the domestic market and exports. One of the problems frequently encountered by cocktail tomato growers is that harvesting takes time because each fruit is picked individually, which increases labor costs. In this context, it can be said that there is a need to develop new varieties suitable for bunch harvesting without damaging the bunch shape in order to shorten the harvest time and reduce labor costs in cocktail tomato cultivation. The research was conducted in the greenhouse belonging to Troya Seed Production Research and Marketing Inc. As a result of the cross-breeding of cocktail type F6 and advanced lines identified as parents in the company's gene pool, 18 hybrid varieties were used as candidate materials. Scala F1, Alkış F1, and Filika F1 varieties were used as controls. Measurements and observations were made on hybrid variety candidates in terms of bunch length, number of fruits ripening in the bunch, degree of fruit detachment from the stem, fruit shape, fruit diameter and length, seed cavity diameter and length, fruit carpel number L*, Chroma (C*), hue angle (h°) color values, average fruit weight, fruit flesh thickness, TSS, fruit flesh firmness, and average cluster weight. As a result of the research, statistically significant differences were found in the observation parameters other than the carpel number of the cocktail type hybrid variety candidates. TH19 (43.56 cm) cluster length, TH19 (18.47 pieces) number of fruits ripening in the cluster, TH04 (39.78 mm) fruit diameter, TH11 (60.63 mm) fruit length, TH02 (29.86 mm) seed cavity diameter, TH11 (38.31 mm) seed cavity length, TH08 (42.35) L*, TH05 (39.75) C*, TH08 (42.83) h°, TH11 (51.47 g) average fruit weight, TH11 (5.67 mm) fruit flesh thickness, TH14 (7.93%) TSS, TH08 (1.22 kg/cm^2) fruit flesh hardness, TH11 (408.94 g) were found to be the hybrid candidates with the highest values in terms of average cluster weight parameters. The shorter cluster lengths and lower fruit counts of the TH01, TH02, TH08, TH06, TH11, TH12, and TH16 candidate varieties compared to the other control varieties, except Scala F1, may indicate that these candidate varieties are suitable for cluster harvesting.

Keywords: Coctail tomato, fruit quality, hybrid tomato breeding, *Solanum lycopersicum*

[Abstract:0118]

Importance of Seed Producibility in Determinate Tomato

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Tomato (*Solanum lycopersicum* L.) is one of the most widely cultivated vegetable species in the world, holding significant economic and strategic importance. Especially, determinate (bush-type) tomato varieties occupy a substantial market share due to their widespread use in open-field production for fresh consumption and their role as a primary raw material in the processed food industry. The relatively low seed prices in field-grown tomatoes highlight the need for efficient and economically viable seed production strategies. Therefore, the genetic performance and seed producibility of determinate tomato lines are critical for the sustainability of breeding programs and commercial production. In plant breeding, seed producibility refers to a plant’s capacity to produce a high quantity of viable and high-quality seeds based on its genetic and physiological traits. This trait is a fundamental standard in developing new cultivars and in commercial seed production. Recent literature emphasizes that seed production capacity is closely associated with physiological parameters such as flower morphology, androgenic potential, pollen viability, and hormonal balance. Additionally, genotypes that exhibit tolerance to environmental stress factors (e.g., temperature, humidity, light intensity) demonstrate superior performance in terms of both production consistency and seed quality. These attributes make the use of high seed-yielding maternal lines particularly valuable in breeding programs. Selecting lines with high seed productivity accelerates genetic progress while reducing production costs, thereby supporting economic sustainability. In crops like tomato, which have high commercial value, such lines also offer agronomic advantages including stress tolerance, disease resistance, and adaptability. In the face of rising seed costs, the use of genotypes with high seed producibility promotes local seed production and provides accessible solutions for small-scale growers. From a corporate perspective, utilizing low-cost yet high-yielding plants maximize seed output per unit area, reduces labor requirements, and lowers overall production expenses. This strategy plays a crucial role in enhancing the economic efficiency of breeding programs and ensuring sustainability in commercial seed production. In this context, exploring how low-cost seed production can be achieved through the evaluation of genetic resources, optimization of production techniques, and implementation of sustainable breeding strategies is expected to contribute meaningfully to both public and private sector breeding initiatives.

Keywords: breeding, seed producibility,tomato.

[Abstract:0165]

Strategies to Prevent Fruit Dropping Tomato Hybrides

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Tomato *Solanum lycopersicum* L. is a major global commercial crop and one of the most widely consumed vegetables worldwide, valued for its economic, nutritional, and cultural importance. It plays a key role in both fresh produce markets and processed food industries, including products like sauces, pastes, and canned tomatoes (1). Turkey plays a significant role in global vegetable production and is particularly prominent in tomato cultivation. According to recent agricultural statistics, Turkey ranks as the third-largest producer of tomatoes worldwide, following China and India (2). Based on physiological responses during the ripening process, especially regarding ethylene production and respiration rate, fruits are generally divided into two main classes: Climacteric and Non-Climacteric Fruits. Tomato is a one of main example of a climacteric fruit. In climacteric fruits During ripening Ethylene production and respiration rate increases. The relationship between ethylene and the developmental factors non-ripening (NOR) and ripening inhibitor (RIN) during ripening is not completely revealed (3). Ethylene seems to be one of the most important factors of the stress response in the tomato Plants which is mediated by Ethylene biosynthesis pathway. in this pathway accumulation of the ACC synthase enzyme and (ACS) mRNA in the tissue lead to ethylene and CO2 production of the tomato fruits. In this study, we focused on reducing ethylene biosynthesis in tomato *Solanum lycopersicum* L.fruits through a backcross breeding program. This approach involved the introgression of the Rin (Ripening-inhibitor) gene into one of the original parental lines, followed by the development of a new hybrid genotype characterized by reduced ethylene production and decreased fruit drop during ripening. The primary objective was to develop tomato cultivars with delayed ripening and improved fruit retention by modulating ethylene biosynthetic pathways. In addition, we demonstrated that external applications, such as aluminum silicate treatment, can further reduce respiration rates, thereby suppress ethylene production and minimize fruit abscission. These combined genetic and physiological strategies offer a promising approach to enhance fruit quality and reduce yield losses in tomato production.

Keywords: Tomato Breeding, Ethylene Production, Fruit dropping, Ripening

[Abstract:0166]

Determination of Hypocotyl Characteristics and Graft Compatibility of Qualified Interspecific Hybrid Tomato (*Solanum lycopersicum* × *Solanum pimpinellifolium*) Rootstock Candidates

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Grafted seedlings have a strong root structure that provides resistance to diseases and pests, positively affecting the yield potential of the crop. Tomato, a member of the Solanaceae family, is one of the most grafted vegetable species worldwide. In the first studies on grafting in vegetables, wild species were used as rootstocks for cultivated forms because of their resistance to certain soil-borne diseases, pests, and other adverse conditions. Currently, the most widely used commercial tomato rootstocks are interspecific hybrids such as *S. lycopersicum* × *S. habrochaites* and *S. lycopersicum* × *S. pimpinellifolium*. In this study, the usability of 39 interspecific hybrid tomato rootstock candidates (*S. lycopersicum* × *S. pimpinellifolium*), developed within an interspecific rootstock breeding program supported by TÜBİTAK TEYDEB in collaboration with the private sector and universities, was investigated for grafted seedling production. These hybrid candidates were developed through selective breeding and were previously identified as resistant to several soil-borne pathogens (*Fusarium oxysporum* f. sp. lycopersici, *Fusarium oxysporum* f. sp. radicis-lycopersici, *Verticillium dahliae*) and root-knot nematodes (*Meloidogyne incognita*). The commercial tomato cultivar Fulya F1 (K) was used as the scion. The control treatments consisted of non-grafted Fulya F1 plants and self-grafted Fulya F1 (S–S) combinations, which were used to compare graft compatibility and seedling performance. The "tube grafting" method was employed to produce grafted seedlings. After grafting, the seedlings were maintained for 10 days in a healing chamber at 25 °C and 85% relative humidity. The hypocotyl length, hypocotyl diameter, and rootstock/scion diameter difference of rootstock candidates were measured; then, the grafting success rate was evaluated based on the results of grafting with the Fulya F1 tomato variety. Statistically significant differences were found between rootstocks and scions in terms of hypocotyl characteristics. In the study, the hypocotyl width values of tomato rootstock candidate genotypes ranged from 2.49 mm (RSP-21) to 3.39 mm (RSP-4). Among the examined *S. lycopersicum* x *S. pimpinellifolium* tomato rootstock candidates, the longest hypocotyl length was determined in RSP-27 (41.69 mm), and the shortest in RSP-9 (28.27 mm). The rootstock genotypes with the highest grafting success rates were determined to be RSP-13/K (100%), RSP-19/K (100%), and RSP-31/K (100%), respectively. The findings indicate that these hybrid rootstock candidates are promising cultivar candidate that could serve as alternatives to existing commercial rootstocks for grafted tomato production.

Keywords: Rootstock breeding, hybridization, grafting, scion, tomato

[Abstract:0196]

Determination of Fruit Quality Parameters of Some Processing Tomato Varieties and Competitor Hybrids

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Tomatoes are among the most widely cultivated vegetables in the world, belonging to the Lycopersicon genus of the Solanaceae family. They can be grown in almost every region of the world. Yield is one of the most important factors in tomato production. However, fruit quality parameters are also crucial in tomato production, marketing, and consumption. In recent years, tomato breeding programs have focused on improving quality traits in response to consumer demands, in addition to objectives such as yield and disease and pest resistance. Quality is particularly prominent in processing tomatoes. Therefore, high-quality tomato varieties have a high competitive advantage. This study aimed to determine the quality traits of five tomato cultivars developed as part of the processing tomato breeding program. Five new tomato cultivars and three currently in production were used in the study, and the cultivars were analyzed for fruit weight, soluble solids, rind color and fruit flesh color, acidity, pH, and flesh firmness. The study determined that the newly developed processing tomato cultivars outperformed competing cultivars in quality traits such as fruit weight, sugar content, and color, while there were no commercially significant differences in flesh firmness, pH, and acidity. The new cultivars, which outperformed commercial varieties in terms of yield and disease resistance, were found to have no significant differences in the measured quality parameters. In the light of the findings obtained from this study, it was concluded that the newly developed varieties can be used in commercial production in Turkey and around the world in terms of yield, quality and disease resistance.

Keywords: Processing Tomato, Hybrid Varieties, Fruit Quality Parameters

[Abstract:0064]

Genetic Diversity and Marker-Trait Associations in Bread Wheat Cultivars of Kazakhstan Using KASP Markers

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Wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide and serves as a staple food for a large part of the global population. In Kazakhstan, wheat plays a strategic role in ensuring food security and export potential, while breeding programs are increasingly directed toward developing high-yielding and stress-resistant cultivars adapted to diverse agro-ecological conditions. In this context, molecular-genetic tools are essential for evaluating genetic diversity and identifying markers associated with agronomically important traits. In this study, a comprehensive genotyping of 143 bread wheat cultivars and breeding lines developed by five major breeding organizations of Kazakhstan: A.I. Barayev Research and Production Center for Grain Farming, Karabalyk Agricultural Experimental Station, A.F. Khristenko Karaganda Agricultural Experimental Station, North Kazakhstan Agricultural Experimental Station, and Aktobe Agricultural Experimental Station was performed. A set of 43 KASP (Kompetitive Allele-Specific PCR) markers, converted from our previously identified SNP markers significantly associated with agronomic traits using GWAS and QTL analyses, was applied. The results demonstrated that 33 KASP markers showed polymorphism and effectively differentiated the collection into allele-specific groups. Genetic diversity parameters were calculated, including the number of effective alleles, Shannon's information index, percentage of polymorphic loci, and Nei's diversity index. The average level of polymorphism reached 85.45%, indicating a high degree of genetic variability within the studied germplasm. Principal coordinate analysis revealed two major genotype groups, with accessions from the Karabalyk station forming a distinct cluster. The dendrogram further divided the collection into seven clusters, the largest of which included accessions from Karabalyk and North Kazakhstan breeding stations. To evaluate marker–trait associations, a Student's t-test was performed using field trial data from four regions of Kazakhstan. Twenty-two markers confirmed their statistical significance under North Kazakhstan conditions, 20 under Karaganda conditions, and 19 each under Karabalyk and A.I. Baraev center conditions. Notably, five markers (ipbb_SH_152, ipbb_SH_219, ipbb_SH_223, ipbb_PAxP_183, ipbb_ta_SH_162) consistently demonstrated significance across all environments. The passport data for all analyzed accessions were performed. In conclusion, this study demonstrated the efficiency of KASP markers for assessing genetic diversity and marker–trait associations in bread wheat. The findings provide a significant resource for advancing regional and national breeding programs focused on developing high-yielding and climate-resilient wheat varieties. This research was funded by the Ministry of Agriculture of the Republic of Kazakhstan (Program No. BR24892821, BR10765056).

Keywords: bread wheat, genotyping, KASP marker, marker assisted selection

[Abstract:0180]

Distribution and Development of Apple Fungal Diseases in the Almaty Region

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Apple is a cornerstone fruit crop in the Almaty region, yet recent shifts in temperature and humidity linked to climate change have increasingly constrained yield and quality. Fungal pathogens-particularly scab (Venturia inaequalis), powdery mildew (Podosphaera leucotricha), sooty blotch, and moniliasis-pose persistent phytosanitary threats, precipitating premature defoliation, fruit rot, canopy weakening, and quality deterioration. This study aimed to characterize the spatial distribution and seasonal development of apple fungal diseases across representative production zones in Almaty, evaluate the phytosanitary status, and generate evidence to inform the selection of cultivars with improved disease resistance. Phytopathological assessments were conducted during 2023–2025 using route and fixed-site surveys. Disease incidence and development were quantified as percent infection and disease index, and interannual differences were statistically compared. Fungal diseases were widespread, with scab and powdery mildew constituting the primary risks. In Aport Almaty and Renet Simirenko, scab severity frequently reached 30–40%, leading to notable downgrades in marketable fruit quality. Golden Delicious and Red Delicious experienced combined pressure from scab and powdery mildew, affecting approximately 20–25% of shoots and leaves. By contrast, Zhetysu, Golden Shafran, and Melba displayed comparatively stable resistance, with scab development limited to roughly 10–15%. Local cultivars such as Kandil-Sinap and Lungo were particularly prone to powdery mildew, with infection affecting up to a quarter of shoots. Preliminary observations in 2025 indicated that in more humid microclimates, early-season scab onset was frequent in Aport Almaty and Red Delicious, adversely impacting external appearance and storage performance; overall, scab intensified in wetter years, whereas powdery mildew was more prominent under drier conditions. Collectively, these results highlight cultivar-dependent vulnerability and environmentally modulated disease pressure. Expanding the cultivation of relatively resistant cultivars (e.g., Zhetysu, Melba, Golden Shafran) alongside sustained phytosanitary monitoring is recommended to mitigate risk and stabilize fruit quality in the Almaty region.

Keywords: Apple, scab (Venturia inaequalis), powdery mildew (Podosphaera leucotricha), phytosanitary monitoring, cultivar resistance, fruit quality

[Abstract:0188]

Identified of the Morphologic, Physiologic and Agronomic Traits of Common Vetch Hybrid Lines with Non-Shattering Pods

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In the Central Anatolia Region of Turkey, which is characterized by semi-arid and arid climates, the common vetch (*Vicia sativa* L.) occupies a significant position among leguminous forage crops. Although this species is predominantly cultivated during the summer months in the region's challenging environment, the development of winter cultivars has provided an alternative. Nevertheless, a major constraint persists in the form of the comparatively lower grain yield of these winter cultivars relative to the established summer cultivars. Consequently, the most critical strategy for overcoming this yield disadvantage involves breeding new cultivars that combine high winter hardiness with maximized biological and grain yield. To date, extensive research has been conducted using a range of genetic resources in order to identify these enhanced characteristics. Among the genetic resources under consideration, the wild lines L-1731 and L-1732 have been found to possess the trait of non-shattering pods. However, their winter hardiness and yields have been found to be weak. The Ayaz-08 cultivar has been found to demonstrate tolerance to cold, with an early maturation cycle and a high biological yield. The crossbreeding process involving wild lines was initiated at the Central Research Institute for Field Crops in 2013 with the objective of enhancing the grain yield of the Ayaz-08. A series of breeding and selection procedures were conducted from 2013 to 2023 with the objective of obtaining a cultivar that is tolerant to cold and non-shattering, with high yield potential. In 2024, the hybrid lines and check cultivars/lines (Alınoglu-2001, Ayaz-08, L-1731 and L-1732) were sown in 2 m² plots with using an augmented experimental design. The resulting dataset was then subjected to a detailed evaluation, utilizing the following parameters: flowering time (FT), plant height (PH), stem diameter (SD), stem number (NS), first pod height (FPH), number of pods per plant (PPP), number of seeds per pod (SPP), seed weight (SW), biological yield (BY), and grain yield (GY). The correlation analysis indicated that FPH, SW, BY and GY exhibited the strongest correlations. In Principal Component Analysis (PCA), the grouping of genotypes based on FPH, SW, BY, and GY accounted for 73.8% of the total explained variation. Consequently, the non-shattering lines AF9, AF67, AF72, and AF75 identified as a significant potential for advancement in both BY and GY.

Keywords: *Vicia sativa* L., hybrid lines, non-shattering pods, correlation between traits.

[Abstract:0049]

Studies on Developing CGMMV (Cucumber Green Mottle Mosaic Virus) Resistant Varieties in Different Cucumber (*Cucumis sativus*) Types

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Cucumber Green Mottle Mosaic Virus (CGMMV) is an important Tobamovirus that causes significant crop losses, particularly in cucurbit species such as cucumbers and melons. It is seed-borne and mechanically transmissible. It is found in countries across Asia, Europe, the Middle East, and North America. Although certain chemicals are used in conjunction with hygiene protocols that inactivate the CGMMV virus, the most important solution is tolerant or resistant varieties. The aim of the research was to identify CGMMV-resistant cucumber varieties for domestic and, in particular, foreign markets. To this end, 40 different types of cucumber varieties with superior agronomic, plant, and fruit characteristics, excluding resistant and susceptible controls, were used in the study. Beith Alpha (9 varieties), 5 varieties each of mini cucumber, American Slicer, and gherkin types, 13 varieties of the Langa-type long cucumber, and 3 varieties of the Pacto-type cucumber (20-28 cm) were tested. Twenty pots were used for each variety in the experiment. Plants grown in pots under nursery conditions were transferred to the growth chamber at the fully cotyledon stage and inoculated with the CGMMV isolate. The resistance status of the varieties was determined three weeks after inoculation. The research identified three tolerant and two highly resistant varieties of Beith Alpha type cucumber, two tolerant varieties of mini cucumber, and five highly resistant varieties of gherkin type cucumber in terms of CGMMV. Particularly important types internationally include: eleven highly resistant and one tolerant variety of the Langa type; two highly resistant and two tolerant varieties of the American slicer type; and two tolerant varieties of the Pacto type. According to the research results, the development of CGMMV-resistant varieties in different cucumber types is important for the successful continuation of production in regions where the virus is prevalent. Resistant and tolerant varieties can be successfully used in regions and countries where CGMMV causes problems.

Keywords: Cucumber, CGMMV, Resistant, Variety

[Abstract:0161]

Effects of Parental Lines on Seed Quality in Cucumber Hybrids

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Cucumber (Cucumis sativus L.) is a widely cultivated vegetable species with high economic value worldwide. Seed quality is one of the most important factors directly affecting yield and seedling development in agricultural production. High-quality seeds ensure rapid and uniform germination, balance seedling growth, and preserve the desired characteristics of the species and variety through genetic purity. Certified and healthy seeds are more resistant to diseases and pests, offering maximum yield potential under optimal conditions. Properly processed and stored seeds maintain viability for longer periods, extending storage and shelf life. Germination tests help monitor seed viability, while selecting varieties adapted to local climate and soil conditions increases success in production.In this study, the effects of parental lines on seed quality traits were investigated in two hybrid cucumber varieties grown under open-field and greenhouse conditions. The experiment included hybrids 14C6768 (Open Field) and 14C3703 (Greenhouse), along with their parental lines FM and M. A total of 150 seeds were sown under sterile conditions in trays filled with a 1:1 mixture of peat and perlite, and all samples were irrigated with well water sourced from Multi Tohum. Germination counts were performed on the 4th, 6th, and 8th days after sowing (24.08, 27.08, and 30.08), and the number of germinated seeds for each line was recorded to evaluate hybrid performance. Genetic effects of FM and M parental lines on hybrids were analyzed, and germination rates and speeds were examined to determine early growth potential. Statistical analyses were conducted to interpret differences among lines and to reveal the impact of parental contributions on hybrid performance.The results showed that parental lines had significant effects on germination traits, and differences were observed between open-field and greenhouse hybrids. In particular, variations in germination speed and rate were closely associated with parental combinations, highlighting the strong relationship between early growth potential and genetic background. These findings emphasize the critical role of parental genetics in seed quality and hybrid performance, demonstrating that selecting appropriate parental combinations is essential for optimizing hybrid outcomes. This study contributes to understanding genetic influences on seed quality in cucumber and provides valuable insights for breeding programs aimed at developing more productive hybrids under different cultivation conditions.

Keywords: Seed quality, Germination rate, Cucumber (Cucumis sativus L.)

[Abstract:0163]

Effect of Salt Stress on Seedling Growth Parameters in Cucumber (Preliminary Evaluation)

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Salt stress is considered one of the most important abiotic factors limiting productivity in agricultural production. Morphological changes that occur especially during the seedling stage play a critical role in determining the tolerance levels of plants to salt at an early stage. During this period, differences such as reduced root development, shortened shoot length, and decreased leaf number are observed. Observations made at the seedling stage are of great importance for selecting salt-tolerant genotypes and developing varieties that will reduce yield loss. Since morphological changes are also the first indicators of physiological and biochemical adaptations, they can be used as rapid screening methods in breeding studies, and early-stage evaluations support sustainability in agricultural production. In this study, the effects of different NaCl concentrations on cucumber (Cucumis sativus L.) seedlings were investigated under controlled greenhouse conditions. Cucumber seeds were sown under sterile conditions in four separate seedling trays containing a peat–perlite (1:1) mixture, and salt treatments were applied on the 6th, 9th, and 12th days after sowing. On the 14th day, seedling height, leaf number, root and shoot fresh weights were measured, and the data obtained were statistically analyzed. The results revealed that the morphological responses of plants to salt stress varied across different parameters. Shoot length emerged as the most sensitive parameter to salt stress, showing significant reductions with increasing salt concentrations. Statistically significant differences observed in T2 and T3 treatments compared to the control groups indicated that shoot growth is highly sensitive to salt stress. In contrast, root length exhibited a more resistant response, with a significant reduction only at the highest salt concentration (T3). Leaf number did not show statistically significant differences among treatments, suggesting that leaf formation is less affected by salt stress in the short term. Over all, shoot length stood out as the most reliable indicator of salt stress, while root length and leaf number showed more limited or delayed responses. These findings demonstrate that shoot length can be used as a primary parameter in determining plant tolerance to salt stress. Thus, shoot length can be considered an effective selection criterion in salt tolerance screening. Moreover, morphological measurements made during the seedling stage serve as an important tool for predicting potential yield losses at later growth stages and for identifying salt-tolerant genotypes. The study highlights that early-stage screenings against salt stress can play a critical role in breeding programs and sustainable production strategies.

Keywords: Cucumber (*Cucumis sativus* L.), NaCl concentration, Salt stress, Morphological changes, Plant breeding

[Abstract:0183]

Genetic Evaluation of Cucumber (*Cucumis sativus* L.) Accessions from Kazakhstan Using SSR Markers

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Cucumber (*Cucumis sativus* L.) is a key vegetable crop in Kazakhstan, playing an important role in both local diets and the agricultural economy. Due to the country's diverse climatic and geographical conditions, cucumbers are cultivated across various regions, exhibiting wide phenotypic and genetic variability in traits such as flavor, texture, and resistance to abiotic and biotic stresses. Recent advances in molecular genetics have facilitated the evaluation of cucumber germplasm to enhance yield, stress tolerance, and disease resistance through selective breeding. This study provides a comprehensive genetic analysis of 60 cucumber accessions from Kazakhstan using 15 Simple Sequence Repeat (SSR) markers, of which 10 were highly polymorphic. A total of 180 samples (in three replicates) were analyzed to assess genetic diversity, allele frequency, and population structure. The number of alleles per locus (Na) averaged 3.9, and the effective number of alleles (Ne) was 2.0. The overall Nei's genetic diversity index (uh) was 0.450, while the mean polymorphism information content (PIC) was 0.592, indicating a high level of marker informativeness. Population structure was analyzed using three approaches: Bayesian clustering (STRUCTURE), Neighbor-Joining (NJ) clustering, and Principal Coordinates Analysis (PCoA). STRUCTURE results suggested an optimal K = 3, revealing three genetic clusters with moderate admixture between outdoor- and greenhouse-type cucumbers. The overall genetic diversity of outdoor and greenhouse groups was comparable but higher than that of the total collection. These findings contribute to the understanding of genetic variability among cucumber accessions in Kazakhstan and provide valuable insights for future breeding and conservation programs. The study also demonstrates the effectiveness of SSR markers for genetic characterization of vegetable crops in diverse agroecological regions. This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Program No. BR28712539).

Keywords: *Cucumis sativus*, accessions, genetic diversity, SSR markers, Kazakhstan

[Abstract:0346]

Pomological Characterization and Quality Assessment of Persimmon (*Diospyros kaki* L.) Genotypes from the Black Sea Region of Türkiye

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This comprehensive research was conducted to evaluate the pomological and biological attributes of local persimmon (*Diospyros kaki* L.) populations and to identify superior genotypes through a systematic selection process. The study focused on Tekkiraz Town, located in the Ünye District of Ordu Province, a region within Türkiye's Black Sea zone where persimmon cultivation has demonstrated significant intensification and ecological adaptation. The primary objective was to distinguish promising types from the existing natural flora that exhibit high commercial potential and desirable fruit quality traits. The research material comprised fifty distinct persimmon types growing naturally within the Tekkiraz vicinity. To ensure consistency in data collection, fruit samples were harvested during the peak physiological maturity stage on November 14–15, 2008. The selected genotypes underwent rigorous laboratory analysis to determine key quality indicators, including fruit weight, morphological dimensions (width and length), Soluble Solid Content (SSC), titratable acidity, pH levels, seed count, and astringency status. These parameters are essential for defining the post-harvest performance and consumer preference for the fruit.The analytical results revealed a profound level of genetic variation among the examined types, reflecting the rich biodiversity of the local population. Notably, fruit weight exhibited a wide range between 114.59 g and 340.07 g, while SSC values fluctuated significantly between 8.0% and 25.4%. A critical finding of this study was that 52% of the sampled population consisted of types categorized as either non-astringent or slightly astringent. This high percentage underscores the region's strategic importance as a source of genotypes suitable for firm consumption, which is a major trend in the global persimmon market. Utilizing a weighted scoring method to synthesize the multi-parametric data, five specific genotypes—52 TKZ 04, 52 TKZ 12, 52 TKZ 15, 52 TKZ 16, and 52 TKZ 20—were identified as "promising" due to their superior pomological profiles. Among these, the 52 TKZ 12 genotype was particularly remarkable, yielding a fruit weight of 340.07 g and an SSC of 21.0%, suggesting excellent potential for high-yield commercial production. It is strongly recommended that these selected genotypes be integrated into advanced adaptation trials and breeding programs to facilitate their registration as new cultivars, thereby enhancing the regional agricultural economy and diversifying the fruit industry in Türkiye.

Keywords: Diospyros kaki, persimmon, pomological traits, quality assessment, astringency

[Abstract:0045]

Applications of Chromosome Doubling in Haploid Squashes and Pumpkins (*Cucurbita*spp.)

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Squashes and pumpkins are important vegetable species belonging to the genus *Cucurbita* of the family *Cucurbitaceae*. The genus *Cucurbita* (2n=40) comprises five cultivated species, the most economically important of which are *Cucurbita pepo* L., *C. maxima* Duch., and *C. moschata* Duch. The dihaploidization technique, which allows the rapid and efficient obtaining of pure lines in variety breeding programs in many plant species, is also successfully applied in the *Cucurbita* genus. The irradiated pollen technique yields successful results in all three squash species in obtaining haploid plants. Successful applications have been made in projects conducted at our company to obtain haploid plants in squash. However, it is not possible to propose a practical protocol for chromosome doubling in squash and obtaining doubled haploid (DH) plants from haploid plants. Although the literature contains successful applications and reports of pure-line seeds, the doubling step remains a key challenge in the production of pure lines in squash. For this purpose, studies were conducted on chromosome doubling in haploid squash plants under in vitro and in vivo conditions. Concentration and duration of colchicine applications were tested, and stomatal examinations revealed diploid plants. The most effective method was determined to be a 3-hour application period using a 0.5% colchicine dose used in acclimated young haploid seedlings at the 3-4 leaf stage. Plants grown from this treatment were self-pollinated to obtain pure-line seeds. However, optimization studies on chromosome doubling in squash varieties are still needed.

Keywords: Squashes and pumpkins, haploid, *C. moschata*, *C. maxima*, colchisine, chromosome doubling

[Abstract:0160]

Phenotypic Profiling of Anchote (7Coccinia abyssinica7 (Lam.) Cogn.) Accessions Through Agro-Morphological and Physiological Markers

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Anchote “(Coccinia abyssinica)” is a neglected high-potential food and nutrition security tuber crop in Ethiopia. Phenotyping core germplasm collections using agro-morphological and physiological markers is essential for effective crop improvement and utilization. A total of 282 anchote germplasms were profiled using six qualitative and twenty-six quantitative agro-morphological and physiological traits. Augmented Block Design was used for the experiment at the Debre Zeit Agricultural Research Center. The chi-square test and Shannon diversity index indicated the presence of substantial phenotypic variation and diversity among the accessions based on the predominant qualitative traits studied. The quantitative agro-morphological and physiological traits showed wider variability and ranges for the accessions. The broad-sense heritability and genetic advance as a percentage of the mean were notably high for quantitative traits such as root yield, vine length, and leaf area index. A significantly positive correlation was observed among agronomically important traits such as root yield and root diameter as well as root yield and leaf area. The principal component analysis for qualitative and quantitative traits found that ten components explained 72.2% of the variation for qualitative traits, whereas nine components accounted for 69.96% of the variation in quantitative traits. The primary contributors to the variations are traits such as root (shape, flesh color, and yield), leaf (color, length, diameter, area) and fruit (length, diameter, and weight). Further, the accessions were grouped into two and three clusters based on qualitative and quantitative traits, respectively, indicating that quantitative characters better differentiated among the accessions. Similarly, the tanglegram showed little similarity between the qualitative and quantitative agro-morphological and physiological traits in clustering the accessions. These findings indicate the presence of sizable trait variation among the accessions that can be exploited as a selection marker to design and facilitate conservation and breeding strategies of anchote.

Keywords: Phenotyping, agro-morphological, physiological, qualitative, quantitative, accessions

[Abstract:0254]

The Effect of Different Plant Growth Regulators on in vitro Double-Haploid Plant Production in *Cucurbitaceae*

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Plant biotechnology encompasses a range of tissue culture and molecular techniques developed to improve the genetic structure of plants (Doe & Smith, 2021). Among these, plant tissue culture is a widely preferred method in modern plant breeding processes (Smith & Jones, 2020). The success of tissue culture applications depends on key components such as the culture medium, explant type, and environmental conditions. One of the most commonly used media is the Murashige and Skoog (1962) medium, which contains inorganic salts, organic compounds, and gelling agents. When combined with plant growth regulators (PGRs), this medium significantly supports regeneration processes. PGRs such as Kinetin (KIN), 2,4-Dichlorophenoxyacetic acid (2,4-D), Gibberellic acid (GA_3), and Thidiazuron (TDZ) regulate physiological events including cell division, embryo development, germination, and organogenesis, thereby promoting plant growth (Dong et al., 2016; Salehian et al., 2023). Notably, TDZ has been reported to enhance callus formation and embryogenic response at low concentrations, while GA_3 positively influences germination rates and seedling development (Acharya et al., 2020; Redhwan et al., 2023). This study investigates the effects of these regulators, applied at different concentrations in MS medium, on the germination and seedling development of species belonging to the Cucurbitaceae family under laboratory conditions. The Cucurbitaceae family includes species of high economic value both in Turkey and globally. The findings contribute to the optimization of tissue culture protocols for these species and support the development of homozygous lines for breeding programs. Techniques such as parthenogenesis and ovule culture have been successfully applied in species like cucumber (*Cucumis sativus* L.), yielding effective results in double haploid (DH) plant production (Claveria et al., 2005; Nyirahabimana et al., 2022; Salehian et al., 2023). DH technology is considered a major innovation in plant breeding due to its ability to rapidly and efficiently achieve genetic purity. The success of this technology depends on the effects of PGRs used in conjunction with MS medium, which vary according to species, genotype, explant type, and culture conditions (Nyirahabimana et al., 2022; Aslibeigi et al., 2023). Recent studies have shown that PGRs play a decisive role not only in germination and seedling development but also in processes such as haploid embryo formation and chromosome doubling. For instance, appropriate doses of 2,4-D support embryo induction, while TDZ and GA_3 enhance regenerative responses (Dong et al., 2016; Acharya et al., 2020; Redhwan et al., 2023). In this context, the development of comprehensive protocols that thoroughly examine the interactions and dose-response relationships of PGRs is essential for improving DH production efficiency in Cucurbitaceae species (Hooghvorst & Nogués, 2020).

Keywords: *Cucurbitaceae*, Double-Habloid (DH), in vitro, Melon, PGR,

[Abstract:0331]

Dihaploidization Studies on Citron Watermelon (*Citrullus lanataus* var. citroides) for Becoming a Rootstock for Watermelon

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Today, biotic and abiotic stress factors significantly impact agricultural production, causing losses in plant growth, development, and productivity. Because popular watermelon varieties used in watermelon production have very limited genetic diversity and are susceptible to many important biotic and abiotic stresses, more than 90% of global watermelon (*Citrullus lanatus* var. lanatus) cultivation is done using grafted seedlings. For this reason, F1 hybrid rootstock breeding has become an industry. Its drought tolerance and high resistance to *Fusarium* and nematodes make citron watermelon a valuable rootstock. Therefore, the development of citron watermelon lines with high rootstock potential is considered an important issue for our country. The first step in obtaining an F1 hybrid variety is the development of pure parental lines, and achieving the desired purity in cross-pollinated species like watermelon requires 6-8 generations of inbreeding. A technique called dihaploidization allows for the production of completely homozygous pure lines within a single generation. By producing doubled haploid (DH) lines with this technique, the process of obtaining recombinant pure lines is shortened, and the development of high-quality F1 hybrid varieties using DH plants can be accelerated. This increases breeding efficiency and accelerates the production of new varieties. This mini-review summarizes studies on dihaploidization techniques (parthenogenesis, gynogenesis, and androgenesis) for breeding drought-tolerant rootstocks in watermelon, and offers suggestions for potential future studies.

Keywords: Watermelon, anther culture technique, haploid plant

[Abstract:0094]

Seed Traits and Root Architecture of Developed Citron Watermelon (*Citrullus lanatus* var. citroides) Lines Used as Rootstocks

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The most commonly used rootstocks in practical watermelon seedling production are interspecific hybrids of *Cucurbita maxima* × *Cucurbita moschata*, as well as Lagenaria siceraria, Benincasa species, and Citrullus species. Citrullus lanatus var. citroides (citron), belonging to the Citrullus genus, is also utilized as a rootstock in grafted watermelon production due to its high resilience to various environmental (abiotic) and biological (biotic) stress factors. A breeding program is being carried out through a university-private sector collaboration to assess the grafting potential of citron (*C. lanatus* var. citroides) as a rootstock for watermelon and to develop improved local lines. This study investigated seed traits and root system architecture of five elite citron lines developed to the S_5 generation within a rootstock breeding program for resistance to nematodes and *Fusarium* wilt. For comparison, commercial interspecific hybrid rootstocks (*C. maxima* × *C. moschata*), Shintoza F1 and Nun 9075 F1, were used. Seed characteristics, including seed length, seed width, seed shape index, seed colour, and 100-seed weight, were determined. Seed width ranged from 0.5 to 1.2 mm, seed length from 1.1 to 2.0 mm, and 100-seed weight varied between 9.89 and 29.8 g. The root architecture of citron lines was determined using the WinRhizo root analysis imaging system. Root analyses were conducted three times, at 10, 20, and 30 days after seedling transplanting. The root scan analysis determined parameters such as root length, root diameter, root volume, root surface area, number of branches, and number of tips. The results indicated that total root length ranged from 864.97 to 1,238.74 cm; root diameter varied between 1.31 and 2.96 mm; root volume ranged from 9.55 to 49.44 cm^3; and root surface area ranged from 326.29 to 637.66 cm^2. Future studies will focus on determining the graft compatibility of citron rootstock candidates with various watermelon cultivars and assessing their potential for use in grafted watermelon seedling production.

Keywords: Citron rootstock, grafted watermelon, rooting, seed characteristics

[Abstract:0190]

Development of Red Lentil Genotypes Tolerant to IMI Group Herbicides

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Lentil (*Lens culinaris* Medik.) plays an important role in human and animal nutrition due to its high protein content. However, one of the major factors limiting lentil yield and production is weed infestation. In many years, weeds caused yield losses of up to 75%. Weed pressure is a major constraint to winter lentil production in the Central Anatolia Region. The aim of this study was to develop lentil genotypes tolerant to IMI herbicides. Lentil genotypes developed by hybridization and maintained in the Legume Breeding Unit of the Field Crops Central Research Institute were used as material. The experiment was conducted with 15 genotypes and 3 control varieties at the İkizce research and production farm in 2025, using a randomised block design with three replications. The genotypes and controls were treated with 40 g/L imazomax during the early growth stage. Herbicide tolerance was assessed 21 days after application using a 1–5 scale. Plant height and first pod height were measured before the herbicide application and at harvest. After harvest, yield and 1000-grain weights were weighed. According to the results, yield ranged between 21 to 118 kg/ha among the genotypes. Among them, AkM 1314 showed the highest yield and was the least affected by the herbicide treatment.

Keywords: Lentil, IMI herbicide resistance, yield, yield components

[Abstract:0306]

Analysis of Tulip Pollen Quality for Parent Selection in Breeding Programs

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Pollen quality is one of the most important factors affecting plant reproduction and propagation success. Pollen viability and germination ability increase the rate of post-pollination fertilization, directly affecting both seed formation and overall yield performance. These traits are critical for the success of breeding programs aimed at obtaining new varieties, particularly in ornamental plants. Determining pollen quality data in ornamental plants with high economic value, such as tulips (*Tulipa* spp.), is helpful in selecting parents for crossbreeding. In this study, viability and germination ability were assessed in pollen from 34 different tulip genotypes. Pollen viability was determined using the 2,3,5-triphenyl tetrazolium chloride (TTC) method, and germination rates were determined by in vitro tests using agar-containing Petri dishes. When pollen from tulip genotypes was evaluated in terms of germination rates, pollen viability rates ranged from 5% (G56) to 94% (G35). Germination rates varied significantly among genotypes, with 16 out of 34 genotypes showing no germination. The highest germination rate was 58.33% in the G35 genotype, while the lowest was 4% in the G39 and G52 genotypes. Overall, the average pollen viability rate was calculated as 39.78%, and the average germination rate was 20.12%. The difference between the two parameters was 49.4%, indicating that pollen viability rates were significantly higher than germination rates. These findings demonstrate that pollen quality is a key trait to consider when selecting parents in tulip breeding programs, and that using genotypes with high viability levels as breeding material can increase the chance of success.

Keywords: *Tulipa* spp., Hybridization, Pollen, TTC test, Germination, Genotype

[Abstract:0055]

SSR-based Analysis of Genetic Diversity in Maize (*Zea mays* L.) Accessions from Kazakhstan

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Maize (*Zea mays* L.) is one of the most important cereal crops worldwide, serving as a source of food, feed, and industrial raw materials. In Kazakhstan, its cultivation is expanding, particularly in southern and southeastern regions. However, local environmental constraints such as drought and temperature extremes limit yield stability, making genetic improvement a priority. Molecular markers, particularly simple sequence repeats (SSRs), provide reliable tools for assessing genetic diversity and informing breeding strategies. This study aimed to evaluate the genetic variability of maize accessions cultivated in Kazakhstan using SSR markers. A total of 21 maize accessions (7 local, 9 Chinese, 5 European) were genotyped with 21 SSR markers. Genomic DNA was extracted from seedlings, amplified by PCR, and analyzed using capillary electrophoresis. Genetic diversity indices, including the number of alleles (Na), effective number of alleles (Ne), Shannon's information index (I), and Nei's diversity index (uh), were calculated with GenAlEx. Population differentiation was assessed by Analysis of Molecular Variance (AMOVA), neighbor-joining dendrogram, Principal Coordinate Analysis (PCoA), and STRUCTURE clustering. SSR markers revealed high polymorphism, with PIC values ranging from 0.557 to 0.962. Kazakh accession ZM001 exhibited the highest diversity (Na = 2.619, uh = 0.629). AMOVA indicated that 66% of total genetic variation was attributable to differences among accessions (Fst = 0.611, Nm = 0.159), suggesting strong population differentiation and limited gene flow. Clustering approaches consistently grouped accessions by geographic origin, with Chinese lines forming a distinct clade and Kazakh and European accessions being more closely related. Several highly informative markers, including umc1327 (PIC = 0.962), umc1265 (0.864), and umc2189 (0.862), demonstrated strong potential for genetic fingerprinting and marker-assisted selection. The study revealed moderate to high levels of genetic diversity among maize accessions in Kazakhstan, with local genotypes demonstrating the greatest allelic richness. The identification of highly informative SSR markers underscores their value for breeding programs aimed at developing climate-resilient and high-yielding maize varieties. These findings highlight the importance of conserving local germplasm and integrating molecular tools into national maize improvement strategies. This study was supported by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Program No. BR24992903).

Keywords: *Zea mays*, SSR markers, genetic diversity, AMOVA, population structure, Kazakhstan

[Abstract:0060]

Obtaining Haploid Seeds in Sweet Corn *Zea mays* saccharata by Haploid Inducer Lines

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In this study, inducing lines (ADAİL-1, ADAİL-2, M741F, and M741H) were pollinated to determine the haploid induction capabilities of different sweet corn (Zea mays saccharata) varieties, and haploid seeds were successfully obtained. The study was conducted under field conditions in a trial plot located in the Sarayönü district of Konya province during the 2025 growing season. A total of 483 controlled pollinations were performed within the scope of the study, resulting in 53 different induced combinations between the inducer lines and the sweet corn genotypes. Sweet corn varieties used in the trial included Princess, Tasty Sweet, Os255Su, Yummy, Inka, Sugrano, Golden Bantam, Ashworth, True Sweet Gold, Sequoia, Elan, Vp Union, Sweet Nugget, Rugby Red, BC 376 susu, Stowell's Evergreen, Calipos, Diego, Mirza, Sherbet, Cajoon, Gucio, Lax, Caramelo, Khan, Fragman, Baron, Performance, Globe, Macaron, Maysu, Vega, Baha, Aurius, Tatonka, Tramunt, Ramondia, Damaun, and Hickory King White, representing both domestic and international registered cultivars. The haploid seeds obtained from these crosses constitute an important genetic resource for the development of doubled haploid (DH) lines in sweet corn breeding programs. The results of this study are expected to contribute significantly to accelerating breeding cycles, enabling early generation selection, and improving genetic purity and uniformity in sweet corn varieties.

Keywords: breeding, inducer, haploid, sweet corn

[Abstract:0081]

Donor-Specific Factors Drive Doubled Haploid Efficiency in Temperate Maize Breeding

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The doubled haploid (DH) method greatly accelerates maize breeding by enabling the production of fully homozygous inbred lines within a single year, compared to at least four years required by conventional selfing. The Maize Research Institute Zemun Polje (MRIZP) established its DH program in 2014 and has since produced nearly 20,000 DH lines from approximately 500 populations representing diverse heterotic groups. A persistent challenge in applying the method under temperate conditions is the strong influence of donor germplasm on DH efficiency. To evaluate the potential of MRIZP's elite materials as DH donors, nine F_1 populations were selected from three heterotic groups—BSSS, IoDent, and Lancaster. These populations were crossed with a standard haploid inducer over two consecutive seasons in Serbia. Putative haploids were identified using kernel color markers and transferred to a winter duplication nursery in Chile for chromosome doubling. A comprehensive set of traits was measured at both stages. In the induction nursery, total kernel number and initial haploid induction rate were recorded. In the duplication nursery, true haploid induction rate, germination, field survival of haploids, false haploid rate, pollination success, duplication success, and the final number of DH lines produced were assessed. Regression analyses were performed to relate these traits to two key indicators of method efficiency for each population: final DH line count and duplication success. The objective was to identify the most sensitive step in the process and to understand how the genetic background of donors, including heterotic group membership, influences the outcome. Regression coefficients between the recorded traits and final DH line count ranged from 0.49 (false haploid rate) to 0.91 (final haploid stand count), indicating that field performance of haploids is a major determinant of DH line yield. In contrast, relationships between these traits and duplication success were negligible. Significant differences were found not only among heterotic groups but also among populations within the same group, suggesting donor-specific effects. Year-to-year variation significantly influenced both population performance and the measured traits. These results emphasize that while heterotic groups contribute to variation in DH efficiency, donor-specific factors are predominant. Understanding these effects can guide the optimization of DH protocols for temperate maize breeding programs and improve predictability and overall success of DH line production. Acknowledge: Acknowledgements: This work was supported by the Project TWINNING GREEN-EDITING VIBES FOR FƟƟD (CREDIT Vibes) (Grant No: 101059942).

Keywords: maize, doubled haploids, breeding

[Abstract:0082]

Selection of Maize Hybrids Adapted to Mediterranean Area using GGE Biplot Analysis

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Six late maturity hybrids, created at Maize Research Institute „Zemun Polje“ were evaluated in multi-locations trials, accoring to RCB design at four locations and two repetitions in Italy and Turkey during 2023-2024. The trial also included two elite commercial check hybrids, well adapted to the agroecological conditions in Mediteranean countries. The aim of the study was to select the best adapted hybrids to the all examined regions and also to detect hybrids speciafically adapted to the certain geographical regions. GGE biplot analysis were used to determine the effect of genotype and genotype-environment interaction. The contribution of GGE interaction in grain yield of examined maize hybrids represented 60.48% of the total variation in the first two components. Strong correlation is observed among all environments in 2024., suggesting that the genotypes performed similarly across all environments and therefore the influence of environment was not strong, while in 2023 the correlation between environments had higher variation. Hybrid Ch-2 had the highest average grain yield among all environments during two years of testing, followed by Ch-1, ZP 8705 and ZP 7900. It is important to point out that the highest yielding hybrid Ch-2 performed very stable, which is important from the aspect of cultivation in unfavorable conditions. Hybrids ZP 7900 and ZP 8705 could be considered as relatively stable, which makes them a good choice for further testing, considering their above-average grain yield. ZP 7902 performed stable in the most of the examined environments, although grain yield was below average at the some of tested locations. This hybrid performed much better in the agroecological conditions of Turkey than in Italy. The genotype × environment interaction was most noticeable at location Lendinara 24, followed by Udine 23 and Lendinara. These environments are discriminative, making it easier to separate hybrids based on their performance. According to the obtained results, it can be concluded that at the Lendinara site there is a significant influence of environmental factors, based on two-year study. Acknowledge: Acknowledgements: This work was supported by the Project TWINNING GREEN-EDITING VIBES FOR FɵɵD (CREDIT Vibes) (Grant No: 101059942).

Keywords: maize hybrids, GGE biplot analysis, genotype × environment interaction

[Abstract:0164]

Development of a Management Model (DOSUYM) Based on Unmanned Aerial Vehicle and Satellite Systems for Variable Rate Irrigation in Mobile Drip Irrigation Systems

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In this study, the use of a newly developed circular-movement mobile drip irrigation system capable of variable rate irrigation in silage maize production was investigated. The research was conducted in the Ladik district of Samsun province, on the experimental fields of Ondokuz Mayıs University. Through the use of digital technologies, less water can be used, higher yields can be obtained, pollution caused by irrigation systems can be reduced, and other natural resources can be preserved. Maize (Zea mays L.) is one of the cereal crops with the highest yield per unit area and can be grown in nearly every part of the world. Maize removes large amounts of water and nutrients from the soil. However, as a C4 plant physiologically, maize produces a very high proportion of dry matter per unit area in return for the water and nutrients it consumes. Due to the high water demand of maize throughout its growth and development period, yield reduction and a decline in cultivated maize areas occur in arid and semi-arid climate regions and under rainfed conditions where irrigation is not practiced. Maize is also an excellent crop for silage production. Using the developed system, four different irrigation levels were applied to silage maize in four replications. Within the scope of the study, meteorological parameters, soil water balance components, morphological characteristics, and yield- and quality-related traits were examined. Specifically, leaf area index, plant height, main stem diameter, leaf number, and green forage yield were determined. The results indicated that plant height, main stem diameter, and leaf number increased up to the tasseling/ear emergence stage and then decreased or stabilized from this stage until harvest. Green forage yield in maize exhibited a significant positive relationship with plant height, leaf number, and leaf area. As in many other crops, water stress negatively affected green forage yield, plant height, main stem diameter, leaf number, and leaf area index. It was found that the irrigation treatments receiving the highest water amounts (MS3 and MS4) belonged to the same statistical group in terms of green forage yield. Consequently, preferring the MS3 treatment instead of full irrigation (MS4) would allow approximately 25% water savings. The results obtained from the study conducted on an area of approximately 50 decares demonstrate that the developed system enables the automatic application of variable rate irrigation over much larger agricultural areas.

Keywords: Maize, Plant breeding, Irrigation level, Precision agriculture practices

[Abstract:0207]

Comprehensive Stability Analysis of Candidate Grain Maize Hybrids for Yield and Quality Traits Across Diverse Environments in Türkiye

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Developing stable maize hybrids that are adaptable to variable environments in terms of yield and quality characteristics is one of the important objectives in corn production. Testing across multiple environments is an ongoing necessity to understand how a hybrid truly performs in diverse environments. Such trials are crucial for ensuring stability and adaptability for yield and quality traits across contrasting agro-ecological zones. The present study was conducted to determine the agronomic performance and stability of 15 candidate maize hybrids developed by Tarım Kredi Tohumculuk against 5 commercial checks across three maize-growing locations of Türkiye (Adana, Mersin and Balıkesir/Altınova). Field trials were carried out during the 2024 growing season utilizing a randomized complete block design with four replications. Data were collected for grain yield, harvest moisture and test weight. The data collected were analyzed using ANOVA and LSD to assess genotype and environment effects. Stability was evaluated through parametric (Shukla's variance, Ecovalence, regression) and non-parametric (Huehn's) methods, complemented by BLUP and Annicchiarico's index. The grain yield of the tested genotypes varied from 484.87 to 1,514.19 kg da^{-1} across environments, while harvest moisture ranged between 14.49% and 24.75%, and test weight between 62.50 and 75.00 kg hl^{-1}. The combined ANOVA revealed significant differences for genotype and location, where the location of Altınova gave the highest mean yield. Among the checks, G19 yielded the highest (1,140.51 kg da^{-1}), followed by G17, and G20, both showing high stability. The candidate G4 (TK2404) yielded 1,057.63 kg da^{-1}, statistically comparable to the top checks, and demonstrated strong stability across environments. Genotypes G10, G11, and G15 had lower harvest moisture (<17%), providing an advantage for early harvest and easier grain drying which offers the significant benefit of reduced drying costs. G1 and G15 also showed high test weight (>72 kg hl^{-1}). Taken together, these results underline the strong influence of environmental factors on yield performance and highlight the importance of multi-location testing when identifying stable and high-performing maize hybrids. Based on the findings, G4 (TK2404) seems suitable for registration, while G10, G11, and G15 could be considered for further breeding efforts focused on improving grain quality.

Keywords: Grain maize, hybrid breeding, multi-location trial, stability indices, yield performance

[Abstract:0209]

Our Silage Corn Variety Candidate: ADA 20S44

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This research was conducted with the aim of developing high-yielding silage maize varieties through a hybridization program using self-pollinated lines derived from breeding materials that have demonstrated superiority particularly in physiological and quality traits. Within the scope of the Marmara Maize Breeding Research Project carried out at our institute, varieties selected from the initial stage trials of hybrid combinations developed in previous years were evaluated across different locations in Turkey. These candidate varieties were subjected to selection through trials established in various locations during 2022 and 2023. A limited number of outstanding candidates were advanced to the official registration trials in 2024. The genotypes were tested in all years and locations using a randomized complete block design with three or four replications. In the trials conducted in Konya and Bursa, morphological traits including days to flowering, plant height, plant-to-ear ratio, leaf-to-stalk ratio, plot weight, and green forage yield were examined. Additionally, observations related to lodging, stay-green, diseases, and pests were recorded. For quality assessment, parameters such as Dry Matter Content, Dry Matter Yield, Acid Detergent Fiber (ADF), Neutral Detergent Fiber (NDF), Acid Detergent Lignin (ADL), and Crude Fiber were analyzed and submitted for registration. In the 2024 registration trials, which were arranged in four rows with four replications, standard varieties registered in the official registration system were included as controls. Our candidate variety ADA 20S44 performed well at both locations, ranking first in combined analysis for green forage yield with 10,737 kg/da. It also ranked first in dry matter yield with 3,684 kg/da and exhibited high quality, with crude fiber and ADF values of 14.9% and 22.1%, respectively. Based on these results, an application for the official registration of the candidate variety ADA 20S44 has been submitted to the Seed Registration and Certification Directorate.

Keywords: Silage Corn, Green Plant Yield, Crude Fiber, ADF and NDF

[Abstract:0253]

Determination of the Effects of Different Pollination Conditions on Seed Formation and Fruit Quality in some Pomegranate Genotypes

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The pomegranate is a fruit species cultivated since ancient times, valued as a religious and social symbol, and used for both therapeutic and industrial purposes. Regardless of the fruit species, hybridization breeding is used in breeding studies. A thorough understanding of the fertilization biology of a particular fruit is crucial for successful breeding. Therefore, it is crucial to identify the distinct pollination characteristics of the genotypes within the Pomegranate Genetic Resource plots for use in future breeding studies. The aim of this study is to determine the effects of different pollination conditions on fruit and seed formation and fruit quality of 7 different pomegranate genotypes that were observed to have differences in fertilization conditions, fruit characteristics and seed numbers. Seven different pomegranate genotypes (33N51, 33N23, 33N24, 33N12, 31N06, 33N52, and 33N16) from the Pomegranate Genetic Resources parcel of the Alata Horticultural Research Institute were used as material in the study. The experiment investigated the self-pollination abilities of the different genotypes under free pollination, B-type flower pollination, and isolation conditions. The results of the different pollination treatments were examined for fruit set and fruit quality traits such as fruit weight, fruit size, number of full and empty seeds, and juice quality. As a result of the study, it was determined that different pollination applications had significant effects on fruit set, seed number and fruit quality.

Keywords: Pomegranate, pollination, seed, breeding

[Abstract:0205]

Genetic Diversity of Moroccan Chickpea Landraces for “*Orobanche*” Tolerance

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Chickpea (*Cicer arietinum* L.) is an important pulse crop in Morocco, valued for its role in nutrition, soil fertility, and smallholder livelihoods. However, its production is severely threatened by *Orobanche* spp., a parasitic weed that causes significant yield losses in infested areas. Exploring the genetic diversity of Moroccan landraces and identifying sources of tolerance to “*Orobanche*” is therefore a priority for sustainable chickpea improvement. In this study, a collection of Moroccan chickpea landraces was evaluated under field conditions in infested and non-infested sites. Agro-morphological traits (growth cycle, plant height, seed size, biomass, and yield components) were recorded alongside “*Orobanche*” incidence and severity. Significant variability was observed among landraces for both agronomic performance and tolerance responses. Multivariate analyses revealed distinct clustering of tolerant landraces, some combining competitive yield potential with reduced susceptibility to “*Orobanche*”. These findings highlight the existence of valuable genetic resources within Moroccan chickpea germplasm that can be harnessed for breeding programs. The identification of tolerant landraces provides a promising pathway for developing improved cultivars adapted to “*Orobanche*”-infested areas, contributing to the resilience and sustainability of chickpea production in Morocco.

Keywords: Chickpea, genetic diversity, landraces, “*Orobanche* “ tolerance, Morocco

[Abstract:0215]

Development of High Yielding Chickpea Varieties Suitable for the Central Anatolia Region

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Chickpea (*Cicer arietinum* L.) is one of the most important legume crops cultivated worldwide. This study was conducted in 2021 at the İkizce Research and Production Farm of the Field Crops Research Institute, located in Ankara, Türkiye. The aim of the experiment was to develop high-yielding and high-quality chickpea varieties productive that are adaptable to the Central Anatolia Region. Thirty-six genotypes, including two checks (Azkan, Akçin 91), constituted the experimental material. The study was conducted in a partially balanced lattice design. Yield components as grain yield per hectare, hundred-seed weight, days to flowering, plant height, and the first pod height were observed and measured throughout the trial. According to the study results, the average grain yield of the genotypes was 127 kg/da, while the average for the standards was 160 kg/da. Three lines in particular (AkN 1228, AkN 1239, and AkN 1256) achieved higher yields than the checks. The average 100-seed weight was 37.00 g, and 14 lines showed values above the average. The 50% flowering time of the genotypes varied between 73 and 84 days, and plant height ranged between 40 and 50 cm. The results demonstrate the potential for developing regionally adapted, high-yielding chickpea cultivars.

Keywords*:* Chickpea (*Cicer arietinum* L.), variety, yield characteristics, adaptation

[Abstract:0159]

Marker Assisted Backcross Breeding For *Fusarium* Wilt (*Fusarium oxyporum* Schlecht. f. sp. melongenae) in Eggplant

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Eggplants are produced in both greenhouse and open field, and disease causes significant yield loss. *Fusarium* wilt (*Fusarium oxysporum* Schlecht. f. sp. melongenae, FOM) is a major soil-borne pathogen, causing vascular wilt disease in eggplant. A molecular marker tightly linked to single dominant gene (FOM) was available for use in marker assisted selection (MAS). The aim of the study was to develop eggplant lines resistant against *Fusarium* wilt using a marker assisted backcross breeding approach. Donor parents were advanced eggplant lines known to have *fusarium* wilt resistance originating from "LS2436" (*Solanum melongenae*) lines. The eggplant breeding materials was first screened with the molecular markers linked to the FOM gene. Then, the 533 young seedlings representing various population claimed to be resistant to the pathogen were both root-dip inoculated with FOM isolate obtained from BATEM. institute (Antalya, Turkey), and screened with the molecular marker. The seedlings identified to be resistant using the markers all survived the inoculation. Marker assisted selection and backcross programme was continued to BC1F1. The seedlings of BC1F1 population along with the parents and checks were again screened with molecular marker and then classical test. Results showed that all the plants selected via MAS showed resistance response to FOM on classical test. Resistance vs susceptible ratio was 1:1 as expected in BC1F1 generation. In conclusion, the marker is reliable for selection against FOM and developing new eggplant cultivars resistant to FOM via marker assisted backcross selection is feasible.

Keywords: Backcross, Disease, Eggplant, *Fusarium* Wilt, Marker Assisted Selection, Resistance

[Abstract:0197]

Development of New Genotypes from Cara Cara Navel Orange (*Citrus sinensis* (L.) Osbeck) (TUR020-438) Using Mutation Breeding-I

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Traditionally citrus breeding is both hard and taking a long time, orange is the one most compelling species in terms of plant breeding. However, In recent years, the method of mutation breeding has been widely utilized to enhancement of variation. In this study, it was aimed to determine the varieties that are superior in yield and quality, more colorful and mature at different times in the red colored Cara Cara Navel (*Citrus sinensis* (L.) Osbeck) (TUR020-438) orange variety, which contains lycopene.To determination of effective mutation doses, 40, 50, 60 and 80 gamma rays (Co60) were treated to budwoods in 2013 and M1V1 population was created by using T budding on Sour orange (*Citrus aurantium* L. var Yerli). In the measurements made two months after the grafting, the dose that reduced the shoot length by 50% compared to the shoot length of the control application was calculated as “Growth Reduction (GR50) or EMD” 43.43 Gy. M1V2 population was developed with bud eye taken from this population and M1V3 population was developed from M1V2 population by the same method. In 2016, 750 saplings were planted 4 X 2 m distance for advanced observation. In fruits, fruit weight, peel thickness, juice content, soluble dry matter content, acid content and fruit flesh colour have been determined. As a result of pomological analyses conducted on the fruits, the fruit weight, peel thickness, juice content, water-soluble dry matter content, and acid content of the control group were 169.97-273.50 g, 5.66-7.39 mm, 34.99-54.34%, 10-11. 5 km, 0.56-1.15%, respectively. In genotypes, these values were determined to be 130.03-319.25 g, 3.64-8.98 mm, 21.48-64.74%, 8-13%, and 0.44-1.25%, respectively. Some genotypes were found to be earlier, later, and redder in colour than the control group, with h values ranging from 68.76 to 111.24, L values ranging from 25.21 to 44.47, a values ranging from -35 to 5.74, and b values ranging from 7.68 to 21.50.

Keywords: Citrus, induced Mutation, gamma-rays, red orange

[Abstract:0172]

Development of a Soybean Variety for Organic Farming in Kazakhstan

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Global production of organic soybeans is projected to rise due to increasing demand from the dairy and confectionery industries and the growing popularity of plant-based and vegan diets, for which soybeans serve as a major protein source. In the United States, organic soybean production for the 2024–2025 marketing period is estimated at about 10.5 million bushels, with a harvested area of 0.29–0.33 million acres. Because soybeans fix atmospheric nitrogen through symbiosis with nitrogen-fixing bacteria, they do not require mineral nitrogen fertilizers, which are often limiting in organic corn and wheat production. For over a decade, the Kazakh Research Institute of Agriculture and Plant Growing (KRIAPG) has conducted breeding research to develop soybean varieties suited for organic farming under programs of the Ministry of Agriculture of the Republic of Kazakhstan. Soybean seeds contain various antinutritional compounds—such as trypsin inhibitors, polyphenols, and tannins—that reduce their nutritional value and limit use in animal feed. Therefore, breeding for reduced antinutrient content is an important direction in soybean improvement. Research on antinutrients in promising soybean breeding lines involved collection accessions and hybrid combinations obtained using the Kazakh varieties Lastochka, Birlik KV, Zara, and Evrika crossed with the foreign varieties Ascacubi and Hilario, both carrying a null allele at the Ti3 locus. As a result, promising F2–F9 hybrid lines were identified with a recessive Ti3 allele, low tannin content (≈0.9 mg/g), and polyphenol content (≈1.71 mg/g). Based on these results, KRIAPG scientists developed a new soybean variety named Milka, designed specifically for organic farming. The seed protein content of Milka exceeds that of the standard variety by 1.9%, and its fat content reaches 21.8%. The concentration of polyphenols (antioxidants that help lower cholesterol) remains at the standard level with only a slight deviation of 0.18 mg/g. Tannin content is 1.96 mg/g—0.52 mg/g lower than the standard—which improves the taste quality of food products made from this variety. From 2022 to 2025, Milka was tested at an organic farming station, showing stable yields ranging from 4.5 to 6.5 tons per hectare depending on the year. In 2025, 10 tons of elite organic seeds of Milka were produced. On April 18, 2025, the Kazakhstan Patent Bureau granted Patent No. 1215 for the new soybean variety Milka. The work is funded by the Ministry of Agriculture within the framework of the program №BR 22885488.

Keywords: soybean, variety, low tannin content, organic farming, selection

[Abstract:0193]

Redefining Soybean Breeding Under Climate Change and Disease Pressure

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Soybean, a leguminous crop of strategic agronomic and economic importance, is increasingly being recognized as a resilient and versatile candidate for future agriculture. As a high-protein, nitrogen-fixing species, soybean has the potential to support global food and feed demands while contributing to sustainable cropping systems. However, the accelerating impacts of climate change—marked by elevated temperatures, altered precipitation patterns, and increased frequency of extreme weather events—pose critical threats to soybean production worldwide. Among the most pressing challenges is the heightened susceptibility of soybean to a broad spectrum of plant pathogens, including fungi, bacteria, and viruses, whose prevalence, virulence, and geographic distribution are being reshaped by changing climatic conditions. In this context, breeding for enhanced disease resistance in soybean has become an urgent priority. The integration of plant pathology insights with modern breeding technologies—such as marker-assisted selection, genomic selection, and CRISPR-based gene editing—has significantly accelerated the development of cultivars with durable and broad-spectrum resistance. Recent studies have demonstrated that climate-responsive breeding strategies not only improve pathogen resistance but also confer greater resilience to abiotic stressors such as drought and heat, which often act synergistically with disease outbreaks. Unlocking its full potential requires a systems-level integration of climate science, plant pathology, and genomics-based breeding pipelines. As global agriculture transitions toward climate-smart strategies, disease-resilient soybean cultivars will play a pivotal role in ensuring food system stability and environmental sustainability in the decades ahead.

Keywords: soybean, climate change, pathological breeding, sustainability

[Abstract:0279]

Exploring Genetic Relationships Among *Trifolium Populations* Using ddRAD Sequencing

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More than 250 forage legume species with notable agronomic and ecological significance are found in the *Trifolium* genus. Due to their ability to fix atmospheric nitrogen and produce high-quality biomass, the annual species *T. incarnatum* L. (crimson clover) and *T. alexandrinum* L. (berseem clover) represent valuable resources for sustainable forage production. Yet, there is currently little genomic data available to enable their genetic differentiation, variety identification, and breeding enhancement. This study aimed to explore the genetic diversity and relationships among forty samples belonging to *T. alexandrinum* (Var-4) and T. incarnatum (Var-1, Var-2, Var-3) using a double digest Restriction-site Associated DNA sequencing (ddRAD-seq) approach. Genomic DNA was extracted, digested with PstI and MspI restriction enzymes, and sequenced using the Ion GeneStudio S5 platform. A total of 1982 high-quality SNP loci were identified and used to estimate population genetic parameters, including observed and expected heterozygosity (Ho, Hs), inbreeding coefficients (Fis), and fixation indices (Fst). Principal Component Analysis (PCA) and UPGMA clustering, based on Nei's genetic distance, were applied to visualize genetic relationships between the accessions. Moreover, STRUCTURE analysis was used to infer population structure and admixture levels across genotypes. The findings clearly confirmed the distinctiveness between *T. alexandrinum* and *T. incarnatum*, revealing a strong genetic differentiation between them. Intraspecific variation was detected within *T. incarnatum*, where Var-2 displayed a distinct genetic profile compared with the more closely related Var-1 and Var-3. This differentiation was supported by its partial separation in the PCA and UPGMA dendrogram, along with higher pairwise FST and Nei's genetic distance values, suggesting moderate genomic divergence within the species. The ddRADseq approach effectively distinguished *T. alexandrinum* and *T. incarnatum* and revealed limited intraspecific variation within *T. incarnatum*. Var-1 and Var-3 showed near-identical genetic backgrounds, while Var-2 displayed greater differentiation, suggesting potential for targeted breeding. Similar variation patterns were observed for Var-4. Even in the absence of a reference genome for *T. incarnatum*, the SNP dataset obtained here provides a useful starting point for future genomic and breeding research. Taken together, the results highlight the potential of molecular markers to complement traditional approaches in *Trifolium* improvement, variety registration, and plant variety protection.

Keywords: ddRADseq,Genetic Diversity, NGS, *Trifolium*

[Abstract:0124]

Yield Performances of Selected Triticale Lines and Varieties in Türkiye's Different Climatic Environments

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Climatic changes throughout the world and in our country have a widespread effect on every living thing, especially in the last 25 years. Climatic difficulties direct researchers to more intensive studies on the development of plants in different climatic conditions. This study is within the scope of "the National Triticale Breeding Project"supported by TAGEM; The results obtained by planting trial material in four different provinces (Konya-Eskişehir-Erzurum & Sakarya) within the project were examined in terms of yield. In the trial, Konya: 3 Lines & 1 Variety, Eskişehir: 3 Lines & 1 Variety, Erzurum: 3 Lines & 1 Variety and Sakarya: 2 Lines & 2 Varieties; was used as material. Trial plantings were carried out between October-November, depending on the conditions of the regions, and harvested in July-August also. According to the results, the highest grain yield was obtained from Sakarya with 1.029 t/ha, and the lowest grain yield was obtained from Konya with 0.2219 t/ha. Erzurum ranked second with 0.5935 t/ha, and Eskişehir ranked 3rd with 0.5100 t/ha. According to the results obtained from the regions, the differences in grain yields are due to the different rainfall regime. In Konya, which is the region most affected by drought and also affected by frost during the development period, it was determined that the lines of Konya, which ranked 2nd and 3rd in the experiment, gave the highest grain yield (0.3121 t/ha). In Eskişehir, which is the Transitional Region, it was determined that the Erzurum line, which ranked 5th in the trial, gave the highest grain yield (0.6046 t/ha). In Sakarya, which is in the Marmara Region, it was determined that the Sakarya line, which ranked 10th in the trial, gave the highest grain yield (1,158 t/ha). Varieties registered according to the regions where they are grown have yielded different grain yield results in each region. In this research, in which the performances of lines and varieties were examined in different regions and under different soil and rainfall conditions, it became clear once again how important rainfall is. According to the results obtained, it can be suggested that the lines included in the trial will be more suitable for growing in those regions and under those conditions, depending on how much grain yield they give in which region.

Keywords: Triticale, line, variety, yield, climate change

[Abstract:0189]

Assessment of the some Agromorphological Characters of Cold Tolerant Forage Pea Lines

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Forage pea (*Pisum sativum* ssp. *arvense* L.) is a highly delicious and nutritious source of feed rich in essential minerals and vitamins. Furthermore, this leguminous plant plays a crucial role in agricultural systems due to its ability to fix atmospheric nitrogen into the soil through a symbiotic relationship with Rhizobium bacteria in its root nodules. This nitrogen-fixing capability becomes forage pea an important forage crop for use in crop rotation systems, particularly in the Central Anatolia Region of Turkey, which is a major grain production area. Despite its significance, the Central Anatolia Region currently faces a significant constraint: a limited availability of high-yield, high-quality forage pea cultivars that are adequately adapted to the local environmental conditions, specifically cold tolerance. Therefore, a dedicated cold-tolerant forage pea breeding program was initiated at the Central Research Institute for Field Crops. The program utilized 146 forage pea populations as the source material. Between 2020 and 2023, a rigorous process of single plant selection was conducted, successfully resulting in the development of 109 lines exhibiting resistance to temperatures as low as −15˚C. In 2024, a preliminary micro-yield trial was established with the lines and five check cultivars (Mir, Nany, Ozkaynak, Taskent, and Tore). The trial was using an augmented experimental design, with each plot that is an area of 1.5 m2 (3×0.25×2). Plant height (PH), stem diameter (SD), number of seeds per pod (SPP), seed weight (SW), biological yield (BY), and grain yield (GY) were examined in the trial. Correlation analysis showed that SD and SW influenced each other, while SW, BY, and GY were closely related. Based on these traits, lines were grouped according to principle component analysis (PCA). Lines PS-9, PS-10, PS-15, PS-69, PS-75, PS-76, and PS-99 were identified as promising in terms of yield.

Keywords: *Pisum sativum* ssp. *arvense* L., cold-tolerant lines, correlation analysis, PCA.

[Abstract:0251]

Determination of Some Agronomic and Quality Traits of Forage Pea *Pisum sativum* L. Advanced Breeding Lines in Bandirma

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Forage pea (*Pisum sativum* L.) is a leguminous forage crop recognized as an alternative protein source with high nutritional value. It performs well in crop rotations, enhances soil fertility through biological nitrogen fixation, and can be grown under rainfed or limited irrigation conditions, making it a suitable alternative to more water-demanding forage crops. Development of new varieties with superior agronomic and nutritional traits is therefore crucial for sustainable forage production. Field experiments were conducted under rainfed conditions in Bandırma during the 2023 and 2024 growing seasons to evaluate the agronomic performance and forage quality of advanced forage pea lines. The trials were arranged in a randomized complete block design with four replications, including 16 advanced breeding lines and four control cultivars (Assas, Taşkent, Töre, Kurtbey). Each plot covered 6 m². Sowing was performed in early November and harvesting in late May. Data were recorded for flowering time, main stem length, plant height, winter hardiness, green and dry forage yield. In addition, nutritional quality parameters were analyzed, including dry matter, crude protein, crude fiber, neutral detergent fiber (NDF), acid detergent fiber (ADF), and acid detergent lignin (ADL). Analysis of variance indicated significant differences among genotypes for green and dry forage yields. According to the combined variance analysis of two years, the highest mean green forage yields were obtained from Line6 (34.69 t/ha), Line12 (32.63 t/ha) and the control variety Assas (32.27 t/ha). Similarly, the highest mean dry forage yields were recorded in Line6 (6.979 t/ha), Line12 (6.679 t/ha) and Assas (6.633 t/ha). Quality traits of the genotypes varied within the following ranges: dry matter (92.7-93.2%), crude protein (17.8-21.3%), crude fiber (27.8-32.4%), NDF (37.3-41.9%), ADF (28.3-31.4%), and ADL (4.9-6.1%). The quality values of Line6 and Line12 were determined as: dry matter (92.8%-93.0%), crude protein (19.1%-18.1%), crude fiber (29.2%-31.6%), NDF (41.9%-37.3%), ADF (29.1%-31.4%) and ADL (5.5%-5.7%), respectively. According to the quality data, the Assas was considered to be high quality, the Tashkent was low quality, Line6 was good quality, and Line12 was low but acceptable quality. As a result, Line6 and Line12 demonstrated higher forage yield, good and acceptable quality and other agronomic traits compared to the control varieties. Therefore, these results strongly revealed that these two candidate lines have potential to provide quality forage and are suitable to apply registration.

Keywords: forage pea, (*Pisum sativum* L.), plant breeding, forage pea breeding,

[Abstract:0328]

Forage Production under Climate Change: Drought- and Heat-Tolerant Alternatives for Mediterranean Coastal Countries

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With global warming, Mediterranean-rim countries are increasingly experiencing drought and high temperature stress, challenging conventional forage (feed crop) production systems. This paper reviews the need for alternative forage species or cultivars that are tolerant to drought and heat, and considers breeding, management and policy approaches applicable in Mediterranean contexts. Key legume and grass species showing resilience in arid Mediterranean climates are identified; traits such as deep rooting, summer dormancy, water-use efficiency and high nutritive value are emphasised. Current breeding projects (e.g., focused on *Medicago sativa* (lucerne/alfalfa), *Hedysarum coronarium* (sulla) and drought-tolerant perennial grasses) are summarised. The review highlights the importance of integrating agronomic selection, irrigation/soil management and supportive policies (such as seed production, subsidies) to ensure sustainable forage supply under Mediterranean climate change. Implications are drawn for Mediterranean agricultural systems—including Turkey—on how to transition towards resilient forage production under increasing aridity and heat stress.

Keywords: Climate change, Drought tolerance, Forage crops, Alternative forage species

[Abstract:0308]

Oat Genotypes Used in Forage and Food Production

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Oat are mostly used as animal feed but are also used food. There has been significant increase in oat cultivation areas in The Trakya-Marmara region in recent years. This study was carried out in 2024-2025 cropping season at The Trakya Agricultural Research İnstitute’s experimental field using a triple alpha lattice experiment design (8 x 8= 64) with three replications in Edirne, Turkiye. The study used with 59 oat advanced lines and 5 control varieties (Kuçukyayla, Kahraman, Elmas, Halkalı ve Haskoy). It was aimed to determine the genotypes suitable for the region in terms of animal feed and food product by examining the grain yield and some characteristics of the genotypes developed as result of breeding studies. In the research, the traits such as grain yield (GY), plant height (PH), grain weight (GW), test weight (TW) and plumpness (P, sieved 2,2 mm slotted) were investigated. The variation among oat genotypes for grain yield and plant height were statistically significant and differences for GW, TW, and P were also determined. The GY, PH, GW, TW and P of oat genotypes ranged between 528,3-840,8 (718,1), 104,5-149,7 (129,1) cm, 26,8-42,9 (32,6) g, 53,3-62,8 (58,8) kg/hl and 23,8-89,3 (67,3) % respectively. The average grain yield of the control varieties in the experiment was determined as (738,2 kg/da), PH (119,7 cm), GW (32,4 g), TW (60,7 kg/hl) and P (67,8%). Of the 59 advanced lines in the trial, 27 (45.7%) were above the average of the varieties in terms of grain yield, 30 (50.8%) in terms of grain weight, 8 (13.6%) in terms of test weight, and 32 (54.2) in terms of 2.2 mm plumpness. The highest grain yield was obtained from genotypes 61 (840,8 kg/da), 33 (838,0 kg/da), 16 (827,3 kg/da) and Elmas variety (787,5 kg/da). The genotypes 9, 12, 16, 33, 44, 46, 51, 53 and 61which were hopeful for examined traits, were included in the oat regional yield trial.

Keywords: Oat (*Avena sativa* L.), grain yield, quality, forage and food product

[Abstract:0129]

Development of Novel Eggplant Hybrids with Diverse Color and Pattern Traits Through Parental Crosses

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Eggplant (*Solanum melongena* L.) is a widely cultivated and economically valuable vegetable crop worldwide. Among the traits influencing consumer preference, fruit color plays a critical role in determining market value. In recent years, there has been a growing demand for aesthetically appealing and visually diverse fruit types. In this context, developing new eggplant hybrids with diverse fruit colors and surface patterns has become a key goal in modern breeding programs. The objective of this study was to develop novel eggplant hybrids through controlled pollination using phenotypically diverse parental lines under greenhouse conditions. The study was conducted during the 2025 growing season in Serik, Türkiye. Six parental lines White, Green, Violet, Black, Stripe, and Pink were selected based on differences in fruit skin color and pattern. A full diallel crossing scheme was employed to create all possible hybrid combinations among these lines. The resulting hybrids were evaluated at commercial maturity for external fruit color, pigmentation under the calyx, and pattern uniformity. Significant phenotypic variation was observed among the hybrids. Notably, the White × Stripe cross produced fruits with a deep pink color, while the White × Violet combination resulted in light violet fruits with a white under-calyx. The Stripe × Pink hybrid exhibited intermediate violet-pink coloration, indicating semi-dominant or intermediate inheritance of pigmentation traits. These results demonstrate the potential to manipulate fruit coloration through strategic parental selection. Specific parental combinations were found to consistently express dominant or intermediate pigmentation traits, emphasizing the importance of careful parental selection in color-focused breeding strategies. The hybrids developed in this study offer valuable genetic material for the creation of visually appealing cultivars that align with consumer preferences. These findings are expected to contribute significantly to future eggplant breeding programs aiming to diversify product lines and enhance market appeal. Further research could focus on genetic mapping of color traits to support marker-assisted selection.

Keywords: *Solanum melongena*, hybridization, fruit color, phenotypic variation, breeding, pigmentation pattern

[Abstract:0140]

Changes in Quality Parameters of Sweet Corn Materials Harvested at Fresh and Dry Stages

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In this study, the changes in quality traits were investigated by harvesting a total of 19 sweet corn materials, including 14 candidate lines and 5 standard varieties, both at fresh and dry stages, under the ecological conditions of Sakarya (central region) in 2024. In this study, it was also aimed to determine the changes in certain quality traits of sweet corn materials during the drying process, both during the breeding phase and under field conditions, as the plants transition from the fresh ear harvest stage to the dry ear harvest stage. In these materials, dry matter (%), crude protein, crude fat, crude starch, and total sugar ratios were analyzed. In fresh ears, the dry matter content ranged from 20.96% to 27.74%, while crude protein content (on a dry matter basis) ranged from 11.1% to 14.5%, with an average of 12.61%. Crude fat content (DM%) ranged between 3.11% and 7.10%, with an average of 5.13%. Crude starch content varied between 2.48% and 6.28%, with an average of 4.4%, and total sugar content ranged from 7.33% to 11.96%, with an average of 9.1%. In dry ears, dry matter content ranged from 88.68% to 89.92%, while crude protein content (DM%) ranged from 13.85% to 17.06%, with an average of 15.48%. Crude fat content (DM%) ranged from 12.24% to 16.54%, with an average of 14.32%. Crude starch content ranged between 31.93% and 39.52%, with an average of 35.68%, and total sugar content (DM%) ranged from 5.69% to 6.88%, with an average of 6.34%. According to these results, compared to fresh ear harvest, crude protein content increased by approximately 23% in dry harvest, crude fat content increased by 179%, and starch content increased by about 8.1 times, while total sugar content decreased by approximately 30%. These findings indicate that as sweet corn ears mature, the total sugar content decreases, while protein and fat levels increase, and sugars are largely converted into starch. This study aimed to identify the differences in quality parameters between harvest stages in sweet corn, and to present the changes in quality components that occur as harvest maturity progresses.

Keywords: Fat, harvest stage, protein, starch, sweet corn, total sugar content

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