REPUBLIC OF TURKEY MINISTRY OF AGRICULTURE AND FORESTRY

bisab

TÜRKTOB
TÜRKİYE TOHUMCULAR BİRLİĞİ

TAGEM
AR-GE & İNOVASYON

IV. INTERNATIONAL PLANT BREEDING CONGRESS

Plant Breeding for the Future: From Local to Global

21-25 November 2022 | Porto Bello Hotel, Antalya, Türkiye

CONGRESS BOOK

www.intpbc2022.org

INVITATION

Plant Breeding plays an important role in the improvement of yield and quality in the field of plant production. Further, Plant Breeding supports economic and national development with its achievements. As far we know and of course up to now advance techniques and tools will assist plant breeders in their work based on different techniques in plant improvement in future.

This oncoming event, the IV. International Plant Breeding Congress, was organized in 2013, 2015 and 2017 with the participation of researchers from different countries all over the world. This coming event will address the latest advances in various plant breeding activities and its achievements. Keynote and invited speakers will present their views and findings in this congress. The congress will provide opportunities and gather as many plant breeders, agricultural scientists, geneticist, researchers, academicians, biotechnologies and students to share their latest knowledge, experience and achievements in plant breeding.

The Congress Topics will cover:

1. Plant Genetic Resources and Landraces

- Pre-Breeding and Germplasm Characterization

2. Conventional Plant Breeding

- Improvement of Neglected and New Crops
- Rootstock Breeding
- Mutation breeding

3. Molecular Plant Breeding

- Plant Breeding and Biotechnological Tool

4. Variety Release and Seed Systems
5. Resistance to Biotic and Abiotic Stresses

- Breeding Pest and Disease Resistance
- Climate Change and Plant Breeding

6. Technological Quality and Functional Foods
7. Phenomics, Remote Sensing and Omics Technologies
8. Tissue Culture and Cryopreservation
9. Bioinformatics and Big Data Processing
10. New Breeding Methods for Future Challenges
11. Intellectual Property Rights (IPRs)

It's our greatest pleasure to welcome you to the 4th International Plant Breeding Congress that aims to provide an international forum for the dissemination of original research results, new ideas and practical development experiences which concentrate on both theory and practices. The congress will be held in November 21-25, 2022, Antalya, Turkey.

We hope to see you and your colleagues in Antalya Turkey.

With our best wishes,

Selami YAZAR	**Fatih SEYİS**
President of BISAB	Head of Organizing Committee

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SCIENTIFIC PROGRAM

	21 November, Monday
14:00	**Welcome** **Registration and Hotel Check-in**

	22 November, Tuesday	**Hall A**
08:00-09:00	**Registration**	
09:00-10:30	**Opening Speeches**	
	Congress Group Photo	
10:30-11:00	**Coffee Break**	
11:00-12:45	**Plenary Session** **Chair:** *Bülent Uzun*	
11:00-11:30	Importance of Plant Genetic Resources for Future Breeding	*Andreas Borner*
11:30-12:00	Role of Agronomy in Biofortification of Food Crops with Micronutrients, and Its Synergism with Breeding	*İsmail Çakmak*
12:00-12:30	Breeding for Resistance - Key to Meet Future Challenges	*Frank Ordon*
12:30-12:45	Discussion	
12:45-14:00	**Lunch**	

		22 November, Tuesday	Hall A
14:00-15:30		**Conventional Plant Breeding I** **Chair:** *S. Ahmet Bağcı*	
14:00-14:30	**OP-01**	Wheat Breeding Studies in Turkey and Its Effects on Yield: Past to Present	*Fahri Altay*
14:30-14:45	**OP-07**	Yield Increase in Last 10 Years of Breeding for Winter Red Wheat	*Muhsin İbrahim Avcı*
14:45-15:00	**OP-04**	Breeding for Improved Technological Quality in Winter Durum Wheat	*Gyula Vida*
15:00-15:15	**OP-05**	Stability Analysis of Some Bread Wheat Genotypes for Grain Yield in Central Anatolian Region Using Regression-Based Stability and AMMI Methods	*Mustafa Serdar Doğan*
15:15-15:30		Discussion	
15:30-16:00		**Coffee Break**	
16:00-17:45		**Conventional Plant Breeding II** **Chair:** *Mesut Keser*	
16:00-16:15	**OP-06**	Grain Yield Stability Analysis of Durum Wheat Genotypes in Dry Areas of the Central Anatolian Region Using AMMI and GGE Biplot Methods	*Mehmet Doğan*
16:15-16:30	**OP-03**	Effect of Drought Stress on Seedling Growth in Bread Wheat (Triticium aestivum L.) Genotypes	*İsmet Başer*
16:30-16:45	**OP-08**	Last 10 years of Winter White Wheat Breeding in Central Anatolia	*Fatma Betül Sade*
16:45-17:00	**OP-09**	A research About Determination of the Grain Yield and Protein Contents of Wheat Genotypes with Different Chromosomes in Ankara Conditions	*Ali Haydar Paksoy*
17:00-17:15	**OP-10**	Evaluating Traits Influencing Hybrid Wheat Seed Production Using a Double Haploid Population Derived from Freeman x Camelot	*Emre Karahan*
17:15-17:30	**OP-11**	Environmental Effect in Two and Six-Rowed Barley (Hordeum vulgare L.) Cultivars on Yield Components and Leaf Diseases under Rainfed Conditions	*İrfan Öztürk*
17:30-17:45		Discussion	
17:45-19:00		Poster Session - 1	Foyer Area

		22 November, Tuesday	Hall B
14:00-15:30		**Conventional Plant Breeding III** **Chair:** *Kazım Abak*	
14:00-14:15	**OP-12**	Identification and Maintenance of Male Sterile Lines using Morphological and Molecular Indices for Development of Onion Hybrids	*Pravin Kumar Sharma*
14:15-14:30	**OP-13**	Establishment and Morphological Characterization of New Interspecies Hybrid Populations Capsicum Annuum and Capsicum Frutescens	*Nihal Denli*
14:30-14:45	**OP-14**	Colchicine Induced Chromosome Doubling in Annual Ryegrass (Lolium multiflorum Lam.) and Identification of Autotetraploid Plants by Flow Cytometer	*Metin Tuna*
14:45-15:00	**OP-15**	Selection for Persistence in Red Clover (Trifolium Pratense L.) Through Improved Tolerance to Northern Anthracnose	*Muhammet Şahin*
15:00-15:15	**OP-16**	Evaluation of Some Silage Hybrid Corn Genotypes in Terms of Yiled and Quality Under Samsun Ecological Conditions	*Erkan Özata*
15:15-15:30		Discussion	
15:30-16:00		**Coffee Break**	

		22 November, Tuesday	Hall B
16:00-17:45		**Conventional Plant Breeding IV** **Chair:** *Baldew Raj Kamboj*	
16:00-16:15	**OP-17**	The Utilizing from Wild Sunflowers (Helianthus spp) for New Anatomical Designs in Sunflower	*Yalçın Kaya*
16:15-16:30	**OP-18**	Morphological and Physiological Responses of Potato Genotypes to Different Water Deficit	*Sani Ibrahim Ibrahim*
16:30-16:45	**OP-19**	Comparative Yield and Quality Traits Stability Estimates of Potato Breeding Lines in the Central Anatolia Region of Türkiye	*Eric Kuopuobe Naawe*
16:45-17:00	**OP-20**	Contrasting Behavior of Potato Breeding Lines to Morpho-Physiological and Agronomic Characteristics in Response Heat Stress	*Eric Kuopuobe Naawe*
17:00-17:15	**OP-21**	Different Maize Breeding Approaches for Tackling Climate Change in Croatia and Turkey	*Zvonimir Zdunic*
17:15-17:30	**OP-22**	Development of Maize Varieties Suitable for Central Anatolian Conditions	*Mehmet Tezel*
17:30-17:45		Discussion	
17:45-19:00		Poster Session - 1	Foyer Area

22 November, Tuesday

Foyer Area

17:45-19:00 **Poster Session 1 - Screen 1**
Moderator: *Mustafa Yıldırım*

PP-28	Evaluation of the Yield, Yield Components and Quality Traits of Faba Bean Genotypes in Aegean Region Conditions	*Selin Eğilmez*
PP-68	Yield and Yield Components of Newly Developed Safflower Lines	*Oğuzhan Aydın*
PP-67	Identification of Superior Winter Wheat Genotypes with High Grain Yield and Quality Combined with Stripe Rust Resistance in Uzbekistan	*Zafarjon Ziyaev*
PP-66	Barley Breeding Studies in Eskişehir Transitional Zone Agricultural Research Institute	*Soner Yüksel*
PP-17	Evaluation of Advanced Barley Lines for Yeld and Yield-Related Traits in Aegean Region Conditions	*Mustafa Cerit*
PP-14	Short Palms for Improved Harvesting Efficiency	*Wan Rusydiah Wan Rusik*

17:45-19:00 **Poster Session 1 - Screen 2** **Foyer Area**
Moderator: *Mustafa Yıldırım*

PP-65	Advances in Industrial Crops Breeding in Transitional Zone Agricultural Research Institute	*Arzu Köse*
PP-19	Breeding for Improved Forage Yield Potential and Digestibility in Tall Fescue (Schedonorus arundinaceus (Schreb.) Dumort.)	*Elif Şahin*
PP-39	Investigation of Root System Architecture of Promising Winter Squash (Cucurbita maxima Duch.) Genotypes for Rootstock Breeding Programme	*Ahmet Balkaya*
PP-64	Pomological and Phenological Characteristics of Promising Sweet Cherry (Prunus Avium L.) Progeny	*İsmail Demirtaş*
PP-61	The Effect of Gamma Irradiation on Groundnut (Arachis hypogaea L.)	*Engin Yol*
PP-59	Study on Some Quality and Morpho-Physiological Traits of Durum Wheat (Triticum durum L. Desf.) Genotypes	*İsmet Başer*

22 November, Tuesday

Foyer Area

17:45-19:00 **Poster Session 1 - Screen 3**
Moderator: *Hakan Aktaş*

PP-37	Effect of Parental Lines on Germination of Avşar F1	*Nur Ülger*
PP-56	Comparison of Two and Six-Rowed Barley (Hordeum vulgare L.) Genotypes under Rainfed Conditions	*İrfan Öztürk*
PP-06	Effects of Tray Conditions For Cucumber Cuttings	*Nur Ülger*
PP-69	Determination of the Seed Yield and Resistance to Broomrape Parasite of Some Hybrid Sunflower Varieties in Different Locations	*Veli Pekcan*
PP-50	Grain Yield Predictions of ZP Maize Hybrids	*Zoran Camdzija*
PP-51	Stability Analysis of Different Maize Hybrids Grown in Serbia	*Jovan Pavlov*

17:45-19:00 **Poster Session 1 - Screen 4** **Foyer Area**
Moderator: *Hakan Aktaş*

PP-20	The Heritability for Flower Productivity and Defoliation in Diploid Roses	*Seza Noyan*
PP-34	Determination of Some Traits in New Purple Sweet Corn Hybrids	*Ahmet Öztürk*
PP-27	Grain Yield and Stability of Some Feed Barley (Hordeum vulgare L.) Lines and Cultivars Under Rainfed Conditions of Central and Transitional Regions of Anatolia	*Namuk Ergün*
PP-71	Revealing Local Wild Plant Species Potential for Microgreens	*Onur Karaağaç*
PP-73	Selection of Advanced Bread Wheat (Triticum Aestivum L.) Lines in Terms of Yellow Rust (Puccinia Striiformis f. sp. Tritici) and Grain Yield in Sakarya Conditions	*Lütfi Demir*
PP-47	Determination of Promising Onion (Allium cepa L.) Genotypes by Selection Method in a Long-Day Breeding Programme	*Arif Bağcı*
PP-72	Population Improvement in Adapop 9e and 9f Sweet Corn (Zea Mays Saccharata) Gene Research	*Mehmet Cavit Sezer*

		23 November, Wednesday	Hall A
09:00-10:30		**Conventional Plant Breeding V** **Chair:** *Yalçın Kaya*	
09:00-09:30		**Keynote Speaker** Deploying Appropriate MAS Technology for Legume Improvement in Sub-Saharan Africa: The Kirkhouse Trust experience	*Robert Koebner*
09:30-09:45	**OP-23**	Towards the Development of Clearfield Red Lentil Cultivars in Turkey	*Abdullah Kahraman*
09:45-10:00	**OP-24**	Determination of Yield Performance of Chickpea Varieties Widely Cultivated in Our Country in Konya Ecology	*Hakan Bayrak*
10:00-10:15	**OP-25**	Selection of Winter-Hardy Genotypes and Determination of Some Agricultural Characteristics in Hybrid Pea Lines (F3)	*Ahmet Tamkoç*
10:15-10:30		Discussion	
10:30-11:00		**Coffee Break**	
11:00-12:30		**Conventional Plant Breeding VI and Molecular Plant Breeding** **Chair:** *Kenan Yalvaç*	
11:00-11:15	**OP-26**	Modifying Flowering Time by Using Vernalization, Photoperiod and Earliness Genes in Winter Wheat to Increase the Adaptability of Wheat in the Era of Climate Change	*Mesut Keser*
11:15-11:30	**OP-27**	CIMMYT's Approach to Speed Breeding for Spring and Winter Breeding Programs	*Beyhan Akın*
11:30-11:45	**OP-28**	Development of Sulfonylurea (SU) Group Herbicide Resistant Ornamental Sunflower Lines	*Bahar Sancar*
11:45-12:00	**OP-29**	Breeding Sterile (Male-Sterile) Ornamental Sunflower Lines Resistance to Imidazolinone (IMI) Group Herbicides and Downy Mildew Disease	*Bahar Sancar*
12:00-12:15	**OP-30**	Determination of Resistance Levels Oo Qualified Tomato Genotypes to (Meloidogyne incognita), Tomato Yellow Leaf Curl Virus, Tomato Spotted wilt Virus, Tomato Mosaic Virus	*Selcan Eroğlu*
12:15-12:30		Discussion	
12:30-14:00		**Lunch**	

		23 November, Wednesday	Hall A
14:00-16:00		**Molecular Plant Breeding** **Chair:** *Vida Gyula*	
14:00-14:30		**Keynote Speaker** Challenges and Opportunities in Breeding Future Proof and Sustainable Crops	*Richard GF Visser* ***(Online)***
14:30-14:45	**OP-31**	QTL Detection of Maturity Timing in Sweet Cherry Using a Multi-Family QTL Approach	*Fatih Topuz*
14:45-15:00	**OP-32**	Cytoplasmic Genome Prediction in Cucumber (Cucumis sativus L.) Hybrid Variety Breeding and it's Usage in Breeding	*Leyla Öztürk Akar*
15:00-15:15	**OP-33**	Moleculer Characterization of Economically Important Some Grape Varieties, Rootstocks and Their Clones Based on AFLP Markers	*Funda Yılmaz Baydu*
15:15-15:30	**OP-34**	Molecular and Morphological Characterisaton and Association Mapping for some Agronomic Characteristics in Different Apple Types And Varieties	*Hasan Pınar*
15:30-15:45	**OP-35**	Determinate Tomato Breeding Using Speed Breeding, Embryo Rescue and Marker Assisted Selection	*Merve Yiğit*
15:45-16:00		Discussion	
16:00-16:30		**Coffee Break**	
16:30-17:45		**Molecular Plant Breeding and New Breeding Methods for Future Challenges I** **Chair:** *Fatih Seyis*	
16:30-16:45	**OP-36**	Comprehensive Genotyping and Diversity Analysis of Maize Inbred Lines Representing Multiple Eras of Germplasm from Southeast Europe	*Domagoj Simic*
16:45-17:00	**OP-37**	Breeding in Ashwagandha (Withania somnifera) in Relation to Molecular Aspects	*Rajesh Kumar*
17:00-17:15	**OP-38**	Phenotypic Diversity and Linkage Disequilibrium for Vitamin B Complex Concentrations in Bean Grain	*Faheem Shehzad Baloch*
17:15-17:30	**OP-39**	Comperison of Index Method and META Analysis for Selection of Winter Feed Barley Genotypes	*Sinan Aydoğan*
17:30-17:45		Discussion	
17:45-19:00		Poster Session - 2	Foyer Area

		23 November, Wednesday	Hall B
09:00-10:30		**Variety Release and Seed Systems** **Chair:** *Oğuz Bilgin*	
09:00-09:30		**Keynote Speaker** Haploidization of Biennial Vegetables	*Agniaszka Kielkowska*
09:30-09:45	**OP-40**	Agricultural and Forestry Research and Development Structures and Systems: A New Approach	*Süleyman Karahan*
09:45-10:00	**OP-41**	Development of Seed Sector and Contribution of the use of Certified Seeds of New Plant Varieties to the Agricultural Production in Türkiye	*Kenan Yalvaç*
10:00-10:15	**OP-42**	Variation of Registered Pepper Varieties on DUS Test	*Güleda Öktem*
10:15-10:30		Discussion	
10:30-11:00		**Coffee Break**	
11:00-12:30		**Resistance to Biotic and Abiotic Stresses I** **Chair:** *İsmet Başer*	
11:00-11:15	**OP-43**	The new Cereal; Tritipyrum; Three Decades of Breeding Challenges for Eating and Feeding in Saline and Brackish Water by Phenotyping, Molecular Markers, Cytogenetics Molecular Markers and Speed Breeding Techniques with the Last Case Study in Turkey	*Hossein Shahsavand Hassani*
11:15-11:30	**OP-44**	Improving Nutrient use Efficiency in Wheat Using Various Breeding Strategies	*Akshay Kumar Vats*
11:30-11:45	**OP-45**	Determination of the Reactions of Some Advanced Yield Trials-Bread Wheat Genotypes to Rust and Bunt	*Nilüfer Akcı*
11:45-12:00	**OP-46**	Breeding for Climate Resilience in Agricultural Crops	*Ajaz Ahmad Lone*
12:00-12:15	**OP-47**	Determination of Heat and Drought Tolerant Lines In Segregating Populations Produced By Interspecific Crosses in Eggplant	*Esra Cebeci*
12:15-12:30		Discussion	
12:30-14:00		**Lunch**	

		23 November, Wednesday	Hall B
14:00-16:00		**Resistance to Biotic and Abiotic Stresses II** **Chair:** *Gönül Cömertpay*	
14:00-14:30		**Keynote Speaker** Breeding Challenges for Wheat, the Cornerstone for Global Food Security	*Hans Braun*
14:30-14:45	**OP-48**	Evaluation of Wheat (T. aestivum L.) Germplasm Under Temperate Conditions and Identification of Sources of Yellow Rust Resistance Genes (yr) Using Molecular Markers	*Shabir Hussain Wani*
14:45-15:00	**OP-49**	Screening of Some Durum Wheat Genotypes to (Warrior) Race of Yellow Rust	*Merve Nur Ertaş Öz*
15:00-15:15	**OP-50**	Comparison of Yield Potentials of Some Triticale Lines and Cultivars Under Different Climatic Conditions	*Emel Özer*
15:15-15:30	**OP-51**	Determination of the Reactions of Some Advanced Yield Trials-Durum Wheat Genotypes to Rust	*Nilüfer Akcı*
15:30-15:45	**OP-52**	Identification of SNP Markers for Grain Quality Traits in A Barley Collection (Hordeum Vulgare L.) Harvested in Kazakhstan	*Yuliya Genievskaya*
15:45-16:00		Discussion	
16:00-16:30		**Coffee Break**	
16:30-17:45		**New Breeding Methods for Future Challenges II** **Chair:** *Nedim Mutlu*	
16:30-16:45	**OP-53**	Effects on the Wheat (Triticum Aestivum L.) Genome From Five Rapid Genomic Selection (GS) Cycles	*Lenin Rodriguez*
16:45-17:00	**OP-54**	Colored Wheat: A Source of Nutrition	*Om Parkash Bishnoi*
17:00-17:15	**OP-55**	Two Different Vernalization Methods Applied in Winter/Facultative Wheat and Their Effects on the Speed Breeding Process	*Emrah Koç*
17:15-17:30	**OP-56**	Genotyping by Sequencing Based SNP Analysis for Discriminating the Heterotic Patterns of Maize Germplasm From Public and Private Sector of Türkiye	*Gönül Cömertpay*
17:30-17:45		Discussion	
17:45-19:00		Poster Session - 2	Foyer Area

Workshop on "Breeding for wheat rust resistance: Recent approaches, and regional collaboration in context of the FAO-Türkiye Partnership Programmes"

	23 November, Wednesday	Hall C
13:30-14:00	**Registration**	
14:00-14:30	**Opening Remarks** - ***Fazıl Düşünceli***, *FAO, Agriculture Officer* - ***Beyhan Akın***, *CIMMYT, IWWIP - CIMMYT Coordinator* - ***Mesut Keser***, *ICARDA, Country Manager* - ***Suat Kaymak***, *Ministry of Agriculture and Forestry, TAGEM, Head of Plant Health Research Department*	
14.30-16.00	**Session 1: Regional Collaboration** **Chair:** *Fazıl Düşünceli*	
14:30-14:45	The FAO – Türkiye Partnership programme project on wheat rust and resistance and support for resistance breeding	*Fazıl Düşünceli*
14:45-15:05	Importance of surveillance and race tracking for developing rust resistant wheat varieties	*Kumarse Nazari*
15:05-15:25	Updates from CIMMYT - Türkiye on developing rust resistant wheat varieties for Central Asia and Caucasus	*Beyhan Akın*
15:25-15:40	Status of wheat rust diseases and resistance breeding work in Türkiye	*Emine Burcu Turgay*
15:40-16:00	Discussion	
16:00-16:30	**Coffee Break**	

Workshop on "Breeding for wheat rust resistance: Recent approaches, and regional collaboration in context of the FAO-Türkiye Partnership Programmes"

23 November, Wednesday		Hall C
16:30-17:45	**Session 2: Past experiences and recent advances in breeding for wheat rust resistance (Panel Discussion)** **Chair:** *Kenan Yalvaç*	
	Global lessons from the past programmes and interventions on breeding for wheat rust resistance	*J. Hans Braun*
	Experiences in breeding for wheat rust resistance in Türkiye and Central Asia: Successes and lessons from International Winter Wheat Programme (IWWIP)	*Mesut Keser*
	Advances in use of molecular tools and approaches for wheat rust resistance	*Robert Koebner*
	Role of genetic resources in wheat rust resistance breeding	*Nusret Zencirci*
	Discussions and conclusions	
17.45	Closing	
17:45-19:00	Poster Session - 2	Foyer Area

23 November, Wednesday

17:45-19:00	**Poster Session 2 - Screen 1** **Moderator:** *Eftal Düzyaman*	**Foyer Area**
PP-25	Infected with ToBRFV (Tomato Brown Rugose Fruit Virus) Disinfectant Efficacy Trial on Tomato Plants	*Özlem Demir*
PP-30	Suitability of Latvian Origin Rye and Wheat Genetic Resources for a Niche Products	*Laila Vilmane*
PP-42	Possibilities to Develop Dry Pea Varieties for Sustainable Agriculture	*Ahmet Ustaoğlu*
PP-52	IPBS-Retrotransposons Variations: DNA Fingerprinting and the Evaluation of Genetic Diversity and Population Structure in International Cowpea Germplasm	*Faheem Shahzad Baloch*
PP-75	Morphological Characterization of Some Local Leek Genotypes Grown in Turkey	*Meryem İpek*

17:45-19:00	**Poster Session 2 - Screen 2** **Moderator:** *Eftal Düzyaman*	**Foyer Area**
PP-74	Use of SSR Molecular Markers to Develop Source Materials in Maize Breeding	*İpek Koca Reçber*
PP-38	Sort-clones of Malus Sieversii (Ledeb.) M. Roem. of Dzungarian Population in the Main Botanical Garden	*Laura Shadmanova*
PP-03	Genome-Wide Association Study for Leaf Rust and Stem Rust Resistance in Bread Wheat Growing in Kazakhstan	*Alibek Zatybekov*
PP-04	QTL Mapping of Agronomic Traits in Wheat Using the Pamyati Azieva × Paragon Mapping Population Tested in Kazakhstan	*Akerke Amalova*
PP-01	Eggplant Genome Editing Using CRISPR/Cas9 Technology	*Vese Pakashtica*
PP-36	Evaluation of Genetic Relationship Among Different Soybean Cultivars in Two Regions of Mazandaran and Alborz Provinces	*Parastoo Majidian*

23 November, Wednesday

Foyer Area

17:45-19:00 **Poster Session 2 - Screen 3**

Moderator: *Ahmet Tamkoç*

PP-62	Determining TSWV Resistance Levels for Some Characteristics of Capia Pepper Lines	*Önder Türkmen*
PP-29	Accelerated Pepper Breeding Studies with MAS and Androgenesis Techniques	*Mesut Nar*
PP-46	New Method in Plant Breeding: CRISPR Technology and its Use	*Kübra Taş*
PP-48	Marker Assisted Selection: An Approach for Improving the Maize Quality	*Marija Kostadinovic*
PP-53	Breeding of Winter Feed Barley Genotypes With High Digestibility Under Turkish Highlands	*Gulizar Manav*

17:45-19:00 **Poster Session 2 - Screen 4** **Foyer Area**

Moderator: *Ahmet Tamkoç*

PP-18	Genetic Mapping of Yield and Yield-Related Traits in a Population Derived from Two Winter Wheat Cultivars	*Mustafa Cerit*
PP-23	Comparison of Pure Lines Developed for Dried Eggplant Breeding in Terms of Quality Characteristics	*Gülsün Elif Vural*
PP-22	The Effects of Open Sun Drying and Oven Drying on Dried Fruit Quality Characteristics in Pure Lines Developed for Dried Pepper Breeding	*Gülsün Elif Vural*
PP-40	Selection of Plants According to Their Resistance to Gamma Radiations, Case of Thapsia Garganica L. (Apiaceae)	*Farid Benkaci Ali*
PP-60	Breeding for Niche Specific Ideotypes in Commercial Agricultural Crops	*Ajaz Ahmad Lone*

		24 November, Thursday	Hall A
09:00-10:30		**Resistance to Biotic and Abiotic Stresses III** **Chair:** *Ahmet Balkaya*	
09:00-09:30		**Keynote Speaker** Importance of Enabling Environment to Promote and Facilitate Innovation in Plant Breeding Worldwide	*Benjamin Rivoire*
09:30-10:00		**Keynote Speaker** Accelerating Genetic Gains in Grain Legume Crops	*Rajeev Varshney* ***(Online)***
10:00-10:15	**OP-57**	Omics in Maize Breeding: Case Studies in Abiotic Stress Tolerance	*Emre Aksoy*
10:15-10:30		Discussion	
10:30-11:00		**Coffee Break**	
11:00-12:30		**Resistance to Biotic and Abiotic Stresses IV** **Chair:** *Hülya İlbi*	
11:00-11:15	**OP-58**	Advances in Climate-Resilient Temperate Tree Breeding: A Case Study in Peach	*Ömer Atagül*
11:15-11:30	**OP-59**	In Silico Analysis of Qtls Associated With İron Efficiency in Soybean Lead to the Identification Of GATA Transcription Factors Involved in Iron Homeostasis	*Emre Aksoy*
11:30-11:45	**OP-60**	Determination of Resistance Levels of Some Bean Genotypes Against Charcoal Rot (Macrophomina Phaseolina (Tassi) Goid) Disease	*Sirel Canpolat*
11:45-12:00	**OP-61**	Determination of Resistance of Some Bean Genotypes to Common Leaf Blight (Xanthomonas Axonopodis Pv. Phaseoli) and Bean Halo Blight (Pseudomonas Syringae Pv. Phaseolicola) Diseases	*Kamil Duman*
12:00-12:15	**OP-62**	Determination of the Reactions of Some Bread Wheat (Triticum Aestivum L.) Genotypes to Waterlogging	*Cemal Şermet*
12:15-12:30		Discussion	
12:30-14:00		**Lunch**	

		24 November, Thursday	Hall A
14:00-16:00		**Resistance to Biotic and Abiotic Stresses V** **Chair:** *Taner Akar*	
14:00-14:15	**OP-63**	Effect of Genotypic Variation on Bread and Flour Quality in Wheat	*Pervin Arı Akın*
14:15-14:30	**OP-64**	Variation of Resistance of Some Downy Mildew Resistance Genes to Downy Mildew Races of Sunflower in Trakya Region, Turkey	*Mehmet İbrahim Yılmaz*
14:30-14:45	**OP-65**	Using Root Criteria in Drought Resistance Selection	*Burak Özdemir*
14:45-15:00	**OP-66**	Overview of Zucchini Yellow Mosaic Virus (ZYMV)	*Akife Dalda Şekerci*
15:00-15:15	**OP-67**	Development of Industrial Type Pepper Lines Resistant to (Phytophthora Capsici)	*Duygu Argün*
15:15-15:30	**OP-68**	Phloem-Mobile Micrornas in the Long-Distance Communication of Pumpkin (Cucurbita Maxima L.) Under Heavy Metal Stresses	*Mehtap Aydın*
15:30-16:00		Discussion	
16:00-16:30		**Coffee Break**	
16:30-17:30		**Intellectual Property** **Chair:** *Ayşe Odman Boztosun*	
16:30-16:45		Turkish Plant Breeders’ Right System	*Mehmet Çakmak*
16:45-17:00	**OP-69**	Evaluation of the Current Situation of the Conditions for Protection of PBR vis-a-vis Recent Developments	*Ayşe Odman Boztosun*
17:00-17:15	**OP-70**	Turkish Plant Breeders' Rights System; Challenges, Opportunities	*Hasan Çelen*
17:15-17:30		Discussion	
17:45-19:00		Poster Session - 3	Foyer Area

		24 November, Thursday	**Hall B**
09:00-10:30		**Conventional Plant Breeding VII** **Chair:** *Abdullah Kahraman*	
09:00-09:30	**OP-71**	**Keynote Speaker** Wheat Response to Individual and Combined Heat and Drought Stress and Breeding for Tolerance	*Rishi K. Behl*
09:30-10:00	**OP-72**	**Keynote Speaker** Participatory Breeding Towards a More Diverse, Resilient and Society-Oriented Organic Farming	*Adrian Rodriguez Burruezo* ***(Online)***
10:00-10:15	**OP-73**	Increasing Breeding Studies Efficiency by Supporting Plant Breeding Software with Data	*Canseri Bozkuş*
10:15-10:30		Discussion	
10:30-11:00		**Coffee Break**	
11:00-12:30		**Tissue Culture** **Chair:** *Şebnem Ellialtıoğlu*	
11:00-11:15	**OP-74**	In Vitro Regeneration of Encapsulated Propagules of Some Cyclamen Species	*Hüsamettin Aycan Alp*
11:15-11:30	**OP-75**	Protoplast Isolation from Leaf Mesophylls of Haploid (Solanum Sisymbriifolium) Lam. Produced Via Anther Culture	*Buse Özdemir Çelik*
11:30-11:45	**OP-76**	HPLC Analysis of Phenolic Compounds from Elicited Hairy Roots of Dracocephalum Kotschyi Boiss and Implications For COVID-19 Inhibition	*Bahman Hosseini*
11:45-12:00	**OP-77**	Production of Durum Wheat Doubled Haploid Lines: A Useful Tools of Breeding	*Olfa Ayed Slama*
12:00-12:15	**OP-78**	Determination of Pollen Viability and Germination of Different Solanum Molengena L. X S. Torvum Sw Hybrids and Crosses on Fertile Hybrids	*Atilla Ata*
12:15-12:30		Discussion	
12:30-14:00		**Lunch**	
14:00-16:00		**Plant Genetic Resources and Landraces I** **Chair:** *Gürbüz Mızrak*	
14:00-14:15	**OP-79**	Genetic Characterizations of Vitis Genetic Resources Belonging Gaziantep and Kilis by Using Simple Sequence Repeats (SSR)	*Kürşat Alp Aslan*

		24 November, Thursday	Hall B
14:15-14:30	**OP-80**	The Potential of Using Landraces in Cassava (Manihot Esculenta Crantz) Improvement Programmes	*Ochanda JB Ogola*
14:30-14:45	**OP-81**	Classification of Pepper Accessions from Turkey and Nigeria for Crop Genetic Improvement and Conservation	*Anjola Samson Aninkan*
14:45-15:00	**OP-82**	Wheat in Different Ploidy Levels (Triticum) Evaluated in Terms of Micro Nutrient Content for Breeding Studies	*Bayram Özdemir*
15:00-15:15	**OP-83**	Increasing Zinc and Iron in Durum Wheat for Central Anatolia Conditions	*Gökhan Kılıç*
15:15-15:30	**OP-84**	A Perspective on the Chromosome Properties of Local Bottle Gourd Landraces	*Ahmet L. Tek*
15:30-16:00		Discussion	
16:00-16:30		**Coffee Break**	
16:30-18:15		**Plant Genetic Resources and Landraces II** **Chair:** *Tahsin Kesici*	
16:30-16:45	**OP-85**	Determination of Effective Dose by Gamma Irradiation in Shoot-Tips of Banana	*Filiz Baysal*
16:45-17:00	**OP-86**	Clarification Optimization in Pomegranate Juices Obtained from Some Pomegranate Cultivars and Genotypes	*Ali Tekin*
17:00-17:15	**OP-87**	Short-Duration Mungbean for Ecologically Oriented Crop Diversification in the Aral Sea Region of Central Asia	*Ram Sharma*
17:15-17:30	**OP-88**	Bread Wheat Landraces of Van Lake Basin	*Mehmet Ülker*
17:30-17:45	**OP-89**	"Characterization and Evaluation of Wheat Landraces Genotypes Root System for Drought Prone Areas and Development of Drought Resistance Varieties"	*Mohd M Alajlouni*
17:45-18:00	**OP-90**	"Improvement of Cotton Varieties Using Modern Genetic and Biotechnological Methods on the Basis of Biodiversity of the Genus Gossypium L"	*Fakhriddin N. Kushanov*
18:00- 18:15		Discussion	
17:45-19:00		Poster Session - 3	Foyer Area

24 November, Thursday

Foyer Area

17:45-19:00 **Poster Session 3 - Screen 1**
Moderator: *Önder Türkmen*

PP-58	Climate Change and Plant Breeding	*Mustafa Demirel*
PP-49	The Biochemical Composition of Maize Hybrids Under the Different Crop Protection Strategies for ECB Attack	*Danijela Ristic*
PP-13	Antioxidant Activity of Phenolic Compounds of Pistacia lentiscus	*Nadia Benzidane*
PP-12	Transcriptional Reprogramming During Developmental and Stress-Induced Leaf Senescence in Barley	*Wiebke Zschiesche*
PP-63	Mapping of Bacterial Wilt and Canker (Clavibacter michiganensis Subsp. michiganensis) Resistance in Tomato Mutant Lines Using Whole Genome Sequence Analysis	*Shabir Hussain Wani*

17:45-19:00 **Poster Session 3 - Screen 2** **Foyer Area**
Moderator: *Önder Türkmen*

PP-45	Molecular Mapping of Leaf Rust and Tan Spot Resistance in the Collection of Wheat Germplasm	*Alma Kokhmetova*
PP-07	Genomic Selection to Predict Fusarium Head Blight (FHB) Resistance of Wheat Lines from the Great Plains Using Ohio Phenotypic Data	*Lenin Rodriguez*
PP-05	SNP Markers for the Resistance of Barley ([i] Hordeum Vulgare[/i] L.) to Spot Blotch, Barley Stripe and Powdery Mildew in South-East Kazakhstan	*Saule Abugalieva*
PP-21	Evaluation of Seedling and Adult-Plant Stripe, Leaf, and Stem Rust Resistance in the A-Genome Diploid Relatives of Wheat	*Buket Şahin*
PP-33	Quality Characteristics of Durum Wheats Grown in Central Anatolia	*Ferda Ünsal Canay*

24 November, Thursday

Foyer Area

17:45-19:00 **Poster Session 3 - Screen 3**
Moderator: *Süleyman Karahan*

PP-32	Evaluation of Quality Parameters of Different Barley Varieties	*Arzu Özer*
PP-31	Effect of Tribolium Confusum's Toxication Infestation on Zea Mays for Human and Animal Nutrition	*Guettaf Sofiane*
PP-15	Toxicological Properties of Flour Beetle's (Tribolium Confusum) Infestation on Hordeum Vulgare Consumption	*Abdelmalek Oulmi*
PP-11	Effect of Flour Beetle's (Tribolium Confusum) Infestation of Wheat Flour's (Triticum Durum) Toxicological Properties for Human Consumption	*Noureddine Laadel*
PP-24	Use of Convolutional Neural Network Model for Detection of Puccinia striiformis f. sp. Tritici and Comparing Disease Severity Monitoring Methods on Scanned Images	*Turan Gökberk Çon*

17:45-19:00 **Poster Session 3 - Screen 4** **Foyer Area**
Moderator: *Süleyman Karahan*

PP-16	Using Newly Developed Proximal Sensors for High-Throughput Phenotyping in Maize Breeding	*Tatjana Ledencan*
PP-70	Determination of the Performance and Quality of Rice (Orzya sativa L.) Genotypes in Samsun Conditions	*Özgür Azapoğlu*
PP-76	Evaluation of Registered Tomato Varieties in Türkiye	*Yıldırım Şamil Özden*
PP-77	Determination of Genetic Relationships in Some Local Lettuce (Lactuca sativa L.) Populations by SSR Primers	*Elif Yetilmezer*
PP-44	Registration of "BAHCIVAN" Runner Bean	*Evren Atmaca*
PP-43	Registration of "ATMACA" Pinto Bean	*Evren Atmaca*
PP-79	Perennial Wheat for Improving Multiple Traits of Bread Wheat for Agro-Pastoral Farming System in Central Asia	*Ram Sharma*

SPEAKER SUMMARY

Importance of Plant Genetic Resources for Future Breeding

Andreas Börner

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

Author for correspondence (boerner@ipk-gatersleben.de)

Ex situ conservation is the most significant and widespread mean of conserving plant genetic resources. Mainly, accessions are maintained in specialized facilities known as genebanks. World-wide 7.4 million accessions are stored in about 1,750 *ex situ* genebanks. Considering major crop groups about 45 percent of all the accessions in the world's genebanks are cereals, followed by legumes (15 percent), fruits and forage crops (each 6-9 percent) as well as roots and tubers, oil crops and fibre crops (each 2-3 percent).

It is estimated that 90% of all genebank holdings are stored as seeds whereas less than 10% and less than 1% are maintained *in vivo* (field genebanks) and *in vitro* (tissue culture and cryo preservation), respectively. Clearly, seed storage is the predominant mode of plant genetic resources conservation.

With a total inventory of 150,000 accessions from 3,212 plant species and 776 genera, the 'Federal *ex situ* Genebank of Germany' in Gatersleben holds one of the most comprehensive collections worldwide. It comprises wild and primitive forms, landraces as well as old and more recent cultivars of mainly cereals but also other crops.

Since the majority of genebank accessions globally are stored in the form of seed, seed longevity is of particular importance for crop germplasm preservation. At the IPK research was initiated for a range of crops stored in the genebank over decades. Variation between crop species was detected. However, there is also intraspecific variation within genebank collections. It was concluded that the differences in germination after long term storage are genetically based. Therefore, genetic analyses of seed longevity were initiated. Genetic mapping was performed for barley, wheat, oilseed rape and tobacco.

In addition, mass spectrometry based untargeted metabolite profiling experiments were performed in order to detect biochemical changes coinciding with loss in seed germination. GC-MS analysis of the polar metabolome of wheat and barley identified glycerol and related intermediates as highly correlated to germination rate. Therefore, the lipidomic composition of a wheat panel was investigated using high-resolution liquid chromatography-mass spectrometry (LC-MS). A high proportion of tentative oxidized lipids was detected, suggesting lipid oxidation as the causal trigger for membrane degradation.

Keywords:

plant genetic resources, seed longevity, genetic mapping, metabolite profiling

Agronomic Biofortification of Food Crops with Micronutrients, and Its Synergism with Breeding.

Ismail Cakmak
Sabanci University, Faculty of Engineering and Natural Sciences, 34956 Istanbul, Turkey

Hidden hunger, also known as micronutrient deficiencies, is old, but still persisting problem globally, especially in developing world. Zinc (Zn), iron (Fe), selenium (Se) and iodine deficiencies are the particular mineral micronutrient deficiencies, leading to various health complications such as impairments in i) brain function and mental health and ii) immune response to viral and bacterial attacks. Hidden hunger problem also represents an important economic burden in the affected countries.

Low phytoavailability of micronutrients in agricultural soils and low micronutrient density in food crops are the underlying causes of the hidden hunger. Soils and fertilizers are the major source of mineral micronutrients entering in the food system. Published evidence from field trials established under the HarvestZinc project (www.harvestzinc.org) demonstrated rapid impact of fertilizer applications (i.e. agronomic biofortification) on concentrations of micronutrients in several food crops. It has been also found that combination of the plant breeding approach with a fertilization strategy create additive and synergistic effects on accumulation of micronutrients in wheat. Zinc-biofortified wheat genotypes by HarvestPlus program respond very positively to Zn fertilizers, more than the local genotypes. Synergism between plant breeding and fertilizer strategies needs to be used extensively in future. It is now time to disseminate and integrate the fertilizer approach into on-going regional and national human nutritional projects and programs.

Key Words: Agronomic Biofortification, Hidden Hunger, Human Nutrition, Micronutrients, Plant Nutrition, Breeding

Breeding for Resistance - Key to Meet Future Challenges

Frank Ordon
Julius Kühn Institute (JKI), Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany

Abstract

Our planet is under pressure. In 2050 about ten billion people have to be fed in the background of climate change and crisis, e.g. the war in the Ukraine. Furthermore, the EU Farm to Fork Strategy recommends a reduction of the use of pesticides, respectively of the risk associated with their use, by 50% up to 2030 and an increase of the acreage of eco farming to 25%. Furthermore, new pathogens, e.g. insect transmitted viruses will gain importance due to rising temperatures especially in the northern hemisphere. In this respect, breeding for resistance is of prime importance to meet these challenges.

Breeding for resistance has been quite successful in the last decades already, as e.g. demonstrated by improving resistance simultaneously to yield in German winter wheat cultivars. This success was mainly based on traditional selection schemes complemented by doubled haploid technologies and marker based selection procedures. Today, high throughput marker systems and knowledge of the genome sequence of many crop plant species on the one hand facilitate new selection strategies, e.g. genomic selection, but also facilitate a more targeted use of genetic resources, which are a treasure trove for improving resistance. They facilitate the efficient development of markers for major genes and quantitative trait loci (QTL) and pave the way for enhanced gene isolation. The isolation of resistance genes will transfer breeding to the allele level and will facilitate the sequenced based identification of novel alleles in large gene bank collections and their directed use in plant breeding as well as the creation of new alleles by genome editing. Examples of using these genomic tools to improve resistance to fungal and viral pathogens as well as to insects are given.

Haploidization of Selected Biennial Vegetables

Agnieszka Kielkowska
University of Agriculture in Krakow, Al. Mickiewicza 21, 31-120 Kraków

The leading method in the modern plant breeding is the F1 hybrid technology. Hybrid varieties based on heterosis, are characterized by abundant high-quality yield and uniformity, which are necessary to meet the requirements of the modern market. The success of hybrid varieties relies on production of homozygous lines with high combining ability. Traditionally, such lines are obtained through inbreeding, which is a long-term process (about 6-8 years on average), especially in biennial plants. Reduction of the time required for obtaining homozygous lines is crucial for accelerating the process of breeding new, improved varieties with high agricultural and health-promoting values. Gametic embryogenesis and haploid technology are valuable biotechnological tools to support plant breeding by fast generation of true homozygous plants. Here a revision of different methods of haploidization such as parthenogenesis induced by pollination with foreign pollen, gynogenesis and androgenesis in selected biennial species i.e. carrot (*Daucus carota* L), cabbage (*Brassica oleracea* L. var. capitata) and onion (*Allium cepa* L.) will be presented.

Keywords: haploid, induced parthenogenesis, androgenesis, gynogenesis

Die Herausforderung im Jahr 2050 zehn Milliarden Menschen zu ernähren

Dr Hans-Joachim Braun, Internationales Mais und Weizenforschungszentrum CIMMYT, Mexiko

H.J.Braun@cgiar.org

Since 1960, on a global scale, yield of all crops has on average tripled. This was achieved through improved cultivars (plant breeding), crop protection, fertilizers, intensive tillage, use of herbicides, irrigation and supporting policies, i.e. through a combination Genetics, Agronomy and Policy (GAP). However, the current crop production systems and practices are not sustainable. Agriculture uses 72% of all water, groundwater tables fall worldwide at alarming speed, N use is 50% beyond sustainable levels and has increased 10 fold since 1960, soil fertility in many regions is degrading, salinization increases. To feed 9 billion people by 2050, crop yields need to increase relative to 2010 by around 60%, since area expansion is in most regions not an option and in some regions agricultural land will have to be turned if the target should be met to protect 30% of all land and sea within the "High Ambition Coalition for Nature and People.

Wheat is grown on the largest area of all a crops and provides 19% of all calories and 20% of vegetable protein to global nutrition and is a major source of Zn, fibre, Vitamin B and other micronutrients. Wheat and wheat products can be easily stored for long time. Around 160 of the 220 million ha are grown in areas where frost occurs during the vegetation period an options to substitute wheat with other crops. Wheat is also the most traded crop and will therefore continue to play a major role for global food security.

Innovations in wheat breeding and agronomy have delivered enormous gains. These gains are threatened by climate change, the rapidly rising financial and environmental costs of fertilizer and pesticides, combined with declines in water availability for irrigation and new emerging diseases. Raising CO2 levels may contribute to yield increases but are likely to have negative consequences on protein quality and nutrition.

Raising temperature and in particular night temperature cause major yield losses due to a shortened and often changing vegetation period - with drastic consequences for established crop rotations - and high night respiration. The progress in global wheat improvement initiatives on raising yield potential (IWYP), heat and drought tolerance (HeDWIC) and disease resistance (BGRI) using latest technologies and new breeding systems is presented.

Breeding is benefitting from rapid technology and knowledge advances in many other scientific disciplines: Genomics, phenotyping, crop and climate modelling, bioinformatics, computing and data analysis, yield mapping and global positioning systems. Rapid generation advancement combined with molecular techniques for early generation selection and pedigree analysis allows to make faster progress. To meet the future challenges will also require Gene editing tools like CRISPR, whose application is currently restricted by lawmakers in particular in Europe. Potential benefits from research in the area of gene-editing is also presented.

Deploying Appropriate MAS Technology for Legume Improvement in Sub-Saharan Africa: The Kirkhouse Trust Experience

Robert Koebner, Norwich UK

The Kirkhouse Trust (KT) is a small UK-based charity founded in 2000 by Ed Southern, following the settlement of a patent dispute with the US tech firm Affymetrix (now part of Applied Biosystems); in 2017, KT's resources were further supplemented as a result of the sale of the company Oxford Gene Technology to the Sysmex Corporation. KT's goal is to address food security of the rural poor in sub-Saharan Africa by supporting the efforts of African crop breeders to generate improved legume varieties. The idea is to enhance the effectiveness and efficiency of local conventional breeding programmes through the implementation of marker-assisted selection. The locally-based and locally-managed marker laboratories established by KT have been and still are supported both materially (through the provision of consumables and the maintenance/replacement of small equipment) and technically (through training and mentoring offered to the breeder and associated staff and students). At the outset, two breeding consortia were set in place, one focusing on cowpea in West Africa, and the other on common bean in East Africa.

For cowpea, the initial aim was to accelerate the introduction into locally favoured varieties of resistance against the parasitic weed *Striga gesneroides*; the rationale for this choice was (1) that infested fields were being abandoned for cowpea production because chemical control of the weed was not an option, (2) that the phenotypic screening method was both cumbersome and somewhat unreliable, and (3) that the existence of major gene-based resistance was known. Over time, the targets have been extended to include resistance against aphids and several fungal pathogens. To date, this programme has generated around twenty improved varieties in Ghana, Burkina Faso, Nigeria and Cameroon.

Unlike for cowpea, in common bean, there was no equivalent clear initial target. Rather the various members of the consortium each chose their own combination of relevant production constraints: these included resistance against the pathogens causing anthracnose, angular leaf spot, bean common mosaic virus and common bacterial blight. Because the bean programme was less sharply focused than was the cowpea one, progress has been slower. However, the release of the first round of improved varieties (in Ethiopia, Uganda, Kenya and Zambia) is now imminent .

The KT model contrasts with that used by the major international funders of crop breeding in Africa. The driver is to encourage each of the breeders to become self reliant and to develop ownership of their programme, so that over time, they will become less dependent on outside support. Its acknowledged downside is that the potential gains in breeding efficiency delivered by accessing a centralized technology hub cannot readily be captured. However, KT has concluded that the continued dependency on outside support inherent in the alternative model represents a major risk in terms of the sustainability of legume improvement programmes in Africa.

Wheat Response to Individual and Combined Heat and Drought Stress and Breeding for Tolerance

R.K. Behl[1]* and Vikender Kaur[2]

[1]Associate Dean (retd.), College of Agriculture, CCSHAU Hisar-125004, Haryana, India

Presently: Prof. R&D, MM (DU),Mullana, District- Ambala, Haryana-133207, India

[2]Senior Scientists, ICAR, NBPGR, New Delhi-110012, India

*IFSDAA-AASF India Chapter, MMDU, Mullana

***Corresponding/presenting author email- rkbehlprof@gmail.com**

Abstract

Wheat is the staple food and element of food security globally. The production of wheat is drastically affected by drought and heat stress. Heat and drought affects are witnessed in major wheat producing region worldwide in recent times. Internationally wheat losses due to heat and drought stresses have encompassed 5.5 and 12%, respectively. Furthermore, the projections that global temperatures may upsurge by 0.6–2.5°C by the year 2050 and 1.4–5.8°C by year 2100 along with increased severity of drought condition may worsen the situation. In India average temperature rise from 1901 to 2018 is recorded as 0.7^{O} C as per reports and world's average warming rate is recorded as 1.1^{O}C in a decade. The effect of heat stress includes increased reproductive rate with decreased photosynthetic rate in plants. Wheat requires 15^{o}C as daytime optimal temperature in its reproductive phase and wheat yield is reduced by 3-4% on every unit (*i.e.*, 1^{O}C) rise in temperature.

Wheat crop is often exposed to drought and high temperature simultaneously, but their effects are usually investigated individually. A small number of studies have documented the impact of combined drought and high temperature on wheat productivity and biological processes. Both drought and high temperatures negatively affect the growth by impairing the photosynthetic system, reduce stomatal conductance, disrupt water relations leading to shortened grain filling duration, reduced grain size, weight and ultimately yield. The effects of these stressors may be synergistic or antagonistic, however their interactive effects are more pronounced, and the synergistic interactions lead to considerably reduced productivity than by either stress alone. Although the major impacts of individual and dual stress of drought and high temperature on wheat productivity are known, there yet the tolerance mechanisms is not properly understood. Systems biology analyses have revealed a complex mode of integration of the different signaling pathways triggered in plants during stress combination. The best step forward is to develop elite wheat varieties with enhanced tolerance against these two robust stresses. Breeding for heat and drought tolerance in wheat is complicated as it is polygenic trait. Stress tolerance in wheat depends on identifying potential cell signaling mechanisms. The strategy to breed for high temperature or drought tolerant genotypes includes identification of potential molecular markers, various quantitative trait loci, association mapping, gene expression profiling studies, cDNA, transcript profiling, proteomics and their applications to develop stay green genotypes which can sustain long photosynthetic activities and translocation of photosynthates into grains. Thus, both source and sink capacity of the plants have to be increased under stress prone environment. Integrated omics assisted approaches can also pay dividend in understanding the tolerance mechanism and thus sustainable yields in challenging environment.

Key words: Heat, drought, interaction, wheat, stress tolerance, breeding strategy

Strategies of Participatory Organic Plant Breeding to Diversify the Agrifood Sector and to Improve its Sustainability and Resiliency

Adrián RODRÍGUEZ-BURRUEZO

[1] *COMAV Institute,Universitat Politècnica de València, Spain*
[*]Corresponding author, e-mail: adrodbur@upvnet.upv.es

Introduction: In the last decades, different Instutions (from FAO or the EU Commission to regional or local councils) have realised the importance of the climate change and the need of more sustainable and resilient production models. In this regard, a range of initiatives considering these goals are being developed to achieve a low-impact and genetically diversified farming sector, particularly in the frame of organic farming.

Aims: To show how participatory plant breeding (PPB), in the context of several European, national, regional or local research projects and initiatives, provide efficient solutions to achieve more diverse, resilient and sustainable agri-food systems, empowering farmers and consumers and increasing social justice.

Materials and Methods: Several living labs including different plant materials (heterogeneous materials, ecotypes, landraces) of target crops (e.g. Solanaceae, carrots, wheat) under a PPB approach aimed at organic farming. According to the socioeconomic context, specificities and breeding goals of each initiative, the number of actors involved may change (breeders, laboratories, farmers, consumers, chiefs, retailers, local governments, etc.) to ensure the highest efficiency.

Results: PPB activities enabled to identify and bred many varieties and plant populations with a satisfactory adaptation to organic farming, quality and/or adaptation to the preferences of a range of socioeconomic actors. Also, these activities have strengthened the links between the actors. Particularly, connecting farmers, breeders and consumers.

Conclusion: PPB has been found an efficient strategy to develop plant materials adapted to organic farming and to diversify the agrifood sector, by widening the number of varieties within each crop and even the diversity within population. Moreover, this approach improves the relationships among the socioeconomic actors and proximity markets.

Keywords: agrobiodiversity, quality breeding, genetic erosion, participatory networks, yield, climate change.

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ORAL PRESENTATIONS

[OP-01]

Wheat Breeding Studies in Turkey and Its effects on Yield: Past to Present

Fahri Altay[1], Seydi Ahmet Bağcı[2]

[1]Bilecik Şeyh Edebali University (Retirement)
[2]Seed Technology, Sarayönü VHS, Selçuk University, Konya Türkiye

Wheat is a very important grain for humanity in terms of its place in nutrition, cultivation area and production, and due to its importance in nutrition and being one of center of origin it is ahead in Turkey rather than most of other countries. Research on wheat began with a series of research stations opened after the founding of the republic of Turkey. In order to meet the variety needs of the farmers working with traditional methods, selection was started with varieties collected from the country or introduced from abroad, and immediately after that, hybridization works were started. Wheat breeding started in Eskişehir in 1925, followed by the work of Istanbul Yeşilköy, Adapazarı and Ankara Research Stations. With the "Wheat Research and Education Project" put into practice in 1969, the number of institutions working increased, and today this number has reached 13, including those in study on the spring wheats. Selection studies were started in 1926-27 and first variety, Karakılçık 1133, was released in 1928. The first successful result of the crossbreeding studies started in 1929-30 was obtained in 1939 with the development of the variety named Melez 13. When the National Project started, this number reached 19 domestic and 12 foreign varieties, and 663 wheat varieties were released up to date. 514 of total registered varieties are currently in the National Variety List. 413 varieties are of bread wheat and 101 of them are durum wheat. Of these varieties, 314 were registered by private sector research institutions, 312 by public research institutes (TAGEM), 14 by the General Directorate of Agricultural Enterprises (TİGEM) and 23 by universities. In 1925, 3 million hectares of cultivation area, 1 million tons of production and an average yield of 340 kg/hectares were set out, today 7 million hectares of cultivation area, 22 million tons of production and an average yield of 2800 kg/hectares have been reached. With a rough calculation, the cultivation area has increased by 2.33 times, the production has increased by 22 times and the average yield has increased by 8.23 times. The increase of The planting area, production and yield values in the 95-year period from 1925, when the researches started, to 2020 are examined three dates draw attention.

The first is the increase in cultivation areas due to the change in agricultural workforce and mechanization in the years 1945-1955 and the increase in production accordingly. The second striking point is the accelerated increase in production and yield since 1965-1970, the years when high yielding varieties were put into production and farmer training on Agronomic Technique within the scope of the Wheat Research and Training Project starting in 1970. Thirdly, "Law No. 5042 on the Protection of Breeder's Rights Belonging to New Plant Varieties" in 2004 and "Seed Law No. 5553" in 2006 came into force. After these laws, it is observed that the private sector's involvement in variety breeding and certified seed production has a significant impact on the country's wheat yield and production.

Keywords: Turkey, wheat, breeding, yield

[OP-03]

Effect of Drought Stress on Seedling Growth in Bread Wheat (Triticum aestivum L.) Genotypes

Ismet Başer, Seher Akseki, Damla Balaban Göçme, Oğuz Bilgin, Alpay Balkan

Tekirdağ namık Kemal Üniversity, Agricultural Faculty, Departmen of Field Crops

The study was carried out in different drought/osmotic stresses (0.00 MPa-control, 0.25 MPa, 0.50 MPa, 0.75 MPa and 1.00 MPa applications) created by using PEG-6000 with 43 genotypes under laboratory conditions, with 5 replications according to a split-plot experiment design. The genotypes constituted the main plots, and the drought/osmotic stress applications constituted the sub-plots.

In the study, plant weight, root number, root length, root weight, shoot length, and shoot weight characters were determined. It was determined that drought stress applications caused statistically significant decreases in root and shoot length development. According to the significance test, the highest root weight was 86.2 mg in Enola genotype, and Bora, Anopa, Ambrogio and Iveta genotypes were in the same statistical group as Enola. The lowest root weight was 21.0 mg in Kavılca genotype, Siyez-1, Siyez-2, Energo and Maya genotypes were then sequenced. is following. Enola, NKÜ Ergene, Bezostoja 1, and Maden genotypes were the best-growing genotypes under drought stress, followed by Aglika, Falado, Anopa, Selimiye, Bora, and Hakan genotypes.

Keywords: wheat, seedling, drought, stress, PEG

[OP-04]

Breeding for Improved Technological Quality in Winter Durum Wheat

Gyula Vida, László Szunics, Ottó Veisz, Mónika Cséplö

Centre for Agricultural Research

The cultivation of winter durum wheat in Hungary dates back only a few decades. Under the climatic conditions of the country, mainly varieties of winter-types are grown, which are able to achieve higher yield than that of spring-types. It is also an important aspect for the players in the cereal sector to grow varieties that meet the quality requirements of the pasta industry. The strength of the gluten and the yellow pigment content are extremely important technological quality characteristics of durum wheat. In durum wheat breeding programs, the former is often determined by measuring the gluten index, while the latter one is estimated by the Minolta b* value. During the decades following the start of the breeding program, both testing methods have been successfully introduced and used in selection aimed at improvement of technological quality. We present the results achieved by using genetically diverse set of varieties, as well as the results of the durum wheat breeding program. With our experiments, we could prove that, based on the repeatability (h2), both traits are genetically well defined (gluten index: 0.949; Minolta b*: 0.978), and a large degree of genetic variability can be observed in the winter and facultative gene pool. As a result of successful selection, the technological quality of winter durum wheat varieties registered in recent years has become competitive with spring ones.

Keywords: Gluten index, Minolta b*, Triticum turgidum ssp. durum, selection, genetic improvement

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[OP-05]

Stability Analysis of Some Bread Wheat Genotypes for Grain Yield in Central Anatolian Region Using Regression-Based Stability and AMMI Methods

Mustafa Serdar Doğan, Gökhan Kiliç, Muhsin Ibrahim Avci, Fatma Betül Sade, Mehmet Doğan, Bayram Özdemir, Ayten Salantur, Mehmet Emin Alyamaç, Kürşad Çiftçi, Selami Yazar

Field Crops Central Research Institute

The present investigations about genotype × environment interaction have assisted breeders to select the best adaptable and stable genotypes for different regions. In this study, twenty promising bread wheat genotypes and four check cultivars in the advanced yield trial were evaluated in thirteen locations of Central Anatolian Region during the 2020-2021 and 2021-2022 cropping seasons by being conducted in a RCBD design with four replications. The joint analysis of variance displayed that the effect of environment (E), genotype (G), and genotype by environment (G × E) interaction had a significant difference at the level of five percent. The multivariate method of Additive Main Effects and Multiplicative Interaction (AMMI) and Regression-Based Stability methods were used to analyze the genotype × environment interactions. Based on the results of the mean comparison analysis, G2, G6, and G3 genotypes for the mean of grain yield were defined as favorable genotypes while G17, G13, and G16 genotypes are identified as unfavorable genotypes in grain yield. According to the regression-based stability, Bayraktar-2000, and Sonmez, G24, and G2, were the most stable genotypes respectively.

On the other hand, the stability performance of other superior genotypes, G6 and G3 was not stable across the environments. Based on the results of the AMMI analysis, the genotypes of G19, G18, G13, and G23 were considered the stable ideotypes among all 24 genotypes however they were lower-yielding genotypes compared with the others.

Keywords: Regression-Based Stability, AMMI Methods, Genotype X Environment Interaction, Bread Wheat, Stability

[OP-06]

Grain Yield Stability Analysis of Durum Wheat Genotypes in Dry Areas of the Central Anatolian Region Using AMMI and GGE Biplot Methods

Mehmet Dogan, Gokhan Kilic, Muhsin Ibrahim Avci, Fatma Betul Sade, Mustafa Serdar Dogan, Mehmet Emin Alyamac, Ayten Salantur, Bayram Ozdemir, Selami Yazar

Central Research Institute for Field Crops, Ankara, Turkiye

Testing the stability of the performances and adaptations of wheat genotypes is crucial to evaluate wheat genotypes under different environments, which allows the development of well-adopted genotypes for large areas to be released as a variety. The objective of this investigation was to determine the stability parameters of the nineteen durum wheat genotypes and five check varieties under different environments in the Central Anatolian Region. Trials were laid out in a RCBD design with four replications during the 2020-2021 and 2021-2022 cropping seasons. The multivariate method of Additive Main Effects and Multiplicative Interaction (AMMI) analysis and GGE Biplot graphic analysis were conducted to interpret the interaction of genotype x environments. The results of the analysis of variance across environments showed that environment (E), genotype (G), and genotype x environment (G × E) interaction was highly significant for grain yield that leads to performing stability analysis. Genotype-18, genotype-4, and the Kiziltan-91 cultivar were superior in grain yield respectively compared to others. Based on the AMMI analysis concept, G8, G21, and Vehbibey cultivar were the most stable genotypes respectively although their yield performances were inadequate in the rank. According to the GGE Biplot graphic analysis concept, G4, G14, Kiziltan-91 cultivar, G1, G22, and Imren cultivar were the most stable genotypes with great means, respectively.

Keywords: AMMI Method, GGE Biplot Method, Genotype X Environment Interaction, Durum Wheat, Stability

[OP-07]

Yield Increase in Last 10 Years of Breeding for Winter Red Wheat

Muhsin Ibrahim Avci[1], Gokhan Kilic[1], Fatma Betul Sade[1], Mehmet Dogan[1], Mustafa Serdar Dogan[1], Mehmet Emin Alyamac[1], Bayram Ozdemir[1], Ayten Salantur[1], Emin Donmez[1], Turgay Sanal[2], Selami Yazar[1]

[1]Wheat Breeding and Genetics Unit, Plant Breeding Department, Central Research Institute for Field Crops
[2]Quality and Technology Department, Central Research Institute for Field Crops

The Wheat Breeding Unit at Central Research Institute for Field Crops is one of the oldest breeding programs in Turkey. Since its establishment, the program aims to develop high-yielding new cultivars that are characterized by high grain quality, and abiotic and biotic stress tolerance for Central Anatolia conditions. Over the years the wheat breeding program has released 35 bread wheat and 15 durum wheat cultivars many of which are cultivated by growers in the Central Anatolia Region in vast areas. These cultivars have not only allowed farmers to achieve good yields with good grain quality but also contributed to the wheat production of the country. In this study, we have analyzed historical data from the last 10 years of red-grained bread wheat preliminary yield trials to assess the yield and grain quality advancement of the breeding program. A total number of 4516 advanced lines and checks grown from 2011 to 2022 growing seasons according to augmented experimental design were utilized for this study. Analysis has shown the trend of increase in grain yield and quality characteristics in the breeding population as well as selected genotypes. This result indicates that the wheat breeding program at Central Research Institute for Field Crops have been steadily increasing the yield potential and quality of the genotypes which eventually turn into new cultivars that serve the people of the country.

Keywords: red winter wheat, genetic gain, yield, seed quality

[OP-08]

Last 10 Years of Winter White Wheat Breeding in Central Anatolia

Fatma Betül Sade[1], Gokhan Kılıç[1], Muhsin Ibrahim Avcı[1], Mehmet Doğan[1], Mustafa Serdar Doğan[1], Mehmet Emin Alyamaç[1], Ayten Salantur[1], Bayram Özdemir[1], Emin Dönmez[1], Turgay Şanal[2], Selami Yazar[1]

[1]Wheat Breeding and Genetics Unit, Plant Breeding Department, Field Crops Central Research Institute
[2]Quality and Technology Department, Field Crops Central Research Institute

Since its establishment, Central Research Institute for Field Crops Wheat Breeding program is aiming to develop high-yielding, abiotic, and biotic stress tolerant plants with high-quality characteristics that are adaptable to Central Anatolia Region. The wheat breeding unit at the CRIFFC is one of the leading wheat breeding programs in the country and achieved quite a success over the years, releasing 35 bread wheat and 15 durum wheat cultivars many of which are grower-favorites, grown extensively in the region. Even though the program is continuously releasing new and superior varieties, there is a need to understand the changes in yield and quality parameters of the genotypes produced by the program over the years. Therefore, this study aims to assess the yield and grain quality advancement of the white-grained bread wheat breeding efforts in the last 10 years. A total number of 2659 advanced lines and checks grown between 2011 to 2022 according to augmented experimental design were utilized in this study. Analysis has shown a trend of increase in grain yield and quality characteristics in the breeding population and selected genotypes. The steady increase in both yield and grain quality over the years indicates that the wheat breeding program is achieving its goals. These genotypes with superior characteristics are eventually released as new cultivars and serve the country's agriculture and its shareholders.

Keywords: white winter wheat, genetic gain, yield, seed quality

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[OP-09]

A Research About Determination of the Grain Yield and Protein Contents of Wheat Genotypes with Different Chromosomes in Ankara Conditions

Ali Haydar Paksoy[1], Mustafa Çölkesen[2]

[1]Ankara Tohumluk Tescil ve Sertifikasyon Merkez Müdürlüğü
[2]Kahramanmaraş Sütçü İmam Üniversitesi

In this research was carried out at Ministry of agriculture and forestry Variety Registration And Seed Certification Center trial areas during 2018-2019 and 2019-2020 growing seasons according to completely randomized block with four replicant. In this study aimed to determine of grain yield and protein content of 3 Triticum monococcum genotypes which has 14 chromosomes, and 3 Triticum aestivum cultivars (Tosunbey, Bayraktar 2000, İkizce 96, Demir 2000) which has 42 chromosomes. Protein content and grain yield of genotypes statisticaly was different to each other in two species. Triticum aestivum genotypes showed higher grain yield while protein content of spices near to each other. This study indicate that Tr. monococcum should be evaluated for special targets in wheat beeding programs.

Keywords: Wheat, Tr. aestivum, Tr. monococcum, Yield, Protein

[OP-10]

Evaluating Traits Influencing Hybrid Wheat Seed Production Using a Double Haploid Population Derived from Freeman x Camelot

Emre Karahan, Peter Stephen Baenziger, Katherine Frels, Reka Howard, Vikas Belamkar

University of Nebraska-Lincoln Agronomy and Horticulture Department

Hybrid wheat (Triticum aestivum L.) cultivars are preferred for their advanced agronomic traits such as a yield improvement increase up to 20%. However, hybrid cultivars remain difficult to produce on a commercial scale due to inadequate pollen dispersal, the closed nature of the wheat floret and the high cost of inducing sterility or restoring fertility in cleistogamous wheat. Redesigning parent-specific traits and understanding their potential interactions with related agronomic traits are needed to breed improved male lines in hybrid seed production fields. To better understand the genetic control of anther extrusion (AE), 174 double haploid lines derived from Freeman (excellent AE) x Camelot (poor AE) were visually assessed in three different environments in 2020 and 2021. Genotypic differences within the DH population were found in 2021. The best linear unbiased estimators found approximately normal distributions with low (AD, PH), moderate (GYLD), and high (AE, LODG) coefficient of variations. Pearson's correlation coefficient results revealed a significant negative correlation (r=-0.39**) between AE and lodging (LOGD). Moderately high broad sense repeatability was calculated (0.66) for AE and other traits in DH population. The contribution of PC1 and PC2 to the total variance were 45.6% and 27.3% respectively and combined explained approximately 70% of the total variance observed in PCA analysis.

Keywords: *Triticum aestivum* L., anther extrusion, hybrid seed production

[OP-11]

Environmental Effect in Two and Six-Rowed Barley (Hordeum vulgare L.) Cultivars on Yield Components and Leaf Diseases Under Rainfed Conditions

Irfan Öztürk[1], Turhan Kahraman[1], Banu Tülek[1], Adnan Tülek[1], Seyit Ahmet Bağcı[2]

[1]Trakya Agriculture Research Institute Edirne, Türkiye
[2]Selçuk University, Sarayönü Vocational Sch., Konya, Turkey

Rainfall and humidity are the main environmental factors that may influence barley yield, biotic and abiotic stress factors from the shooting up to the grain filling period in the Trakia region (Türkiye). It compared the effect of the rainfall and humidity from shooting to the end of the grain-filling phase, on yield and agronomic characteristics of two and six-rowed barley cultivars. Rainfall and mean humidity data from shooting up to the grain filling period were taken from the meteorological station in the experimental area. This research was established with 25 barley genotypes in a randomised complete block design (RCBD) with 4 replications in the Edirne location, Trakia region (Türkiye) ten consecutive growing cycles from 2006-2007 (E1) to 2015-2016 (E6). Two-rowed winter barley cultivar Bolayır and six-rowed winter barley cultivar Martı were selected from this experiment. Grain yield, 1000-kernel weight, test weight, protein ratio, days of heading, plant height, Scald and Net blotch leaf diseases were investigated. According to the parameters investigated, there was a significant difference between years in both cultivars. Across ten years of environments, in a two-rowed cultivar, the mean grain yield was in the range of 4480 - 8773 kg ha-1. In the research, while E2 was the highest productive environment, the lowest yield was in E9. The 48% difference between the highest and lowest yields showed the importance of environmental factors. The highest TKW (47.4 g) was in E9 and the minimum (30.4 g) was in environment E2. TW varied from the lowest 63.8 kg in E2 to the highest 75.7 kg in E5. The lowest (9.5%) and highest protein ratio (14.1%) was determined in environments E1 and E3. In six-rowed cultivar, across ten years environments, the mean grain yield was in the range of 5203 - 9167 kg ha-1, and the highest yielding crop season was E1 and the lowest was in E10. The yield difference between the highest and lowest year was 43.2%. There was a very wide variation in a thousand-grain weight. The highest TKW (45.0 g) was in E9 and the minimum (26.4 g) was in environments E2 and E6. TW varied from the lowest 56.6 kg in E2 to the highest 71.0 kg in E8. The lowest (8.9%) and highest protein ratio (12.9%) was determined in environments E1 and E2. There was a significant difference between years in both cultivars in Scald and Net blotch leaf disease.

Keywords: Barley, environmental effect, rainfall and humidity, yield, quality characters

[OP-12]

Identification and Maintenance of Male Sterile Lines using Morphological and Molecular Indices for Development of Onion Hybrids

Pravin Kumar Sharma

Department of Agriculture, Maharishi Markandeshwar (deemed to be university) Mullana, Ambala, Haryana, INDIA, 133207

Onion (Allium cepa L.) is the most diversified crop of the family Alliaceae; it is in cultivation since ancient era for its edible bulbs and verdant foliage due to the immense nutritional and medicinal properties. An experiment was conducted at Research Farm of Department of Vegetable Science, CCS Haryana Agricultural University, Hisar during winter season over two years to identify male sterile lines using morphological and molecular markers for their maintenance and hybrid production of onion. The male sterile line were developed in the genetic background of variety of Onion namely Hisar 2. Eight cytoplasmic male sterile line (MS 20, MS 21, MS 22, MS 23, MS 34, MS 35, MS 37and MS 40) and two maintainer line (Pollinator 5 and Pollinator 11) were identified on the basis of flower morphology and test cross with fertile pollen donor plant (Maintainer line). Identified male sterile lines were crossed with three restores to develop hybrids. A field trail was conducted to evaluate the performance of male sterile lines, maintainer lines and hybrids. Observations were recorded, bulb yield attributes like plant height, plant height, bulbs size, diameter of bulb, average weight of bulb, total bulb yield, marketable bulb yield, moisture content of bulb, dry matter content of bulb, total soluble solids of bulb. The analysis of variance exhibited significant genotypic difference, showing considerable amount of genetic variability among the genotypes. PCV were observed to be higher than GCV for all the characters studied, High estimates of PCV and GCV was observed for number of 'D' grade bulb followed by number of 'C' grade bulbs and number of 'A' grade bulbs. Among all eight lines, the line MS 20 was found good general combiner for more number of traits studied. Line MS 34 was found good general combiner for number of leaves per plant, average weight of bulb, total bulb yield, marketable yield, moisture content of bulb (%) and dry matter content of bulb (%). Among the tester Pusa Red showed good general combiner for plant height, diameter of bulb (polar & equatorial), average weight of bulb, total bulb yield, marketable yield, moisture content of bulb (%), dry matter content of bulb (%) and total soluble solids of bulb (%). Tester Pusa Red was observed as good combiner for plant height, number of 'B' grade bulb and polar diameter of bulb. Crosses MS 35 x Hisar- 3, MS 37 x Hisar-3, MS 22 x Agrifound Dark Red, MS 40 x Pusa Red and MS 21 x Pusa Red could be exploited for the development of onion hybrids and also for selecting desirable segregants to develop pure line varieties. The preponderance of both additive and non-additive gene actions for yield, its components and quality parameters suggests for both selection and heterosis breeding for the improvement of onion crop. The hybrid programme in onion is being further strengthened by use of DNA molecular markers and marker assisted selection (MAS). The QTLs governing male sterility have been identified for rapid selection of male sterile lines and pollinators.

Keywords: Allium cepa L., Alliaceae, cytoplasmic male sterile, marker assisted selection, PCV and GCV

[OP-13]

Establishment and Morphological Characterization of new Interspecies Hybrid Populations Capsicum Annuum and Capsicum Frutescens

Nihal Denli[1], Atilla Ata[1], Nedim Mutlu[2], Emre Öztürk[1], Hasan Pınar[3], Davut Keleş[4]

[1]Alata Horticultural Research Institute
[2]Akdeniz University
[3]Erciyes University
[4]General Directorate of Agricultural Research and Policies

Pepper is grown in all regions of Turkey and is among the species with high commercial potential. Although Turkey has a great diversity in terms of pepper genetic resources, the use of standard and especially hybrid varieties in production reduces this diversity. Interspecific hybridization is intensively carried out to increase the existing genetic variation, extend of genetic bases of cultivar varieties and biotic/abiotic stress tolerance in pepper breeding programs. This study, it was aimed to expand the existing genetic base by crossing a cultivar and 2 genotypes belonging to Capsicum annuum species and the PI 281420 genotype belonging to Capsicum furtescens species. The embryo rescue technique has been applied to prevent embryo abortion caused by interspecific

hybridization. Transformation rates from recovered embryos to plants varied between 0.16% and 20%. A total of 54 morphological features were evaluated in the three F2 populations created in the study, and the genetic variation in the populations in terms of these features was found to be between 53% and 76%.

Keywords: Capsicum annuum, Capsicum frutescens, embriyo rescue, variation, morphologic characterization

[OP-14]

Colchicine Induced Chromosome Doubling in Annual Ryegrass (Lolium multiflorum Lam.) and Identification of Autotetraploid Plants by Flow Cytometer

Batuhan Tuna[1], Hande Terzioglu[1], Veli Barak[1], Gulsemin Savas Tuna[2], Metin Tuna[1]

[1]Department of Field Crops, Faculty of Agriculture, Tekirdag Namik Kemal University, TURKEY
[2]Tekirdag Anatolian High School, Ministry of National Education, TURKEY

The production of animal based foods has been threatened in Turkey by insufficient forage production which is one of the long standing problems of the industry. Therefore, alternative forage species for each ecological region of the country must be determined and their higher performing cultivars must be developed. Annual ryegrass (L. multiforum Lam.) is one of the most commonly grown forage grass species in temperate regions of the world. In recent years, its cultivation has been started in Turkey as well, and its acreage has been increasing rapidly. However, except only a few, all of the ryegrass cultivars grown in Turkey have been developed in other countries with different climatic conditions than Turkey. Therefore, it is our own national interest to develop high performing new annual ryegrass cultivars for local conditions.

Induced polyploidy by application of mutagens such as colchicine is a well-known technique with a long history. It has been used successfully on many plant species. Induced polyploids generally have different morphological, physiological, and genetic characteristics than their diploid progenitors. As a result of these differences, they have higher biomass yield than their diploid progenitors as they are more tolerant to biotic and abiotic stress. Therefore, induced polyploidy is an important breeding method, especially for forage species. Approximately, 50% of the annual ryegrass cultivars registered in the world are autotetraploids, although it is a natural diploid with 2n=14 chromosome. Based on the results of previous studies, it has been determined that characteristics and performance of autopolyploids depend greatly on their diploid progenitors. Therefore, it has critical importance to evaluate diploid germplasms in the conditions of target regions and select the best performing ones for ploidy induction. However, we have not come across any similar type of study carried out on annual ryegrass in Turkey so far.

The objective of this study is to develop an efficient method for our laboratory to induce chromosome doubling in annual ryegrass and identify autotetraploids. Approximately 1200 seeds of a diploid population developed by selecting from an annual ryegrass collection including approximatelly 120 accessions based on their performance in Tekirdağ conditions. Five different doses of colchicine (0.05, 0.1, 0.2, 0.3, 0.4 %) and 3 different periods of application (4, 8 and 24 h) were used in the study. Flow cytometry was used in ploidy analysis after 8 weeks of colchicine application. The highest recovery of autotetraploids (15%) was obtained by treatment of one week old germinating seedlings with 0.2% colchicine for 8 hours. A high incidence of mixoploidy was obtained following colchicine treatment. Hexaploids were also rarely encountered. It was found out that ploidy varied among the tillers of the same plants when ploidy analysis is repeated after 4 months of colchicine applications. Autotetraploid tillers were propagated vegetatively, and used in polycrosses.

Acknowledgement: This study was supported by the Tubitak grants (Tubitak- 2209-A and Tubitak-1220242).

Keywords: Plant breeding, chromosome doubling, poliploidy, ploidy, ryegrass, flow cytometer

[OP-15]

Selection for Persistence in Red Clover (Trifolium pratense L.) Through Improved Tolerance to Northern Anthracnose

Muhammet Şahin[1], Steve Reid[2], Elif Şahin[1], Serkan Ateş[3], Sabry Elias[4], David B. Hannaway[4]

[1]Black Sea Agricultural Research Institute, Samtun, Türkiye
[2]USA DLF Pickseed USA, Corvallis, OR
[3]Department of Animal and Rangeland Sciences, OSU, Corvallis, OR
[4]Faculty, Department of Crop and Soil Science, OSU, Corvallis, OR

Red clover is one of the most important forage legumes, used extensively in European and North American farming systems as a short-lived perennial species (Smith, et al., 1985). This study was conducted with 23 red clover genotypes to evaluate tolerance of northern anthracnose (NA) and yield in Boyd, Kentucky and for agromorphological characteristics in Philomath, Oregon. Red clover cultivars and accessions were evaluated for NA tolerance of naturally occurring inoculum, using phenotypical selection techniques. Plants were rated for disease tolerance on a scale of 1 to 9, with 1 being necrotic (susceptible) and 9 being no visible symptoms (tolerant). Dry matter production was determined for each cutting by harvesting whole plots in 2018 and 2019. Results revealed significant differences ($P<0.05$) for disease severity and yield. In 2018, 'Evolve' and 'Redkin' had the highest dry matter yields (5078 and 4917 kg/ha, respectively), while in 2019, 'Helike' and 'Evolve' had the highest dry matter yields (9923 and 9843 kg/ha, respectively). The NA disease tolerance ranged from 2.6 to 7.8, with 'Kenland' being most tolerant. Agromorphological characteristics (plant height, spring growth, and growth habit) were determined in 2019 for the same 23 red clover genotypes grown under irrigated conditions at Philomath, Oregon. Significant differences ($P<0.05$) were observed among genotypes for plant height, spring growth, and growth habit, indicating potential for developing new cultivars suitable for both grazing and hay/silage systems. Future work will include rating cultivars in spaced-plants nursery in Oregon.

Keywords: Red clover, Northern anthracnose, Disease selection

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[OP-16]

Evaluation of Some Silage Hybrid Corn Genotypes in Terms of Yiled and Quality Under Samsun Ecological Conditions

Erkan Özata

Blacksea Agricultural Researc Instutute

İn this study, it was aimed to determine the yield and quality characteristics of silage hybrid maize genotypes for two years (2018 and 2019). The experiment was carried out according to the randomized complete blocks design with three replications. 25 genotypes (21 candidates and 4 standards) were used in both years of the experiment. In the first year of the experiment, green plant yields varied between 4470-5967 kg da-1, dry matter yields ranged between 1564-1986.5 kg da-1. In the second year, green plant yields ranged from 5571-7246 kg da-1, dry matter yields ranged between 1870-2643 kg da-1. The ranges of variation in quality characteristics of genotypes on a weight basis; ADF (%), NDF (%) crude protein ratio (%) and metabolic energy (mj/kg) were 28.5%-33.4%, 48.7-55.6%, 5.10-6.25% and 8.08-9.42 mj/kg in the second year, respectively. It was measured as 27.4-33.8%, 49.8-56.7%, 5.46-6.72% and 7.96-8.82 mj/kg. Similar results were obtained in both years in terms of mineral content (Ca, K, Mg and P) in dry matter. When two years are evaluated together; TTM2017-135 and TTM2017-136 genotypes took the first place in terms of green plant and dry matter yields. It was determined that both genotypes were within acceptable limits in terms of quality.

Keywords: Silage Maize, ADF, NDF, ME, dry matters

[OP-17]

The Utilizing from wild Sunflowers (*Helianthus spp*) for New Anatomical Designs in Sunflower

Yalcin Kaya

Department of Genetic and Bioengineering, Engineering Faculty, Trakya University, TURKEY

Sunflower is a native crop to North America continent then have started to cultivate at the beginning of 19th century in Europe after redeveloped as oil crop by Russian researchers. As an oil crop, sunflower grows widely in the world due to higher adaptation capability in different environments because sunflower conserves higher the genetic backgrounds from wild relatives surviving in severe climatic conditions from desserts to higher mountains. However, sunflower could not compete well with other crops in the rotations such as wheat in rainfed areas and corn and sugar beet in irrigated lands. Then sunflower is pushed to grow into poor soils with feeling great pressure for drought stress due to both global warming. Therefore, sunflower need new plant anatomical designs to increase seed yield capacity as having more plants per area, more seeds per head as well as higher seed weights. Furthermore, maybe it should have different root design as well as leaf number and areas. Wild sunflowers have great potentials for these important anatomical yield traits as consisting 51 species plus some subspecies growing in different climatic zones as well as having different plant anatomies. As a summer crop, sunflower production influences more from environmental conditions then it has had similar plant yield for 50 years in the Black sea areas and Europe. Therefore, sunflower breeders should seek different plant designs and anatomies as well as physiological traits and breeding methods to develop new better varieties. The wild sunflowers have many different desired traits for these specification so breeders should consider and screen these genetic resources utilizing their genetic diversity of these wild species as well as interspecific hybrids then determine these genes and add into to their new developed hybrids. Recently, molecular tools present great opportunities for screening these useful genes widely. As conclusion, wild sunflowers are the main sources for new plant anatomical designs and these genes need to transfer accurately then develop higher yielding varieties by sunflower breeders.

Keywords: Sunflower, Wild species, Helianthus, Plant Anatomy, Yield description

[OP-18]

Morphological And Physiological Responses of Potato Genotypes to Different Water Deficit

Sani Ibrahim Ibrahim, Eric Kuopuobe Naawe, Mehmet Emin Caliskan

Nigde Omer Halisdemir University

Potato is an important global crop for human life sustainability. Potato is characterized by shallow root architecture that makes it a drought-sensitive crop. Drought stress causes severe loss of yield and the quality of potatoes. There is a need to produce drought-tolerant potato breeding lines by breeders to meet ever-rising human demands. The present study was conducted to assess the response of 25 potato breeding lines and 4 check cultivars under two different irrigation regimes; fully watered as control and drought stress treatment. The research was set up in a randomized complete block design with four replications over two potato growing seasons: from May to October 2021 and June to October 2022. The experimental setup was irrigated using a drip irrigation system and the control was irrigated twice weekly while the water stress site was irrigated once a week. The morpho-physiological traits assessed were planted height, and the number of stems per plant, and traits included emergence times, stand establishment, leaf canopy temperature, leaf area index, leaf chlorophyll, growth duration, and physiological maturity. There were high significant ($p <= 0.01$) differences for the stem number, leaf area index, leaf chlorophyll, plant height, and yield between the genotypes. There were also highly significant disparities between the drought and control treatment for the yield, dry matter content, and specific gravity. Some genotypes exhibited tolerant responses to drought stress.

Keywords: Potato, breeding lines, drought stress, water deficit morpho-physiological

[OP-19]

Comparative Yield and Quality Traits Stability Estimates of Potato Breeding Lines in the Central Anatolia Region of Türkiye

Eric Kuopuobe Naawe, Sani Ibrahim Ibrahim, Mehmet Emin Çalişkan

Nigde Omer Halisdemir University

In crop breeding, the success of plant breeding programs depends on the ability to provide farmers with genotypes having superior performance in terms of yield across a range of environmental conditions. Stability analyses are important for sustainable production and food security in the era of climate change. The study of crop stability is important as it helps breeders and farmers to identify crop varieties with specific and general adaptabilities. Potato is the most important tuber crop and the 3rd most important food crop globally due to its economic value. This study was conducted in the Central Anatolia region of Türkiye to estimate the adaptation and stability of potato breeding lines aiming to identify superior varieties for yield and quality traits using different stability models for comparison. The study was conducted from May to October 2019 potato growing season. The study consisted of 12 potato breeding lines and 3 standard cultivars in a randomized complete block design in three different environmental locations with four replications. The analysis of variance results showed highly significant ($p<= 0.01$) effects of genotype (G), environment (E), and GEI on yield, phenotypic traits, and quality traits of potato breeding lines tested except for stand establishment where there was no significant difference. The mean marketable tuber yield and total tuber yield ranged from 16.66 to 41.60 t/ha, and 17.03 to 41.77t/ha respectively. The different stability models showed that MEÇ1407.17, MEÇ1407.05, MEÇ1407.08, and MEÇ1411.06) were high-yielding and stable genotypes and thus considered candidates for cultivar release. The result showed that MEÇ1405.06, MEÇ1405.07, MACAR1409.09, and MACAR1406.04, were high yielding with narrow stability (specific adaptation) while other genotypes were generally stable (general adaptation). The study recommended the combined use of Finlay and Wilkinson's regression model, and the Additive Main Effects and Multiplicative Interactions (AMMI) model for crop yield and quality stability studies.

Keywords: Potato breeding lines, adaptation, AMMI, Finlay and Wilkinson stability, stability estimation

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[OP-20]

Contrasting Behavior of Potato Breeding Lines to Morpho-Physiological and Agronomic Characteristics in Response Heat Stress

Eric Kuopuobe Naawe, Sani Ibrahim Ibrahim, Mehmet Emin Caliskan

Nigde Omer Halisdemir University

Abiotic stresses are the major factors that influence the growth and development of plants resulting in devastating yield losses and poor-quality traits. Heat stress studies are important in breeding programs and necessary for the development of heat-tolerant breeding lines that fit well to the ever-changing climate. Potato is an important cool-temperature vegetable crop consumed globally however its productivity is threatened by warmer climatic zones due to heat stress. The development of heat-tolerant potato varieties is one of the key breeding priorities in recent times. Therefore, the current study was devised to evaluate and screen the morpho-physiological responses of 25 potato breeding lines and 4 commercial cultivars to high temperature with the aim of identifying heat tolerant breeding lines. The study was conducted under field conditions in a split-plot design in the randomized complete block with four replications from May to August 2022. Morphological traits such as the number of stems per plant, plant height, physiological traits such as gaseous exchange, chlorophyll index, leaf temperature, leaf area index, and relative water content, and field agronomic traits such as stand establishment, emergence time, and growth duration were assessed. There were significant differences in the morpho-physiological traits between the heat stress treatment and control treatment. In the agronomic traits, there were no significant differences in the stand establishment, and the number of stems per plant between the treatment, except for the physiological maturity date where the control treatment matured earlier than the heat-stress treatment. For plant height and leaf temperature, there were highly significant differences between the heat and control treatments. The photosynthesis analysis also showed significant differences between the treatment. The photosynthetic rate declined significantly in 10 breeding lines whereas a non-significant reduction was noticed in the remaining breeding lines. It suggested their tolerant nature. This study showed that potato breeding lines have differential responses to heat.

Keywords: abiotic stress, heat stress, potato, morphological, physiological

[OP-21]

Different Maize Breeding Approaches for Tackling Climate Change in Croatia and Turkey

Zvonimir Zdunic[1], Vlatko Galic[2], Antun Jambrovic[1], Tatjana Ledencan[2], Andrija Brkic[2], Kamil Yılmaz[3], Ersan Atakul[4], Ülkü Er[4], Domagoj Simic[1]

[1]Agricultural Institute Osijek, Juzno predgradje 17, Osijek, Croatia; Centre of Excellence for Biodiversity and Molecular Plant Breeding, Zagreb, Croatia
[2]Agricultural Institute Osijek, Osijek, Croatia
[3]TAREKS, Genel Müdürlük: Kazakistan Caddesi (4.Cad) No: 136/4-5-6 Emek, Ankara, Turkey
[4]TAREKS, Altınova Selimiye Mah. Topçukuru Mevkii Belediye Otogarı Arkası, Ayvalık, Turkey

The framework of genotype × environment × management (G×E×M) interactions in maize breeding enables integration of all available information in the range of environment types that characterize target production regions also in the context of climate change. Integrating environmental data, the estimated phenotypic value of traits, and relations to trait genetic architecture may be used to conduct studies on trait physiology, phenotyping, and genomic prediction/ selection on how to cope with single and/or multiple stress. Maize growing conditions differ considerably in Croatia and Turkey resulting in particular G×E×M interactions. In Croatia, maize is grown in continental temperate regions mostly under rainfed conditions. On the other hand, in Turkey, maize is grown in several climate zones applying irrigation routinely. The objective of this study was to compare different maize breeding approaches for adapting to climate change using environmental parameters in Croatia and Turkey. According to our long-term trials set across Croatia and Turkey together with data simulations, environmental parameters such as stress degree days (SDD) and vapor pressure deficit (VPD) play critical role in yield development. In Croatia, heat stress represented by SDD along with duration of maize life cycle affected grain yield considerably, whereas VPD was of major importance throughout Turkey. Current status and predictions for Croatia suggest that the right choice of maize maturity to attain higher yields in future is not straightforward and it is not made only according to prevalent climate change expectations. In Turkey, two cycles of selection for yield was beneficial taking into account increased VPD. Experimental results from long-term maize variety trial network in Croatia and Turkey will be presented and discussed.

Keywords: breeding, maize, Croatia, Turkey, environmental parameters, climate change, yield

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[OP-22]

Development of Maize Varieties Suitable for Central Anatolian Conditions

Mehmet Tezel, Erdal Gönülal, Ramazan Çağatay Arıcı, Gazi Özcan

Bahri Dağdaş Uluslararası Tarımsal Araştırma Enstitüsü

TThis study was obtained from the trials established in 2019 of maize breeding studies carried out in Central Anatolian conditions. In the study, 20 single hybrid maize combinations and 5 standard maize varieties (P0937, DKC5741, P0900, DKC5364 and P0573), which were crossed using inbred lines in 2018, were used. In the study carried out in the randomized blocks trial design in Konya Bahri Dağdaş International Agricultural Research Institute fields, grain yield, number of flowering days, grain moisture, plant height and ear height observations and measurements were taken. In the study, the average grain yield was obtained as 11900 kg ha-1, the average of the standards was 12880 kg ha-1, while the average yield of single hybrid maize combinations was 11660 kg ha-1. In the study, 5 single hybrid maize combinations (KTM 18.39, KTM 18.46, KTM 18.44, KTM 18.47 and KTM 18.68) reached higher yields than the yield standard maize varieties. Number of flowering days in the study was between 76.7 days (KTM18.45 and P0937) / 79.3 days (KTM 18.66), grain moisture at harvest was between 14.1% (DKC5364) / 23.2% (KTM 18.65) and plant height was 242 cm (KTM 18.67) / 294 cm (KTM 18.44). With this study carried out in Central Anatolian conditions since 2008, it has been seen that productive varieties suitable for the region can be developed.

Keywords: Maize breeding, local variety, single hybrid, yield

[OP-23]

Towards the Development of Clearfield Red Lentil Cultivars in Turkey

Abdullah Kahraman[1], Ahmet Cakmak[1], Murat Tunc[1], Belgin Sahin[1], Caner Pac[1], Abdullah Birisik[1], Varma Penmetsa[2]

[1]Department of Field Crops, Faculty of Agriculture, Harran University, Osmanbey Campus, Sanliurfa, Turkey
[2]Department. of Plant Sciences, University of California - Davis,1210 PES Building, 387 North Quad, One Shields Ave, Davis, CA 95616, USA

Weeds are one of the most important factors limiting the yield of lentil. Herbicides developed for lentils are insufficient in the fight against broad-leaved weeds. With the development of clearfield varieties, fields remain clean, yield loss due to weeds is prevented, a high market price is achieved by obtaining clean products free of weeds, and as a result, high yields and income opportunities are obtained. In this study, it was aimed to develop varieties resistant to imidazolinone herbicides from cultivar Firat 87 seeds by mutation breeding. Sodium Azide (NaN3) and EMS (Ethyl Methane Sulfonate) were applied to the seeds as chemical mutagens. As a result of different dose trials to determine the effective mutation dose, it was determined that 5 mM EMS concentration for two hours was suitable for lentil seeds In field and laboratory studies, herbicide resistant lentil lines were determined by applying 2x dose of imazamox herbicide and selections were made from amongst approximately 3 million lentil plants. Herebicide resistant lines were retested in both field and greenhouse trials and proved to be herbicide tolerant. In order to determine the resistance of imazamox herbicide at the molecular level, changes in the ALS (Acetolactate synthase) gene region in the lentil genome was examined. It was determined that it changed from Guanine to Adenine at base 1630 in the ALS region. On the other hand, it was determined that the AAG sequence in the control plant DNA was converted to AAA in the mutant individual, and Ser653 was converted to Asn653 at the amino acid level with reference to the Arabidopsis thaliana ALS region. Mutations in the ALS region provide tolerance to high herbicide doses in plants, and it has been determined that the mutant individuals obtained in this study show resistance up to 3 times the recommended dose (160 ml/da with 25% a.i. imazamox). Candidate lines for variety registration were determined and selected candidate lines were compared with some standard cultivars in terms of yield and agronomic characters. It is planned to submit two imazamox herbicide tolerant lentil genotypes as candidates for cultivar registration. Clearfield cultivars offer an alternative and economical solution for lentil growers to control weeds and increase yields.

Keywords: Lentil, clearfield, imidazolinone tolerance, herbicide resistance, mutation breeding

[OP-24]

Determination of Yield Performance of Chickpea Varieties Widely Cultivated in Our Country in Konya Ecology

Hakan Bayrak

Hakan Bayrak Bahri Dağdaş UTAEM Konya

This study was carried out to determine the performance of chickpea cultivars, which are extensively cultivated in our country, in terms of yield and yield criteria in Konya ecology. The study was carried out in barren conditions for two years in 2016-2017.

In this study; A total of 9 Azkan, Çakır, Akça, Gökçe, Akçin 91, İnci, Çağatay, Sezenbey and Zuhal varieties were used as materials. Trials were conducted in Bahri Dağdaş U.T.A.E.M. carried out in experimental fields. In the experiments, observations were taken and determinations were made about emergence time, flowering time, vegetation period, anthracnose, plant height, first pod height and grain yield. As a result of the experiment, the grain yield changed from 41.3 to 149.6 kg/da. Flowering period is 41.9-54.5 days, vegetation period is 93.2-101.2 days, first pod height is 17.5-19.9 cm, plant height is 28.1-51.2 cm, Anthracnose scale value is 1-3.5 was detected.

Keywords: Chickpea, variety, grain yield, yield characteristics

[OP-25]

Selection of Winter-Hardy Genotypes and Determination of Some Agricultural Characteristics in Hybrid Pea Lines (F3)

Ahmet Tamkoç[1], Özkan Taşpınar[2], Ahmet Konuk[2], Tuba Uzun[2], Saliha Mutlu[3], Bilal Mohammed Abbas Al Rubaye[4], Ilker Topal[5]

[1]Department of Field Crops, Faculty of Agriculture, Selcuk University, 42250 Konya, Turkiye
[2]Taspinar Tarim Industry and Trade Limited Company, 42050 Konya, Turkiye
[3]Department of Plant Breeding and Genetics, Institute of Sciences, Selcuk University, 42130 Konya, Turkiye
[4]Department of Field Crops, Institute of Sciences, Selcuk University, 42130 Konya, Türkiye
[5]Bahri Dagdas International Agricultural Research Institute, 42020 Konya, Turkiye

This study was carried out to select winter-hardy pea genotypes and to determine some agricultural characteristics. In the study, lines in the F3 generation obtained by crossing the wild pea genotypes collected from nature with the bred varieties and lines were used (91 lines). Planting of the lines was done in rows with a length of 2 m in 50 cm row spacing, 20 cm in row spacing, and 5 cm planting depth. The experiment was carried out in the experimental field of Selçuk University Faculty of Agriculture in the growing season of 2020/2021. Maintenance procedures such as irrigation, fertilization and weed control, which are necessary for the healthy growth of plants, have been carried out. In this study; Winter damage, disease damage, number of flowering days, number of main branches, plant height, number of pods per plant, number of seeds per pod, number of plants reaching harvest maturity and seed yield were emphasized. Winter damage was not seen in 38 lines; disease damage was not seen in 72 lines; the number of flowering days varied between 146-176 days; the number of main branches varied between 1-10; plant height varied between 45-125 cm; the number of pods per plant varied between 10-39; the number of seeds per pod varied between 2.67-7.67; The number of plants reaching the harvest maturity ranged from 1-10 and the seed yield per plant was between 4.29-101.2 grams.

Keywords: peas, seed yield, number of seeds, number of main branches

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[OP-26]

Modifying Flowering time by Using Vernalization, Photoperiod and Earliness Genes in Winter Wheat to Increase the Adaptability of Wheat in the Era of Climate Change

Mesut Keser[1], Beyhan Akın[2], Fatih Özdemir[3]

[1]International Center for Agricultural Research in the Dry Areas, Ankara Turkey
[2]International Maize and Wheat Research Center, Izmir Turkey
[3]Bahri Dagdas International Agricultural Research Center, Konya Turkey

Global warming is expected to change the duration of the vegetation period that would also lead a shift in the timing of phenological phases resulting a drastic impact on the productivity of winter crops. The wide adaptability of wheat is largely controlled by three genetics factors; vernalization (Vrn), photoperiod (Ppd) and earliness per se genes including plant status. The combinations of these alleles effect the adaptability of wheat by affecting heading time and altering the phenological phases. Flowering date in bread wheat is determined by Vrn, photoperiodic sensitivity (Ppd) and earliness per se (Eps) genes. The aim of this study was to study the effect of Vrn, Ppd and Eps genes on heading date (HD) in winter wheat in controlled environment and exploring the possibility of altering the phenological phases of the winter wheat. The allelic composition of two winter wheat cultivars, Karahan and Sönmez for above mentioned genes were determined and each of them were crossed with two different unknown genetic make-up of winter wheat genotypes. Though Sonmez and Karahan are winter wheat cultivars, their allelic combinations for the above-mentioned genes are different. Both cultivars do not have 1B1R rye translocation which is associated with good adaptability but with bad grain quality. F1 and F2's of the crosses was grown in the field and 200 F2:3 randomly selected seeds of each 4 populations were grown under controlled environment. Plants were vernalized for 4 weeks in a cold chamber under 4 0C degree before transplanting into the controlled conditions. After the vernalization treatment completed, the plants were transplanted into greenhouse (GH). Heading dates of each plant in the populations after transplanting into GH were determined at the stage ears emerged fully from the boot. Wide range of heading dates were observed in each populations indicating it was possible to select early or later genotypes.

In populations when one parent was Karahan, while the HD range was 43-72 days in one population, it was 54-68 days in the second populations. In one parent Sonmez populations, HD range was 46-72 days and 29-70 days in the first and second population respectively. In all populations, some plants did not reach to heading; their percentages in the populations were different changing from 20.7 % to 37.5 %. The results indicate that the suitable genotypes can be selected for different Agro-Ecological Zones (AEZ) to increase the adaptability of the genotype to that AEZ. Purity of cultivars used in this study for Vrn, Ppd and Eps genes is questionable due to high variation both in Karahan and Sonmez in HD.

Keywords: Winter wheat, Vernalization, Photoperiod, Earliness

[OP-27]

CIMMYT's Approach to Speed Breeding for Spring and Winter Breeding Programs

Beyhan Akın, Emrah Koç, Fehmi Kozveren

International Maize and Wheat Improvement Center

In recent breeding efforts, a significant amount of time, space and resources are used to find effective ways to develop best varieties in as short a time as possible. Speed breeding (SB) achieves this shorter cycle for breeding through rapid generation advancement and thereby accelerates the research. The combined effect of prolonged exposure to light under controlled conditions together with early harvesting of fast-maturing plants shortens the generations. Hence, the SB method becomes a promising approach contributing to nutritional security and sustainable agriculture for food and industrial crop enhancement.

After having long years of studies on Spring Wheat Breeding, CIMMYT established its well-designed its rapid breeding facility at Toluca in 2020. Using a low-cost operation, scientists use an in-field screenhouse spanning 2 hectares, and obtained 4 generations of spring wheat per year, thereby reducing the time needed for the development of new germplasm ready for yield testing to under 2 years. CIMMYT integrate different traditional and advanced genomics-assisted breeding technologies in their research like Genomic Selection (GS) and Genomic Estimated Breeding Values (GEBVs) to achieve faster and more accurate results and serve as a decision-making tool for breeders.

In winter wheat breeding, classic breeding methods take 12-13 years from initial crossing to obtaining variety candidate lines, and this time can increase to 15 years in total when the registration of the new variety from these lines and the process of delivery to the farmers are considered. Using the rapid breeding technicques, it becomes possible to obtain 6 generations per year in plants such as spring wheat, durum wheat, barley and peas and 4 generations in canola. 6 generations in a year can be ensured with spring wheat as the need for cooling, which is absent or very little. However, unlike spring wheats, winter wheat requires 4-6 weeks of vernalization to pass from the vegetative period to the generative period and this differs between varieties. The initiatives to apply speed breeding to winter wheat was started by the International Winter Breeding Program at a greenhouse facility established at the Aegean Agricultural Research Institute in 2018. The greenhouse provides controlled consitions for 25,000 single plants. With winter wheat lines which were planted at controlled greenhouse conditions – exposed to LED Lightening System for 22h/per day for 10 weeks reaching harvest maturity, only 3 generations were obtained within 13 months. According to the initial results obtained from the spring and winter wheat speed breeding activities, it is seen that the rapid breeding can accelerate obtaining new varieties by shortening the generation process, give a different dimension to the research and development studies achieving the result promptly, and contribute economically in the long run despite the high initial establishment costs.

Keywords: Speed breeding, winter wheat, spring wheat, genome selection, vernalization

[OP-28]

Development of Sulfonylurea (SU) Group Herbicide Resistant Ornamental Sunflower Lines

Bahar Sancar[1], Songül Sever Mutlu[2], Nedim Mutlu[2], Ayşe Nuran Çil[3], Alparslan Karabeniz[2], Mamoudou Zonon[2], Ahmet Barkan Bostan[2]

[1]Kocaeli University
[2]Akdeniz University
[3]Eastern Mediterranean Agricultural Research Institute

Sunflower (Helianthus annuus L.) is an annual species of Helianthus genus belonging to the Asteraceae family. It is widely grown for oil or confectionery. However, sunflower has been used as an ornamental plant throughout history. It is used as cut flower, potted ornamental plant and outdoor landscape plant. The cytoplasmic male sterility (CMS) offers breeding sterile hybrids and relatively easy, inexpensive hybrid seed production. Weeds are one of the most important parameters limiting the widespread production of ornamental sunflower in open fields and greenhouses. The non-transgenic ALS-based Imidazolinone (IMI) and Sulfonylurea (SU) group herbicide resistance is widely used commercially in sunflower breeding and production. The aim of this study is to develop ornamental type CMS and maintainer sunflower lines resistant to SU group herbicides suitable for hybrid sunflower breeding. The study is carried out in Akdeniz University Ornamental Plants Greenhouse. The plant materials included commercial 15 Fertile F1 ornamental sunflowers having different growth forms, colors and flower characteristics, ornamental type maintainers from the Eastern Mediterranean Agricultural Research Institute (Adana) sunflower breeding program, and SU herbicide resistant restorer donor lines. The SU resistant Restorer (R) line was first crossed to sterile hybrid "Sunrich Orange F1" ornamental sunflower. The resulting F1 plants were used as pollen source and backcrossed to both maintainer (B) and Sunrich Orange F1. Single plant selections are made for flower color/structure in segregating BC populations and resistant plants are determined by applying. It has been observed that the SU resistant BC2F1 plants began to resemble the related ornamental hybrid in terms of plant height, flower color and structure Backcrossing will continue until BC3 or BC4 generations. The SU resistant maintainer and CMS lines will be used to develop new ornamental hybrids.

Keywords: Ornamental sunflower, Sulfonylurea herbicide, Cytoplasmic male sterility, Ornamental Plant Breeding

[OP-29]

Breeding Sterile (Male-Sterile) Ornamental Sunflower Lines Resistance to Imidazolinone (IMI) Group Herbicides and Downy Mildew Disease

Alparslan Karabeniz[1], Songül Sever Mutlu[1], Nedim Mutlu[1], Ayşe Nuran Çil[3], Bahar Sancar[2], Barkan Bostan[1], Mamoudou Zonon[1]

[1]Akdeniz University
[2]Kocaeli University
[3]Eastern Mediterranean Agricultural Research Institute

Sunflower (Helianthus annuus L.) is a annual plant which belongs to Asteraceae family. As well as being cultivated as oil crop and confectionary, sunflower has been also used as ornamental plant throughout history. Hybrid and steril (male-sterile) sunflower cultivars are in high demand in world market as cut flower. Cytoplasmic Male Sterility (CMS) method provides quick and low-cost hybrid seed production. One of the most important factors which restricts ornamental sunflower production is weeds and downy mildew infection. Both in greenhouses and in fields, seeds are directly sown in ornamental sunflower cultivation. The most effective weed control strategy, Imidazolinone (IMI) and Sulfonilurea(SU) groups herbicide resistance, are commercially used for oil and confectionary sunflower production. However, it is yet to find common use in ornamental sunflowers. The downy mildew disease (Plasmopara halstedii) can cause full crop failure in infected fields. Aim of this study is to obtain CMS and maintainer lines resistant to IMI herbicide and downy mildew. The plant materials included 17 commercial sterile (male-sterile) F1 cultivars with different growth forms, colors and flowers, ornamental type maintainer, and IMI + downy mildew resistant restorer (R) line from Eastern Mediterranean Agricultural Research Institute (Adana). The R line was crossed with commercial hybrids, then F1 plants as pollen source were backcrossed to both maintainer and sterile hybrids. The seedlings of segregating populations were biologically tested by mixing downy mildew spores collected from sunflower production fields. Then, downy mildew resistant seedlings were sprayed with IMI herbicide at 4-6 and 7-8 leaf stage. Some of the IMI + downy mildew resistant BC2 plants showed ornamental characteristics. Populations will be advanced to BC3 or BC4 to obtain ornamental type

resistant A and B lines. Advanced lines are expected to yield improved ornamental sunflower hybrids suitable to greenhouse as well as open field cultivation.

Keywords: Ornamental Sunflower, Imidazolinone Herbicide, Downy Mildew Resistance, Cytoplasmic Male Sterility, Ornamental Plant Breeding

[OP-30]

Determination of Resistance Levels Oo Qualified Tomato Genotypes to *Meloidogyne Incognita*, Tomato Yellow Leaf Curl Virus, Tomato Spotted Wilt Virus, Tomato Mosaic Virus

Selcan Eroğlu[1], Ali Tevfik Uncu[2], Ayşe Özgür Uncu[2], Neslihan Issı[1], Banu Çiçek Arı[1], Gülbanu Kıymacı[1], Önder Türkmen[3]

[1]Selcuk University, Faculty of Agriculture, Department of Horticulture, Konya/Turkey
[2]Necmettin Erbakan University, Faculty of Science, Department of Molecular Biology and Genetics, Konya/Turkey
[3]Selcuk University, Faculty of Agriculture, Department of Horticulture, Konya/Turkey; Necmettin Erbakan University, Eregli Faculty of Agriculture, Konya/Turkey

Tomato (*Solanum lycopersicum* L.), one of the vegetable species, is one of the vegetables that covers an important area in terms of reproduction both in Turkey and in the world. Although Turkey is not among the gene centers, it ranks 4th in the world in terms of production after China, India and the USA. According to consumer demands, tomato varieties such as pink, beef, bunch, cocktail are grown. In recent years, an important production potential of pink tomatoes has started to emerge in Turkey, and breeding programs are carried out in this context. The main goals in breeding are high yield, quality and resistance to stress factors, and molecular assisted selection is a fast and reliable method, especially in determining the levels of resistance to biotic stress factors. In this study, the determination of the resistance levels of 339 tomato genotypes, which have the potential to become parent lines due to their agromorphological characteristics, against *Meloidogyne incognita* (Nematode), Tomato Yellow Leaf Curl Virus (TYLCV), Tomato Spotted Wilt Virus(TSWV), Tomato Mosaic Virus (ToMV) in the S6 stage was the subject of this study. When the results of the study were examined, 235 resistant lines to *Meloidogyne incognita*, 175 resistant to TYLCV, 201 resistant to TSWV and 211 resistant to ToMV lines were determined among 339 genotypes and they were included in the breeding process in order to develop resistant varieties against these biotic stress factors.

Keywords: eloidogyne incognita, Tomatoes, ToMV, TSWV, TYLCV

[OP-31]

QTL Detection of Maturity Timing in Sweet Cherry Using a Multi-Family QTL Approach

Fatih Topuz[1], Cameron Peace[2]

[1]Alata Horticultural Research Institute, Erdemli, Turkey
[2]Department of Horticulture and Landscape Architecture, Washington State University, Pullman, Washington, United States of America

In sweet cherry production, maturity timing is important trait that defines market class. Early and late varieties can be more profitable for sweet cherry growers. Thus, the maturity timing of sweet cherry in breeding programs is one of the main consideration. The use of DNA information in tree fruit species is promising because DNA-informed breeding can decrease cost and time needed in tree fruit breeding efforts. The maturity timing of sweet cherry is highly heritable, and several research has reported QTLs from bi-parental families. However, the genetic dissection of sweet cherry maturity timing has not been fully discovered. The objective of this study was to determine QTLs associated with sweet cherry maturity timing. The RosBREED Crop Reference Set with SNP with High density SNP marker data were used. The set consist of 528 individuals representing Washington State University Pacific Northwest Sweet Cherry Breeding Program. QTL analysis using the Bayesian approach implemented by FlexQTL™software revealed 9 major QTLs on linkage groups 1, 3, 4, 5, 6, and 7 explaining the ~66% of the phenotypic variation. These QTLs were on the same chromosomes as reported in the literature from bi-parental analyses, confirming their relevance for U.S. breeding germplasm. This study showed that the pedigree-connected multi-family approach can successfully detect breeding-relevant QTLs associated with sweet cherry maturity timing. Once the effects and germplasm distribution of their functional alleles are determined, these QTLs could be useful for DNA-informed breeding applications.

Keywords: *Prunus Avium*, Fruit Maturity, QTL Discovery, FlexQTL ™

[OP-32]

Cytoplasmic Genome Prediction in Cucumber (*Cucumis sativus* L.) Hybrid Variety Breeding and it's Usage in Breeding

Osman Gülşen[1], Leyla Öztürk Akar[2], Sinan Zengin[3], Gülsün Elif Vural[3]

[1]Department of Horticulture, Erciyes University, Melikgazi, Kayseri, Turkey
[2]Agromar Marmara Tarım Ürünleri A.Ş., Bursa, Turkey
[3]Antalya Tarım A.Ş., Antalya, Turkey

Cucumber (*Cucumis sativus* L.), which is among the top 10 most cultivated products among fruits and vegetables, has a production value of 87.8 million tons in the world according to the latest statistics and Turkey ranks second after China with 1.9 million tons of production. It is necessary to carry out effective and rapid breeding studies in order to develop domestic hybrid varieties with productive and resistance to both abiotic and biotic stress factors in cucumber cultivation. Breeding studies in Cucurbitaceae species take a long time. It has become necessary to shorten the time and support traditional breeding methods with modern biotechnological methods to get qualified domestic cucumber varieties. Obtaining haploid plants from female gametes by using double haploid technique in cucumber achieved successfully and rapid selections after hybridization can be made by using molecular markers. Additionally, cytoplasmic genome prediction within the scope of molecular-based breeding is a very important application. To get heterosis in test crosses, reciprocal (double way) crosses can be made as well as single crosses. Reciprocal crosses are made based on the idea that the cytoplasmic organelles (plastid and mitochondria) between individuals are different from each other significantly increases the labor. In case where the origins of individuals whose cytoplasm can be estimated by molecular methods are not different, the need for reciprocal crosses will be eliminated, and a significant labor and time savings will be provided. In this study, 4 plastid genome regions (rbcL, psb-trnS, trnHK, trnST) of 50 donor genotypes were sequenced and cytoplasmic genome prediction was made. The PCR products obtained by using specific primers designed for this purpose, were sequenced. The resulting band sizes are approximately about 900, 1500, 3000 and 1400 base pairs. The sequences of 50 genotypes were analyzed by MEGA Genetic Analysis Program. According to the alignment results of the obtained sequences, no nucleotide variation exists among the donor genotypes. Since these results were assumed that there was no cytoplasmic genome difference between the hundreds of inbred lines obtained from 50 genotypes, reciprocal crosses were excluded. This analysis can provide rapidity and savings in breeding by eliminating unnecessary reciprocal test crosses.

Keywords: Breeding, Cucumber, *Cucumis sativus* L., Cytoplasmic Genome Prediction, Double Haploid, Hybrid Variety Breeding

[OP-33]

Moleculer Characterization of Economically Important Some Grape Varieties, Rootstocks and Their Clones Based on AFLP Markers

Funda Yilmaz Baydu, Gokhan Soylemezoglu

Department of Horticulture, Agriculture Faculty, Ankara University, 06110 -Ankara, Turkey

This research was conducted to characterize economically important grape varieties, rootstocks and their clones by AFLP Thecniques. The major problem in defining grape varieties is the huge morphological and genetic variability in the genus Vitis, which also leads to confusion and uncertainty. In this study, a total of 154 individuals were identified with AFLP technique, including grape varieties selected in Türkiye and grapevines and American rootstocks and their clones and known varieties as central. In this technique, restriction enzymes (EcoRI / MseI) and double (di) selective primers for cutting regions (ESEL32-MSEL2, ESEL32-MSEL6, ESEL32-MSEL7, AFLPC- MSEL6, AFLPC- MSEL7, AFLPD- MSEL7, AFLPD-ESEL22-MSEL2, ESEL22-MSEL6, ESEL22-MSEL7) are used. Polymorphism rate was found as 87,8%. It was observed that the similarity rates between genotypes and clones varied between 99% and 39%. The highest similarity rate among the different genotypes was found in the genotypes of Bilecik İri Karası and Kozak Siyahı with 84%. The lowest similarity rate was found in the genotypes of Hafızali and Siyah Razakı with 39%. The highest similarity rate among the clones was found in clones 15 and 30 of the Karaerik variety with 99%. In this study, clonal polymorphism was provided. Technical progress in moleculer phylogenetics (SNP: Single Nucleotide Polymorphism) will provide prospective contributions in clonal assays of the present material.

Keywords: Viticulture, Vitis vinifera L., Grape, Clone, Rootstock, AFLP, Türkiye

[OP-34]

Molecular and Morphological Characterisaton and Association Mapping for Some Agronomic Characteristics in Different Apple Types and Varieties

Hasan Pinar

Erciyes Universty Department of Horticultur

In apple breeding, morphology, flower and fruit related features are the most important factors in terms of breeding criteria. Although genetic mapping studies in the world, including apples, accelerated, populations of F1 individuals generally obtained as a result of crossings have been studied is used in studies. With the association mapping technique that emerged with the development of molecular techniques, DNA markers associated with phenotype can be detected by establishing a link between phenotype and genotype. With this technique, genetic diversity can be achieved without the need for time-consuming processes such as the development of mapping populations. In this study, morphological, phenological, pomological and molecular characterization processes were performed on apples using 120 apple genotypes consisting of four different species, and DNA markers associated with some important agronomic traits in the apple population were determined by applying association mapping technique. SSR, ISSR, SRAP and RAPD techniques were used for molecular characterization. Similarity coefficients between 0.60-0.89 were determined in apple genotypes. As a result of the relationship mapping with SSR, ISSR, SRAP and RAPD markers, the GLM (Q) model, which gave the best results in 5 parameters, and the MLM (K) and MLM (K+Q) models, which gave the best results in the others, were applied. The obtained results will make very important contributions to apple breeding programs.

Keywords: Apple, morphological features, characterisation, association mapping

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[OP-35]

Determinate Tomato Breeding Using Speed Breeding, Embryo Rescue and Marker Assisted Selection

Merve Yiğit[1], Emre Şeker[1], Ayşe Şeker[1], Nedim Mutlu[2], Ergün Doğangüzel[1], Fatma Nur Altındağ[1]

[1]United genetics turkey seed company
[2]University of Akdeniz

Conventional breeding techniques take a long time to develop parental lines and new varieties. To expedite plant breeding, speed breeding has been proposed and shown to be effective for some plant species. The molecular markers linked to genes for disease resistance and major agronomic traits have been used for the selection within segregating populations. The objective of the study was to test if determinate tomato is amenable to speed breeding coupled with marker assisted backcross and embryo rescue. The photoperiod was extended to 22 h light and 2 h dark with 8 C cooler atmosphere on average. Disease resistant donor parents were crossed with susceptible recurrent parents (RP) to generate F1s that was backcrossed to the RPs. The 30-day-old fruits were harvested and embryos rescued in tissue culture lab. The seedlings derived from the embryos were tested with molecular markers for the trait of interests. And the resistant ones were taken back to the speed breeding greenhouse where they were grown, backcrossed or selfed and immature fruits harvested for embryo rescue. With this combined system, 80 to 90 d was sufficient to reach from seed to seed for determinate tomato. The results showed that using the speed breeding technique coupled with marker assisted backcross selection and embryo rescue, four generations of tomato can be advanced in one year.

Keywords: Speed breeding, marker-assisted backcrossing, pyramiding, embryo rescue

[OP-36]

Comprehensive Genotyping and Diversity Analysis of Maize Inbred Lines Representing Multiple Eras of Germplasm From Southeast Europe

Vlatko Galic[1], Antun Jambrovic[2], Zvonimir Zdunic[2], Tatjana Ledencan[1], Andrija Brkic[1], Violeta Andjelkovic[3], Alain Charcosset[4], Zlatko Satovic[5], Domagoj Simic[2]

[1]Agricultural Institute Osijek, Osijek, Croatia
[2]Agricultural Institute Osijek, Osijek, Croatia; Centre of Excellence for Biodiversity and Molecular Plant Breeding, Zagreb, Croatia
[3]Maize Research Institute "Zemun Polje", Belgrade, Serbia
[4]Génétique Quantitative et Évolution - Le Moulon, Université Paris-Saclay - INRAE - CNRS – AgroParisTech, Gif-sur-Yvette, France
[5]Faculty of Agriculture, University of Zagreb, Zagreb, Croatia; Centre of Excellence for Biodiversity and Molecular Plant Breeding, Zagreb, Croatia

Available data about molecular diversity of maize genetic material in Southeast Europe (SEE) is limited. Nonetheless, utilization of the SEE maize for its favorable alleles and diversity has been long speculated, with most of the materials still deposited in gene banks. Further, no comprehensive molecular data is available on elite genetic material currently used in SEE. The objective of this study is to present and discuss data on genotyping and diversity analysis of more than 1800 maize inbred lines from two panels representing multiple eras of germplasm from SEE. The first genotyping panel included 572 accessions of the historical inbreds from Maize Research Institute Zemun Polje genotyped using the Axiom 600k maize genotyping array. The second panel comprised 1300 inbred lines traced back from other two breeding eras (until 2011/after 2011) which were genotyped by Illumina MaizeSNP50 technology with 56000 polymorphic SNP markers. In the first panel, genetic structure and diversity were analyzed using neighbor-joining cladogram, PcoA, Admixture, Structure and sNMF. The best number of ancestral populations was K=7, whereby one of them is a subpopulation containing inbreds belong exclusively to the SEE panel. The prevalence of inbreds linked to historical US inbred lines Wf9, Oh43, Pa91 and A374 was detected. In the second panel, admixture analysis was performed using Admixture 1.3.0 software. Number of ancestral populations (K) was set from 1 to 15 and quintuple cross validation was performed. Cross validation error was the lowest in K=7. The next steps would be to combine the data of the two panels and to identify genomic regions that have undergone selection (selective sweeps) in response to adaptation to SEE conditions.

Keywords: genetic diversity, genotyping arrays, inbred lines, maize, Southeast Europe

[OP-37]

Breeding in Ashwagandha [Withania somnifera] in Relation to Molecular Aspects

Rajesh Kumar, Somveer Nimbal, Ganesh Kumar Koli

Department of Genetics and Plant Breeding, CCS HAU, Hisar, India

India is home of herbal medicines. Ashwagandha (Withania somnifera (L.) Dunal (2n=48), is one of the most valuable medicinal plant used in the Indian and Unani systems of medicine. It is also known as gooseberry or winter cherry and belongs to the family Solanaceae. The India, North-Western and Central parts in Africa, the Mediterranean region are the native palaces of ashwagandha. The most suitable climatic region for its growth and development is the dry and subtropical type. In India, it is mainly cultivated in the states of Madhya Pradesh, Rajasthan, Gujarat, Maharashtra, Punjab, and Uttar Pradesh. India is also an exporter of ashwagandha roots in the international market. In Ayurvedic era, it was mainly consumed as a health tonic for fitness, longevity and vitality. It is also very important stimulation of the human body immune system cells, phagocytes and lymphocytes, which also assist to manage the effects of stress and encourage wellness. It is also utilized to treat asthma, bronchitis, emaciation, dementia, insomnia, inflammation, neurological disorders, and Parkinson's disease. The main chemical constituents are alkaloids and steroidal lactones. The medicinal properties of the plant are due to the presence of withanolides (withaferin A and withanolide D). As per Indian chemotype, it has 12 types withanolides, five unknown alkaloids, several free amino acids, glycosides, tannins, chlorogenic acid, glucose, and several flavonoids in the leaves. Earlier, the medicinal herbs and shrubs were available effortlessly in the nearby jungles and on mountains. Presently, due to constant utilization of these natural plants with alarming speed reduced their accessibility.

Therefore, it is an insistent need to evolve the high yielding superior cultivars of essential medicinal flora to manufacture the superior quality raw drugs. Moreover, sufficient genetic diversity is available in this crop, and very little work has been done on its genetic improvement in spite of the long history of its domestication. A large portion of it still comprises wild, semi-wild plants or primitive cultivars which have not acquired genes for high productivity under cultivation and have great potential to improve the yield and quality. Medicinal plants are generally cultivated under harsh climatic conditions; therefore, identification of the superior genotypes for high temperature tolerance is essential for effective manipulation through breeding techniques. The male and female parts are present in same flower and pistil is surrounded by anthers and both mature at same time, which fevers self pollination. But, natural crossing is also observed in some conditions. Therefore, any breeding methods may be applied as per suitability and availability of resources. In addition, molecular breeding to enhance the specific bio-molecules through marker assisted technique is an excellent way for its genetic improvement.

Keywords: Withania somnifera, Ashawgandha, breeding aspects, root yield, bio molecules

[OP-38]

Phenotypic Diversity and Linkage Disequilibrium for Vitamin B Complex Concentrations in Bean Grain

Faheem Shehzad Baloch[1], Muhammad Azhar Nadeem[1], Emre Aksoy[2], Tolga Karaköy[1], Sertaç Özer[3]

[1]Faculty of agricultural sciences and Technologies, Sivas University of science and Technology, Sivas, Türkiye
[2]Department of Biological sciences, Middle east Technical University, Ankara, Türkiye
[3]Department of Food science, Faculty of agriculture, university of çukurova, Adana, Türkiye

Vitamin deficiencies are major forms of micronutrient deficiencies, insufficient intake of vitamins threatening billions of people, and causing nutrition-related poor growth and referred as 'hidden hunger'. Biofortification is an important technique aimed to improve the vitamins and nutrient contents in plants. Vitamin B is essential for maintaining normal life activities in humans and animals who have to intake the microelement from the outside. Common bean is a significant source of protein, carbohydrates, vitamins, minerals, and considered as an important plant for biofortification. The present work aimed to investigate the variation in common bean seeds for Vitamin, B1, B2 and B9 contents. 188 common bean landraces, representing various geographical regions of Türkiye were used as plant material and field experiments were conducted under 5 environments at Sivas and Bolu provinces aiming to perform seed vitamin profiling for B1, B2 and B9 contents. Analysis of variance revealed the significant effects of genotypes, and genotype × environment interaction on the studied vitamin contents in common bean seeds. A plentiful variation was observed for studied vitamins in Turkish bean germplasm showing its potential for Biofortifying the bean grain with enriched vitamin B complex contents. Genotyping by sequencing was performed and a total of 7900 high quality DArTseq markers were used for marker-trait association using MLM (Q-metrics + Kinship) approach in TASSEL software. Genome wide association studies revealed 2 SNPs for each vitamin B1 and vitamin B2 and 3 SNPs for vitamin B9. Linear regression analysis showed a significantly positive correlation of the number of favorable alleles with vitamin B1 and B2 contents. Common bean genotypes with higher vitamin B contents under different environments were also identified. This is the first report claiming the markers associated with vitamin B1 and B2. The loci identified in this work and associated SNPs with vitamin B1, B2, B9 and genotypes with superior vitamin B contents in seeds will serve as genetic and genomic resources for the marker-assisted breeding of common bean.
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Keywords: GWAS, vitamin B complex, selection, DArTseq, SNP, diversity, genomics

[OP-39]

Comperison of Index Method and META Analysis for Selection of Winter Feed Barley Genotypes

Sinan Aydoğan, Namuk Ergün, Ismail Sayim, Melih Bilir

Central Research Institute for Field Crops, Ankara, TURKIYE

This research aims to determine Linear Phenotypic Selection Index (LPSI) method and Multi-Environment Trials Analysis (META) for the selection of advanced feed barley lines. Multi-environment trials were conducted in five locations (İkizce- Ankara, Altınova-Konya, Gözlü- Konya, Malya- Kırşehir and Ulaş-Sivas) during the 2020-2021 growing season. Five trials were conducted including four controls (Burakbey, and Tosunpasa, Tarm 92 and Larende) and twenty advanced feed barley lines under a randomized complete block design with four replications The results showed significant effects of environment (E) and genotypes (G) and G by E interaction on grain yield. For selection, and comparison LPSI and META methods, both methods could not change the rank of some genotypes while some genotypes were significantly affected by using a different method.

Keywords: Barley, Index Selection, Grain yield, META Analysis

[OP-40]

Agricultural and Forestry Research and Development Structures and Systems: A new Approach

Mesut Keser[1], Suleyman Karahan[2], Lutfi Tahtacioglu[3], Sahin Anil[4], Mete Aydemir[5], Ibrahim Gucdemir[6], Yavuz Er[7]

[1]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Research, Eskişehir, Türkiye
[2]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Research, Ankara, Türkiye
[3]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Research, Erzurum, Türkiye
[4]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Research, Osmaniye, Türkiye
[5]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Research, YENİMAHALLE-Ankara, Türkiye
[6]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Reform,Gaziantep, Türkiye
[7]Retired From The Ministry Of Agriculture And Forestry, The General Directorate of Agricultural Reform,Ankara, Türkiye

As a consequences of the rapidly developing technologies, in the era of climate change and environmental awarenes and sensitivity of the public, significant changes have been observed in today’s understanding of agriculture, and concepts such as “science-based agriculture”, “conservative agriculture”, “digital-smart agriculture” and “green agriculture” have emerged that define these changes and transformations. In other words, agriculture is in a steady progress and transformation, and it is expected that transformation and progress in the agriculture would be guided through the outputs of agricultural R&D systems. Almost all developed countries have restructured their R&D systems and created an efficient and competitive visionary structure that can produce quick solutions to current and expected future problems. Although there is a very good scientific agricultural research background and technical equipment and infrastructure have been established in Turkey compared to other sectors, it is thought that both organizational restructuring and human resource development are needed for the progress and establishment of “R&D Culture”. In Turkey, there has not been a significant change in the agricultural R&D system, which has maintained its traditional structure in the public sector since its establishment. Quantitative R&D outputs put forward within the current system can be misleading. When the outputs and current problems are evaluated together, the need for restructuring in agricultural R&D can be seen. In the light of these evaluations and in the era of new world, a new structure is needed for Agricultural R&D system in order to coordinate and establish the cooperation among public R&D, universities, NGOs, private organizations, and the most importantly for human resource capacity development and coordination of them among the sector. An initiative group has been established to develop and raise awareness for the proposed new agricultural R&D system and to provide the organizational structure of the system to the related units. In this context, a survey form was developed by examining the R&D systems of

nearly 60 countries with agricultural production capacity on the scale of Turkey. While developing system and model suggestions; establishing an R&D structure, innovative, competitive, egalitarian, participatory, multi-disciplinary, output-oriented, committed to vision-mission-goals and targets, accountable, based on decentralization, aiming at preventing repetitions,an environmentally friendly structure are envisaged. As a start, this survey form was sent to more than 100 researchers and managers experienced in this field and the responses started to come. In the following stages, the R&D structure will be finalized in view of forward looking vision by discussing the issue thoroughly with stakeholders through workshops or conferences.

Keywords: Agriculture, Forestry, Research, Structures and Systems

[OP-41]

Development of Seed Sector and Contributtion of the use of Certified Seeds of New Plant Varieties to the Agricultural Production in Türkiye

Kenan Yalvaç

Turkish Seed Industry Association Türkted

Agricultural Research and Development activities have been carried out since 1880's in Türkiye. New Agricultural Research Institutions have been established right after the foundation of the Turkish Republic in 1923. Establishment of GD of State Farms have increased the procuction and the use of certified seeds in Türkiye. The seed supply system used to be a formal system where public sector dominated the seed system. However, in 1984, the government has issued legislations to allow the private sector to take part in the seed sector. Since then the seed sector has been progressing significantly. The amount of seeds produced, the number of private seed companies and the use of certified seeds by the farmers have been increasing regularly. Turkey has been harmonised with UPOV 1991 act. There are two main legislation applied in Turkey. These are namely Seed Law Numbered 5553 and Plant Breeders Rights Law numbered 5042. Registration of new plant varieties and certification of the seeds are performed in accordance with the legislation mentioned above and their secondary implementing legislations. Turkey is eligible to issue OECD and ISTA certificates as well as national seed certificates. Total certified seed production has been over 1,300,000 tonnes in 2021. Farmers use of certified seeds of certain species have been supported by the Ministry since 2005. Production of certified seeds by the seed companies of certain species has been supported by the Ministry since 2008. These efforts in turn, has increased total certified seed production in Turkey and the share of the certified seeds produced by the private sector has increased considerably. The contribution of certified seeds in agricultural production is enormous.

Keywords: Agricultural Research and Development, Seed Sector Development, Production and Use of Certified Seeds

[OP-42]

Variation of Registered Pepper Varieties on DUS Test

Güleda Öktem[1], Sıtkı Ermis[2], Şakır Berktaş[1]

[1]Variety Registration and Seed Certification Centre, Ankara
[2]Eskisehir Osmangazi University, Faculty of Agriculture, Department of Horticulture, Eskisehir

One of the most significant vegetables grown in Turkey and around the world is pepper. Pepper, which belongs to Capsicum genus of Solanaceae family, is one of the most freshly consumed vegetables in our country, and it is also one of the most diverse vegetable species due to the variation in other eating habits. The suitable climatic conditions in our country also allow pepper cultivation throughout the year, and pepper cultivation can be done all year long in different regions both in the open field and greenhouses.

Variety Registration And Seed Certification Center directorate became a member of UPOV (The International Union for the Protection of New Varieties of Plants) on November 18, 2007. Beginning in 2008, DUS tests were conducted in accordance with UPOV criteria as part of variety registration procedures. In this study, morphological observations of the pepper species registered by performing DUS tests from 2008 to the present are discussed. The pepper species was investigated and a proportional evaluation of the situation in the registrated types was made based on these observations, which were especially qualitative and pseudo-qualitative in nature.

Keywords: DUS Test, Morphological Characterization, Pepper, Registration, UPOV

[OP-43]

The new Cereal; Tritipyrum; Three Decades of Breeding Challenges for Eating and Feeding in Saline and Brackish Water by Phenotyping, Molecular Markers, Cytogenetics Molecular Markers and Speed Breeding Techniques with the Last Case Study in Turkey

Hossein Shahsavand Hassani[1], Ayten Saluntur[1], Cuma Karoglu[1], Khalid Mahmood Khawar[2], Hossein Shahsavand Hassani[3], Solmaz Nacafi[4]

[1]Field Crops Central Research Institute, Department of Biotechnology, Ankara, Türkiye
[2]Department of the Field Crops The Faculty of Agriculture Ankara University, Ankara, Türkiye
[3]Department of Crop production and Genetics, School of Agriculture Shiraz University, İran
[4]Department of the Field Crops The Faculty of Agriculture Yüzüncü Yıl University, Van, Türkiye

Bread wheat (2n=6x=42, AABBDD, Triticum aestivum) is an 6x species that originated 10,000 years ago from polyploidization events involving three species. During domestication, both revolutionary and evolutionary changes led to allopolyploid formation, species diversification, chromosomal re-patterning, introgression of alien chromosome segments and formation of recombinant genomes. The strong human selection for yield and adaptation to different environments and agricultural practices indicate strong structural rearrangements of chromosomes to shape different cultivars. Soil salinization is a serious problem world over and in Turkey could result in a loss of arable land as much as 50% by the middle of the 21st century which will damage the yields, growth and development of many crops. The EC of saline soils in the book “Turkey’s Barren Breeding Guide” varies from 5.55 ds/m2 in Konya–Ereğli to 17.62 ds/m2 in Samsun-Bafra. A comprehensive survey of salt tolerance of crops and pasture species published by the US Salinity Laboratory (USDA-ARS, 200510) mentions that the yield of wheat declines at 6–8 ds/m2. Furthermore, there is an urgent need to take measures and protect the yield of crops against loss due to global warming. These measures can include breeding and the introduction of new crop cultivars with enhanced tolerance to salt. Wild relatives of wheat offer a wide range of useful traits such as resistance abiotic stresses and continue to offer new genes for introducing desirable agronomic traits into bread wheat. The first new primary Tritipyrums (2n=6x=42, AABBEbEb) was produced from a cross between Triticum durum (4x=28, AABB) cultivars and Thinopyrum bessarabicum (2x=14, EbEb) species in UK. These are being evaluated for their field adaptation traits in UK (1997) and Iran (1999-2022). In order to remove a few undesirable traits of Primary Tritipyrum lines such brittle rachis and late maturity, the secondary Tritipyrum (AABBEb(1-7)”D(1-7)”) lines were produced by crossing with Iranian bread wheat cultivars at Shiraz Universities (2012-2022) to replace the Eb genome chromosomes with the D genome chromosomes of hexaploid wheat. The Eb genome is known for its high tolerance to 350 mM NaCl. The Iranian primary and secondary Tritipyrum lines were evaluated under 150 to 250 mM NaCl; respectively, which suggests these lines have potential to become a new cereal for feed/food industry under saline soils and brackish waters. Their field adaptation trials in Iran have shown the comparable agronomical behavior of them with Iranian bread wheat cultivars. From last year the production of Turkish/Iranian primary and secondary lines in collaboration with the Central Field Crops Research Institute and Ankara University Turkey under the TÜBİTAK 2020 horizon 121CO36 project sponsored by Mary Curie fellowship program (2021-2023) has been started. In this studies vernalization, chromosome rearrangements, adaptation and genome sequences of the selected lines under salinity conditions will be studied for the first time. This is also the first report of 3 decade of breeding challenges for production Tritipyrum, as a new salt tolerant cereal in the world and its first year adaptation potentials as a new crop for the first year in Hayman field station, Turkey.

Keywords: Primary Tritipyrum, speed breeding, Haymana, Secondary Tritipyrum, FISH, bread wheat

[OP-44]

Improving Nutrient use Efficiency in Wheat Using Various Breeding Strategies

Akshay Kumar Vats, Rishi Kumar Behl

Department of Agriculture, Maharishi Markandeshwar (deemed to be university) Mullana, Ambala, Haryana, INDIA, 133207

Production of wheat is recorded 765.77 million tonnes in the world and 103.60 million tonnes in India in the year 2019. Production in wheat is determined by a genotype and environment input. Not all the genotypes have the same NUE despite the common environment due to genetic and physiological mechanism. When crop is supplied with lesser nutrients, nutrient use efficiency of the crop rises at its maximum. Nutrient use efficiency in case of wheat remains less than 50 percent and approximately 33 percent at global scale and P use efficiency on global scale was recorded upto 16 percent in cereals, which indicates scope of more research in this area. Although, genes related to nutrient use efficiency are being very well studied, yet studies in mechanism of direct influence are still lacking. More attention is focused on engineering transcription factors and identification of miRNA influencing expression of nutrient use efficiency related traits. Gene pyramiding is effective to enhance NUE in wheat. Gene transporters of NUE related traits includes two affinity systems HATS (high affinity transporter systems) and LATS (low affinity transporter systems). The transporter genes like NTR (NRT 1, NRT 2, CLC and SLAC 1/ SLAH 1) and AMT gene TaAMT1;1 have been reported to be functional in NUE. Genetic potential of only higher root biomass or root surface can't contribute to increasing NUE. However, the genetic potential of quicker and earlier uptake is essential to achieve higher NUE, which could be attributed to faster root growth at the early vegetative stage to capture the nitrate before it moves away from rooting profile. Our investigation refers to screen germplasm of four groups i.e. T.aestivum, T.durum, synthetic wheat and triticale comparing A, B, D and R genome for NUE related traits. Observations were recorded for grain yield and its attributes. Promising genotypes to be utilized under MAGIC population were screened for various NUE related traits. Genotype X Fertilizer interaction was found significant for majority of characters except plant height, chlorophyll content and number of tillers per plant. Experimental findings showed considerable variability among genotypes for NUE related traits, which indicate scope of developing MAGIC population for further breeding programme. Most of the emphasis was given to genotypes performing best in low input conditions. These genotypes were WH 1105, HD 2967, DBW 17, WH 147, PBW 373, PBW 644, LOK 54, WH 1127, TL 2963 and DPW-621-50 for grain yield and its attributes. Intercrossing these genotypes would lead to accumulation of genes influencing NUE in one way or the other in a common background, which could be in agronomically superior variety for raising the ceilings upwards for sustainable wheat production.

Keywords: Nutrient Use Efficiency, NUE Wheat, NUE related traits, MAGIC population, Triticale NUE, low input conditions

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[OP-45]

Determination of the Reactions of Some Advanced Yield Trials-Bread Wheat Genotypes to Rust and Bunt

Nilüfer Akci[1], Kadir Akan[2], Bayram Özdemir[3], Selami Yazar[3], Ayten Salantur[3], Gökhan Kılıç[3], Mehmet Emin Alyamaç[3], Emin Dönmez[4], İrfan Öztürk[5]

[1]Plant Protection Central Research Institute,Yenimahalle, Ankara
[2]Kırşehir Ahi Evran University, Agricultural Faculty, Plant Protection Department, Kırşehir
[3]The Central Research Institute for Field Crops, Sehit Cem Ersever Cd. No. 9-11, Yenimahalle, Ankara
[4]Hektaş Ticaret T.Ş Gebze, Kocaeli
[5]Thrace Agricultural Research Institute, Kocasinan Mahallesi, Atatürk Bulvarı 167/A Edirne

Rusts *(caused Puccinia spp.)* and bunt *(caused Tilletia spp.)* can reason different level economical loss on bread wheat. This loss increases especially in susceptible genotypes of environmental conditions suitable for disease development. The goal of this research 24 bread wheat genotypes (19 Lines (Advance Yield stage) and 5 standard cultivars (Rudo, Eser, Carisma, Alpu 2001, Jaguar) in advance yield trials improvement by Central Research Institute for Field Crops (CRIFC) the Wheat Breeding Part. Seedling stage tests were evaluated for all materials YR, LR and SR (Ankara/ Yenimahalle locations) in February-April. Adult plant stage reactions, Ankara (İkizce location- Yellow Rust (YR/Pst) and Bunt (BT/Bt;)), Edirne (Merkez location- Leaf Rust LR/Pt)), Kastamonu (Seydiler location- Stem Rust (SR/Pgt)) in October. For all seedling test genotypes were sown in plastic pots with 3 replication and for all adult plant test materials were sown 1 meter and 3 replications. The Pst (avirulent on; Yr5, 8, 10, 15, 24, 26 and 27 resistance genes) and Bt (virulent on Bt0, 2, 3, 4, 6 and 7 resistance genes) adult plant reactions of the research were carried out under artificial epidemic condition. The Pt (avirulent on; Lr9, 11, 19, 20, 24 and 28 resistance genes) and Pgt (avirulent on; Sr24 and 31 resistance genes) adult plant reactions of the research were carried out natural epidemic condition. For seedling test, infections were be fruitful and disease severity was observed as 3-4 in susceptible check genotypes. For adult plant test, infections were be fruitful and disease severity was observed as 80-100S in susceptible check genotypes in June-August. Genotypes with a coefficient of infections of 20 and below were considered to be resistant. For Bunt, the infection was considered successful since

the number of diseased ears in susceptible control genotypes was 80-100% in the evaluations made in August. Less 25% were well-considered to be resistant. When both seedling and adult plant tests are together (not include 5 standard cultivars) 3 (16%) line for YR, 3 (16%) line for LR, 4 (21%) line for SR, 15 (79%) line for BT were included in the resistant group. As a result of this study, lines determined to be resistant are registered as disease resistant cultivars or may be resistant parents as a source of resistance.

Keywords: Bread wheat, rusts *(Puccinia spp.)*, bunt *(Tilletia spp.)*, reaction test, seedling stage reaction, adult plant reaction

[OP-46]

Breeding for Climate Resilience in Agricultural Crops

Ajaz Ahmad Lone[1], Zahoor A Dar[1], Shabir H Wani[1], Faik Kantar[2], Audil Gul[1], Munazah Rashid[1], Asmat Ara[1], Ozer Callis[2]

[1]Dryland Agriculture Research Station, Sher-e-Kashmir University of Agriculture Sciences & Technology of Kashmir INDIA
[2]Akdeniz University-Antalya Turkey

Climate change impacts agriculture in numerous ways including rising average temperatures, rainfall, changes in pests and diseases, rise in atmospheric carbon dioxide, ozone concentrations at ground level and changes in the nutritional quality of certain foods. Therefore, achieving global food security for rising global population under limited arable land is a major challenge in the twenty-first century. Farmers are advised to use climate-resilient crops and crop types as a means of coping with or adapting to climate change. As the primary source of protein and minerals for vegetarians, pulses are typically grown on marginal land with minimal inputs in a number of resource-poor nations around the world. They are subjected to a variety of abiotic and biotic challenges as a result of their growing in resource-limited circumstances, which results in severe production losses. Additionally, the effects of climate change brought on by global warming have made them more susceptible to fresh biotic and abiotic pressures that could get considerably worse in the years to come. Climate-resilient smart pulse and cereal crop breeding and development have become more difficult as a result of the changing climate situation. Although pulses are climate smart, adapting to the consequences of climate change while also reducing them, their limited genetic variety has always been a key barrier to their ability to become more adaptable. For the development of cultivars that are climate-resilient, however, the genetic variety that currently exists still offers chances to take advantage of unique traits. Additionally, maize, a C4 plant, has a high yield potential as evidenced by the highest compound annual growth rate. However, due to the full exploitation of hybrid and manufacturing technology, maize production has plateaued in many nations. Therefore, it is necessary to generate maize ideotypes with favourable trait architecture for greater stress resistance and higher yield under changing climatic conditions. Abiotic stress in maize, such as drought, causes a delay in silking, which increases the anthesis-silking gap and is a key contributor to yield losses. Every crop improvement programme must inevitably put a strong emphasis on making significant use of wild germplasm and unlocking the genetic diversity store. However, current developments in genomics, high-throughput phenomics, sequencing, and breeding methods, as well as state-of-the-art genome-editing tools coupled with artificial intelligence, open up new directions for the enhancement of climate-resilient crops. Adaptive characteristics that confer tolerance or resistance to climate-smart pulses and maize can be mined and exploited more quickly by applying cutting-edge biotechnological techniques including transgenics, genome editing, and epigenetics. In order to combat climate change and create new crop types that are better suited to the changing climate, holistic smart breeding approaches may be a feasible solution.

Keywords: Climate Resilient crops, Biotic stress, Abiotic stress

[OP-47]

Determination of Heat and Drought Tolerant Lines in Segregating Populations Produced by Interspecific Crosses in Eggplant

Esra Cebeci[1], Hatice Filiz Boyacı[2], Yıldız Doğan[1], Laura Toppino[3], Giuseppe Leonardo Rottino[3]

[1]Bati Akdeniz Agricultural Research Institute, (BATEM), Vegetable Breeding and Ornamentals, Antalya, Türkiye
[2]Food Control Laboratory Directorate, Antalya, Türkiye
[3]Council for Agricultural Research and Agricultural Economy Analysis, Montanaso, Lombardo, Italy

Nowadays abiotic stresses originated by climate change is one of the main factors which reducing the agricultural production. Heat and drought are the most prominent abiotic stress factors that threat to eggplant production worldwide and food security.. Although eggplant is known as tolerant compared to the other vegetables, its quality and yield suffers from severe stress conditions. In this research, 256 F2 plants developed by interspecific crosses between the wild relative of Solanum insanum L. and the pure line (BATEM-TDC47) from BATEM eggplant genepool were used as plant materials. Seedlings with 3-4 true leaves were subjected to drought stress test. For this, deficit irrigation at 75% was applied to the plants in three-liter pots filled with a 1:1 mixture of peat and perlite. Control plants were watered by required irrigation at 100% ETp of full as appropriate management strategy. The stress symptoms of plants were determined by morphological and chemical characteristics. Plant heights were measured on the 25th day of the experiment and visual evaluation stress symptoms was observed according to the 0-5 scale. Morphological observations, MDA (malondialdehyde) and proline analysis of selected 50 plants were performed to confirm their heat and drought tolerance levels. Following the drought test, the plants were transferred to the greenhouse for the determination of heat tolerant individuals.

Keywords: abiotic stress, drought, eggplant, heat, MDA, proline, tolerance

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[OP-48]

Evaluation of Wheat (T. aestivum L.) Germplasm Under Temperate Conditions and Identification of Sources of Yellow Rust Resistance Genes (yr) using Molecular Markers

Basharat Ul Islam[1], Shabir Hussain Wani[2], Gazala H Khan[2], Saba Mir[2], Mohammad Saleem Dar[2], Najeeb Ul Rehman Sofi[2], Asif B Shikari[1], Fayaz Mohiddin[2], Ajaz A Lone[1], Mumin Ibrahim Tek[3], Ozer Calis[3], Gyanendra P Singh[4]

[1]Mountain Research Centre for Field Crops, Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology, Srinagar, Jammu and Kashmir,India
[2]Division of GPB, Faculty of Agriculture, Wadura, Sopore, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu and Kashmir, India
[3]ICAR-Indian Institute of Wheat and Barley Research, Karnal India
[4]Department of Molecular Plant Pathology, Faculty of Agriculture, Akdeniz University, 07070 Campus-Antalya/Turkey.

The present study was conducted with an objective to identify potential resistant genotypes that could be used in yellow rust resistance breeding programs as an effective gene deployment strategy. 192 elite wheat genotypes, including 6 checks were evaluated in an augmented block design for resistance against yellow rust disease at Mountain Research Center for Field Crops (MRCFC) Khudwani, SKUAST Kashmir. Among 192 genotypes of wheat evaluated against yellow rust disease under field conditions, 53 genotypes, including those cultivars whose resistance reaction towards the pathogen was already established, showed resistance reaction. Similarly, 40 wheat genotypes were moderately resistant. Further, a subset of 115 wheat genotypes were tested against the six most virulent races viz., 7S0, 238S119, 110S119,110S84, 47S119 (T), 46S119, of yellow rust pathogen under controlled conditions. Among the subset, only 12 wheat genotypes were showing resistance against all these six races. Another subset of ninety-seven wheat genotypes were substantiated at the molecular level for the presence of four effective yellow rust resistance genes viz., Yr5, Yr10, Yr15, and Yr17 by using their respective linked gene-based markers namely STS7/8, XPSP3000, Xbarc-8 and VENTRIUP / LN2 respectively. Molecular validation revealed that Yr5 gene was present in 16 genotypes, out of which 7 genotypes were heterozygous

for Yr5 gene as well. Yr10 gene was found in 29 entries of which 9 entries were heterozygous for the gene. Yr15 was found in 16 entries of which 6 were found to be heterozygous for the Yr15 gene. Similarly, Yr17 was found in 37 genotypes of wheat and the in rest of the remaining 60 genotypes, the yellow rust resistance gene was absent. The yellow rust resistance (Yr) genes studied in the current research program are effective in conferring resistance against the yellow rust disease. The genotypes identified as resistant both under field and controlled conditions and possessing Yr genes shall be used as genetic stocks in yellow rust resistance breeding programs for effective gene deployment.

Keywords: Molecular markers, Puccinia striformis, Stripe rust, Wheat, Yr genes

[OP-49]

Screening of Some Durum Wheat Genotypes to *Warrior* Race of Yellow Rust

Merve Nur Ertaş Öz, Emine Burcu Turgay, Sibel Bülbül, Öztekin Urla, Selami Yazar, Bayram Özdemir, Ayten Salantur, Mehmet Emin Alyamaç, Gökhan Kılıç, Muhsin Ibrahim Avcı, Fatma Betül Sade

Field Crops Central Research Instititute

Wheat, having large cultivation areas both in Türkiye and in the world, is a significant crop for human nutrition. Yet, biotic and abiotic factors limit the quality and production of wheat. Of these factors, yellow rust (*Puccinia striiformis* fsp. *tritici*) leads to economic losses, in particularly moisture and humid regions. Fungicide use is one of the efficient way to combat with the disease. However, due to detrimental effects of fungicides to human and environment health, causing resistance of pathogen populations and overcost of fungicide application, developing disease-tolerant varieties has been popular, recently. Here, 606 durum wheat genotypes (Preliminary Trials-1 and 2), developed by Wheat Breeding Unit of Field Crops Central Research Institute, were tested for all-stage-resistance (seedling stage resistance) and adult plant resistance (APR) using *Warrior* race (PstS7; *1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,Amb* effective on these resistance genes) during 2020-2021 season. All-stage-resistance reactions of the genotypes were assessed using 0-9 McNeal Scalea and 86% of those reacted as resistant, scored between 0-6 while 4% was assessed as susceptible. APR were evaluated through Modified Cobb-Scale and nearly 18%, 57%, 3% found resistant, moderately resistant and susceptible, respectively. Resultingly, genotypes identified as resistant in all-stage-resistance and in APR has been suggested using as tolerant source material and/or developing new varieties.

Keywords: yellow rust, *Puccinia striiformis* fsp. *tritici*, durum genotypes, APR, all-stage-resistance

[OP-50]

Comparison of Yield Potentials of Some Triticale Lines and Cultivars Under Different Climatic Conditions

Emel Özer[1], Ramazan Keleş[1], Sait Çeri[1], Musa Türköz[1], Şah Ismail Cerit[1], Meltem Yaşar[1], Murat Nadi Taş[1], Ibrahim Kara[1], Cevat Eser[1], Aysun Akcaçık[1], Yılmaz Yıldırım[2], Lütfü Demir[3]

[1]Bahri dagdas ınternational agricultural research instute-Konya/Türkiye
[2]Tansitional zone agricultural research institute-Konya/Yürkiye
[3]Maize research institute-sakarya/Türkiye

Rising agricultural supply and increasing demand for arable land heighten the occurrence of abiotic stresses. Drought is one of the most important factors limiting crop production all over the world compared to other abiotic stresses. Drought as an abiotic stress reduces food production in the world and in our country as well. Drought stress occurring in any period of grow has negative effects on morphological, physiological and biochemical activities and ultimately leads to low yields. Triticale is a strong plant with efficient growth and adaptability to various environmental conditions. Triticale production in our country is increasing every year. It is used in animal feed such as poultry feed, silage, as well as in human nutrition, in making blended flour and in biscuit flour mixtures. Triticale varieties, which are known for their compatibility with marginal conditions, need to receive the necessary precipitation in order to obtain optimum yield, which corresponds to an average seasonal precipitation of 230-250 mm. Even though triticale is below this precipitation average, sufficient grain yield cannot be reached as a cereal type. In recent years, where the impact of climate change has increased, it is one of the main subjects of Research Institutes to develop varieties that are compatible with climate change

and have high tolerance to abiotic-biotic stresses. This study was carried out in 20 lines and 4 varieties (TATLICAK-97, ALPERBEY, ÖZER & MİKHAM-2002) in a randomized block trial design with 4 replications in 6 different locations in 2020-2021, in Konya and its Konuklar district, Kayseri, Eskişehir & Sakarya provinces. The precipitation of each planted location during the season was determined as Konya: 214.7 mm, Konuklar: 200 mm, Eskişehir: 347,0 mm; Sakarya: 826.4 mm. (MGM-2021). Plant growth is not achieved due to poor soil conditions as well as insufficient rainfall in Karapınar location has been cancelled. The average grain yield of the trial was determined as 3.494 t/ha. As a result of the variation analysis, the variance between locations and lines was found to be statistically significant. ($p<0.01$). Among the locations, Sakarya location gave the highest grain yield (6.214 t/ha), while Konya location gave the lowest grain yield (1.446 t/ha). Among the lines, line 16 gave the highest grain yield. According to the quality analyzes made on the samples taken from Konya, Kayseri and Konuk locations, the thousand grain average of the trial was 34.35 g; Hectoliter: 71.81 kg; Protein content: 13.36%; SDS; 20.37 mm & Cellulose: 2.97%. When all results are analyzed together, according to yield and quality; despite different climatic data, lines 1, 7,8,11,12,21 & 24 have been determined to give high quality values as well as high yield, and it is recommended to work on these lines for Central Anatolia and Transition Regions in cultivar breeding studies.

Keywords: Triticale, breeding, quality, climate change

[OP-51]

Determination of the Reactions of Some Advanced Yield Trials-Durum Wheat Genotypes to Rust

Nilüfer Akci[1], Kadir Akan[2], Bayram Özdemir[3], Selami Yazar[3], Ayten Salantur[3], Gökhan Kılıç[3], Mehmet Emin Alyamaç[3], Emin Dönmez[4]

[1]Plant Protection Central Research Institute, Yenimahalle, Ankara, Turkey
[2]Kırşehir Ahi Evran University, Agricultural Faculty, Plant Protection Department, Kırşehir- Turkey
[3]The Central Research Institute for Field Crops, Yenimahalle, Ankara, Turkey
[4]Hektaş Ticaret T.Ş Gebze, Kocaeli, Turkey

Durum wheat is among the most grown field crops in Turkey. Rusts (caused *Puccinia spp.*) is the important fungal diseases limits grain different level quality and yield and in Turkey. The goal of this study 24 durum wheat genotypes (19 Lines (Advance Yield stage) and 5 standard cultivars (Kızıltan 91, Eminbey, Çeş it 1252, Ankara 98, Mirzabey 2000) in advance yield trials improvement by Central Research Institute for Field Crops (CRIFC) the Wheat Breeding Part. Seedling stage tests were evaluated for all materials YR and SR (Ankara/Yenimahalle locations) in February-April. Adult plant stage reactions, Ankara (İkizce location-Yellow Rust (YR/Pst), Kastamonu (Seydiler location-Stem Rust (SR/Pgt)) in October.

For all seedling test genotypes were sown in plastic pots with 3 replication and for all adult plant test materials were sown 1 meter and 3 replications. The Pst (avirulent on; Yr5, 8, 10, 15, 24, 26 and 27 resistance genes) adult plant reactions of the research were carried out under artificial epidemic condition. The Pgt (avirulent on; Sr24 and 31 resistance genes) adult plant reactions of the research were carried out natural epidemic condition. For seedling test, infections were be fruitful and disease severity was observed as 3-4 in susceptible check genotypes. For adult plant test, infections were be fruitful and disease severity was observed as 80-100S in susceptible check genotypes in June-July. Genotypes with a coefficient of infections of 20 and below were considered to be resistant. When both seedling and adult plant tests are evaluated together; 15 (79%) and 3 (16%) genotypes were resistant to Pst and Pgt respectively. The resistant lines will be beneficial to achieve resistant cultivars.

Keywords: Durum wheat, rusts (*Puccinia spp.*), reaction test, seedling reaction, adult plant reaction

[OP-52]

Identification of SNP Markers for Grain Quality Traits in a Barley Collection (*Hordeum vulgare* L.) Harvested in Kazakhstan

Yuliya Genievskaya, Shyryn Almerekova, Yerlan Turuspekov

Laboratory of Molecular Genetics, Institute of Plant Biology and Biotechnology, Almaty 050040, Kazakhstan

Barley (*Hordeum vulgare* L.) is a cereal crop grown all over the world and used for animal feed, malting, brewing, and food production. In Kazakhstan, barley is the second most cultivated cereal grain, after wheat. Barley grain quality traits are highly variable and the requirements for their level depend on the breeding directions. For example, the raw protein content in malting barley grain should be less than 11.5 %, while in the grain for animal feed this component should exceed 13.0 %. In order to assess grain quality and identify genetic markers associated with them, a collection of barley consisiting of 658 barley accessions from the USA and Kazakhstan was analyzed using key quality traits: raw protein content (GPC) and raw starch content (GSC) in the grain, total extractivity (EX), and grain test weight per liter (TWL). These complex traits are quantitative and controlled by many genetic factors, as well as by environmental conditions. In this study, we applied a genome-wide association study (GWAS) that was used for the identification of quantitative trait loci (QTLs) associated with GPC, GSC, EX, and TWL. This collection was grown at three breeding organizations in Kazakhstan (Karabalyk Agricultural Experimental Station (north), Karaganda Agricultural Experimental Station (center), and Kazakh Research Institute of Rice Growing (south)) in 2010 and 2011 and genotyped using the 9K SNP Illumina chip. As a result, 18 marker-trait associations (MTAs) for GPC, 19 MTAs for GSC, 12 MTAs for EX, and 27 MTAs for TWL were detected, resulting in 30 identified QTLs. The genetic positions of 25 out of these 30 QTLs were close to the QTLs and genes previously reported in the scientific literature, suggesting that the 5 remaining QTLs are novel putative loci for studied grain quality traits. Five of the most significant SNP markers ($P<2.6E-5$) identified in the GWAS were used for the development of informative kompetitive allele-specific PCR (KASP) genotyping assays. The effectiveness of two assays (*ipbb_hv_6* and *ipbb_hv_128*) was confirmed in a separate barley breeding lines collection grown in northern Kazakhstan. The genotype "A:A" of *ipbb_hv_6* provided an average 1.88% increase in GSC ($P<1.2E-05$), a 1.02% increase in EX ($P<2.9E-04$), and a 1.87% decrease in GPC ($P < 3.5E-04$). The genotype "T:T" of *ipbb_hv_128* increased the GSC and decreased the GPC values by 1.26 % ($P<0.05$) and 0.89 % ($P<0.01$), respectively. Thus, MTAs and KASP assays identified in this study can be efficiently used in breeding barley for malting, food production, and animal feed. The study was supported by grants AP08052804 (2020-2022) and AP14871383 (2022-2024) from the Ministry of Education and Science of the Republic of Kazakhstan.

Keywords: GWAS, KASP, grain quality, marker-assissted selection

[OP-53]

Effects on the Wheat (Triticum aestivum L.) Genome from Five Rapid Genomic Selection (GS) Cycles

Maria Nelly Arguello Blanco, Clay H Sneller

The Ohio State University, Department of Horticulture and Crop Science, Wooster, OH, USA

Genomic selection (GS) is a molecular breeding tool that models and predicts the genomic estimated breeding value (GEBV) of a individual. The predicted GEBV is then used to select parents for the subsequent breeding cycle. Wheat breeders can use GS to reduce the duration of the breeding cycle to 1 year, as opposed to 7 years when using the traditional phenotypic selection method. The shortening of the cycle is known as "rapid cycling". The wheat genome changes resulting from rapid cycling have not been characterized. The OSU (Ohio State University) soft red winter wheat breeding program has completed five cycles of GS in five years. The OSU program initiated GS from a training population (TP) of 470 wheat varieties that were phenotyped for grain yield. Our objective was to assess the effect of this molecular breeding selection method on the wheat genome, using marker information in the TP as the initial and reference genome (We define genome as the collection of markers used for selection). We genotyped the TP and individuals from the five cycles with 3927 single nucleotide polymorphism markers to assess the dynamics of allele frequencies, genetic diversity (simple matching coefficient, SMC), population structure (Fst), and linkage disequilibrium (LD). We quantified a reduction in genetic diversity, an increase of the genetic differentiation of cycles from the TP, and changes in the LD patterns. About 27% of the markers had a significant change in allele frequency relative to the TP, with 18% of these attributed to selection: the others could be due to drift or selection as these did not meet the model criteria to be considered for either genetic drift or directional selection. Of all markers, 18.5% were fixed by cycle 5. The SMC increased 0.02 units per cycle, revealing a reduction of genetic diversity. The TP and cycles significantly differentiated from one another at 0.046 Fst units per cycle. The correlation between the LD matrices of each cycle decreased -0.057 units per cycle indicating that the LD pattern in the TP was changing through the cycles. The prediction accuracy of GS depends on similarity of the genome of the TP and the genome of the prediction population. Our findings suggest that rapid cycling causes significant genome changes that could quickly decrease the accuracy of GS in the subsequent cycles. Although the change in the genome is desired for breeding purposes, they can also reduce GS accuracy that could hamper genetic gain and the benefits of GS rapid cycling. Molecular wheat breeders using GS and rapid cycling can combine population genetics analysis such the one presented here, to partially drive the crossing schemes when using GS and to control for the reduction in diversity, changes in LD and population structuring. Maintaining the genome similarity between the TP and GS cycles is crucial for GS accuracy and hence short and long term genetic gain. Our findings should be complemented with estimating the accuracy of GS at predicting field performance of wheat lines derived from the rapid cycles of GS.

Keywords: Wheat breeding, genomic selection, rapid cycling, genome changes

[OP-54]

Colored Wheat: A Source of Nutrition

Om Parkash Bishnoi, Harsh Chaurasia

Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana, India (125004)

In the world of rapid economic growth, food security in terms of nutritional profile began to receive greater interest, especially in underdeveloped or developing countries. As wheat is an important cereal crop and have major contribution in daily dietary requirements, development of biofortified bread wheat emerged with an idea of ensuring nutritional security. The anthocyanin-rich wheat developed through conventional breeding contains anthocyanins which are antioxidants capable of neutralizing the detrimental effects caused by destructive free radicals induced by various physiological processes going on in our body. The anthocyanin present in colored wheat has a broad spectrum of health implications such as protection against various metabolic syndromes like obesity, diabetes, hypertension and dyslipidemia. The idea of developing anthocyanin-biofortified wheat is believed to shape the lifestyle of human beings as it is a staple food crop in many parts of the world. Grain yield of amber wheat has been increased many folds due to the introduction of semi-dwarf wheat varieties which are responsive to inorganic fertilizers but these amber colored wheat varieties are unable to meet the nutritional requirements. So, colored wheat was developed by using Japanese colored wheat parents in crossing programme with amber wheat genotypes by National Agri-Food Biotechnology Institute (NABI), Mohali (Punjab). These colored wheat genotypes (Purple and Black Wheat) were evaluated along with amber wheat genotypes under timely and late sown conditions for yield assessment at CCS Haryana Agricultural University, Hisar (Haryana) during rabi 2019-20 and 2020-21. The data were recorded on days to heading, days to maturity, plant height, tillers number per meter length, lodging %, 1000 grains weight and grain yield. Though, there was yield penalty of 10-15 percent of black wheat as compared to amber wheat under timely sown conditions and under late sown conditions yield reduction was less in colored wheat, but colored wheat have high nutritional quality as compared to amber wheat in relation to anthocyanins content, total dietary fiber, iron and zinc content. This high nutritional quality fetch high market price of colored wheat. If colored wheat is included in the public distribution system, it will overcome the problem of malnutrition.

Keywords: Anthocyanin, Colored Wheat, Grain Yield and Malnutrition

[OP-55]

Two Different Vernalization Methods Applied in Winter/Facultative Wheat and Their Effects on the Speed Breeding Process

Emrah Koç, Fehmi Kozveren, Beyhan Akın

International Maize and Wheat Improvement Center (CIMMYT), Turkey

Speed breeding (SB) is a new method successfully used in the breeding of self-pollinated plants. SB is a method that shortens the generation period of crops grown in a controlled greenhouse (GH) or growth room (GR) by the combination of manipulated environmental conditions and early seed harvesting, to cycle quickly from seed to seed. Day length, temperature, and humidity are the most substantial environmental factors that can be manipulated with the SB method to force plants for earlier flowering and seed forming. SB method has been used for following cereals and up to six successful generation advancements per year have been reported for spring wheat (Triticum aestivum), durum wheat (T. durum), and barley (Hordeum vulgare). In terms of winter/facultative wheat, by controlling these factors, up to three generation advancements per year have been achieved in the GH by International Winter Wheat Improvement Program (IWWIP). The key difference between spring, facultative, and winter wheat is the vernalization requirements of these subtypes. Winter wheat needs exposure to low temperatures to initiate flower development, while spring wheat does not and facultative wheat needs very weak. In this study, two different vernalization methods were examined in order to eliminate the loss of time caused by the vernalization requirements, which is one of the reasons why fewer generation advancements are obtained in winter/facultative wheat compared to spring wheat. The first method is to meet the vernalization requirements of the seeds placed in petri dishes by keeping them in a deep freezer. Once the germination activity was observed on seeds kept at room condition in the petri dishes for one-two days to activate germination, the seeds were kept at 4 °C for 4 weeks in a deep freeze to meet the vernalization needs. At the end of the 4th week, germinated seeds were transplanted into the viols and moved to the GH. These seeds in the viols have been headed in the 5-6th week, completed the grain-filling stage in the 8-9th week, and harvested in the 10-12th week after the vernalization. The second method is to meet the vernalization requirements of seeds sown in viols while continuing their growth in the GR. Seeds sown in the viols have been kept in the GR at 22 °C for one-two days to activate germination. Once the germination activity was observed, the GR temperature was gradually decreased to 8 °C and daily light was set up to 10 h. At the end of the 4th week, it was observed that the seeds planted in the viols were not only vernalized but also reached the form of seedlings with at least 2-3 leaves. These seedlings in the viols moved to the GH have been headed in the 4-5th week, completed the grain-filling stage in the 6-7th week, and harvested in the 8-9th week after the vernalization. As a result, sowing seeds directly into viols and keeping them in the GR for vernalization resulted in a gain of 15-20 days per cycle, which equates to about 60 days per year.

Keywords: Speed breeding, winter/facultative wheat, vernalization methods, manipulation of environmental factors

[OP-56]

Genotyping by Sequencing Based SNP Analysis for Discriminating the Heterotic Patterns of Maize Germplasm from Public and Private Sector of Turkiye

Gönül Cömertpay[1], Nergiz Çoban[1], Ibrahim Cerit[1], Faheem Shahzad Baloch[2]

[1]Eastern Mediterranean Agricultural Research Institute, Yuregir, Adana, Turkiye
[2]Sivas Science and Technology University, Sivas

In the maize breeding programs, knowledge of genetic diversity and population structure is essential for the development of new varieties equipped with many desirable traits for commercialization. The Eastern Mediterranean Agricultural Research Institute (EMARI) has a collection of advanced elite inbred lines from different sources and these sources are used for improving new silage hybrids with high quality together with commercial companies (Polen, TAREKS, Biotek and Zeagen). In this study, population structures of 358 maize inbred lines from public and private companies was obtained to define their heterotic groups using 15425 DArT seq based single nucleotide polymorphism (SNP) markers. Polymorphic information content (PIC) ranged from 0.1 to 0.49. Based on SNP markers, estimates of the genetic distance between inbred lines ranged from 0.16 to 0.72 with an average of 0.247, indicating a plentiful diversity harbored by our inbred lines indiacting the potential for developing elite hybrids using genomic data. The highest genetic

distance was observed between inbred lines C16IH4 and LH216 (exPVP) and the least between 16AH1 and 16AH28. Cluster analysis based on SNP data divided 358 inbred lines into various clusters which was highly compatible with their pedigrees. Based on a population structure analysis, the 358 maize inbred lines were divided into five population (K=5) corresponding to their heterotic groups: Stiff Stalk, Lancaster, Iodent, tropical and miscellaneous. The findings of this study showed that knowledge of genomic diversity have important implication for identification of heterotic groups, which will enable for effective and efficient usage and management of the germplasm to produce new 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:TOVAG-121O313

Keywords: DArT SNP, corn, inbred line, genetic diversity, structure, heterotic group

[OP-57]

Omics in Maize Breeding: Case Studies in Abiotic Stress Tolerance

Emre Aksoy[1], Faheem Shahzad Baloch[2]

[1]Biological Sciences, Middle East Technical University, Ankara, Turkey
[2]Department of Plant Protection, Sivas University of Science and Technology

Maize (*Zea mays* L., corn) is a C4 crop grown in diverse climate zones, ranging from 45° N to 45° S in the world. Maize is one of the world's most important crops used for direct human consumption, animal feed, and chemical feedstock. The maize genome is organized into 10 chromosomes (2N = 20), and is about 2400 Mb of DNA per haploid nucleus in the B73 inbred, which is approximately six times larger than rice and six times smaller than wheat, although a large proportion of the genome represented by repetitive elements. Its genome contains 42 000–56 000 genes. Maize genetics took the advantage of an outbreeding reproduction system with the tolerance of inbreeding. Multiple breeding products of maize have been developed, including inbreds, hybrids, synthetic cultivars, open-pollinated varieties (OPVs), and improved landraces, and it shows wide adaptability including good sources of resistance to environmental stresses. Maize breeding requires an integrated approach including pan-genome analyzes and functional annotations, high-throughput and precise phenotyping, targeted gene identification, and editing. Recent developments in next-generation sequencing improved the quality of the B73 reference genome and showed that structural variations play important roles in trait differences. Finally, the combination of genome-wide association studies (GWAS) and transcriptome-wide association studies (TWAS) determined novel quantitative trait loci (QTL) and expression QTL (eQTL) related to abiotic stress tolerance in maize. Significantly associated genes identified by the combination of GWAS and TWAS explain more heritable variation for a majority of a trait than do TWAS or GWAS alone. In recent years, maize genomics research canalizes its efforts in understanding the epigenomic variations linked with previously unnoticed slight phenotypic differences through epigenome-wire association studies. Several examples from the maize abiotic stress tolerance perspective will be highlighted in the presentation in conjunction with their importance in genomics and breeding.

Keywords: breeding, maize, genomics, GWAS, TWAS, pan-genome, epigenome

[OP-58]

Advances in Climate-Resilient Temperate Tree Breeding: A Case Study in Peach

Omer Atagul[1], Alejandro Calle[2], Ksenija Gasic[2]

[1]East Mediterranean Transitional Zone Agricultural Research Institute, 46060 Kahramanmaras, Turkey
[2]Department of Plant and Environmental Sciences, Clemson University, 105 Collings St., Clemson, SC, USA, 29634

Fluctuations in the climate and their influence on peach [Prunus persica (L.) Batsch] production have highlighted the need to incorporate adaptive phenotypic plasticity in newly developed cultivars. In temperate fruit trees, including peaches, the adaptive mechanism includes genotype-specific chill requirement (CR) and heat requirement (HR) as cues for bloom date (BD). In peach, BD is determined by the dynamic relationship of CR and HR during dormancy. Understanding these two thermal requirements would enable breeders to develop new cultivars adapted to new climatic scenarios. Genetic variability in HR was observed in peach germplasm. Still, the variation of this requirement and its interaction with CR and BD has received less attention due to the difficulty in

methodological implementation. The HR is estimated by counting the thermal time using the growing degree hour (GDH) model at a threshold base temperature (Tb) from chilling fulfillment until full bloom. We hypothesize that peach germplasm varies in HR and that variability can be used in breeding for delayed BD. Therefore, an opportunity exists for breeding peaches with high Tb and/or HR for delayed bloom and avoidance of late spring frosts. In this study, we focused on estimating the HR of 136 peach cultivars and 269 F2 peach progeny over eight (2014-2021) growing seasons to evaluate the feasibility of breeding for climate resilience. The peach germplasm used in the study included accessions with a wide CR range, from less than 400 to more than 1000 chill hours. We used Best Linear Unbiased Prediction (BLUP) for each accession to compare traits' variation over the seasons. The BD BLUP ranged from 62 to 80 Julian days and was skewed to mid and late-season blooming. The HR BLUP ranged from 4808–7721 growing degree hours (GDH), with most accessions accumulating from 6000–7000 GDH. In addition, the interaction between these traits manifested a high positive correlation between BD and CR and a negative correlation between CR and HR, with a seasonal effect on the correlation between BD and HR. Different climate influences on CR, HR and BD observed in peach germplasm will be discussed in the context of enabling breeding for climate resilience.

Keywords: Heat Requirement, Chill Requirement, Bloom Date, Climate Change, Dormancy, Growing Degree Hour, Peach [Prunus persica (L.) Batsch]

[OP-59]

In Silico Analysis of QTLs Associated With Iron Efficiency in Soybean Lead to the Identification of GATA Transcription Factors Involved in Iron Homeostasis

Amir Maqbool[1], Allah Bakhsh[2], Emre Aksoy[3]

[1]Department of Agricultural Genetic Engineering, Nigde Omer Halisdemir University
[2]Centre of Excellence in Molecular Biology, University of the Punjab
[3]Department of Biological Sciences, Middle East Technical University

Alkalinity induced iron deficiency chlorosis (IDC) is a major problem leading to massive yield losses and poor nutritional quality in many crop species. Some plants, including soybean (*Glycine max*), are inefficient in iron uptake from the alkaline soils, and they can be exploited as model plants to study iron deficiency responses in plants. Although a number of quantitative studies were done related to iron deficiency tolerance in soybean, the genes in the QTL regions have not been identified and characterized yet. We have done comprehensive in silico analysis of all the genes present in these soybean QTLs. We found 6465 genes in 39 QTL linked with IDC tolerance in soybean. Bioinformatic analyses of these genes lead to the identification of a sub-set of GATA transcriptions factors (TFs) co-express together with known iron homeostasis genes, which suggests the involvement of GATA TFs in IDC tolerance. GATA-binding elements were characterized in the promoter regions of all known iron homeostasis genes in the co-expression network. Therefore, we characterized orthologs of GATA TFs in Arabidopsis thaliana under iron deficiency. GATA family mutants are more tolerant to iron deficiency than the wild type since they induce higher FRO enzyme activity, release more protons, and accumulate more iron in the roots. However, overexpression lines show the opposite responses in iron deficiency. Taken together our data prove that the GATA TFs are involved in IDC tolerance and they can be used as the targets to develop soybean lines tolerant to IDC.

Keywords: iron, QTLs, soybean, GATA, soil alkalinity, bioinformatics

[OP-60]

Determination of Resistance Levels of Some Bean Genotypes Against Charcoal Rot (Macrophomina phaseolina (Tassi) Goid) Disease

Sirel Canpolat[1], Abdulaziz Yağmur[1], Senem Tülek[1], Evren Atmaca[2], Abdullah Taner Kılınç[2]

[1]Directorate of Plant Protection Central Research Institute, Ankara, Türkiye
[2]Directorate of Transitional Zone Agricultural Research Institute, Eskişehir, Türkiye

Macrophomina phaseolina (Tassi) Goid. is a fungal pathogen that causes significant economic losses, including root and hypocotyl rot, root collar and stem blight, which are common in bean production areas. In this study, 24 bean genotype developed by the Transitional Zone Agricultural Research Institute and M. phaseolina isolate (M8 isolate) were used. This research was carried out with pot experiments in climatic chamber conditions to determine the reactions of some bean (Phaseolus vulgaris L.) genotypes against

M. phaseolina, which causes charcoal rot disease in beans. Among the bean genotypes evaluated within the scope of the study, 19-Kuru Fasulye Melez Bahçesi-3, 19-Kuru Fasulye Melez Bahçesi-5, 19-Kuru Fasulye Melez Bahçesi-11, 19-Kuru Fasulye Melez Bahçesi-14, 19-Kuru Fasulye Melez Bahçesi-47, 19-Kuru Fasulye Melez Bahçesi-51, 19-Sırık Bölge Verim Denemesi-3 genotypes were found to be tolerant, while the 19-Kuru Fasulye Melez Bahçesi-10, 19-Kuru Fasulye Melez Bahçesi-12, 19-Kuru Fasulye Melez Bahçesi-13, 19-Kuru Fasulye Melez Bahçesi-40, 19-Kuru Fasulye Melez Bahçesi-41, 19-Kuru Fasulye Melez Bahçesi-50, 19-Sırık Bölge Verim Denemesi-1, 19-Sırık Bölge Verim Denemesi-6 genotypes was found to be resistant.

Keywords: Bean, charcoal rot, disease reaction, Macrophomina phaseolina

[OP-61]

Determination of Resistance of Some Bean Genotypes to Common Leaf Blight (Xanthomonas axonopodis pv. phaseoli) and Bean Halo Blight (Pseudomonas syringae pv. phaseolicola) Diseases

Kamil Duman[1], Evren Atmaca[2], Sirel Canpolat[1], Abdullah Taner Kılınç[2], Mesut Topal[2], Aynur Karahan[1]

[1]Plant Protection Central Research Institute
[2]Eskişehir Transitional Zone Agricultural Research Institu

This study was carried out jointly with the Transition Zone Agricultural Research Institute Directorate (GKTAEM), Eskişehir, and the Bean Common Leaf Blight [Xanthomonas axonopodis pv. phaseoli (Xap)] and Bean Halo Blight Disease [Pseudomonas syringae pv. phaseolicola (Psp)] strains of advanced bean lines were phenotypically characterized. In the field trials, 82 bean genotypes developed by GKTAEM and Xap and Psp agents, which were isolated from the production areas in previous studies and determined by the Agricultural Protection Central Research Institute (ZMMAE), Ankara, were used. As a result of the study, 20-SBVD-22 and 20-SBVD-21 were found to be the most tolerant lines against Psp from 82 different bean genotypes used in the trials, while these lines were 20-BBVD-5, 20-SBarBVD-8, 20-SBarBVD-5, 20 -SBarBVD-9, 20-BBVD-9, 20-BBarBVD-5 and 20-BBarBVD-12 lines followed. The 20-BBVD-4 line was determined as the most sensitive line against the Psp. The 20-SBVD-6, 20-SBVD-10, 20-SBVD-2, 20-SBVD-10, 20-SBVD-18 and 20-SBVD-11 lines were subsequently included among the sensitive lines. 20-SBVD-13, 20-SBarBVD-8 and 20-BBarBVD-14 lines were determined as the most tolerant lines against Xap, followed by 20-BBVD-8, 20-SBarBVD-3 and 20-BBarBVD-12 lines. followed the 20-SBarBVD-4 and 20-BBarBVD-9. The 20-BBVD-4 line was determined as the most sensitive line to Xap. Following this line, 20-SBVD-19 and 20-SBVD-17 lines were determined as the next sensitive lines. Testing of selected lines with markor assisted selection based on SCAR markors still continues.

Keywords: common blight, halo blight, bean, disease reaction, Pseudomonas, Xanthomonas

[OP-62]

Determination of the Reactions of Some Bread Wheat (Triticum Aestivum L.) Genotypes to Waterlogging

Cemal Şermet[1], Yavuz Balmuk[1], Hasan Orhan Bayramoğlu[1], Mehmet Karaman[2]

[1]Blacksea Agricultural Research Institute-Samsun-Türkiye
[2]Alparslan University-Muş-Türkiye

Waterlogging is one of the important factors limiting wheat yield. It is known that around 10-15 million hectares of wheat growing areas around the world are affected by waterlogging every year and it is a common limiting factor for wheat production. Wheat is a plant that is vulnerable to waterlogging. However, it has a wide genetic variation that affects tolerance and sensitivity. Resistance to waterlogging in wheat and barley is governed by a dominant gene. Parental selection should be considered more in providing tolerance to waterlogging in breeding studies. In this study, it was aimed to determine the reactions of some bread wheat genotypes against waterlogging and to contribute to breeding programs. 27 genotypes (15 local bread wheat pure lines and 12 varieties) were used as material in the study. The test run was conducted in a fully controlled plant growth chamber. A pool was created in order to create waterlogging stress conditions. The experiment was planned as 3 repetitions of stress application inside the pool and 3 repetitions of control application outside the pool. There were 5 plants in each plot. Growing conditions were artificially created with 16 hours of light/22 0C and 8 hours of darkness/17 0C. Ambient humidity is set to 75%. Soil mix was used for the plant growing. Before sowing, the seeds of the genotypes were germinated in sterilized

petri dishes. Seeds that germinated at the same time were selected and planted in viols (5x5x12 cm). With the planting, 6 kg of pure nitrogen, phosphorus and potassium (15-15-15 compound fertilizer) was applied by the calculation of per decare. Plants were watered every other day until water stress was applied. When the first tillering was seen in the plants (Zadoks 21), stress conditions were created by giving water to the pool where the viols were located. The water level is adjusted to be 5 cm above the ground level. Stress conditions were maintained until the stem elongation (Zadoks 34). In this process, the plants planted as control were watered to maintain the soil moisture. After the stress application was completed, the plants were allowed to recover for 5 days. Then, wet root weight, wet biomass weight, dry root weight, dry biomass weight, root length, number of tiller and root element content (Fe, Mn, P, Cu and Zn) analyses were performed on the plant samples of each genotype. According to the results obtained, YP-25, YP-67 and YP-69 local bread wheat pure lines and Sakin, Nevzatbey, Müfitbey and Daphan varieties were found to be tolerant against waterlogging. YP-28 and Bezostaya, İkizce-96 and Köse 220/33 cultivars were found to be susceptable to waterlogging.

Keywords: Bread wheat, waterlogging, root weight, biomass weight, element content

Keywords: Bread wheat, biomass weight, element content, root weight, waterlogging

[OP-63]

Effect of Genotypic Variation on Bread and Flour Quality in Wheat

Pervin Ari Akin, Arzu Özer, Canan Göksu Sürücü, Selim Uygun, Hümeyra Yaman

Central Research Institute for Field Crops

The basic requirement for producing high-quality bakery products is knowledge of the quality parameters of raw materials used in the production process, as well as the ability to maximize their potential. Ten Turkish wheat cultivars (Tosunbey, Şanlı, Kışla, Demirhan, Ayten Abla, Çavuş, Selamibey, Bayram, Ayaz and Kürşad) grown in the İkizce location (Ankara, Türkiye) were used during the 2021-2022 growing season in this study. Hectolitre (kg/hL), moisture content (%), protein content (%) wet gluten (%), dry gluten (%), gluten index (%), sedimentation (mL), farinograph and alveograph parameters of these varieties were evaluated. Among all cultivars, cv. Çavuş had the highest protein content (16.2 %), wet gluten content (39.4%), Zeleny Sedimentation (67 mL), water absorption (62%), dough strength (292 J), and bread volume (900 cm3). Based on the results, cv. Çavuş was the most suitable cultivar for bread production.

Keywords: Wheat, Genotype, Flour, Dough, Bread, Quality Parameters

[OP-64]

Variation of Resistance of Some Downy Mildew Resistance Genes to Downy Mildew Races in Trakya Region, Turkey

Mehmet Ibrahim Yılmaz[1], Veli Pekcan[1], Samet Sağlam[1], Bayram Serkan Cabar[1], Göksel Evci[2], Yalçın Kaya[3]

[1]Trakya Agricultural Research Institute,Edirne, Türkiye
[2]Trakya Birlik, Edirne, Türkiye
[3]Trakya University Engineering Faculty, Genetic and Bioengineering Dept, Edirne, Türkiye

Sunflower is the most important oil crop in the Balkans and Blacksea region which has over 60% of world sunflower production. Biotic stress are the main limiting factors reducing sunflower yield. Broomrape parasite and sunflower mildew (Plasmopara halstedii (Farlow) Berlese & de Toni) are the main problems in sunflower production areas in this region. Downy mildew fungal disease has developed over 20 races in sunflower and exist almost all parts of the world. Therefore, resistance to downy mildew is one of the main targets in sunflower breeding programs. It has been determined that there are some races of downy mildew in the Trakya region which is European part of Turkey and has more than 50% of sunflower planted areas of Turkey and resistant varieties have been developed and planting widely in the region. However, in recent years, mildew disease has started to be seen again in planting varieties widely used in the region. In this study, it was aimed to determine the changes in resistance status of the Pl 6, Pl 8 and Pl 13 resistance genes, which provide resistance to downy mildew races in the Trakya Region, in recent years (2012-2021). In the study, HA 335 lines containing the P1 6 gene, RHA 437 lines containing the P1 8 gene and HAR5 lines containing the P1 13 gene were used. In the HA 335, RHA 437 and HAR 5 lines, 12.6%, 2.3% and 0% symptoms were observed in 2012, respectively, while 96.1%, 47.5% and 4.7% of the disease symptoms were observed in 2021. As a result, it could be concluded that new downy mildew breeds have started to appear in the Trakya Region and the resistance of the Pl 13 gene continues to the new races in the region.

Keywords: downy mildew, hybrid breeding, races, resistance, sunflower

[OP-65]

Using Root Criteria in Drought Resistance Selection

Burak Özdemir, Sana Jamal Sailh, Mehmet Ülker

van yüzüncü yıl university faculty of agriculture department of field crops

Increasing drought stress with global climate change causes serious yield losses in different crops in our country as well as all over the world. Since it is predicted that the effects of drought will increase in the future, the duties of plant breeders and physiologist will become more intensive. Most of the physiological and morphological parameters used in the selection process for drought resistance are related to above-ground parts of the plant, whereas root parameters are not. The reason for that might be due to the unanswered questions related to root system such as which root characteristic is more effective and in which type of drought, or whether deep or branched root is more efficient. Therefore, it is necessary to define the relationship between the root system and the above-ground part. Root characteristics are important for maintaining vegetative yield under drought. Roots found in deep soils with thin root diameter and high specific root length and low xylem diameter for water uptake in the lower layers of the soil might be effective for late drought. In areas with episodic drought, root types that continue to grow rapidly with the moisten of the soil is preferred. In recent years, various root studies have been carried out with the help of imaging systems. Especially in the last 10 years, many studies have been carried out on many root characteristics of rice crop and the genes that affect these characteristics. Root phenotypes were determined through examining parameters such as total root length, root architecture in the first development period, root diameter and root density distribution in later periods. Similar studies are needed in other plants.

Keywords: Drought tolerance, root architecture, root bimass, root morphology

[OP-66]

Overview of Zucchini Yellow Mosaic Virus (ZYMV)

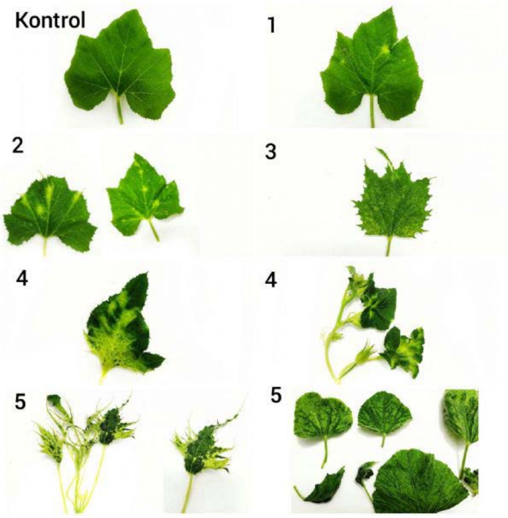
Emre Öztürk[1], Akife Dalda Şekerci[2]

[1]Alata Horticultural Research Institute, Erdemli, Mersin, Turkiye
[2]Agriculture Faculty, Department of Horticulture, Erciyes University, Kayseri, Turkiye

The Cucurbitaceae family, which has more than 800 species, members have long been cultivated to be used as food, medicinal and also ornamental purposes. However, many plant diseases and pests cause losses of yield and quality in cucurbits and one of them is viral diseases. Zucchini Yellow Mosaic Virus (ZYMV) which causes serious yield losses in cucurbits production worldwide is a viral disease. It is often non-persistently transmitted by aphids and is also transmitted by seed in cucurbits, which may contribute to its rapid spread around the world. Zucchini Yellow Mosaic Virus shows symptoms such as mosaics, yellowing, clogs, curling at the leaf edges, deformation, vein opening, fragmentation of leaves, threading, shortening and thickening of the internodes, and also may result to loss of yield, quality and plant death. As it is known, there is no effective chemical control of virus diseases and the use of resistant/tolerant varieties is the most effective solution. For this reason, it is a very important criterion that the developed cucurbits F1 hybrid varieties are resistant/tolerant to ZYMV. In this study, about ZYMV is given, which is very common in cucurbit cultivation in our country and in the world and causes serious production and quality losses also, awareness is aimed to provide an overview of ZYMV resistant cucurbit breeding practices.

Keywords: Cucurbitaceae, ZYMV, breeding

Fig. 1. Scale of damage caused by ZYMV in Cucurbita pepo (original: Dalda-Şekerci A., 2020)



cale of damage caused by ZYMV in Cucurbita pepo (original: Dalda-Şekerci A., 2020)

[OP-67]

Development of Industrial Type Pepper Lines Resistant to *Phytophthora capsici*

Duygu Argün[1], Mine Bulut[1], Ayşegül Çolak Ateş[2], Davut Keleş[4], Hasan Pınar[3], Sevinç Tekin[1], Mustafa Ünlü[1], Nihal Denli[1], Atilla Ata[1]

[1]Alata Bahçe Kültürleri Araştırma Enstitüsü Mersin
[2]Biyolojik Mücadele Araştırma Enstitüsü Adana
[3]Erciyes Üniversitesi Kayseri
[4]Tarımsal Araştırmalar ve Politikalar Genel Müdürlüğü Ankara

Pepper, which is one of the most important vegetable types in a balanced diet, also has an important commercial potential. Root blight (*Phytophthora capsici* L.) is the leading factor limiting pepper production. The most effective method in the fight against the disease in question is genetic resistance. This study is to provide resistance to root collar blight on the productive and high quality varieties developed by Keleş et al., (2013) in Karaisalı pepper, which is an important industrial variety for Adana and Mersin regions. The material of the study; Among the Karaisalı pepper lines, the disease-susceptible Hayriye cultivar and the K9 pepper genotype and the resistant CM 334 and P1401 genotypes are formed. Molecular marker selection and biological testing techniques were used in our study, which created a population by crossbreeding, backcrossing and inbreeding. As a result of the study, 82 half-way materials of industrial pepper type resistant to root collar blight with high fruit yield and quality were developed.

Keywords: Pepper, *Phytophthora capsici*, Molecular marker selection, biological testing

[OP-68]

Phloem-Mobile MicroRNAs in the Long-Distance Communication of Pumpkin (Cucurbita maxima L.) Under Heavy Metal Stresses

Mehtap Aydın[1], Hüseyin Tombuloğlu[2], Güzin Tombuloğlu[3]

[1]Yeditepe University, İstanbul
[2]Imam Abdul Rahman bin Faisal University, Saudi Arabia
[3]Adnan Kahveci Mah., Mimar Sinan Cad., Mavisu evleri, 7/28Beylikduzu-, Istanbul

Plant cells and organs communicate with each other using specific signal molecules such as proteins, metabolites, small RNAs, etc. While cells neighboring each other interact with plasmodesmata, organs or tissues in distant locations can communicate through the vascular system. Mobile microRNAs (miRNAs) travel from root-to-leaf or vice versa through phloem and xylem and play important roles at distant organ such as regulating biological processes under stress conditions. This study aims to identify mobile miRNAs having role in the long-distance communication of plants under various heavy metal stresses. For this purpose, pumpkin (Cucurbita maxima L.) seedlings grown in hydroponic culture were subjected to Cd, Ni, and Pb (200 µM). The phloem sap was collected, and the mobile miRNAs were determined by using quantitative stem-loop RT-PCR (stem-loop RT-qPCR) and semi-quantitative PCR methods. Furthermore, functional characterization of those miRNAs was identified by grafting the stressed plants to the control rootstocks. Results showed that miRNA genetic expression is increasing under Ni toxicity and some miRNAs were found to be selectively induced upon toxic Cd, and Pb. Overall, this study suggested mobile miRNAs which are functional in the long-distance communication strategy

of plants under different heavy metal stresses.

Keywords: Mobile miRNA, Heavy metal stress, Long distance communication, stem-loop RT-qPCR

[OP-69]

Evaluation of the Current Situation of the Conditions for Protection of PBR vis-a-vis Recent Developments

Ayşe Odman Boztosun

Akdeniz University Law Faculty

The Law No. 5042 on the Protection of Breeders' Rights of New Plant Varieties (Law) entered into force by being published in the Official Gazette dated January 15, 2004. This regulation, which provides intellectual property protection to new plant varieties in our country, envisages four conditions for granting protection: novelty, distinctness, uniformity and stability. Controversial issues in the context of the novelty condition revolve around cases that do not affect the novelty of the variety. In this context, it will be determined which acts should be considered as making public. In terms of the distinctness condition, the criteria and methods (phenotypical/genotypical) used in the determination of the difference will be evaluated in the light of the latest developments. In this context, the concept of "essentially derived variety" will also be defined. In the evaluation of the condition of uniformity, within the framework of the definition, "A variety showing uniformity in terms of relevant characteristics is considered uniform, excluding possible variations depending on the reproduction method used" in the Law, the scope of "possible variations depending on the reproduction method used" and the criterion of "showing uniformity in terms of the relevant characteristics" criteria will be discussed. In terms of the stability condition, the criterion of "remaining uniform without changing its relevant characteristics during successive reproductions or at the end of certain reproduction periods" will be evaluated in terms of different plant species. Thus, the developments in terms of the conditions sought for granting breeder's right on new plant varieties in the eighteen years since the entry into force of the Law will be examined in detail in the light of jurisprudence, doctrine and technical developments.

Keywords: New Plant Varieties, Breeders' Rights, Conditions for Protection, Essentially Derived Varieties, Phenotype/Genotype Evaluation

[OP-70]

Turkish Plant Breeders' Rights System; Challenges, Opportunities

Hasan Çelen

TAGEM, Alata Horticultural Research Institute

The plant breeder's rights law has been in effect since 2004, and Turkey has been a member of the UPOV since 2007. The Turkish Plant Breeder Rights System is still a young system. This youth brings with it many challenges and opportunities. In this study, the Turkish Plant Breeder Rights system is briefly explained. Then challenges of system and what the Turkish and international plant breeder community should do in order to turn these challenges into opportunities are explained together with the gains that will be made. The acceptance of the DUS reports carried according to the UPOV technical guides, the waiting for the DUS results of the applications to the CPVO without the need for a second DUS report, the cheapness of the official fees are basic opportunities. In addition, the acceptance of the using of molecular techniques as valid evidence in varieties comparison in some court decisions has also been presented as an important opportunity. Preservation of reference plants, as well as the lack of development of a molecular database of varieties, were explained as challanges. It is a significant challenge is breeders as experts of case to present their opinion to the courts as identification and comparison as the same concepts. In order to overcome these challenges; Turkish breeders should carry the experiences of their international colleagues on infringement cases and molecular varieties database; create a molecular variety database as in the examples of some other UPOV member countries; train whole sector on differences of "variety identification and comparison" along with case studies; has been suggested.

Keywords: PBR, Molecular Varieties Databases, Infringement Case

[OP-71]

Wheat Response to Individual and Combined Heat and Drought Stress and Breeding for Tolerance

Rishi Kumar Behl

Department of Agriculture, Maharishi Markandeshwar (deemed to be university) Mullana, Ambala, Haryana, INDIA, 133207

Wheat is the staple food and element of food security globally. The production of wheat is drastically affected by drought and heat stress. Heat and drought affects are witnessed in major wheat producing region worldwide in recent times. Internationally wheat losses due to heat and drought stresses have encompassed 5.5 and 12%, respectively. Furthermore, the projections that global temperatures may upsurge by 0.6–2.5°C by the year 2050 and 1.4–5.8°C by year 2100 along with increased severity of drought condition may worsen the situation. In India average temperature rise from 1901 to 2018 is recorded as 0.7O C as per reports and world's average warming rate is recorded as 1.1OC in a decade. The effect of heat stress includes increased reproductive rate with decreased photosynthetic rate in plants. Wheat requires 15oC as daytime optimal temperature in its reproductive phase and wheat yield is reduced by 3-4% on every unit (i.e., 1OC) rise in temperature. Wheat crop is often exposed to drought and high temperature simultaneously, but their effects are usually investigated individually. A small number of studies have documented the impact of combined drought and high temperature on wheat productivity and biological processes. Both drought and high temperatures negatively affect the growth by impairing the photosynthetic system, reduce stomatal conductance, disrupt water relations leading to shortened grain filling duration, reduced grain size, weight and ultimately yield. The effects of these stressors may be synergistic or antagonistic, however their interactive effects are more pronounced, and the synergistic interactions lead to considerably reduced productivity than by either stress alone. Although the major impacts of individual and dual stress of drought and high temperature on wheat productivity are known, there yet the tolerance mechanisms is not properly understood. Systems biology analyses have revealed a complex mode of integration of the different signaling pathways triggered in plants during stress combination. The best step forward is to develop elite wheat varieties with enhanced tolerance against these two robust stresses. Breeding for heat and drought tolerance in wheat is complicated as it is polygenic trait. Stress tolerance in wheat depends on identifying potential cell signaling mechanisms. The strategy to breed for high temperature or drought tolerant genotypes includes identification of potential molecular markers, various quantitative trait loci, association mapping, gene expression profiling studies, cDNA, transcript profiling, proteomics and their applications to develop stay green genotypes which can sustain long photosynthetic activities and translocation of photosynthates into grains. Thus, both source and sink capacity of the plants have to be increased under stress prone environment. Integrated omics assisted approaches can also pay dividend in understanding the tolerance mechanism and thus sustainable yields in challenging environment.

Keywords: Heat, drought, interaction, wheat, stress tolerance, breeding strategy

[OP-73]

Increasing Breeding Studies Efficiency by Supporting Plant Breeding Software with Data

Canseri Bozkuş

Beautifulmind Yazılım ARGE, Plant Breeding Software, ANTALYA TEKNOKENT

Plant breeding is the art and science of improving important agricultural plants for the benefit of humankind. Breeders work to make our food, fiber, forage, and industrial crops more productive, nutritious, more resistant to diseases, better phenotype and better genotype. Breeders reduce the pesticide use and they protect the environment by developing resistant varieties. The most important thing that breeders do is developing crops which has good yield to be able to feed expanding human population in the world. In today agricultural business plant breeding have become quite difficult. One of important reason is companies not pay enough attention to data management, storing and analysis by software. Using software determines and shows whether the breeding strategies are effective or not. It can be obtain more succesfull hybrids than usual by using the plant observation, resistance and genetic information datas. Plant breeding software is important to make plant breeders work easier and make seed business sustainable.

Keywords: Plant, Breeding, Software

[OP-74]

In vitro Regeneration of Encapsulated Propagules of Some Cyclamen Species

Hüsamettin Aycan Alp[1], Serap Balık[1], Yeşim Yalçın Mendi[2]

[1]Alata Horticultural Research Institute, Vegetables and Ornamental Crops Department, Mersin, Turkey
[2]Cukurova University, Faculty of Agriculture, Horticulture Department, Adana, Turkey

Cyclamen is a genus of 22 species of perennial flowering plants in the family Myrsinaceae. Cyclamen species are native to Europe and the Mediterranean Basin. Ten Cyclamen species, 6 of them are endemic, grow naturally in Turkey. Cyclamens are important as ornamental plant as well as medicinal and aromatic plant. Biotechnology, specially in vitro studies, are very important tools to preserve genetic resources, micro propagation and producing the secondary metabolites in bioreactors. In this study, regeneration capability of in vitro-derived propagules of some cyclamen species were investigated. The somatic embryos of C. percicum, C. persicum cv Melodi and C. mirabile in globular stage and the shoot tips of C. pseudibericum transformed on callus tissues were selected for encapsulation attentively. Sodium alginate in 3% concentration was used as the coating material and was prepared in two different ways using pure water as a control and ½ liquid MS medium. In addition to the encapsulation process, the effects of benzyl adenine, indole butyric acid, gibberellic acid, proline and spermin on regeneration rate were also investigated. Regeneration rates were recorded in 4-week periods for 20 weeks. The differences among the PGRs concentrations and also the control were compared. The germination ratio and the vigor of the C. persicum and C. persicum cv. Melodi were notably increased. The somatic embryos of C. mirabile tended to produce somatic embryos in each treatment however the numbers of somatic embryos were increased through PRGs. And also the shoot regeneration ability of C. pseudibericum affected positively by the help of coating agent supplied by PGRs. At the end of 20th week, the highest germination rate was observed in the encapsulated embryos which were coated by alginate prepared with 0.6 mg l-1 GA3, 0.3 mg l-1 BA, 3 gl-1 proline and 0.2 mg l-1 spermidin. For C. pseudibericum, the highest shoot regeneration ratio was observed in the coating media supplied with 3.0 mg l-1 BA and 0.3 mg l-1IBA. As a result, the PGRs added into the capsulation agent were improved the regeneration capacities of the propagules of each studied cyclamen species significantly.

Keywords: artificial seed, synthetic seed, coating agent

[OP-75]

Protoplast isolation from leaf mesophylls of haploid Solanum sisymbriifolium Lam. produced via anther culture

Buse Özdemir Çelik[1]*, Hatice Filiz Boyacı[2], Esra Cebeci[3], Metin Tuna[4], Ahmet Naci Onus[5]

[1]Elmalı Vocational School, Akdeniz University, Antalya, Türkiye

[2]Republic of Türkiye Ministry of Agriculture and Forestry Antalya Food Control Laboratory Directorate, Antalya, Türkiye

[3]Bati Akdeniz Agricultural Research Institute, Department of Vegetable Crops and Ornamentals, Antalya, Türkiye

[4]Department of Field Crops, Faculty of Agriculture, Namik Kemal University, Tekirdag, Türkiye

[5]Department of Horticulture, Faculty of Agriculture, Akdeniz University, Antalya, Türkiye

Abstract: While the cultivated eggplant genotypes are susceptible to many biotic and abiotic stress factors the wild relatives of eggplant can be resistant to more than one factor. Nevertheless, the success in interspecific cross between cultivated form and wild relatives of eggplant is very limited because of incompatibility. Hence, using biotechnological approaches such as somatic hybridization can be useful tool to overcome this problem. This study aimed to achieve protoplast isolation, which is the first step for an alternative method for creating hybrid plants using haploid protoplasts for fusion that results directly with creation of a diploid plant. The use of haploid plants as a source of protoplasts is of great importance in terms of the ploidy level of the hybrids to be obtained in somatic hybridization, and no study has been found in eggplant on using haploid cells as a source of protoplasts and isolating them. The present study reports the isolation of viable protoplast from anther-derived haploid leaves of Solanum sisymbriifolium, which is the wild species, a useful material in eggplant plant improvement. Haploid plant leaves obtained by culturing anthers of Solanum sisymbriifolium Lam. yielded quality protoplasts after isolation and found to be useful as a protoplast source for further somatic hybridization studies.

Keywords: Solanum *sisymbriifolium*, protoplast isolation, haploid protoplast, eggplant.

[OP-76]

HPLC Analysis of Phenolic Compounds From Elicited Hairy Roots of Dracocephalum Kotschyi Boiss and Implications for COVID-19 Inhibition

Bahman Hosseini[1], Fatemeh Naseri[1], Lotfali Naseri[1], Raheleh Tahmasebi[2]

[1]Department of Horticulture, Faculty of Agriculture, Urmia University, Urmia, Iran
[2]Food and Chemical Analysis Research Laboratory, Jahad-e-Daneshgahi, Urmia, Iran

Phenolic compounds are a group of small molecules known for their anti-inflammatory, antibacterial, antiviral, antioxidant and anticancer properties. As Dracocephalum kotschyi Boiss is rich in valuable phenolic compounds, it can be a good candidate to inhibit the activity of the novel SARS-CoV-2 virus. In the present study, a nano elicitor was used to increase the precious compounds in hairy roots of D. kotschyi. The effectiveness of these compounds on COVID-19 6LU7 protease was also evaluated through the molecular docking method. D. kotschyi hairy roots were obtained from the inoculation of 3-week-old cotyledons with Agrobacterium rhizogenes strain ATCC15834. Transgenic roots were elicited with nano copper oxide (nano-CuO) at different concentrations (0, 5, 10, and 15 µM) and exposure times (24 and 48 h). Nano-CuO (10 µM) increased the expression levels of rosmarinic acid synthase (ras) and phenylalanine ammonia-lyase (pal) genes during 24 and 48 h exposure times, respectively. According to high-performance liquid chromatography (HPLC) results, rosmarinic acid (RA) production was maximized in the treatment with nano elicitor (10 µM) during 48 h. RA content was 8.4 times higher (308.57 µg g-1 FW) than that of the control samples (36.53 µg g-1 FW). Besides, increases were observed in other phenolic compounds such as caffeic acid, chlorogenic acid (CGA), cinnamic acid, coumaric acid, gallic acid, quercetin and rutin. The standard inhibitor N3 (4′-[(2-phenylethyl)carbamoyl][2,2′-bipyridine]-4-carboxylic acid) was used to compare the results of molecular docking. Out of the eight phenolic compounds studied, only RA and CGA showed better results than the standard N3. MolDock score of the inhibitor N3 was -138.635 versus those of -182.610 and -139.674 for RA and CGA, respectively

Keywords: Dracocephalum kotschyi Boiss, Gene expression, Molegro Virtual Docker, Nano copper oxide, 6LU7 protein

Figure 1. (A and B) Inoculation of D. kotschyi cotyledons by A. rhizogenes strain ATCC15834 to obtain hairy roots; (C) Emergence of hairy roots from the site of wounds; (D) PCR analysis of the rolB gene in D. kotschyi hairy roots. M, 1 Kb molecular s

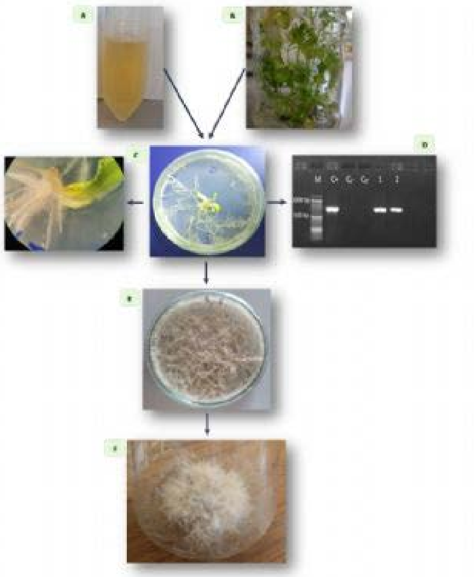
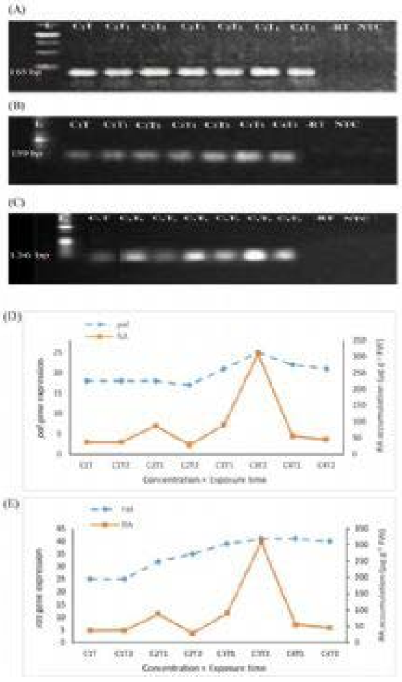


Figure 2. Effects of nano copper oxide on transcripts of the pal and ras genes in D. kotschyi hairy roots at various concentrations and treatment times; (A) Bands of 18S rRNA gene (housekeeping gene); (B) Effect of nano-CuO on the pal gene expression



Phenolic compounds studied by the HPLC method in the hairy roots of D. kotschyi, their retention time, and wavelengths.

Substance	RT	Wavelength (λmax)
Gallic acid	4.1	272
Caffeic acid	8.6	310
Chlorogenic acid	9.1	250
Rutin	10.3	310
Coumaric acid	10.7	310
Rosmarinic acid	11.19	250
Quercetin	13.31	250
Cinnamic acid	14.3	272
Apigenin	14.56	272

[OP-77]

Production of Durum Wheat Doubled Haploid Lines: A Useful Tools of Breeding

Olfa Ayed Slama, Hajer Slim Amara

University of Carthage/National Agronomic Institute of Tunisia/Department of Agronomy and Plant Biotechnology/ Genetic and Cereal Breeding Laboratory

The production of double haploid lines is used by breeders to produce homozygous lines in a single generation as opposed to conventional line production, which requires several cycles of self-pollination. The major problem with this approach is the low efficiency of green plants regeneration particularly for durum wheat (Triticum turgidum subsp. durum Desf.). In order to compare the efficiency of two haplodiploidization technics (androgenesis by isolated microspores culture, gynogenesis by unpollinated ovaries culture), three tunisian durum wheat varieties (Hmira, Khiar and Razzek) was used. The results showed that the best induction, calli or embryos formation and plant regeneration rates for all genotypes were obtained with gynogenesis (49.01, 8.6, 17.2 %) compared to isolated microspore culture (10.99, 4.80, 2.85%). Interestingly, all plants regenerated by gynogenesis were green. Whereas plants obtained by isolated microspore culture were either albino either greens depending on the genotypes used. The low regeneration rate and the high frequency of albino plants hinder the application of androgenesis for durum wheat. In the haploid production system, we conclude that genotypes with good capacity of induction have not necessarily a good capacity of haploid plantlets regeneration and vice-versa. However, calli or embryos formation seems to be an indicator of the haploid production. Although gynogenesis is the less used method for durum wheat, it has proved to be a successful approach for green haploid plant production. It is important to perform new experiments to advance its response.

Keywords: haplodiploidization, androgenesis, gynogenesis, durum wheat

[OP-78]

Determination of Pollen Viability and Germination of Different *Solanum Molengena* L. X *S. Torvum* Sw Hybrids and Crosses on Fertile Hybrids

Atilla Ata[1], Nihal Denli[1], Hatıra Taşkın[2]

[1]Vegetables and Ornamental Plants, Alata Horticultural Research Institue, Mersin, Türkiye
[2]Department of Horticulture, Faculty of Agriculture, Çukurova University, Adana, Türkiye

S.torvum is a source of resistance to Fusarium, Verticillium wilting and root-knot nematode of eggplant. The species is also used as rootstock due to its strong root structure. Hybrids of S.melongena x S.torvum are infertile, preventing the transfer of desired characters. To have fertile S.melongena x S.torvum hybrids, 7 S.melongena and 5 S.torvum genotypes were used to have 35 crossing combinations. Embryos of the hybrid fruits which were on the 21st day were rescued in MS containing 0.05 mg/L NAA, 0.5 mg/L Gibberellic acids (GA3), 15 mg/L AgNO3, 30 g/L sucrose, %0.25 activated charcoal and 8 g/L agar. Hybrids were obtained from 33 crossing combinations. Hybrid individuals were cultivated to test the viability of pollens which was determined by the Tetrazolium (TTC) test and to see the germination rate of pollens by using agar in a petri dish method. While there was no viability and germination of pollens in one-year-old hybrids, the germination rate and viability were 18.8-9.2 %, respectively, in two years of Sm1 x St5 hybrid combinations. By using those hybrids backcrossings were done in which the S.melongena genotype was used as the female parent, and the fruit set formation was observed. On the other hand, no fruit set formation was observed in the backcrossings obtained from fertile hybrids and S.torvum and the selfing of fertile hybrids. The plants obtained from the backcrossing in which S.melongena was used as a female parent showed similar characteristics to the female parent.

Keywords: Eggplant, intercrosses, S.torvum

[OP-79]

Genetic Characterizations of Vitis Genetic Resources Belonging Gaziantep and Kilis by Using Simple Sequence Repe (SSR)

Kürşat Alp Aslan[1], Hakan Usanmaz[1], Belgin Akça İzci[1], Mehmet Uzun[1], Ali Ergül[2]

[1]Pistachio Research Instıtue, Gaziantep, Turkey
[2]Ankara University Biotechnology Institute, Ankara, Turkey

Studies on genetic characterization are useful way to determine genetic diversity within species as well as between species and identify species. Grown almost everywhere in Turkey vine has abundance of local varieties and kinds. However, as a result of different denomination and variation within varieties, there is confusion of grape varieties. Moreover, some varieties which is out of production nowadays have risk of extinction Aiming to overcome problems mentioned above, SSR markers method has been used. In this study, belonging Gaziantep and Kilis 17 variety and kind from Pistachio Research Center Southeast Anatolian Vitis Genetic Sources Vineyards and together with 2 reference variety, 17 varieties (Vitis vinifera L.) were analyzed for genetic characterization by using 6 microsatellite markers (VVS2, VVMD5, VVMD7, VVMD27, ZAG62, ZAG79). In 6 loci, 46 alleles were designated. Genetic relationship dendogram has showed that varieties used as reference had independent branch from studied varieties and within 2 branches 3 synonyms were found. Genetic findings as research results belong to Pistachio Research Center Southeast Anatolian Vitis Genetic Resources Vineyards were integrated with Turkish Vitis Genetic Resources Databases created by Ankara University Faculty of Agriculture Department of Biotechnology. Employing SSR markers, this study reveals the first identification results of genetic Vitis resources of Gaziantep and Kilis in Southeast Anatolia. Obtained by this study, the results have value in better identification of varieties in Pistachio Research Center Southeast Anatolian Vitis Genetic Resources Collection Vineyards, regulation the number of varieties in National Collection and new breeding studies.

Keywords: TUrkey, Southeast Anatolia, SSR, Vitis

[OP-80]

The Potential of Using Landraces in Cassava (Manihot esculenta Crantz) Improvement Programmes

Ochanda JB Ogola, Petros K Malele

University of Venda

Climate change and increasing population growth will place more pressure on agriculture to produce more food using less resources. This requires development and adoption of climate-smart cropping systems. Cassava (*Manihot esculenta* Crantz) is a root crop of importance in tropical and subtropical regions and is generally regarded as drought resistant and capable of doing well in poor soils. However, low cassava yields due to biotic and abiotic stresses are common. Local cassava landraces my provide useful genetic resources in cassava improvement programmes aimed at improving yield and consumer preference. This study assessed the variation in water use, chlorophyll fluorescence, chlorophyll content, gas exchange and root yield of four cassava landraces (ACC#1, ACC#2, ACC#3, and ACC#4). A field experiment was conducted in the north-eastern part of South Africa in 2016/2017 (wetter) and 2017/2018 (drier) cropping season under rainfed conditions. Soil moisture content was measured at weekly intervals using a neutron probe and the data used to determine water use (WU), water-use efficiency for root yield (WUErt) and water use of biomass production (WUEb). Chlorophyll fluorescence and leaf chlorophyll content were measured using a PAM2100 portable chlorophyll fluorometer and chlorophyll content meter, respectively. Root yield and yield components were determined at 311 days after planting. (WUErt) and (WUEb) varied with landraces in season I from 37.0 kg ha^{-1} mm^{-1} (ACC#4) to 46.60 kg ha^{-1} mm^{-1} (ACC#3), and between 71.30 kg ha^{-1} mm^{-1} (ACC#2) and 86.0 kg ha^{-1} mm^{-1} (ACC#1), respectively. Photosynthesis did not vary with landraces, however, stomatal conductance varied with landraces from 0.08 mmol m^{-2} s^{-1} (ACC#4) to 0.2 mmol m^{-2} s^{-1} (ACC#2). The effective quantum yield of PSII photochemistry (ΦPSII) did not vary with landraces but chlorophyll fluorescence (Fv/Fm) varied with landraces from 0.652 (ACC#4) to 0.792 (ACC#3) in the drier season. A similar trend was observed with chlorophyll content. Root yield and total biomass varied with landraces from 9.5 t ha^{-1} (ACC#4) to 11.9 t ha^{-1} (ACC#3) and 18.2 t ha^{-1} (ACC#4) to 22.0 t ha^{-1} (ACC#1), respectively in the wetter season but landraces did not affect root yield and aboveground biomass in the drier cropping season. Although the

genotype x cropping season interaction did not affect root yield and yield components, root yield and yield components were greater in the wetter compared to the drier season as expected. These preliminary results suggest that ACC#3 and ACC#1 may have some useful traits that may be exploited in cassava improvement programmes for this region. However, there is a need for further studies, incorporating more landraces as well as improved cultivars, over several seasons, before any definite conclusions on their suitability in cassava improvement programmes can be drawn

Keywords: Aboveground biomass, cassava, photosynthesis, root yield, water use and water use efficiency

[OP-81]

Classification of Pepper Accessions from Turkey and Nigeria for Crop Genetic Improvement and Conservation

Anjola Samson Aninkan, Hulya Ilbi

Ege Üniversity, Dept. of Horticulture, Bornova-Izmir/TURKEY

The main of this research was to determine the genetic relationships based on morphological and molecular markers between 60 pepper accessions obtained from Turkey-İzmir Aegean Agricultural Research Institute Gene Bank and Nigeria-Ibadan National Genetic Resources and Biotechnology Center (NACGRAB) Gene Bank. The pepper accessions were grown in greenhouses in Antalya to characterize the agro-morphological traits. Morphological evaluation was made according to 41 criteria defined by the International Union for Conservation of New Plant Varieties (UPOV), As well as morphological evaluation, ten pepper-specific SSR markers were used to determine the genetic differences among the accessions. The Principal Component Analysis (PCA) was performed by using 33 morphological traits that varied between accessions. PCA analysis based on morphological traits generated 9 PC axes representing 77.64% of the total variation between pepper accessions, the majority containing fruit traits. In the dendrogram based on morphological data, it was determined that the genetic distance of pepper accessions varied between 1% and 25%. The pepper accessions were classified under four main groups, based on plant growth habit and fruit characteristics. SSR analysis yielded an average of 7.9 alleles per locus with a total of 79 polymorphic alleles and an average polymorphic information content of 0.664. PCA analysis generated 17 PC axes representing 82.17% of the total variability between accessions. In the dendrogram created based on SSR data, it was seen that pepper accessions were classfied under 7 main groups. It was observed that the genetic distance between the accessions varied between 18% and 98%. The study was able to determine the genetic distances both morphologically and molecularly in the sixty pepper accessions collected from Nigeria and Turkey and a basis was formed for their future use in breeding programs.

Keywords: Plant characterization, genetic resources, Capsicum spp and SSR markers

[OP-82]

Wheat in Different Ploidy Levels (Triticum) Evaluated in Terms of Micro Nutrient Content for Breeding Studies

Bayram Özdemir[1], Saime Ünver Ikincikarakaya[2]

[1]Wheat Breeding Unit, Plant Breeding & Genetics Department, Field Crops Central Research Institute
[2]Field Crops Department, Faculty of Agriculture, Ankara University

This research was carried out at the Research and Production Farm of Field Crops Central Research Institute located near İkizce Village in Ankara Province, Gölbaşı District, during the 2016-2017 and 2017-2018 growing seasons. In the study; It was aimed to determine the differences between wild, local and commercial varieties of wheat (7 different genotip) at 2 different ploidy levels in terms of microelement contents which are important in human diet. The experimental design was the split plots design with four replications and traits; heading days, plant height, number of fertile ears per square meter, grain yield per unit area, harvest index per unit area, thousand grain weight, hectoliter weight, protein content and sedimentation (Zeleny) were evaluated. Since the significant statistical difference between years was found for all the examined characters, the years were evaluated separately. In the first year of the trial; the variety named Sönmez-01 had the highest unit area for grain yield with an average 255 kg/da in biofortification application, followed by the variety, while Sünter cultivar with an average 139 kg/da showed the lowest unit area for grain yield in the no-applied biofortification. In the second year of the trial; Bayraktar 2000 variety showed the highest unit area grain yield with an average 338 kg/da, followed by

Sönmez variety with an average of 286 kg/da whereas Sünter with an average 141 kg/da demostrated the lowest unit area for grain yield, respectively. In terms of microelement content, local and wild varieties had high values, while the difference for element content between varieties was statistically insignificant.

Keywords: wheat, micro element, iron (Fe), zinc (Zn), sulfur (S), selenium (Se)

[OP-83]

Increasing Zinc and Iron in Durum Wheat for Central Anatolia Conditions

Gokhan Kilic[1], Muhsin Ibrahim Avci[1], Saime Unver Ikincikarakaya[2]

[1]Wheat Breeding and Genetics Unit, Plant Breeding Department, Central Research Institute for Field Crops
[2]Field Crops Department, Faculty of Agriculture, Ankara University

Wheat is one of the most important staple crops in the world, providing a substantial amount of proteins and calories for millions. However, due to its low levels of essential micronutrient contents such as zinc and iron, it leads to deficiency of these elements, especially in developing countries where the diet is mostly based on cereals. Wheat wild relatives with high iron and zinc content are great genetic resources to transfer these desirable characteristics to modern cultivars. Thus, in this study, 19 genotypes derived from interspecific hybridization as well as 5 check varieties were utilized in order to determine the iron and zinc content along with grain yield. The study was carried out according to a randomized complete block design with 4 replications during the 2019-2020 and 2020-2021 growing seasons in Ankara, Konya, Kirsehir, and Sivas locations. The zinc and Iron content of the genotypes ranged between 34.06-45.63 mg/kg, and 15.8-21.07 mg/kg, respectively while grain yield ranged between 164.43-268.5 kg/da. Interspecific hybrids have resulted in higher Zinc and Iron content compared to modern durum cultivars. These genotypes will be valuable for future breeding efforts as parent lines to achieve high-yielding and iron and zinc-rich genotypes.

Keywords: zinc conent, iron conent, durum wheat, grain yield, micro nutrient, wheat wild relatives

[OP-84]

A Perspective on the Chromosome Properties of Local Bottle Gourd Landraces

Ahmet L. Tek

Department of Agricultural Genetic Engineering, Ayhan Sahenk Faculty of Agricultural Sciences and Technologies, Niğde Ömer Halisdemir University, 51240, Niğde, Turkey

Landraces with a broad genetic diversity are important genetic resources for plant breeding. Initial tapping this genetic diversity requires efficient and robust tools to determine possible chromosomal variations. Fluorochrome banding with CMA$_3$/DAPI and fluorescence *in situ* hybridization (FISH) with ribosomal genes (rDNA) can be used to compare morphological differences with possible chromosomal changes among landrace populations. Bottle gourd (*Lagenaria siceraria*) is the only cultivated species (2n = 2× = 22) in its genus with high genetic diversity. We collected landraces from geographically distinct regions in Turkey. The CMA$_3$/DAPI banding showed four signals on the GC- and AT-rich regions on interphase nuclei and somatic metaphase chromosomes. Interestingly, FISH with the 45S ribosomal genes indicated a colocalization of four signals with the CMA$_3$/DAPI. On the other hand, FISH with the 5S rDNAs probes showed a signal at the termini of another pair of chromosomes. Overall, two chromosome pairs can be identified individually with cytogenetic markers, and there is no chromosomal level changes among five different bottle gourd landraces.

Keywords: bottle gourd, CMA$_3$/DAPI, FISH, fluorochrome staining, landrace, ribosomal DNA

[OP-85]

Determination of Effective Dose by Gamma Irradiation in Shoot-Tips of Banana

Filiz Baysal[1], Güçer Kafa[3], Nihal Denli[2], Onur Uysal[4], Haluk Ihsan Tekin[2]

[1]Alata Horticultural Research Institute, Department of Fruit Growing and Viticulture, Erdemli, Mersin, 33740, Türkiye
[2]Alata Horticultural Research Institute, Department of Vegetable and Ornamental Plants, Erdemli, Mersin, 33740, Türkiye
[3]Directorate Of Provincial Agriculture And Forestry, Herbal Production and Phytosanitary Branch Directorate, Kadıköy, İstanbul, 34728, Türkiye
[4]Alata Horticultural Research Institute, Department of Production and Business, Erdemli, Mersin, 33740, Türkiye

Banana is a type of fruit that shows absolute parthenocarpy in terms of fertilization biology. Mutation breeding is used as an alternative breeding method for obtaining new varieties and hybrids to solve the problems experienced in breeding. A mutation breeding project has been designed to develop new varieties with superior characteristics that can compete with imported bananas to support banana cultivation and increase yield. In the study, the GP23 banana clone obtained by selection was used. The suckers removed from the greenhouse were shrunk to be explanted, with 8-10 leaf layers on them, and were taken to the Türkiye Atomic Energy Agency for irradiation by taking them into autoclavable bags. 50 explants were used at each dose administration, including the control group. After the application of acute gamma rays at doses of 0 (Control), 10, 20, 30, 40, 50, 60, 70, 80, 90, and 100 grays, the explants were cultured in the initial medium specified. The explants were planted in nutrient media with a 0.5-1 cm length of growth cones. The number of plants that died and the number of plants that survived was determined for each dose of radiation on the 45th day following the application. After the data was obtained, the proportions of living plants with the formula (number of dead plants/number of surviving plants) x 100 were determined according to the doses. By evaluating these viability rates, the LD50 radiation dose at which 50% viable and reproducible plants can be obtained as a result of irradiation was determined. After acute gamma ray application, the LD50 dose was determined as 38.5 gray. As a result of the study, very prominent swelling occurred in the leaf layers of the explants transferred to the nutrient medium immediately after irradiation. In addition, explants that developed vertically after the shoot tip growth started in explants did not survive, while explants that formed a slightly horizontal shoot tip were able to till their development in a healthy way.

Keywords: banana, breeding, explant, LD50 dose, mutation

[OP-86]

Clarification Optimization in Pomegranate Juices Obtained from Some Pomegranate Cultivars and Genotypes

Zeynettin Baysal[1], Ali Tekin[1], Nesrin Karataş[1], Rıdvan Arslan[2], Evren Çağlar Eroğlu[1], Mustafa Ünlü[1], Tuğçe Göktürk Taşkın[1], Halil Esimek[1], Hacı Ibrahim Ekiz[2], Erdal Ağçam[3]

[1]Alata Horticultural Research Institute
[2]Mersin University, Engineering Faculty, Department of Food Engineering
[3]Cukurova University, Engineering Faculty, Department of Food Engineering

In pomegranate juice production, pomegranates; are pressed directly with their shells or by graining. The pomegranate juices obtained after pressing are quite turbid. For this reason, the most important process in the production of pomegranate juice and concentrate is clarification. In this study, pomegranate juice samples were obtained by using different pomegranate cultivars and genotypes and it was aimed to obtain optimum clarification conditions in these samples.

Besides, pomegranate concentrate (pomegranate syrup) was obtained by thickening pomegranate juice samples that were rinsed under vacuum, and it is aimed to reveal the local and international suitability of these pomegranate juice concentrate samples and some bioactive component contents. Pectolytic enzyme, gelatin and bentonite were used for clarification. These agents were used at different temperatures, durations and dosages. NTU values in pomegranate syrup samples ranged from 0.06 to 0.94. While the lowest NTU value was obtained in Hicaznar variety, the highest NTU value was obtained in Onurnar5 variety. As a result, it has been determined that all varieties and genotypes used in the study can be used for pomegranate juice production by providing optimum clarification conditions.

Keywords: PomePomegranate (Punica granatum Linn.)., Pomegranate juice, Clarification, Pomegranate Syrup

[OP-87]

Short-Duration Mungbean for Ecologically Oriented Crop Diversification in the Aral Sea Region of Central Asia

Ram Sharma[1], Akmal Akramkhanov[1], Ravza Mavlyanova[2], Yulduz Djumaniyazova[3], Bekjon Matjonov[3], Esbosin Sadikov[4], Zafar Ziyaev[5]

[1]International Center for Agricultural Research in the Dry Areas (ICARDA), 6 Osiyo Street, Tashkent, Uzbekistan
[2]Research Institute of Vegetable, Melon Crops and Potato, Tashkent, Uzbekistan
[3]Urgench State University, 14 Hamid Alimjan, Urgench 220100 Uzbekistan
[4]Grain and Rice Research and Production Association in Nukus, Karakalpakstan, Uzbekistan
[5]Institute of Plant Genetics and Experimental Biology, Tashkent, Uzbekistan

Land degradation is a constraint to sustainable crop production across Central Asia including the cold-arid Aral Sea region due to increasing salinity, extreme heat and cold, and limited crop diversification caused by predominant wheat-cotton rotation. Winter wheat is planted in September-October and harvested in June-July. Spring wheat is planted in March-April and harvested in June – July. Cotton is planted in March-April and harvested in September-October. Frost occurs in September-October. In some years, when cotton harvested is delayed and frost occurs early, it may not be possible to plant winter wheat. Considering that farmers must grow cotton and wheat as strategic crops there is a limited window of a maximum of 3 months to grow an additional crop after the wheat harvest. On a limited scale, farmers have been growing fodder crops such as maize and halophytes after wheat harvest. However, these fodder crops further impoverish the soil. An alternative for sustaining soil health remains either cultivation of a short-duration leguminous crop for grain or green manure. A sole green manure crop can also be grown for improving soil health. ICARDA with funding support from GIZ has started alternative crop rotations in the Aral Sea region with the potential of growing up to three leguminous crops – one grain and two green manure – in the present one cycle of wheat–cotton rotation.

Short duration (70 days) grain-purpose mungbean variety “Durdona” which has already been successfully produced in other parts of Uzbekistan and Tajikistan between two crops of winter wheat was grown in the rotation. Besides, a green manure winter pea crop has also been utilized in the rotation. Spring wheat was included in the rotation for conditions where winter wheat can’t be planted in autumn. The experiments were conducted in 10 farmers’ fields in the Aral Sea region. Each crop was planted in an RCBD in two replicates using 1,500 m^2 individual plots. To determine profit from traditional and new rotations, economic analyses are being conducted for each crop. Soil analyses before and after each rotation are included in the experiments to assess soil health.

Both winter wheat and spring wheat followed by mungbean have been successfully grown in the farmers’ fields and cotton will be planted in the spring of 2023. Both winter wheat and spring wheat were successfully grown allowing ample time for the cultivation of mungbean. The highest grain yields of winter wheat and spring wheat were 6.2 and 3.2 t ha^{-1}, respectively. The rates of economic return were higher for winter compared to spring wheat. Mungbean planted in June yielded higher compared to early July planting. An economic analysis of mungbean production is being conducted. Previous work in Uzbekistan had that mungbean could bring up to USD 2,000 ha^{-1}. The successful cultivation of mungbean demonstrates that it is possible to diversify wheat-cotton rotation both for economic, soil health and environmental benefits. The findings bear far-reaching implications for economic, soil, and environmental benefits in the Aral Sea region with spillover benefits for entire Central Asia.

Keywords: Aral Sea, crop rotation, Durdona mungbean variety, land degradation, soil health, Uzbekistan, wheat

[OP-88]

Bread Wheat Landraces of Van Lake Basin

Mehmet Ülker[1], Fevzi Altuner[3], Burak Özdemir[1], Sana Jamal Salih[1], Erol Oral[1], Siyami Karaca[2], Solmaz Najafi[1], Selami Yazar[5], Şadiye Demir Atmaca[1], Durmuş Deniz[5], Bulut Sargın[2], Mehmet Alp Furan[4]

[1]Van Yüzüncü Yıl University, Faculty of Agriculture, Field Crops Department, Van/Turkey
[2]Van Yüzüncü Yıl University, Faculty of Agriculture, Soil Science Department, Van/Turkey
[3]Van Yüzüncü Yıl University, Gevaş Vocational School, Crop and Animal Production, Organic Agriculture Program, Van/Turkey
[4]Van Yüzüncü Yıl University, Faculty of Agriculture, Agricultural Biotechnology Department, Van/Turkey
[5]Ministry of Agriculture and Forestry, Field Crops Central Research Institute, Ankara/Turkey

As the wheat spread from the fertile crescent to other regions, it was shaped according to the human and geographical conditions of each region where it was cultivated. In the process until today, the culture and expectations of the people who shape it in every period and the changing environmental conditions of the region have made small touches to local varieties. In addition to the plant characteristics preferred by the growers, the palate tastes of those who consume it have also been an essential factor in shaping the local wheat varieties. Thus, local varieties have been transformed into valuable genetic material with a broad genetic base, well adapted to the region in which it was grown. In this respect, each local variety has become a cultural heritage of the region in which it developed.

Lake Van Basin is next to the Fertile Crescent and is Turkey's second-largest closed basin. The climate of the basin, where the continental climate prevails, is softer due to the effect of Lake Van. Annual precipitation in the basin varies between 380-1000 mm, and the annual average temperature is 8.9 0C. Local bread wheat varieties such as Karakılçık, Tir, Geverik, Hevidi, Kirik and Toptopik are grown in the region where low-input agriculture is dominant. Since the first studies by Zhukovsky and then Gökgöl in 1925 to preserve the genetic materials of wheat grown in the region, very few of the collected materials have been preserved. As a result, a limited part of the bread wheat genotypes collected in the last hundred years are protected and accessible in certain seed gene banks.

Within the project started in the Van Lake basin (going a little further out of the basin in some places) in 2019, the spikes of local bread wheat were collected from the farmer fields. The seeds of the lines were multiplied by the spike-to-row method, and characterisation was made in terms of some traits in two locations. Furthermore, samples representing farmer fields were delivered to the Ankara Seed Gene Bank and taken under protection.

In this paper, the current situation of local bread wheat varieties in the Van Lake Basin will be evaluated together with the bread wheat collection studies carried out in the last hundred years.

Keywords: Bread wheat, Landraces, Van Lake Basin, Collection, Characterisation

[OP-89]

Characterization and Evaluation of Wheat Landraces Genotypes Root System for Drought Prone Areas and Development of Drought Resistance Varieties

Mohd M Alajlouni

Plant Production Department, Faculty of agriculture, Jordan University of Science and Technology, Irbid, Jordan

This study designed to evaluation group of wheat landraces genotypes that has been collected early from Jordan for the root traits that will enable the plants to utilize more water and nutrients from the top and subsoil profile. Improving the root characteristics will lead to reduction in the farm input and improve the water use efficiency and productivity of these genotypes. In other word this study will lead to "more crop per water drop" and more crop per unite of nutrient. Landraces genotypes that have extensive root system which grow very fast during high soil availability to explore more water and support the above ground plant growth and can limited the growth when water is short in rainfed areas will be of high interest. The other aspect that this study will concentrate on is identification of genotypes that have contrasted root and shoot characteristics phenotypes which will be used in cross to produce new drought resistance wheat varieties. The selection process and testing of the new varieties will be on the basis of its ability to have efficient water and nutrient uptake, its ability to have efficient carbon investment in roots and have good plant strategy in utilizing water for crop production. Therefore, the specific objectives of this study will include evaluation of wheat landraces root characteristics; identify the genotypes that have diverse root system;

and crossing and testing the identify genotypes to produce new drought resistance wheat varieties. The experiment was planted at the green house in 50 cm diameter glass cylinders and Soil mix used was 1:1:1 Soil, peat mouse and sand to facilitate the root washing. The number of landraces genotypes used was 120. The root system has been classified according to the root angle and biomass to four categories: (i) narrow root angel high root biomass, (ii) wide root angel high root biomass, (iii) narrow root angel low root biomass, and (iv) wide root angel low root biomass. The results shows that the 36% of the genotypes has a wide root angle and high biomass which was the most dominant and the second category was the narrow root angle and high biomass with 31%, while the third category was the narrow angle and the low biomass with 20%, the wide angle and low biomass was the least dominant with only 12%. To test the drought resistance of these genotypes, next season they will be planted in three locations with moderate to low rain fall average (between 450 and 200 mm).

Keywords: Wheat landraces, Root system, Drought

[OP-90]

Improvement of Cotton Varieties Using Modern Genetic and Biotechnological Methods on the Basis of Biodiversity of the Genus Gossypium L

Fakhriddin N. Kushanov[1], Ozod S. Turaev[2], Dilrabo K. Ernazarova[1], Ziroatkhon A. Ernazarova[1]

[1]Institute of Genetics and Plant Experimental Biology, Academy of Sciences of the Republic of Uzbekistan, Qibray QFY, Yuqori-Yuz, Qibray district, Tashkent region, 111226 Uzbekistan
[2]Department of Biology, National University of Uzbekistan, University Street-4, Olmazor district, Tashkent, 100174 Uzbekistan

Plant genetic diversity and resources are one of the most important resources for food security and agriculture. Many crop species especially their wild ancestors are responsible for the genetic variation associated with world food production. Creating a new variety using traditional breeding methods requires some hard work and a long time. Modern, marker-based selection (MAS) technology is somewhat more efficient than conventional selection methods in terms of resource efficiency and less time required for creating a new variety.

Cotton (Gossypium) is the main cash crop that supplies the world's textile industry with natural fiber. The genus Gossypium L. belongs to the small taxonomic tribe (Gossypieae) with nine genera in total, eight of which are classically recognized. The haploid set of cotton chromosomes is 13, and in nature, they occur as diploid ($2n=26$) and tetraploid ($2n=52$) species. At present, the genus Gossypium includes seven allotetraploid and 50 diploid species distributed among eight genome groups (A-G and K genomes). The natural biodiversity of cotton - its wild relatives - is the richest source of genetic resources, the smallest part of which is used in breeding programs.

Much of the gene pool is still waiting to be recognized. The rich potential of the Old-World species has been used extremely little; they are used mainly in the countries of Asia and India. In breeding terms, many forms of subspecies of these species, as well as New World species (G. herbaceum L., G. arboreum L.), are of great practical interest, possessing a number of very valuable economic traits: high early maturity, resistance to water deficiency, disease, good fiber quality, fiber hygroscopicity.

The reasons for the extremely low use of the available intraspecific diversity are, first of all, the insufficiently high level of development of theoretical issues of taxonomy and phylogeny, as well as a number of objective problems that arise during hybridization, biotechnology, genetic engineering and other attempts to involve and transfer valuable germplasm into the genome of cultivated varieties.

The involvement of new alleles of genes of wild-growing relatives in the selection process greatly increases the prospect of creating unique source materials with useful properties and with a new gen-immune system of potential resistance to agricultural diseases and pests.

However, due to the difference in the number of chromosomes, the possibility of obtaining hybrids based on cross-breeding of diploid species and tetraploid species, in particular G. hirsutum, is limited

Since, under the influence of colchicine it is possible to double the number of chromosomes of diploid species and crossbreed with G. hirsutum varieties and thereby create starting materials for cotton breeding research.

One of the modern approaches to the study of plant genomes is the technology of molecular markers, which make it possible to fully assess phylogenetic relationships and relationships, identify varieties, and identify DNA markers associated with economically valuable traits. Once identified, these molecular markers allow faster and more efficient plant breeding with a significant reduction in financial costs.

Keywords: Cotton, Gossypium L., genetic diversity, marker-assisted selection

[OP-91]

Perennial Wheat for Improving Multiple Traits of Bread Wheat for Agro-Pastoral Farming System in Central Asia

Amir Amanov[1], Dilshod Musirmanov[1], Safar Alikulov[1], Ram Sharma[2]

[1]Research Institute of Plant Genetic Resources, Kibray, Uzbekistan
[2]International Center for Agricultural Research in the Dry Areas (ICARDA)

Wheat and meat production is directly linked with food security and nutrition in Central Asia. There are a number of abiotic and biotic constraints to wheat production in Central Asia with heat, drought and yellow rust of particular significance. Dwindling rainfall and irrigation water availability to wheat production and terminal heat stress have become primary concern to wheat growers in Uzbekistan. Two of the above three factors also affect natural pasture making it necessary to think about additional source of grazing vegetation. In the above contexts of stresses faced by wheat crop and natural pastures, perennial wheat offers promise by introgression of its stress tolerance, extensive root system and ratooning ability into modern varieties of bread wheat.

A set of 32 experimental genotypes and Bezostaya-1 were obtained from the International Winter Wheat Improvement Program (IWWP), which is a joint program of the Government of Turkey, CIMMYT and ICARDA. Perennial wheat had been received from Kansas State University, USA. Field experiments were conducted at the Research Institute of Plant Genetic Resources in Kibray, Uzbekistan in three years, 2018 to 2020. Sixteen plant traits were evaluated. One of the 32 lines showed 100% regrowth after summer harvest; this line had been utilized in the partial backcross breeding.

Perennial wheat significantly differed from Bezostaya-1 for several traits. Compared to Bezostaya-1, the perennial wheat showed significantly higher number of tillers per plant (20 vs. 12), taller plants (124 cm vs. 97 cm), lower yellow rust severity (0% vs. 40%), longer spike (16.3 cm vs. 11.4 cm), fewer spikelet per spike (16.7 vs. 19.2), less kernel per spike (44 vs. 54), lighter kernel (25 g vs. 40 g), and lower grain weight per spike (1.3 g vs 2.5). The magnitudes of the differences for root length and root mass were significantly and visibly higher for perennial wheat compared to Bezostaya-1. Rood distribution of Bezostaya-1 was primarily in the upper 15 cm soil surface compared to 57 cm for perennial wheat.

Through three backcrossing with bread wheat, a number of agronomic traits were improved. One-thousand kernel weight was improved from 22 g to 40 g in the BC3F3 generation. Regrowth trait was successfully transferred into the bread wheat, and aboveground biomass was harvested in October 2022 from the ratoon crop. A number of BC3F3 lines have also shown resistance to yellow rust and performed well under soil salinity in the cold arid region of Aral Sea. The long and profuse rooting system of the perennial wheat was substantially transferred into the bread wheat. The value of the new root system in extracting water from the deeper soil levels under rainfed and limited irrigation condition needs to be assessed. Comparative economic analysis of new wheat lines in comparison to other annual crop rotations needs to done. The new perennial-wheat-derived lines have implications for improving stress tolerance of bread wheat as well as provide grazing opportunities in the mixed agro-pastoral farming systems in Central Asia and beyond.

Keywords: Perennial wheat, bread wheat, wheat-livestock farming system, stress tolerance, Uzbekistan

POSTER PRESENTATIONS

[PP-01]

Eggplant Genome Editing Using CRISPR/Cas9 Technology

Vese Pakashtica[1], Nedim Mutlu[1], Hasan Pinar[2], Inanc Soylu[3], Cansu Bulbul[4], Selcen Dogan[1], Alparslan Karabeniz[1], Fatma Akcakale[1], Adem Kaba[1], Aidai Muratbek Kyzy[1], Mamoudou Zonon[1], Ahmet Barkan Bostan[1]

[1]Akdeniz University, Department of Agricultural Biotechnology, Antalya, Turkey
[2]Erciyes University, Department of Horticulture, Kayseri, Turkey
[3]University of Nebraska, Department of Plant Pathology, Nebraska, America
[4]Areo Seed Company, Antalya, Turkey

Eggplant (Solanum melongena L.,) is one of the main used vegetables in many countries. It has a long growth period which makes as one of the vegetables that is more exposed to pests, disease infestation, environmental stresses and parasitic weeds.

Orobanche spp. known as broomrape is one of the parasitic weeds that can cause huge damages to yields off eggplant. It is a well- known fact that these parasite seeds for germination need to be exposed to specific chemicals called strigolactones [SLs], which are released by the host roots.

The CCD8 gene is involved in the synthesis of strigolactones and plays an important role in controlling growth and development. CRISPR-Cas9 has been applied to manipulate the SlCCD8 gene in eggplant (Solanum melongena).

Using the Agrobacterium-mediated plant transformation method gRNA and Cas9 were transferred to eggplant. As the material was used eggplant cotyledons. The successful editing of eggplant lines was confirmed by Sanger sequencing. The induced mutations were stably inherited in the T1 progeny. Our findings based using CRISPR-Cas9 technology opens the way to the development of eggplant genotype's resistance to parasitic weeds

Keywords: Agrobacterium tumefaciens-mediated, CCD8, CRISPR-Cas9 technology, Eggplant, Orobanche spp

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[PP-03]

Genome-Wide Association Study for Leaf Rust and Stem Rust Resistance in Bread Wheat Growing in Kazakhstan

Alibek Zatybekov[1], Yuliya Genievskaya[1], Aralbek Rsaliyev[2], Akerke Amalova[1], Moldir Yermagambetova[1], Saule Abugalieva[1], Yerlan Turuspekov[1]

[1]Laboratory of Molecular Genetics, Institute of Plant Biology and Biotechnology, Almaty 050040 Kazakhstan
[2]Laboratory of Phytosanitary Safety, Research Institute of Biological Safety Problems, Gvardeisky 080409, Zhambyl Region, Kazakhstan

Common wheat (Triticum aestivum L.), is one of the main cereal crops cultivated around the world and is important for food security. Kazakhstan is among the ten largest exporters of wheat, with a volume of 11.4 thousand tons produced in 2019. According to the Bureau of National Statistics of Kazakhstan, the sown area under wheat was 12.2 million hectares in 2021, which represents about 76.7% of the total area used for cereal crops in the country. One of the largest problems in wheat production all over the world is foliar diseases, in particular Puccinia graminis f. sp. tritici (Pgt), causing stem rust (SR), and Puccinia triticina Eriks. (Pt), causing leaf rust (LR). One of the most effective ways to prevent wheat rust epidemics is the development of cultivars with durable resistance to pathogens. The development of new cultivars with high productivity and LR and SR disease resistance, including using marker-assisted selection, is becoming an important priority in local breeding projects. Therefore, the search for key genetic factors controlling resistance in all plant stages, including the seedling stage, is of great significance. LR and SR resistance is controlled by a diverse group of genes, designated as Lr and Sr, respectively. In the literature, approximately 80 Lr and about 60 Sr genes have been identified and described in bread wheat, durum wheat, and diploid wheat species. In this work, we applied a genome-wide association study (GWAS) approach using 212 local bread wheat accessions that were phenotyped for resistance to specific races of Pt and Pgt at the seedling stages. The collection was genotyped using a 20 K Illumina iSelect SNP assay, and 11,150 polymorphic SNP markers were selected for the association mapping. Using a mixed linear model, we identified 11 quantitative trait loci (QTLs) for five out of six specific races of Pt and Pgt. The comparison of the results from this GWAS with those from previously

published work showed that nine out of eleven QTLs for LR and SR resistance had been previously reported in a GWAS study at the adult plant stages of wheat growth. Therefore, it was assumed that these nine common identified QTLs were effective for all-stage resistance to LR and SR, and the two other QTLs appear to be novel QTLs. In addition, five out of these nine QTLs that had been identified earlier were found to be associated with yield components, suggesting that they may directly influence the field performance of bread wheat. The identified QTLs, including novel QTLs found in this study, may play an essential role in the breeding process for improving wheat resistance to LR and SR. This research was funded by the Ministry of Agriculture of the Republic of Kazakhstan, grants number BR10765056, and by the Ministry of Education and Science of the Republic of Kazakhstan grant number AP08855387.

Keywords: wheat, rust diseases, GWAS, QTL, marker assisted selection, crop genetics

[PP-04]

QTL Mapping of Agronomic Traits in Wheat Using the Pamyati Azieva × Paragon Mapping Population Tested in Kazakhstan

Akerke Amalova[1], Simon Griffiths[2], Saule Abugalieva[1], Yerlan Turuspekov[1]

[1]Laboratory of Molecular Genetics, Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2]Department of Crop Genetics, John Innes Centre, Norwich, United Kingdom

Wheat is one of the three most important food crops in the world. Although genome-wide association studies are an increasingly informative tool in the mining of new quantitative trait loci (QTLs), a classical biparental mapping approach is still a widely used powerful method to search the unique genetic factors associated with important agronomic traits in bread wheat. In this study, a newly constructed mapping population of Pamyati Azieva (Russian Federation) × Paragon (UK) consisting of 94 recombinant inbred lines (RILs) was tested in three different regions of Kazakhstan with the purpose of QTL identification for key agronomic traits. The RILs were tested in 11 environments of two northern breeding stations (Petropavlovsk, North Kazakhstan region, and Shortandy, Akmola region) and one southeastern station (Almalybak, Almaty region). The following eight agronomic traits were studied: heading days, seed maturation days, plant height, spike length, number of productive spikes, number of kernels per spike, thousand kernel weight, and yield per square meter. The 94 RILs of the PAxP cross were genotyped using Illumina's iSelect 20K single nucleotide polymorphism (SNP) array and resulted in the identification of 4595 polymorphic SNP markers. The application of the QTL Cartographer statistical package allowed the identification of 53 stable QTLs for the studied traits. A survey of published studies related to common wheat QTL identification suggested that 28 of those 53 QTLs were presumably novel genetic factors. The SNP markers for the identified QTLs of the analyzed agronomic traits of common wheat can be efficiently applied in ongoing breeding activities in the wheat breeding community using a marker-assisted selection approach. The Ministry of Education and Science of the Republic of Kazakhstan grant number AP08855387, and by the Ministry of Agriculture of the Republic of Kazakhstan funded this research grants number BR10765056.

Keywords: *Triticum aestivum* L., quantitative trait loci, mapping population, recombinant inbred lines

[PP-05]

SNP Markers for the Resistance of Barley (*Hordeum vulgare* L.) to Spot Blotch, Barley Stripe and Powdery Mildew in South-East Kazakhstan

Yuliya Genievskaya, Alibek Zatybekov, Yerlan Turuspekov, Saule Abugalieva

Laboratory of Molecular Genetics, Institute of Plant Biology and Biotechnology, Almaty 050040, Kazakhstan

Fungal diseases of barley, including spot blotch (*Cochliobolus sativus* (Ito et Kurib.) Drechsler ex Dastur.), barley stripe (*Bipolaris sorokiniana* (Sacc.) Shoemaker), and powdery mildew (*Blumeria graminis* f. sp. *hordei*) are important biotic stress factors all over the world. Each of them may cause grain yield losses up to 30-40% in susceptible barley cultivars. In Kazakhstan, particularly in southeastern part of the country, these three fungal diseases are common and occur periodically under conditions favorable for the development and reproduction of pathogens. One of the most effective ways to protect crops from massive disease outbreaks is growing of genetically resistant cultivars. Disease resistance is a genetically complex trait controlled by several genes in barley genome. There are 3 *Rdg (Rhg)*, 5 *Rcs*, and 23 *Ml (Reg)* genes responsible for the resistance to barley stripe, spot blotch, and powdery mildew, respectively, as well as hundreds quantitative train loci (QTL) described in literature earlier. In this study, we applied a genome-wide association study (GWAS) for the identification of marker trait associations (MTAs) in a world collection of spring barley (n=415). This collection was grown in 2020 in experimental field of Kazakh Research Institute of Agriculture and Plant Growing (Almaty region) under natural infectious conditions and genotyped using the 9K SNP Illumina chip. As a result, we identified seven MTAs for the resistance to barley stripe, two MTAs for the spot blotch, and one MTA for powdery mildew resistance (P<1.00E-4). MTAs for barley stripe resistance were observed on chromosomes 1H, 2H, 3H, 4H, and 6H; spot blotch resistance MTAs were identified on chromosomes 1H and 2H; powdery mildew resistance MTA was found on the chromosome 4H. MTA for powdery mildew resistance demonstrated high genetic effect explaining 44 % of phenotypic variance and likely, that the SNP was associated with the resistance gene *Reg2*. Other SNPs associations identified for spot blotch and barley stripe were located away from known resistance genes and could be considered as novel for these traits. MTAs identified in this study can be efficiently used in breeding barley cultivars with broad genetic resistance to fungal diseases or for gene (QTL) pyramiding. The study was supported by the Program "Biological safety of the Republic of Kazakhstan: assessment of threats, scientific and technical bases of their prevention and elimination" (2021-2023) from the Ministry of Education and Science of the Republic of Kazakhstan

Keywords: barley spot blotch, barley stripe, powdery mildew, GWAS, marker-assisted selection

[PP-06]

Effects of Tray Conditions for Cucumber Cuttings

Nur Ülger[1], Özlem Ertem[2]

[1]Nur Ülger, R&D Department, Multi Tohum Tar. San. Tic. A.ş., Antalya, Turkiye
[2]Özlem Ertem, R&D Department, Multi Tohum Tar. San. Tic. A.ş., Antalya, Turkiye

Cucumber (Cucumis sativus L.) is one of the most economically important crops consumed worldwide. Seedling quality is one of the most significant parameters on the process of vegetable production. Therefore, many researches have been done on the optimization of nursery conditions. For research and development processes in production, plant cuttings are utilized. This study is performed to evaluate the effects of different tray soil contents for cucumber cuttings from different varieties. Bereket F1 and two different Multi Tohum F1 varieties were used to understand the effects of pearlite and peat-pearlite mixture (1:1) on rooting. The study has been done in 2021 at Multi Tohum A.Ş greenhouses located in Antalya, Turkey. Three replications have been done for this experiment. It is observed that plant growth rate of cuttings was slower than the standard growth of hybrids sown from seeds. As a consequence of this experiment, the cuttings which were planted in the peat-perlite mixture performed higher survival rate compared to only perlite use. Therefore, for cucumber cuttings peat-perlite mixture should be used during production.

Keywords: Cucumber, Cutting, Nursery

Figure 1. Bereket F1

[PP-07]

Genomic Selection to Predict Fusarium Head Blight (FHB) Resistance of Wheat Lines from the Great Plains Using Ohio Phenotypic Data

Lenin Rodriguez, Carlos Ignacio, Nelly Arguello, Corinne Marfori, Clay Sneller

The Ohio State University

Fusarium head blight (FHB) is a prevalent disease in the Midwest and the great plains of the United States that can make wheat inedible due to deoxynivalenol (DON) toxin accumulation from infection of the fungus Fusarium graminearum. However, unlike in the Midwest, low humidity in the great plains lowers the FHB disease pressure needed to evaluate FHB resistance. Genomic prediction and selection (GS) can help in this scenario since it estimates the performance of lines that have not been phenotyped using genomic data. This research aims to measure how accurately FHB resistance of hard red winter wheat (HRWW) in the great plains can be predicted using GS with phenotypic data gathered from the Midwest. Using a randomized complete block design, we evaluated 373 HRWW lines from the University of Nebraska and 434 from South Dakota State University (SD) in 2020 and 2021 FHB nurseries at the Ohio Agricultural Research and Development Center, The Ohio State University. DON accumulation, Fusarium damaged kernel, and disease index were used with Genotyping by Sequencing data to train the GS model. Results showed that the correlation of the phenotypes of the SD lines with their predicted value based on Ohio (OH) data was 0.30, similar to the correlation of OH phenotypes and SD Genomic Estimated Breeding Values with SD phenotypes. These outcomes indicate that we can obtain OH phenotypes that predict FHB resistance in HRWW.

Keywords: Fusarium Head Blight, Genomic Selection, Deoxynivalenol, Genotyping by Sequencing

[PP-11]

Effect of Flour Beetle's (Tribolium confusum) Infestation of Wheat Flour's (Triticum Durum) Toxicological Properties for Human Consumption

Noureddine Laadel[1], Abdelmalek Oulmi[2], Cyntia Mekideche[3], Zouhir Boulgueraguer[4], Sofiane Guettaf[5], Akram Akram[6], Nadia Benzidane[7]

[1]Noureddine Laadel Laboratory of Improvement and development of plant and animal production, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[2]Abdelmalek Oulmi Laboratory for the Valorization of Natural Biological Resources (LVNBR), Faculty of Nature and Life Science, Ferhat ABBAS University Sétif-1, 19000 Setif, Algeria
[3]Cyntia Mekideche Department of Biology and plant Ecology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[4]Zouhir Boulgueraguer Department of Geology, Laboratory of water resources and sustainable development REDD,, BADJI Mokhtar, Annaba University. Algeria
[5]Sofiane Guettaf Laboratory of Applied Microbiology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[6]Akram Kout MISC Laboratory. Abdelhamid Mehri Constantine 2 University. Algeria
[7]Nadia Benzidane Laboratory of Applied Biochemistry, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

Wheat is one of the most consumed cereals in the world. It comes from a type of grass (Triticum) that is grown in countless varieties around the world. large quantities of flour are stored in open shounas and/or blinds. Under these conditions, the flour is attacked by various biological factors including insects. Flour beetle (Tribolium confusum) attack stored grain products such as flour, cereals, meal, crackers, beans, spices, pasta, cake mix, dried pet food, dried flowers, chocolate, nuts, seeds, and even dried museum specimens. These beetles have chewing mouthparts, but do not bite or sting. The red flour beetle may elicit an allergic response. Over the past three decades, the presence and adverse effects of certain toxic compounds in flour as a result of insect pest infestation during storage has been of growing international concern. Previous studies have indicated that flour extracted from wheat that has suffered infestation by insect pests such as Tribolium confusum could be affected in its nutritional, chemical and rheological characteristics. Each change

in these factors depends on many variables, such as wheat type, pest species, level of infestation and environmental conditions. previous studies have indicated that infestations by insect pests and their influence on the hygienic parameters of wheat flour. Fifty bowls, 1 kilogram, of flour were used filled with wheat flour 80 % extraction. A 50 larvae of Tribolium confusum were put into each bowl and 15 jars, for 2 months at 25 0C and 50% of relative humidity. At the end of this period, all samples were sieved to recover the insects and then analyzed. Mutagenic and Carcinogenic compounds, increased by the rate of 211.22 and 21.83% compared to 1.29 and 2.17% for the uninfected samples, respectively.

Keywords: wheat flour, insects’ infestation, flour beetles, Mutagenic and Carcinogenic

[PP-12]

Transcriptional Reprogramming During Developmental and Stress-Induced Leaf Senescence in Barley

Klaus Humbeck, Wiebke Zschiesche

Martin-Luther-University Halle-Wittenberg

Leaf function dynamically alters during development and in response to environmental cues, from being a source of assimilates in photosynthetically active leaves to a source of valuable resources in senescing leaves. In this work we analyze reprogramming of gene expression at early and late stages of developmental and stress-induced senescence, i.e., drought stress-induced senescence and N-deficiency- induced senescence. The data show that there is a hierarchical structure of the pathways leading to senescence. At early stages, overlap between the different conditions is low and most genes regulated are specific for the different stress-conditions, e.g., early down-regulation of photosynthesis related genes at onset of developmental senescence, induction of genes encoding osmotic regulators after decrease in soil water content and regulation of genes involved in N metabolism when availability of N is decreasing. At later stages, specific pathways flow into a common senescence pathway which involves typical senescence-associated genes. Knowledge about the structure and function of the complex, dynamic, environment-sensitive and highly flexible regulatory senescence-networks helps to identify key factors of plant performance under changing environment.

Keywords: Barley, transcriptional reprogramming, drought-stress, nitrogen deficiency

[PP-13]

Antioxidant Activity of Phenolic Compounds of Pistacia Lentiscus

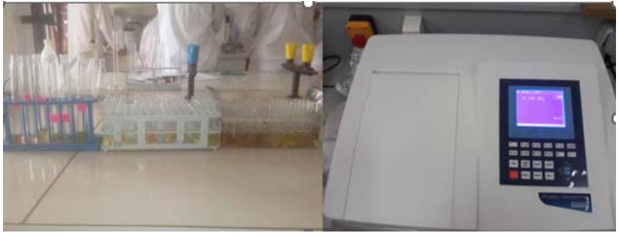
Nadia Benzidane[1], Sofiane Guettaf[2], Lekhmici Arrar[1], Chaima Djehiche[1], Noureddine Laadal[3], Abdelmalek Oulmi[4]

[1]Laboratory of Applied Biochemistry, Department of Biochemistry, Faculty of Nature and Life Science, University Ferhat Abbas, Sétif, ALGERIA
[2]Department of Natural Sciences, Faculty of Natural and Life Sciences Kouba High School 1University, Algiers-ALGERIA
[3]Department of Biology and Plant Physiology, Faculty of Natural and Life Sciences, Ferhat Abbas Sétif-1University, Setif-ALGERIA
[4]Department of Biology and Animal Physiology, Faculty of Natural and Life Sciences, Ferhat Abbas Sétif-1University, Setif-ALGERIA

Objective: To investigate antioxydant activity, total phenolic and flavonoid content of methanol and aqueous extracts of Pistacia lentiscus root, stem and leaf parts selected from Ain Arnat Setif regions of Algeria. Methods: The antioxydant activity of different extracts (aqueous and Methanol fractions) from Pistacia lentiscus was evaluated by the DPPH scavenging test. The total phenolic and total flavonoid content of these extracts was determined according to the Folin-Ciocalteu procedure and Aluminum chloride colorimetric assay respectively. Total phenolic content was measured by Folin Ciocalteu reagent. Results: All the extracts showed significant antioxydant activities and contained important levels of phenols. The methanol extract from Pistacia lentiscus showed the greatest antioxydant capacity, which was probably due to its high content of polyphenols. Total flavonoid content was found equal for all extracts. Conclusions: Our results of antioxydant assays were justified and partially supported the popular usage of the tested plants. The high antioxydant activity found in the plant in this region suggested that Pistacia lentiscus is a good source of natural compounds which might have benefits for health. Keywords: Pistacia lentiscus, Folk medicine, Flavonoids contents, Polyphenols, Antioxidant activity:

Keywords: Pistacia lentiscus, Folk medicine, Flavonoids contents, Polyphenols, Antioxidant activity

Dosage of polyphenole



[PP-14]

Short Palms for Improved Harvesting Efficiency

Siti Khadijah Mohd Rais[1], Wan Rusydiah Wan Rusik[1], Teh Chee Keng[2], Harikrishna Kulaveerasingam[1]

[1]Sime Darby Research Sdn Bhd, KM10, Jalan Banting-Kelanang, PO Box 207, 42700, Banting, Selangor, Malaysia
[2]Sime Darby Plantation Technology Centre, 1st Floor, Block B, UPM-MTDC Technology Centre III Malaysia, Lebuh Silikon, Putra Square, 43400 Serdang, Selangor, Malaysia

The most crucial operation in oil palm plantation is harvesting of fresh fruit bunches that known to be a labour and energy intensive process. The economic life of the oil palm is mainly determined by the height of the palms, when the palm is too tall it becomes uneconomical to harvest either due to unavailability of skilled harvesters, cost or duration taken to harvest the bunches and safety issue to the harvesters. Shorter palms may help to address these four issues. In breeding, progeny and individual palms selection are the most suitable approach for improvement of secondary traits in oil palm because their phenotypic expression strongly influenced by environment factors. Crosses between Kulai-Nigerian dura with URT-Calabar pisifera resulted into 8 full-sib DxP progenies with total of 108 palms and another 8 full-sib progenies comprised 120 palms for crosses from Kulai-Nigerian dura with AVROS pisifera in the progeny testing. Data were collected for four consecutive years on fresh fruit bunch yield and bunch components while vegetative traits were recorded 3 times at 5,7 and 12 years old. Progenies performance of FFB varied significantly and it ranged from 193.8 kg/p/yr to 254.8 kg/p/yr. 8 short height progenies produced moderate FFB yield (ranged from 185.7 to 233.3 kg/p/yr), moderate bunch weight (ranged from 9.3 to 11.8 kg/palm) and higher bunch number (ranged from 17 to 23 bunches/palm/year). Mean progeny of palm height increment was below than 40.8 centimetres per year at age of 12 years old in Kulai Dura-Nigerian x URT-Calabar population and this result showed that this population have slow height increment over the years. The height data showed that short palms have 28% shorter than normal palms. These short palms also produced higher oil to dry mesocarp (O/DM) of 70.6% and oil to bunch (O/B) ratios of 26.0% that contributed to higher oil extraction rate (OER) indirectly. OER is important parameter that is directly related to the profitability of an oil palm plantation. The results from fresh fruit bunch (FFB) yield performance, bunch components and vegetative traits showed that the Kulai-Nigerian dura and URT-Calabar pisifera has potential to be utilized as parental palms of short height materials in future commercial production.

Keywords: oil palm breeding, short palms, high oil yield

[PP-15]

Toxicological Properties of Flour Beetle's (Tribolium Confusum) Infestation on Hordeum Vulgare Consumption

Abdelmalek Oulmi[1], Noureddine Laadel[2], Cyntia Mekideche[3], Zouhir Boulgueraguer[4], Sofiane Guettaf[5], Akram Kout[6], Nadia Benzidane[7]

[1]Abdelmalek OULMI, Laboratory for the Valorization of Natural Biological Resources (LVNBR), Faculty of Nature and Life Science, Ferhat ABBAS University Sétif-1, 19000 Setif, Algeria
[2]Noureddine LAADEL, Laboratory of Improvement and development of plant and animal production, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[3]Cyntia MEKIDECHE, Department of Biology and plant Ecology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[4]Zouhir BOULGUERAGUER, Department of Geology, Laboratory of water resources and sustainable development REDD,, BADJI Mokhtar, Annaba University. Algeria
[5]Sofiane GUETTAF, Laboratory of Applied Microbiology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[6]Akram KOUT, MISC Laboratory. Abdelhamid Mehri Constantine 2 University. Algeria
[7]Nadia BENZIDANE, Laboratory of Applied Biochemistry, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

Barley (Hordeum vulgare), a member of the grass family, is a major cereal grain grown in temperate climates globally. It was one of the first cultivated grains, particularly in Eurasia as early as 10,000 years ago. In 2020, world production of barley was 157 million tonnes, led by Russia producing 13% of the world total. Spain, Germany, Canada, and France were major producers. It can be susceptible to many diseases, but plant breeders have been working hard to incorporate resistance. The devastation caused by any one disease will depend upon the susceptibility of the variety being grown and the environmental conditions during disease development. Serious diseases of barley include powdery mildew caused by Flour beetle (Tribolium confusum). The presence and adverse effects of certain toxic compounds in flour as a result of insect pest infestation during storage has been of growing international concern. Previous studies have indicated that flour extracted from wheat that has suffered infestation by insect pests such as Tribolium confusum could be affected in its nutritional, chemical and rheological characteristics.. Fifty bowls, 1 kilogram, of flour were used filled with wheat flour 80 % extraction. A 50 larvae of Tribolium confusum were put into each bowl and 15 jars, for 2 months at 25 0C and 50% of relative humidity. At the end of this period, all samples were sieved to recover the insects and then analyzed. Mutagenic and Carcinogenic compounds, increased by the rate of 231.87 and 23.55% compared to 1.87 and 2.99% for the uninfected samples, respectively.

Keywords: Hordeum vulgare, Insects’ infestation, Flour beetles, Mutagenic and Carcinogenic

[PP-16]

Using Newly Developed Proximal Sensors for High-Throughput Phenotyping in Maize Breeding

Tatjana Ledencan[1], Vlatko Galic[1], Josip Spisic[2], Zvonimir Zdunic[1], Ivana Podnar Zarko[3], Domagoj Simic[1]

[1]Agricultural Institute Osijek, Osijek, Croatia
[2]Faculty of Electrical Engineering, Computer Science and Information Technology, J.J. Strossmayer University, Osijek, Croatia
[3]Faculty of Electrical Engineering and Computing, University of Zagreb, Zagreb, Croatia

Proximal sensors are increasingly used for high-throughput phenotyping as part of plant breeding process. They include handheld sensor devices, indoor platforms and field-based sensor devices. In our project, we aimed to compare handheld and field-based high-throughput techniques for quantifying photosynthetic efficiency in maize according to their applicability and accuracy. We developed a low-cost proximal sensing node retrieving reads at six wavelengths in red (610 and 680 nm), near infra-red (730 and 760 nm) and infrared (810 and 860 nm) to capture important plant reflectance indices and fluorescence signals. The six reads are further arranged to obtain normalized difference vegetation indices (NDVIs). Several maize experiments with 10 to 61 hybrids with FAO maturity from 200 to 700 were measured during the 2021 growing season. The reads were collected and coupled with reads from a commercial multispectral sensing device and a handheld fluorimeter, measuring plant photosynthetic efficiency in a JIP-test framework. Tight correlations were obtained between vegetation indices (VIs) retrieved from our sensor and NDVI measured by a commercial device, reaching R2>0.91. Correlation analysis also showed strong link between VI810610 and primary electron transport, vanishing between VIs and higher order photosynthetic reactions. It indicates high applicability and accuracy of newly developed proximal sensors for high-throughput phenotyping in maize breeding. Additionally, results on leaf rolling occurrence as a heat stress related trait causing visible changes in spectral responses and VIs were combined with several machine learning (ML) approaches. It was demonstrated that ML algorithms were able to use simple multispectral reads for efficient classification of leaf rolling in maize germplasm.

Keywords: maize breeding, high-throughput phenotyping, proximal sensors, photosynthetic efficiency, heat stress, leaf rolling

[PP-17]

Evaluation of Advanced Barley Lines for Yeld and Yield-Related Traits in Aegean Region Conditions

Aydin Imamoglu, Seda Uces, Mustafa Cerit

Aegean Agricultural Research Institute, Ministry of Agriculture and Forestry, İzmir - Turkey

This study was conducted to find out enhanced barley (H. Vulgare L.) lines suitable for Aegean ecological conditions in Soke (Aydin), Gonen (Balikesir), and Menemen (Izmir) during the 2020-2021 growing seasons. The aim of present study was to select

superior barley lines with high quality and yield potential. The experimental material included 20 advanced barley lines and 5 check varieties (Sancak, Bayrak, Imbat, Aybar, and Hilal). Experimental design was Randomized Complete Block Design using four replications for the field trials. Data were recorded for grain yield, thousand kernel weight, >=2,5 mm particle size, hectoliter weight and crude protein content for investigated genotypes. Over all lines 15, 16, and 17 out yielded the checks (536 kg/da), with 702, 697, and 637 kg/da respectively. Based on the statistical analysis, two advance lines were found out promising lines for Aegean region. Therefore, these lines could be registered as new variety or used in barley breeding programs to improve grain yield.

Keywords: Barley, Grain yield, Yield components, Advanced lines, Quality

[PP-18]

Genetic Mapping of Yield and Yield-Related Traits in a Population Derived from Two Winter Wheat Cultivars

Mustafa Cerit[1], Zhen Wang[3], Shuhao Yu[2], Jorge Valenzuela Antelo[3], Mehmet Dogan[3], Shichen Wang[4], Paul St Amand[5], Qingwu Xue[2], Jackie C. Rudd[2], Amir M.h. Ibrahim[3], Geraldine B. Opena[3], Shuyu Liu[2]

[1]Aegean Agricultural Research Institute, Ministry of Agriculture and Forestry, İzmir - Turkey
[2]Texas A&M AgriLife Research and Extension Center, Amarillo, Texas, USA
[3]Deparment of Soil and Crop Sciences, Texas A&M University, College Station, Texas, USA
[4]Genomics and Bioinformatic Service Center, College Station, Texas, USA
[5]USDA, Hard Winter Wheat Genetics Research Unit, 4008 Throckmorton Hall, Manhattan, Kansas, USA

Wheat (Triticum arestivum L.) is one of the largely grown cereal. Understanding the genetic basis of yield and yield components under dryland and irrigated conditions can help to develop enhanced germplasms and cultivars. This study aims to construct a genetic map and detect quantitative trait loci (QTL) linked to yield and its components using a biparental population comprised of 191 recombinant inbred lines (RILs) derived from a 'TAM 113'/'Gallagher'. Data for agronomic and yield-related traits were collected at McGregor, College Station, and two different locations at Bushland, TX in 2019, 2020, and 2021. A high-density genetic map covering all 21 chromosomes was constructed using 8,075 single nucleotide polymorphisms (SNPs) markers. A total of 119 QTL regions were detected for all traits. Three QTL clusters on chromosome 2B, 2D and 7D were identified, each of them associated with more than three traits. One cluster on 2D was located in the flanking region of Ppd-D1, a major gene that regulated photoperiodism.

Keywords: Wheat, QTL, Grain yield, Genetic

[PP-19]

Breeding for Improved Forage Yield Potential and Digestibility in Tall Fescue (*Schedonorus arundinaceus* (Schreb.) Dumort.)

Elif Şahin[1], Steve Reid[2], Muhammet Şahin[1], Serkan Ateş[3], Sabry Elias[4], David B. Hannaway[4]

[1]Black Sea Agricultural Research Institute, Samsun, Türkiye
[2]DLF Pickseed USA, Corvallis, OR
[3]Faculty, Department of Animal and Rangeland Science, OSU, Corvallis, OR
[4]Faculty, Department of Crop and Soil Sciences, OSU, Corvallis, OR

Tall fescue is a perennial forage grass widely used in areas not well-suited to perennial ryegrass due to climatic or edaphic stressors including drought and low or high pH. Although tall fescue has many agronomic attributes that make it well suited to a wide range of environments, it is lower in palatability and digestibility than Lolium species. The goal of this study was to improve fiber digestibility and yield of early and medium maturing tall fescue genotypes through recurrent phenotypic selection. Improving fiber digestibility and yield concurrently is a challenge because yield and fiber content are positively correlated.

Plants were selected from both an early maturity source population and a medium maturity source population. Using resulting half-sib seeds, spaced-plant nurseries were established in Philomath, Oregon to evaluate forage and seed yield and agro-morphological characteristics. In addition, small plot trials were established in Boyd, Kentucky in 2018 to quantify forage yield and estimate forage quality. In the spaced-plant nurseries, some agro-morphological traits were significantly different ($P<0.05$) among genotypes. In the small plot trials, significant differences were found for forage yield and quality traits in the first cutting. Thus, although

there is a positive correlation between forage yield and fiber (NDF and ADF), concurrent improvements can be obtained for yield and digestibility through recurrent phenotypic selection. Since tall fescue does not produce culmed (jointed) vegetative shoots in regrowth, quality evaluation from the first cutting is most critical in selecting for improved digestibility.

Keywords: Tall fescue, digestibility, fiber, recurrent phenotypic selection, yield

[PP-20]

The Heritability for Flower Productivity and Defoliation in Diploid Roses

Seza Noyan[1], David H. Byrne[2], Oscar Riera Lizarazu[2], Stella Kang[2], Ellen Young[2], Jeekin Lau[2], Natalie Anderson[2], Pam Hornby[2]

[1]Aegean Agricultural Research Institute, Menemen-İzmir/Turkey
[2]Deparment of Horticultural Sciences, Texas A&M University, College Station, Texas/USA

Roses were domesticated several thousand years ago for various purposes. Garden roses are one of the important woody ornamental plants in the USA. For a garden rose, two highly valued traits are high continuous flower productivity and excellent plant health throughout the season. In this study, flower productivity was measured by rating flower intensity (percent canopy covered with flowers) on a weekly basis and plant health was assessed monthly by rating the defoliation. This study estimated the heritability of flower productivity and defoliation in 10 inter-related diploid rose families in the field using a random effects model Restricted Maximum Likelihood (REML) analysis. Traits were evaluated from Spring 2019 to November 2019 on a percentage-based rating scale of 0-9 (0=no flowers/defoliation and 9=foliage covered with flowers/percent of leaves fallen) throughout the growing season on 662 diploid plants in College Station, TX. Narrow sense (h2) and broad sense (H2) heritabilities were estimated to be 0.10 and 0.81, respectively, for flower intensity, and 0.44 and 0.90 for defoliation.

Keywords: Rose, Heritability, Flower, Defoliation

[PP-21]

Evaluation of Seedling and Adult-Plant Stripe, Leaf, and Stem Rust Resistance in the A-Genome Diploid Relatives of Wheat

Buket Şahin[1], Duane Wilson[2], John Raupp[3], Robert Bowden[4], Jesse Poland[5], Bernd Friebe[2]

[1]Regional Cereal Rust Research Center, Aegean Agricultural Research Institute, 35660 Menemen, Izmir, Türkiye
[2]Department of Plant Pathology, Kansas State University, Manhattan, Kansas 66502, USA
[3]Wheat Genetics Resource Center (WGRC), Kansas State University, Manhattan, Kansas 66502, USA
[4]USDA/ARS/Hard Winter Wheat Genetics Research Unit, Kansas State University, Manhattan, KS 66506, USA
[5]Center for Desert Agriculture, King Abdullah University of Science and Technology, Thuwal 23955, Saudi Arabia

Wheat (*Triticum aestivum* L.) is one of the most significant cereal crops worldwide, ranking third following rice and maize. The rust diseases that attack this crop – leaf rust (*Puccinia triticina*), stripe rust (*Puccinia striiformis* f. sp. *tritici*), and stem rust (*Puccinia graminis* f. sp. *tritici*), are an important limitation for increasing wheat production. Resistance genes to these rusts were identified and are used by wheat breeders, however, achieving long-term resistance has been difficult. In order to stay ahead of constantly evolving rust pathogens, identifying genetic resistance from sources other than common wheat is necessary for increasing genetic diversity. The wild relatives of wheat are an important source of wheat rust resistance genes. Indeed, the use of resistance genes transferred from wild relatives to wheat is one technique that helps breeders in developing resistant cultivars. Previously, genes with wheat rust resistance were introgressed from *Triticum monococcum* to wheat. For additional resistance genes, we screened a mini-core collection of diploid A-genome species, covering about 90 percent of the genetic variation, including 59 accessions of *T. monococcum* subsp. *aegilopoides*, 24 accessions of *T. monococcum* subsp. *monococcum*, and 25 accessions of *T. urartu*. These accessions were evaluated for their seedling resistance to leaf rust, stripe rust, and stem rust under greenhouse conditions and were screened for adult-plant resistance under both greenhouse and field conditions. Among the evaluated accessions, *T. monococcum* subsp. *monococcum* showed a higher number of resistant accessions, followed by

T. monococcum subsp. *aegilopoides*, and *T. urartu*. Consequently, these species may have a high potential as donors of resistance to stripe, leaf, and stem rusts. This information will be crucial for directed gene transfer from these accessions into advanced wheat breeding lines.

Keywords: wheat, stripe rust, leaf rust, stem rust, *Triticum monococcum*, *Triticum urartu*

[PP-22]

The Effects of Open Sun Drying and Oven Drying on Dried Fruit Quality Characteristics in Pure Lines Developed for Dried Pepper Breeding

Gülsün Elif Vural[1], Cafer Doğanlar[1], Ali Kün[1], Sinan Zengin[1], Özge Meral[1], Şeküre Şebnem Ellialtıoğlu[2]

[1]Antalya Tarim Co. R & D Center, Antalya, Turkey
[2]Ankara University Technopolis Doqutech Academy Ltd.Şti., Ankara, Turkey

Pepper (Capsicum annuum L.), which originates from the Americas and is grown in every region of the world, has great commercial importance, both fresh and processed (spices, tomato paste and pickles). Turkey is the fourth largest producer country in world pepper production with a share of 7.3%. 8.17% of this production is dry pepper and 91.83% is fresh pepper production. Although dried pepper has a unique and important place in traditional Turkish cuisine, our high quality commercial F1 hybrid varieties developed for this purpose are almost non-existent. For this reason, variety development studies have been accelerated in recent years. It is also common to dry pepper as a whole, in addition to processing it as powdered pepper and chili pepper. Developing varieties suitable for all these uses will fill an important deficiency in the pepper seed market in our country and especially in other countries where the culinary culture is similar. For this purpose, as a result of the studies carried out for the collection of local dried pepper genotypes in our country and the development of pure lines with the folded haploidy (Doubled Haploid: DH) technique, more than 200 pure lines were examined. 20 pepper lines selected from among them formed the plant material of this research. For 20 DH dried pepper lines, trials were set up in 3 different locations, Adana / Tuzla, Antalya / Serik and Manisa / Turgutlu, and three harvests were made during the growing period. Harvest time was determined by measuring the amount of water-soluble dry matter during harvest periods. Conventional drying method (under 50% shade net in sunny weather) and drying method in tunnel type ovens were used to determine the drying performance of DH pepper lines whose pre-washing and filtration processes were completed. Drying processes were carried out in İzmir / Kemalpaşa location. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. Fruit samples obtained in each harvest were taken to drying tests. In these tests, the values of parameters such as moisture, ash, oil, pH, processing efficiency, sensory evaluations (color, juiciness, crispness, flavor, general acceptability) and dry product shelf life were calculated separately for both sun drying and oven drying methods. In dry product shelf-life studies, the samples dried in the sun and in the oven were stored at room conditions (24°C). On the 32nd, 48th and 64th days, the weights, color parameters (L*(brightness), a*(redness), b*(blueness)), shape and taste characteristics of the products were evaluated as packed in vacuum and normal bags. As a result of the evaluations, prominent pure lines were determined in order to develop hybrid varieties for drying.

Keywords: Capsicum annum L., Drying techniques, Fruit quality, Local genotypes, Pure lines

[PP-23]

Comparison of Pure Lines Developed for Dried Eggplant Breeding in Terms of Quality Characteristics

Gülsün Elif Vural[1], Cafer Doğanlar[1], Sinan Zengin[1], Tuncay Karakuş[1], Şeküre Şebnem Ellialtıoğlu[2]

[1]Antalya Tarim Co. R & D Center, Antalya, Turkey
[2]Ankara University Technopolis Doqutech Academy Ltd.Şti., Ankara, Turkey

Turkey ranks fourth in world vegetable production. According to the 2021 data of the Turkish Statistical Institute (TUIK), Turkey produced approximately 32 million tons of vegetables. Eggplant constitutes 2.6% of vegetable production. Turkey is the fourth largest producer country in world eggplant production after China, India and Egypt. Although eggplant is mostly used for fresh consumption, its use takes its place in Turkish cuisine with different recipes thanks to processing techniques such as canning and drying. Especially in the gastronomic culture of certain geographical regions such as Southeastern Anatolia, the position of eggplant, both fresh and dried, is very important. Dried eggplant production is common in provinces such as Adana and Gaziantep, and the drying process is traditionally done outdoors and under the sun. However, there are technologically developed technical drying methods as an alternative to this traditional method. In the studies carried out within the scope of the project, populations were collected from the regions in Turkey where the local dried eggplant genotypes were grown, and doubled haploid (DH) pure lines were obtained from them by anther culture. By examining criteria such as yield, fruit characteristics and growth strengths, 44 eggplant pure lines were selected among more than 200. The material of the study presented here consists of 44 selected DH eggplant lines. Harvesting was done three times during the growing period in 3 different locations, Adana / Tuzla, Antalya / Serik and Manisa / Turgutlu. Before drying, the amount of water-soluble dry matter in the fruits was determined with a refractometer device. Conventional drying method (under 50% shade net in sunny weather) and drying method in tunnel type ovens were used to determine the drying performance of DH eggplant lines whose pre-washing and filtration processes were completed. Drying processes were carried out in İzmir / Kemalpaşa location. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. Various drying tests were applied to dried fruit samples. In these tests, the values of parameters such as moisture, ash, oil, pH, processing efficiency, sensory evaluations (color, juiciness, crispness, flavor, general acceptability) and dry product shelf life were calculated separately for both sun drying and oven drying methods. In dry product shelf-life studies, the samples dried in the sun and in the oven were stored at room conditions (24°C). On the 32nd, 48th and 64th days, the weights, color parameters (L*(brightness), a*(redness), b*(blueness)), shape and taste characteristics of the products were evaluated as packed in vacuum and normal bags. At the end of the study, prominent dried eggplant DH lines were determined to be used for test hybridizations.

Keywords: Drying techniques, Fruit quality, Hybrid variety, Solanum melongena

[PP-24]

Use of Convolutional Neural Network Model for Detection of *Puccinia striiformis f. sp. Tritici* and Comparing Disease Severity Monitoring Methods on Scanned Images

Turan Gokberk Con[1], Alexey Mikaberidze[2]

[1]Aegean Agricultural Research Institute, Menemen-Izmir/TÜRKİYE
[2]School of Agriculture, Policy and Development, University of Reading, Reading-United Kingdom

Wheat is one of the most produced and consumed cereals in the World, therefore, it is necessary to take some actions against yellow rust disease in order to ensure sustainability in production. Yellow rust is a fungal disease that causes yield decreases in wheat crops during epidemic periods. To get prevention against this disease damage, early detection of the disease and cultivation of resistant varieties can be preferred. In favor of the innovations brought by science and technology, artificial intelligence and digital image analysis can be used against yellow rust disease.

In this research, artificial intelligence that can detect yellow rust on scanned wheat leaf images has been developed. Moreover, Visual data were reproduced in different colors and shapes with the augmentation method, increasing the number of data. The Convolutional Neural Network (CNN) model was trained to distinct yellow rust-infected or non-infected on scanned sheets. The Model training with these images provided 0.91 validation accuracy in the end and 86% successful prediction was seen in the tested scans. The Model succeeded in separating yellow rust not only from healthy leaves but also from plants with other diseases. This research indicates that yellow rust can be diagnosed with a disease detection program. The detection success of the model can be improved by increasing the number of data in future studies.

In the second part of the research, different observation methods were tried on software to find out the severity of pustules in the scanned leaf images of yellow rust disease. The severity of yellow rust disease was compared from the images using two methods, the ZymoMacro Scanner, which was previously used in the evaluation of Septoria tritici blotch disease, and ImageJ software HSB color space adjustments. In the measurements made with the HSB color space, the Spearman correlation coefficient was found to be 0.77 for the pustule severity and 0.72 for the area of the pustules on the leaf. In the measurements made with the ZymoMacro Scanner, the Spearman correlation coefficient was 0.69 when no adjustment was made in the macro settings, 0.92 when the macro was changed, and 0.85 when the changes were made in other images. While the areas of the pustules measured with the HSB color space settings were found to be smaller than the real areas, the areas were actually wider in the measurements made with the Zymomacro Scanner. The success of the edited version, especially in the Zymomacro Scanner tests, has shown that a yellow rust-specific macro can be developed. Tests with the HSB color space did not show the desired level of correlation, but it is possible to repeat the study by using another software or color space.

Keywords: yellow rust, wheat, convolutional neural network, disease severity, disease detection

[PP-25]

Infected with ToBRFV (Tomato Brown Rugose Fruit Virus) Disinfectant Efficacy Trial on Tomato Plants

Özlem Demir, Damla Ulusoy

Anamas Seed Company, Serik, Antalya

In this study, it was aimed to determine the effectiveness of disinfectants against ToBRFV under controlled and farmer conditions. A trial of 160 plants was established using the Samyeli F1 cultivar of Anamas company with the randomized blocks trial design. A total of 4 blocks were created, with 4 blocks in each parcel of the experiment and 10 plants in each block. In addition, plants known to be infected with ToBRFV were planted as a source of infection in row 5, at the beginning of each row and at the end of row 3. To ensure that these plants are infected with ToBRFV; When the tomatoes reached the true two-leaf stage, mechanical inoculation was applied 3 times with the "soft sponge pad" method at regular intervals with the "ToBRFV-Ant-Tom: MT107885" isolates we have. In the evaluation of the effectiveness of disinfectants in farmer conditions against ToBRFV; Disinfectants with active substances such as 0.5-1% HCl, 11.2% Hydrogen peroxide and vein glow (300 cc/100 lt) were found to be effective. It has been observed that these disinfectants, which are applied from above with hand sprayers, have a preventive effect on the spread of the virus in an uncontaminated greenhouse as a result of regular use once a week. It has been observed that these disinfectants, which are applied from above with hand sprayers, have a preventive effect on the spread of the virus in the greenhouse as a result of regular use once a week. At the end of the experiment, the plants in the greenhouse were subjected to molecular tests. The bands seen in the gel electrophoresis show that the disinfectants are not effective on the related virus agent and the plants are 100% infected with ToBRFV. In addition to the early diagnosis of the presence of virus diseases and the removal of diseased plants from the greenhouse, routine hygiene procedures in the greenhouse are also very important. For this reason, disinfectant studies to prevent ToBRFV from infecting tomato production areas come to the fore. As a result, it has been observed that disinfectants, which are effective in controlled conditions, delay the epidemic in the greenhouse but do not prevent ToBRFV infection in studies conducted under farmer conditions.

Keywords: Disinfectant, Tomato, ToBRFV, Virus infection

[PP-27]

Grain Yield and Stability of Some Feed Barley (Hordeum vulgare L.) Lines and Cultivars Under Rainfed Conditions of Central and Transitional Regions of Anatolia

Namuk Ergün, Ismail Sayim, Sinan Aydoğan, Melih Bilir

Central Research Institute for Field Crops

In this study, the grain yield of eighteen feed barley lines was compared to six feed (Tarm-92, Burakbey, Sayim 40, Tosunpaşa, Asil, and Larende) barley cultivars, as well as their response to diverse ecological conditions, in nine locations throughout Central and Transitional Regions of Anatolia (İkizce, Altınova, Gözlü, Malya, Ulaş, Sarkışla, Konya, Karapınar, and Afyonkarahisar) during the 2019–2020 growing season. The grand mean of the yield trials over nine sites was 3545 kg/ha, while cv. Sayim 40 outyielded all genotypes with 4392 kg/ha grain yield, followed by cv. Larende with 4076 kg/ha and advance line 123 with 3959 kg/ha, respectively. The high yielding environment was Konya with 5206 kg/ha while Afyonkarahisar was the unfavorable condition with 2113 kg/ha. Stability analysis based on regression revealed that the most stable and high yielding genotypes were cv. Asil, cv Tosunpaşa, and advance feed line 113. Furthermore, advance feed barley lines 103, 107, 108, cv. Tarm-92, and cv Larende were more stable and especially for unfavorable conditions however, advance feed line 104, cv. Burakbey and cv. Sayim 40 were in good adaptability to favorable conditions. Tarm-92, the most widely cultivated cultivar in Central Anatolia, remained the most stable genotype with yield potential near to the grand mean. Among the new varieties, Sayim 40 had a higher grain yield potential in Central Anatolia and Transition Regions. According to the findings of this study, advance line 123, which has a high and stable grain yield, is the most promising feed barley line for central and transitional ecological zones of Anatolia.

Keywords: Feed barley genotypes, grain yield, environments, adaptability and stability, Rainfed, Central Anatolia and Transition Regions

[PP-28]

Evaluation of the Yield, Yield Components and Quality traits of Faba Bean Genotypes in Aegean Region Conditions

Damla Uncuer, Eylem Tugay Karagül, Firdevs Niksarlı Inal, Erkan Kaya, Selin Egilmez

Aegean Agricultural Research Institute

This study was carried out in 3 years in Menemen (Izmir) conditions from 2018 to 2020 to develope new varieties of Faba bean (Vicia Faba L.) with small grains and multi-purpose, efficient, high protein content, suitable for the consumption characteristics of the Aegean Region. As the experiment is a part of a continuous project, it was established using 13 lines and 4 standards (Giza3, Giza4, Nubarie, Eresen87) varieties were selected from the previous project period and the ICARDA-sourced observation garden in a Complete Block Design (RCBD) with 4 replications.

As a methodology plant height (cm), first pod height (cm), number of branches (cm), number of pods and seeds per pod, yield of single plant (g), yield of parcel (g), hundred-seed weight (g) observed and protein ratios were analysed in all the 13 lines and 4 standard varieties. Results were analysed by applying LSD test and using Microcomputer statistical program.

Based on statistical analysis, significant differences were detected between lines and varieties over the three-year period. The performances of the lines and varieties differ statistically according to the years as well. While the 3-year average yield of all lines and varieties was 274,3164kg/da, the lines with the highest and lowest yields varied according to years. Furthermore, hundred-grain weights, plant height, initial pod height, number of branches, pods, and pods per plant, and interactions between lines and cultivars within years were found statistically significant. The cultivars had an average hundred-grain weight of 82.21 g and an average plant height of 63,318 cm. The initial pod's average height is 22,761 cm, while there are 2.84 average grains in each pod. Protein ratios vary from 25% to 32% on average depending on the line and variety, although there are no statistically significant variances based on years.

The lines that were determined and assessed to be suitable for breeding purposes and stability performances will therefore by transferring them to variety registration in the following years of the continued project in accordance with the data received.

Keywords: Faba bean Breeding, Stability, Advanced lines, Yield

[PP-29]

Accelerated Pepper Breeding Studies with MAS and Androgenesis Techniques

Mesut Nar[1], Hande Nur Albezirgan[1], Burcu DemirKaya[1], Hakan Fidan[2], Hakan Aktaş[3], Ş. Şebnem Ellialtıoğlu[4]

[1]AG Seed Industry Trade Inc., Antalya, Turkey

[2]Akdeniz University, Faculty of Agriculture, Plant Protection Department, Antalya, Turkey

[3]Isparta University of Applied Science, Faculty of Agriculture, Horticulture Department, Isparta, Turkey

[4]Ankara University, Technocity Doqutech Academy Ltd. Şti. Ankara, Turkey

By using molecular techniques and tissue culture studies together in plant breeding, it can produce superior with desired characteristics plants in a short time. By applying molecular markers in gene pools with relevant traits in the early period, new individual plants with desired genetic structure can be produced with reduced labor, time and costs. Determining the presence of the relevant resistance gene in plants at the seedling stage is easier within molecular markers than traditional methods such as artificial inoculations which requires time, labor and space. For determination of whether the resistance gene is either homozygous or heterozygous provides great knowledge to the breeder.

Another area for accelerating breeding studies in plant tissue cultures in biotechnology where double haploidy technology reduced time at least 5-8 times to obtain pure lines. Combinations of MAS and androgenesis techiniques have resulted in F1 hybrids and all relevant tests have also been conducted in 3 years.

According to statistics, the importance of pepper cultivation in Turkey is increasing day by day, and interest local varieties are gaining more interest due to their agronomic richness. The local varieties for instance, Hatay (Samandağ) pepper, are preferred in terms of quality characteristics e.g. hot, fresh and suitable for dried consumption, but it does not contain any disease resistance genes. Within the scope, we established the project is aiming to develop resistant hybrid varieties to Tomato Spotted Wilt Virus (TSWV)

is causing high yield and quality losses in pepper production areas. For this purpose, studies are carried out to obtain pure resistant lines in a short time, a *Tsw* gene found in *Capsicum* chinence, which provides resistance to TSWV, was combined with Hatay pepper lines by crossbreeding. First of all, 20 of the Hatay pepper lines from the gene pool were selected according to weighted grading criteria, then the number was reduced to 4. In *C. chinense* lines, molecular screening was performed with SCAC568 primers (Moury et al., 2000) and individuals with *Tsw* gene were determined from donor parents and crosses. After then, backcrosses to Hatay peppers were conducted and GM1F1 was generated. Their seed samples were sown from them and brought until the first true leaves during the transition from seed to seedling stage. Meanwhile, molecular analyses were applied to find resistant individuals with *Tsw* gene. The homozygous and heterozygous plants were planted in a greenhouse and used in anther culture study.

In anther culture, haploid plants were developed using the protocol described Alremi et al. (2014). Whole study takes 22 months from the initiation of hybridization to the emergence of androgenic embryos and acclimatization to external conditions and development of DH seeds. Here, these findings are presented as a case study in biotechnology and the combined teqhniques are an indispensable part of accelerated breeding processes.

Keywords: Anther culture, Capsicum spp., Tsw, Hatay pepper, Molecular marker

[PP-30]

Suitability of Latvian Origin Rye and Wheat Genetic Resources for a Niche Products

Laila Vilmane, Vija Strazdina, Ligita Salkovska, Valentina Fetere

Institute of Agricultural Resources and Economics, Stende Research Centre, Latvia

In Latvia the first experiments and breeding work with rye and wheat started 100 years ago – 1922. During this year's more than 30 local rye, winter and spring wheat varieties were developing. One of the first and oldest Latvian rye varieties 'Stende' was created in 1929. Later (1949) this variety was improved and named 'Stendes II', grown up to the end of 1960. Breeding of wheat in Stende and Priekuļi in the period 1923-1950 was successful. The first local winter wheat varieties were 'Viestura', and 'Zemgale' registered in 1929, later 'Viestura II' (1937), 'Kursas' (1940), Milturum 5 (1949), and spring wheat 'Stendes 5' (1951). Registered Latvian plant varieties and some breeder lines considered as important for future utilisation for a long time were kept in several Gene Banks. The first initial samples of rye and wheat were received from Latvian Gene Bank and the former Soviet Union – the N.Vavilov All-Union Plant Industry Institute in St. Petersburg, also from Genbank Gatersleben in 2020. Further seed multiplication and evaluation was carried out at Institute of Agricultural Resources and Economics Stende Research Centre. The main task of the studies was to investigate agronomic traits (yield, grain quality, and resistance to the most dangerous diseases) of Latvian PGR – (ancient rye, winter and spring wheat varieties) under the organic farming conditions and also to determine the suitability for creation a new products. After evaluation the best varieties and lines will be register in Latvian Plant varieties catalogue and will be accessible for farmers. The first results of winter rye 'Stendes II' showed that variety is suitable for Latvian climatic conditions: good winter hardiness (7-9 point), grain yield 2.0 t ha-1 and grain quality was corresponding to food (Volume weight 70. 31 kg L-1, Falling number 160 s). Grain yield of winter wheat varieties and breeder lines varied from 1.60 to 3.31 t ha-1 in 2021. The highest winter hardiness, yield and grain quality showed variety 'Milturum' (yield 3.1 t ha-1,Volume weight 77.99 kg L-1, protein content 107.7 mg kg-1, Gluten content 210.2 mg kg-1, Zeleny index 31.92, Falling number 341 s. Varieties 'Kurzeme', 'Viestura' and 'Zemgale' had a lower grain yield, due to high infection of snow mould. All bread samples from rye floure has irregular shape, small and dense pores and small specific volume.

Keywords: rye, wheat, genetic resources

[PP-31]

Effect of Tribolium Confusum's Toxication Infestation on Zea Mays for Human and Animal Nutrition

Guettaf Sofiane[1], Laadel Noureddine[2], Oulmi Oulmi[3], Mekideche Cyntia[4], Benzidane Nadia[5]

[1]Laboratory of Applied Microbiology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[2]Laboratory of Improvement and development of plant and animal production, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[3]Laboratory for the Valorization of Natural Biological Resources (LVNBR), Faculty of Nature and Life Science, Ferhat ABBAS University Sétif-1, 19000 Setif, Algeria
[4]Department of Biology and plant Ecology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria
[5]Laboratory of Applied Biochemistry, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

Maize (Zea mays) is the third most important cereal grain in the world, after wheat and rice, providing nutrients for humans and animals and serving as a basic raw material for production of starch, oil, protein, alcoholic beverages, food sweeteners, and fuel. It has the greatest global production of any crop species around 800 million tonnes was produced worldwide in 2013, accounting for 32% of the total cereal production. The top three producers include the United States, China, and Brazil. Large quantities of flour are stored in open shounas and/or blinds. Under these conditions, the flour is attacked by various biological factors including insects. Flour beetle (Tribolium confusum).These beetles have chewing effects of certain toxic compounds in maize as a result of insect pest infestation during storage has been of growing international concern. Previous studies have indicated that flour extracted from maize that has suffered infestation by insect pests such as Tribolium confusum could be affected in its nutritional, chemical and rheological characteristics. Fifty bowls, 1 kilogram, of maize were used filled with maize flour 80 % extraction. A 50 larvae of Tribolium confusum were put into each bowl and 15 jars, for 2 months at 25 0C and 50% of relative humidity. At the end of this period, all samples were sieved to recover the insects and then analyzed. Mutagenic and Carcinogenic compounds, increased by the rate of 199.11 and 15.73% compared to 1.02 and 1.68% for the uninfected samples, respectively.

Keywords: maize, insects' infestation, flour beetles, Mutagenic and Carcinogenic

[PP-32]

Evaluation of Quality Parameters of Different Barley Varieties

Arzu Özer, Pervin Arı Akın, Selim Uygun, Hümeyra Yaman

Central Research Institute for Field Crops,Ankara,Türkiye

In this study, the grain quality parameters of 13 barley variety were studied. The barley varieties (Yalın, Burakbey, Anka 06, Misket, Zeynelağa, Aydanhanım, Tarm 92, Beşparmak, Bozlak, Tosunpaşa, Sinanbey, Akar, Sayım 40) collected from Central Research Institute for Field Crops, Ankara. The samples were grown in İkizce location during the 2021– 2022 growing season. Varieties were evaluated in terms of moisture content, hectoliter weight, grain protein content, thousand grain weight, starch content, HS (crude fiber), NDF (cellulose, hemiselulose, lignin), ADF (cellulose, hemicellulose) and ADL (Acid Detergent Lignin) values and sieve analysis. Yalın (hull-less barley) had the highest mean protein content (15,8%) and hectoliter weight (80,5 kg/hl). The moisture content varied from 10,5 to 14,4% and starch content from 59,4 to 62,3%. Malting barley varieties had the highest amount of starch content.

Keywords: Barley, Quality Parameters, Hull-less barley, Malting barley, Grain Quality

[PP-33]

Quality Characteristics of Durum Wheats Grown in Central Anatolia

Ferda Ünsal Canay, Arzu Özer, Pervin Arı Akın, Selim Uygun

Central Research Institute for Field Crops

Durum wheat (Triticum durum) is primarily used for the production of high-quality pasta products because of its color, flavor and cooking properties.

Color and protein characteristics, kernel size and vitreousness are important in durum wheat quality, as they are strongly related to semolina yield, bright yellow appearance of semolina and cooking properties of pasta products. Quality of durum wheat can be affected by environmental conditions such as location, rainfall, soil fertility and temperature.

The objective of this study was to determine some quality characteristics in durum wheat cultivars.Five durum wheat cultivars (Kızıltan 91, Eminbey, Ç-1252, İmren, Vehbibey) which were grown in İkizce location during the 2021-2022 growing season were used. In the study, cultivars were evaluated in terms of thousand kernel weight, vitreousness, grain hardness (determined by Single Kernel Characterization System - SKCS), protein content, b*(yellowness), SDS sedimentation values.

According to results; Eminbey and Vehbibey cultivars gave better results in terms of SDS sedimentation value; Kızıltan-91 cultivar gave better results in terms of the b*(yellowness) value and protein content. There were also significant differences between the samples in terms of thousand kernel weight, vitreousness, grain hardness, protein content, b*(yellowness) and SDS sedimentation values. The results might be beneficial for breeders for improving quality characteristics of durum wheats.

Keywords: Durum wheat, Cultivar, Pasta, Quality characteristics

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[PP-34]

Determination of Some Traits in New Purple Sweet Corn Hybrids

Ahmet Öztürk[1], Bülent Uzun[2]

[1]Karaman Directorate of Provincial of Ministry of Agriculture and Foresty
[2]Department of Field Crops, Faculty of Agriculture, Akdeniz University

Purple sweet corn can be used as functional food thanks to significantly higher anthocyanin concentration, phenolic content and antioxidant activity than uncolored corn. There is no any registered purple sweet corn variety in Turkey. To develop new varieties and to register in Turkey, breeding studies were started and purple sweet corn inbred lines during the consequent of 2017-2021 years. To obtain new purple sweet corn hybrids, fifteen purple sweet corn inbred lines were used as parent lines. The aim of this study was to determine some traits of new purple sweet corn hybrids. This study was carried out in Antalya Turkey under greenhouse and field conditions in 2020 and 2021 years. The twenty-one hybrids were obtained in greenhouse in 2020-21 greenhouse season. Total twenty-seven genotypes (21 hybrids, 3 inbred lines and 3 commercial check yellow sweet corn hybrids) were evaluated in this experiment that was carried out according to randomized complete block design with three replications in Antalya in 2021. The number of days to anthesis (DtoA), plant height (PH), ear height (EH), ear length (EL), ear with (EW) and yield (Y) were evaluated in order to determine the performance of hybrids. All of them were statistically significant at $P < 0.001$ across the hybrids. The DtoA, PH, EH, EL, EW and Y varied between 52.3 and 60.7 days, 131.7 and 199.3 cm, 51.7 and 88.3 cm, 10.6 and 18.5 cm, 3.3 and 4.5 cm and 5086 and 14986 kg ha-1, respectively. The number 13, 14, 15 and 18 hybrids were found as promising for yield. This is first report on evaluation of purple sweet corn hybrids in Turkey.

Keywords: Hybrids, purple sweet corn, purple inbred lines, yield

[PP-36]

Evaluation of Genetic Relationship among Different Soybean Cultivars in Two Regions of Mazandaran and Alborz Provinces

Parastoo Majidian[1], Bahram Masoudi[2]

[1]Crop and Horticultural Science Research Department, Mazandaran Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO), Sari, Iran.

[2]Seed and Plant Improvement Department, Seed and Plant Improvement Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

In order to determine genetic diversity among new soybean germplasm, 119 and 124 new soybean imported genotypes with four control samples (Saman, Katol, Kosar and Sahar) in Alborz province and (Telar, Sari, Wiliams and Sahar) in Mazandaran province were investigated based on augmented design project respectively. The genotypes studied were assessed according to different agronomical and morphological traits such as days to flowering, days to maturation, plant height, number of node, number of secondary branch, number of null pod, number of pod in whole plant/secondary branch, number of seed per plant, seed yield per plant, plant biological yield, seed oil and protein percentage. The results showed that the highest amount of phenotypic variation coefficient were related to seed yield (84.23), number of null/infertile pod (75.8) and number of seed in plant (75.28) and the lowest amount of phenotypic variation coefficient belonged to protein percentage (3.96), oil percentage (4.27) and days to full maturation (9.33) in Alborz province. In Mazandaran province, the highest amount of phenotypic variation coefficient were belonged to seed yield (89.93), number of null pod (85.9), number of pod in secondary branch (74.3) and the lowest one was considered as oil percentage (2.99), protein percentage (3.25) and days to full maturation (14.01). The mean comparison of seed yield indicated that the genotypes of Clark curly pubesce, GH 66-6-14, Seedmakers 1-E, Delmar and Valder had the highest seed yield in Alborz province. In addition, the genotypes of Alaric, Mediachev, Chico, Telar and Dakota No. 3338 exhibited the most seed yield per plant in Mazandaran province. Thus, it could be suggested that the superior genotypes compared to control samples had capability to make use of them in further breeding programs.

Keywords: New soybean genotypes, morphological and agronomical traits, genetic relationships

[PP-37]

Effect of Parental Lines on Germination of Avşar F1

Nur Ülger[1], Zehra Nur Arda[2]

[1]Nur Ülger, R&D Department, Multi Tohum Tar. San. Tic. A.s., Antalya, Türkiye
[2]Zehra Nur Arda, R&D Department, Multi Tohum Tar. San. Tic. A.s., Antalya, Türkiye

Pepper (Capsicum spp.) is one of the most important crops for production worldwide due to its consumption as a vegetable and spice. Seeds quality has an important role in the production process of crops. Therefore, many researches has been done to analyze and improvement of germination. For pepper seeds production, seed quality is one of the major properties considered during the breeding process. This study is performed to evaluate the effects of parental line seed quality property affect on the hybrid. Avsar F1 (Multi Tohum Tar. San. Tic. A.S.) and its parental lines were used to understand parental effects on the germination of the hybrid. The study has been done in 2021 at Multi Tohum R&D center which is located in Antalya, Türkiye. Four replications have been done in this experiment. It is observed that hybrid germination quality is between parental lines. As a result of this experiment, germination levels of the parental lines affect the hybrid, and growth vigor and rate are high for the hybrid and its parental lines. Therefore, the hybrid is suitable for commercial production and sale in germination aspects.

Keywords: Pepper, Seed, Germination

[PP-38]

Sort-Clones of Malus Sieversii (Ledeb.) M. Roem. of Dzungarian Population in the Main Botanical Garden

Laura Shadmanova[1], Laura Shadmanova[2], Gulnara Sitpayeva[1], Gauhar Mukanova[1]

[1]Institute of botany and phytointroduction, Timiryazev str. 36 d, Almaty, 050040, Republic of Kazakhstan.
[2]Al-Farabi Kazakh National University, Timiryazev str.71, 050038, Almaty, Republic of Kazakhstan.

Kazakhstan possesses a unique genetic resource of a wild apple species Malus sieversii, which is the main ancestor of the cultivated apple tree [1; 2]. Natural populations are found in the mountainous regions of Kazakhstan, Kyrgyzstan, Uzbekistan and Western China [3; 4]. The largest natural populations of "M. sieversii" were found in the Zhungar Alatau. In the 1960s, academician A. Dzhangaliyev created a unique collection fund of wild M. sieversii (more than 200 forms and sort-clones) in the Main Botanical Garden of Almaty [5]. To create this collection, valuable forms of M. sieversii were selected as a stock according to the phenotype, and brought to the sort-clones by means of occultation method on the stock of M. sieversii. Studying this collection made it possible to give a selection assessment and identify sort-clones with the greatest manifestation of valuable features [6]. The introduction test and pre-breeding of M. sieversii cultivars-clones in the conditions of the Main Botanical Garden testifies to their high frost resistance; M. sieversii sort-clones are distinguished by uniform long-term growth of shoots and active leaf formation.

Keywords: Biochemical evaluation, genetic resource, sort-clones, Malus sieversii

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[PP-39]

Investigation of Root System Architecture of Promising Winter Squash (*Cucurbita maxima* Duch.) Genotypes for Rootstock Breeding Programme

Ahmet Balkaya[1], Hatice Şeyma Yücel[2], Onur Karaağaç[3], Dilek Kandemir[2]

[1]Ondokuz Mayıs University, Faculty of Agriculture, Department of Horticulture, Samsun, Türkiye
[2]Ondokuz Mayıs University, Department of Crop and Animal Production, Samsun, Türkiye
[3]Seed Certification and Variety Test Station, Ministry of Agriculture and Forestry, Samsun, Türkiye

Root system architecture of plants can significantly influence various physiological functions such as water and nutrient uptake, and plays an important role productivity. The rootstock breeding studies based on strong root improvement are very limited in Türkiye. Due to the difficulty of examining the root development and root morphology of plants within the soil, these features have generally been excluded or neglected in rootstock breeding programmes. As a result of the rootstock breeding studies carried out since 2010, promising six winter squash genotypes were determined from the gene pool in terms of rootstock potential. In this study, it is aimed to investigate and compare the root system architecture of these genotypes with WinRhizo root analysis program. The total root length (cm), average root diameter (mm), root surface area (cm^2) root volume (cm^3) and forks were examined. Moreover, root dry weight and vine weight were determined. All traits were evaluated on the 30th and 50th days from seedling planting date. As a result of the 50th day experiment, it was determined that there were significant differences between vine weight (966.8 - 2301.8 g), fresh root weight (21.0 - 34.5 g), root length (3888.5 - 4667.6 cm), surface area (722.8 - 1001.3 cm^2) and root volume (21.40 - 29.1 cm^3) of genotypes. In all genotypes, the highest vine and root weight was determined in 55BA08 genotype. As a result of the current study, 55CA08 and 55BA08 genotypes showed better performance according to the traits of root system architecture.

Keywords: *Cucurbita maxima*, breeding, rootstock, root system

[PP-40]

Selection of Plants According to Their Resistance to Gamma Radiations, Case of Thapsia Garganica L.(Apiaceae)

Farid Benkaci Ali[1], Abir M. Mohamed Ibrahim[2], Henrik T. Simonsen[3]

[1]Laboratory of Organic and Functional Analysis, Faculty of Chemistry, University of Sciences and Technologies Houari Boumediène, USTHB, BP 32 El Alia, Bâb-Ezzouar,Algiers, Algeria
[2]Department of Food Technology, Laboratory of Food Technology and Humane nutrition, National School Agronomic (ENSA) Avenue Hassan Badi,16000, El - Harrach,Algiers, Algeria
[3]Department of Plant Biology and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg, Denmark

Thapsia garganicaL. roots are used in Algerian traditional medicine for a numberof ailments. It is used in a poultice as an antitussive treatment of acute bronchitis and pneumonia, in preparations with milk or oil taken orally to treat common lung diseases, and with the direct application of root sections for the soothing of dental pains. The objective of this study was to evaluate the combined effect of microwave assisted extraction and gamma irradiation on sesquiterpene lactones in T. garganica extracts. To evaluate the combined effect of microwave assisted extraction and gamma irradiation on the highly bioactive compounds found in extracts of Algerian T. garganica, samples from different locations in Algeria were prepared by extraction from dried leaf and root samples of dried plant material, using different extraction methods. Quantification of the compounds of interest was done using an HPLC. The antioxidant activity extracts was determined using the two free radical scavenging assays: the 2,2-diphenyl-picryl-hydrazyl (DPPH) and the 2,2’-azino-bis(3-ethylbenzothiazoline-6-sulphonic acid) diammonium salt (ABTS). It was found that location and extraction method had significant impact on the phytochemical composition of extracts. Gamma irradiation was found to have no effect on the phytochemical composition of the plant extracts or on their antioxidant properties. The study has shown that microwave assisted extraction is an effective method for investigating chemical compounds in T. garganica and the results support the notion that gamma irradiation for sterilisation do not alter the chemical composition.

Keywords: Thapsia garganica, Gamma irradiation, Microwave assisted extraction, Thapsigargin, Antioxidant

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[PP-42]

Possibilities to Develop Dry Pea Varieties for Sustainable Agriculture

Ahmet Ustaoğlu

Selcuk University, Institute of Sciences, Plant Breeding and Genetics, Konya, TÜRKİYE

With the rapidly increasing world population, it is predicted that there may be problems in meeting the food need in the coming years. The importance of plant-based proteins instead of animal proteins is increasing for the nutrition of the human population. For this, it becomes a necessity to change agricultural production patterns. The need for protein in human nutrition can be met directly with legume plants (soybean, chickpea, pea, lentil and beans), as well as by the inclusion of these plants in other food products as industrial additives. Considering these problems, dry peas increase soil fertility in our improvement studies and reduce the fertilizer cost of the crops planted after it. It is necessary to develop large and high yielding varieties from dry pea and forage pea genotypes suitable for human consumption. According to the study we carried out in two different locations in Konya in 2017 growing seasons, the grain yields of 7 different pea genotypes (*Pisum sativum ssp.*) were determined as line and culture varieties selected from the population. According to the averages of the two locations; Grain yield in pea genotypes were obtained from *Pisum sativum* cv Salamanca, *Pisum sativum* cv Astronaute, *Pisum sativum* cv Guiduro, *Pisum sativum* cv Green Wood, *Pisum sativum* cv Whero, *Pisum sativum* cv PS306, *Pisum sativum* cv PS317. According to results in the trials, the yield ranking was as follows 5328 kg/ha, 4953 kg/ha 4744 kg/ha, 4161 kg/ha, 4113 kg/ha, 3773 kg/ha, 3437 kg/ha. It has been determined that line and pea varieties with high grain yield can be used as genetic soutce in breeding studies in the development of edible dry pea types. With breeding new dry pea varieties adaptable to central Anatolia and transition regions, and to increse their production in the future in those regions, we believe that the foreign dependency of the food and livestock sectors will decrease.

Keywords: dry pea, breeding, sustainable agriculture, vegetable protein

[PP-43]

Registration of "ATMACA" Pinto Bean

Evren Atmaca, Abdullah Taner Kılınç, Ramazan Akın, Sabri Çakır, Mesut Topal

Transitional Zone Agricultural Research Institute

"Atmaca" pinto bean variety was developed by Transitional Zone Agricultural Research Institute and registered in 2020. Among the aims of the Bean breeding program carried out in our institute, it is aimed to develop varieties that can be resistant to diseases which are problematic in the production areas of barbunya and which can be cultivated in large grains, early and large production areas. In line with the improvement studies carried out for these purposes, our Istanbul-coded pinto bean genotype is obtained as a result of cross-linking to our genus of halo blight (Pseudomonas syringae pv.) In the form of a dwarf plant. Modified Bulk Method was brought up to F5 and Pinto bean line was obtained from the single plants selected from the selected parcels.

Keywords: Pinto bean, breeding, halo blight (Pseudomonas syringae pv.)

[PP-44]

Registration of "BAHCIVAN" Runner Bean

Evren Atmaca, Abdullah Taner Kılınç, Ramazan Akın, Sabri Çakır, Mesut Topal

Transitional Zone Agricultural Research Institute

Bahçıvan" runner bean variety was developed by Transitional Zone Agricultural Research Institute and registered in 2020. In the study carried out for the purpose of evaluating the breeding programs in the local varieties in the scope of Dry Bean breeding programs conducted in TZARI, the seeds obtained from this population named as "BOMBA" which is cultivated in the central villages of Erzurum province, were grown in the trial and application area of the TZARI and the line was developed with pure-line selection breeding method.

Keywords: Runner bean, selection, land race

[PP-45]

Molecular Mapping of Leaf Rust and Tan Spot Resistance in the Collection of Wheat Germplasm

Alma Kokhmetova[1], Deepmala Sehgal[2], Makpal Atishova[1], Angelina Malysheva[1], Madina Kumarbayeva[1], Susanne Dreisigacker[2]

[1]Laboratory of Breeding and Genetics, Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2]Global Wheat Program, International Maize and Wheat Improvement Center, Texcoco, Mexico

Leaf rust, caused by Puccinia triticina and tan spot, caused by Pyrenophora tritici-repentis, is an economically important disease in most wheat-growing regions worldwide, including Europe, North and South America, Australia and Kazakhstan. In average, the leaf rust causes 21.5% of yield losses in wheat globally, losses due to tan spot reach up to 50% during epidemic years. Here, we report evaluation of a collection of 194 spring and winter hexaploid wheat cultivars and promising lines from Kazakhstan, Russia and CIMMYT, for tan spot resistance and identification of genomic resistance conferring resistance to the disease using a genome wide association study (GWAS) approach. The panel was genotyped using genotyping-by-sequencing (GBS) markers which revealed high diversity in the panel (PIC 0.33), moderate population structure and a genome wide linkage disequilibrium decay at 8 cM. GWAS identified 34 marker-trait associations for resistance to tan spot with percentage variation from 4 to 13.7%. Our results suggest the existence of novel valuable resistant alleles on chromosomes 3BS, and 3AS and 6AL for resistance tan spot races 1 and 5, respectively, in addition to known genes tsn1 and tsc 2. On chromosome 6A, a genomic region spanning 380 Kb was identified conferring resistance to both races 1 and 5. Epistatic interaction of associated loci was revealed on chromosomes 1B, 5B, 7B, 5AL and 6AL contributing to additional variation of 3.2 to 11.7%. Twenty-five lines with best allele combinations of SNPs associated with both resistance to races 1 and 5 have been identified. Individual high-density map was built for the RIL population Almaly x Anza phenotyped for leaf rust in the QTL study. The final data consisted of 1,969 polymorphic SNP markers located on chromosome 21 with an average number of SNP markers per chromosome 93.76. The lengths of genetic maps for individual chromosomes ranged from 617 cM (chromosome 7D) to 132 cM (chromosome 4B). Markers were mainly distributed among genomes

A and B (40.98 and 40.83%, respectively), the smallest number of markers was presented in genome D (18.18%). The largest number of polymorphic markers was found on chromosome 7D (617; 14.35%), followed by chromosome 5D (577; 19.23%) and 6D (540; 12%). The smallest number of markers was found on chromosome 4B (132; 2.13%).

Keywords: Triticum aestivum, Puccinia triticina, Pyrenophora tritici-repentis; GBS; GWAS; RILs

[PP-46]

New Method In Plant Breeding: Crispr Technology and Its Use

Kübra Taş

Selcuk University, Institute of Sciences, Plant Breeding and Genetics, Konya, TÜRKİYE

In order to increase access to nutritious foods around the world, innovative technologies need to be developed and integrated into agricultural production systems. The new plant breeding techniques developed offer many advantages for making modifications in the plant genome. The availability of genome sequences for plants and advances in genome editing technology have increased breeding possibilities for virtually every agricultural character. Advances in genome editing technologies such as ZFN (Zinc Finger Nucleas) and TALEN (Transcription Activator Like Effector Nuclease) have made it possible to edit any gene of interest at the molecular level. On the contrary, the CRISPR / Cas9 genome editing method includes simple design and easy cloning methods. With different guide RNAs targeting more than one region in the Cas9 genome, multiple different gene regions can be intervened. CRSPR/Cas9, one of the genome editing technologies, is an efficient system with high potential that allows the formation of target-oriented mutations in many agricultural products and allows the mutation of new and desired characters to be obtained through breeding programs without the use of foreign genetic elements. In this study, the current situation of the CRISPR/Cas9-based genome editing technique in plant breeding is summarized, the genome editing studies of CRSPR/Cas9 technology in plants and the strong potentials of the technique for plant breeding and the advantages that genome editing technologies will bring to plant breeding are summarized.

Keywords: Biotechnology, CRSPR/Cas9, Genome Editing, Plant Breeding

[PP-47]

Determination of Promising Onion (*Allium cepa L.*) Genotypes by Selection Method in a Long-Day Breeding Programme

Arif Bağcı[1], Onur Karaağaç[2], Ahmet Balkaya[1], Dilek Kandemir[3]

[1]Department of Horticulture, Faculty of Agriculture, Ondokuz Mayıs University, Samsun, Türkiye
[2]Seed Certification and Variety Test Station, Ministry of Agriculture and Forestry, Samsun, Türkiye
[3]Vocational High School of Samsun, Ondokuz Mayıs University, Samsun, Türkiye

This study aimed to select the superior onion genotypes based on certain selection criteria, bulb shape index, bulb skin digital color (hue°), bulb weight (g), yield (t/da), harvest time (day), bulb neck width (mm), single centeredness, pungency, and total soluble solids (%). Onion genetic resources consisting of 55 yellow, 14 red, and 9 white were obtained from the USDA ARS National Plant Germplasm System. The experiment was carried out in the landraces and laboratories of Faculty of Agriculture (Ondokuz Mayıs University, Samsun, Türkiye), between February - September 2021. All cultural practices (irrigation, pests and diseases control, fertilization) were carried out regularly during the growing period. Bulb shape index and bulb weight varied between 0.6 (R4) - 1.2 (Y50) and 36.67 g (R8) - 281.30 g (Y8), respectively among onion genotypes. Bulb skin digital hue color values ranged between 359°-61° in white onions, 344°-2° in red onions, and 9°-92° in yellow onions. Bulb neck width values of genotypes changed from 4.5 mm (W6) to 28.3 mm (Y8). The highest yield was found in Y8 (11.3 t/da) and the lowest yield was found in R8 (1.5 t/da) and averaged yield as 4.5 t/da was determined for all genotypes. Harvest time of the genotypes were between 129 and 150 days. The genotypes exhibited a range of 6.7% (Y44) - 17.1% (R8) for the total soluble solids. Pungency of the onion genotypes were ranged 56.41% sweet and 43.59% pungent. All of the genotypes were determined as single center. The weighted-ranking method was employed to select the most promising onion genotypes for Samsun ecological condition. The total scores of the genotypes varied between 242 (W8) and 452 (Y9). According to the evaluations, five yellow (Y9, Y13, Y3, Y46, and Y42), one red (R13), and one white (W2) onion genotypes were selected with 10% selection efficiency. Y9, the best yellow onion has a bulb weight of 202 g, a round shape, a single center, dark yellow skin color, long day

harvest, bitterness, and 8.1 t/da yield. R13 has bulb weight of 127 g, round shape, single center, red skin color, long day harvest, sweet, and 5.1 t/da yield. W2 has a bulb weight of 154 g, round shape, single center, white skin color, long day harvest, sweet, and 6.2 t/da yield. These selected promising onion genotypes will be use in hybrid variety programme in the near future.

Keywords: Breeding, method, onion, selection, weighted-ranking, yield

[PP-48]

Marker Assisted Selection: An Approach for Improving the Maize Quality

Marija Kostadinovic, Danijela Ristic, Jovan Pavlov, Zoran Camdzija, Dragana Ignjatovic Micic, Jelena Vancetovic

Maize Research Institute Zemun Polje, Belgrade, Serbia

Marker assisted selection has gained considerable importance as it increases efficiency, reduces time and costs taken to obtain desirable genotypes. Molecular markers can aid selection of all target alleles that are difficult to assay phenotypically, in less time and with minimum linkage drag. Simple sequence repeats (SSR) are being used efficiently for introgressing a target allele, without any intermediate field selection. These markers can be used for direct selection of the target gene (foreground selection), as well as for fast recovery of recurrent parent›s genome (background selection). Maize Research Institute Zemun Polje has a breeding program aimed at conversion of standard quality maize to quality protein maize (QPM), as well as β-carotene (BC) rich genotypes, adapted to temperate regions. As gene-specific SSR markers in foreground selection, phi057 and umc1066 were used for QPM lines, while crtRB1-3'TE marker was used for BC lines. Being the codominant markers, they successfully detected homozygous dominant, heterozygous and homozygous recessive plants separately. Percentage of heterozygous plants identified in BC1 and BC2 generations and homozygous recessive in BC2F2 was in accordance with the expected Mendelian ratio in backcross generations. Background selection was performed on BC2 heterozygous plants. SSR markers evenly distributed throughout the genome (at least three per chromosome) were efficiently used for identification of the genotypes with the highest proportion of recurrent parent's genome (RPG). The recovery of the recipient genome in our best lines varied from 93% to 99% for QPM and from 85% to 99% for BC. Homozygous recessive genotypes with the highest RPG content were screened for biochemical and phenotypic traits to verify their nutritional and agronomical superiority. These newly developed lines are being used for developing high-yielding maize hybrids with improved nutritional benefit adapted to temperate regions.

Keywords: marker assisted selection, nutritional quality, quality protein maize, β-carotene rich maize, simple sequence repeats

[PP-49]

The Biochemical Composition of Maize Hybrids Under the Different Crop Protection Strategies for ECB Attack

Danijela Ristic, Snezana Gosic Dondo, Dragan Grcak, Jovan Pavlov, Zoran Camdzija, Marija Kostadinovic

Maize Research Institute „Zemun Polje‟, Belgarde, Serbia

Maize is one of the three most economically important cereal grains exposed to abiotic stress which affects the occurrence and intensity of ECB attacks. Ostrinia nubilalis Hübn. may attack the maize plants causing the characteristic symptoms of elongated tunnels and circular holes, that can promote the progression of stalk rot. During 2021, the response of three maize hybrids to the different crop protection strategies for ECB attack (insecticides and bioinsecticides) was done. The aim of this work was to evaluate the whole grain biochemical composition of three maize hybrids belonging to different FAO maturity groups. In the experimental field, maize ears were sampled at a moisture content of 14%. Phytochemical characterization was conducted for total protein and amino acid content, as well as for the sugar content (e.g. sucrose, fructose, glucose, lactose and maltose). Statistical data analysis was performed using Microsoft Excel. The results showed lower protein content in untreated control for all tested hybrids, while bioinsecticide treatment showed higher protein content in two hybrids. In contrast, the sugar content was higher in untreated control for most tested hybrids, except for H2 where the highest sugar content was with insecticides treatment. Leucine and cystine content was lower in untreated control for all analyzed hybrids. Variations in phytochemicals in maize grain under the different strategies in ECB control can be one of the important directions in choosing a sustainable pest control strategy.

Keywords: protein content, sugar content, amino acid, European corn borer, Zea mays L

[PP-50]

Grain Yield Predictions of ZP Maize Hybrids

Zoran Camdzija, Milomir Filipovic, Nenad Delic, Jovan Pavlov, Nikola Grcic, Danijela Ristic, Marija Kostadinovic

Maize Research Institute "Zemun Polje", Belgrade Serbia

Maize hybrids are created by crossing inbreds of opposite heterotic groups, where the discovery of genetic distances (GD) is of great significance. With the presence of modern breeding tools for discovering heterotic pairs and GDs in used material an efficiency in breeding can be increased for more precisely planned field work.

For this study 11 crosses were made in order to compare the prediction of data obtained by GDs between crossed inbreds with the results of same hybrids from field testing. Crosses were done in 2020 according to the GD suggestions which ranged from 0.386 to 0.465 to check out is it possible to predict specific superior hybrid performance before the field results itself. 25k SNP Ilumina Infinium Array for maize was used to determine GD values.

As a check ZP 457-market accepted hybrid (registered in 2018 in Republic of Serbia) was used together with 10 other hybrids. All 11 hybrids shared the same female component (Lancaster Sure Crop heterotic group), while male components from opposite heterotic groups (BSSS and Iowa dent) were used. GD values of used males ranged from 0.190 to 0.412 clearly stating one broad heterotic group. The most famous heterotic pair B-73 x Mo-17 as well as two Institute's top selling hybrids (ZP 434 and ZP 606) were also included for GD comparison with test hybrids with the GD values of 0.488, 0.466 and 0.462 respectively.

Review of B-73 x Mo-17 through ZP 434 and ZP 606 to the newly created hybrids suggests GD values are decreasing with every new cycle of selection between crossed material. Results from field testing compared to GD values show somewhat positive correlation as for ZP 3 exp which ranked 2nd highest GD value and 3rd rank in grain yield outyielding ZP 457 significantly, but ZP 457 GD value of 0.458 (ranking third in GD) suggests higher yielder should be though to find. Grain yield results proved same hybrid ZP 457 to be one of the lowest yielders being superior only to ZP 4123 despite high GD value. In top three yielders GD values were in great correspondence for only one mentioned combination ZP 3 exp, but for the ZP 4 exp and ZP 457 taking first and third position according to the GD rank proved to be good only for 5th and 10th rank within field results, while the lowest yielder ZP 4123 took 4th position according to GD values, having very high value of 0.457.

This result proves SNP to be powerful tool in predicting herotic pairs in maize and must be considered for more precise planned field work. Even though GD values being so informative on one side they do not specifically imply to the solution for detecting the most superior hybrid combination therefore leaving field observations to confirm start assumptions.

Keywords: maize hybrid, grain yield, genetic distance

[PP-51]

Stability Analysis of Different Maize Hybrids Grown in Serbia

Jovan Pavlov, Nenad Delic, Srboljub Zivanov, Zoran Camdzija, Nikola Grcic, Danijela Ristic, Marija Kostadinovic

Maize Research Institute "Zemun Polje", Belgrade, Serbia

Maize is the most important field crop in Serbia. The total surface area under maize production is in range from 800.000 to 900.000 hectares annually, which encompasses 25% of the total agricultural land area. The majority of the production is without irrigation, therefore there is a high variation in total annual production, depending on the amount and distribution of precipitations.

The main challenge for maize breeders in Serbia is to develop high yielding and stable hybrids for diverse environmental and climate conditions. Different response of genotypes to diverse environmental conditions is a result of genotype x environment (G x E) interaction. Several statistical methods have been developed for testing G x E interaction. Parametric methods are based on variance components and regression, while non-parametric methods are based on the ranks of genotypes in each environment.

In order to evaluate stability of different maize hybrids, seven commercial ZP maize hybrids within maturity range FAO 400-700 were tested at nine different locations across the Serbia for two years period. Selected locations represent the main growing regions

in Serbia. Three parametric (Eberhart and Russel model (bi), Shukla's stability variance (ri2), Francis and Kanneberg coefficient of variation, CVi) and two non-parametric approaches (Huhn rank stability measures Si1 and Si2) were used for the evaluation of the hybrids based on their stability.

Average yield for all hybrids tested in 2020. was 10,92 t/ha, while average yield in 2021. was 6,74 t/ha. The highest yielding hybrid was ZP 5601 and this hybrid showed above average stability measured by different parameters. Hybrids ZP 606 and ZP 6263 were also high yielding and both showed above average stability according to the majority of used parameters. Hybrids from FAO 400 maturity group had lower yield than the hybrids from other maturity groups and also performed less stable compared to late maturity hybrids.

Significant positive rank correlations were found between grain yield and CVi (0.93*), grain yield and ri2 (0,75*), as well as between CVi and ri2 (0,75*). For all other pairs of parameters positive non-significant correlation was observed, except between bi and Si1 and bi and Si2.

Based on the results obtained in the study, application of both parametric and non-parametric methods is useful for stability analysis in maize.

Keywords: maize hybrids, grain yield, stability

[PP-52]

iPBS-Retrotransposons Variations: DNA Fingerprinting and the Evaluation of Genetic Diversity and Population Structure in International Cowpea Germplasm

Faheem Shahzad Baloch, Muhammad Tanveer Altaf, Mehmet Bedir, Muhmmad Azhar Nadeem, Tolga Karaköy, Muhammad Aasim

Faculty of Agricultural Sciences and Technologies, Sivas University of Science and Technology, Sivas 58140, Turkey

Cowpea belongs to the Leguminosae family, originated in Africa, and grown in subtropical and tropical areas worldwide. Cowpea seeds contain high nutritional contents and play a vital role in nutritional feed for animals and humans in many countries. The present investigation aimed to check the genetic variations among cowpea germplasm collected from 6 countries using iPBS-retrotransposons markers system. Twelve highly polymorphic iPBS-retrotransposons primers were used for PCR amplification. These primers generated 200 total bands of which 188 were highly polymorphic and 94.30% polymorphism was observed. Mean values of genetic diversity indices i.e., Shannon's information index (I = 0.452), effective number of alleles (ne = 1.501), overall gene diversity (ht = 0.236), gene diversity (h = 0.298), polymorphism information content (PIC = 0.308), and average genetic distance 0.61 confirmed a great level of genetic variations in studied germplasm. Analysis of molecular variance revealed 96 percent variation within the population. (The STRUCTURE analysis divided germplasm into 2 populations according to geographically. The Neighbor-joining tree and Principle coordinate analysis (PCoA) divided the germplasm into 3 groups and the grouping was mostly aline with STRUCTURE-based clustering. This study revealed high genetic variability in cowpea germplasm and the high values of diversity indices revealed the utility and efficiency of iPBS-retrotransposons marker system. The PCoA, Neighbor-joining tree and STRUCTURE analysis separated the accessions geographically.

Analysis of molecular variance revealed 94% genetic variation within a population and Ghana 1 and Turkey 4 had the greatest genetic distance and could be recommended for breeding activities.

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Keywords: iPBS-retrotransposons, Cowpea germplasm, Leguminosae, Population Structure, Genetic diversity

[PP-53]

Breeding of Winter Feed Barley Genotypes With High Digestibility Under Turkish Highlands

Aytekin Aksoy[1], Gulizar Manav[1], Fatma Uygunsoy[1], Fatih Demirkutlu[1], Ismet Aykol[1], Serdar Ural[1], Mehmet Tekin[2], Taner Akar[2]

[1]TASACO Seed Company, Antalya, TURKIYE
[2]Akdeniz University, Faculty of Agriculture

This research was carried out to develop new winter type feed barley cultivars with high digestibility during the last six years under highland condition of Turkey. For this aim, 1100 single spike from 110 Turkish landraces were selected in the first year. Then, 130 line based on their cold tolerance, disease resistance, earliness and lodging resistance were determined in the second year. These lines together with for common checks such as Tarm, 92, Aydanhanım, Burakbey and Tosunpasa were experimented under Augmented design in 2019-20 season and they were characterized both genetically by using 21 diverse SSR markers and phenotypically by using 1000 kernel weight, volume weight, grading, starch, crude cellulose and protein, ADF, NDF so totally, 20 advanced lines were selected further evaluation in 2020-21 season. These genotypes were experimented under RBCD at two locations of Konya province and 11 candidate cultivars were selected based on yield and advanced feed quality parameters for regional yield trials in 2021-2022. These together with the four common checks under RCBD at 4 locations of Konya, Ankara and Eskisehir provinces and three candidate lines were nominated for registration trial. There was great variation in terms of digestibility parameters and grain yield among candidate lines compared to common checks. Among these, candidate line 148 with reasonable physical parameters such as 54,2 1000 kernel and 61,2 volume weights and 1,5 g under sieve and superior advanced feed quality parameters compared to the common checks such as 49,8 % starch, 2,8 % crude cellulose, 12,2 % crude protein, 3,5% ADF, 15,0% NDF was one of the most promising genotypes. This study showed importance of Turkish barley landraces and these candidate cultivars can be used parental lines as progenitors for further breeding studies.

Keywords: feed barley, digestibility, crude cellulose and protein, ADF, NDF

[PP-56]

Comparison of Two and Six-rowed Barley (Hordeum vulgare L.) Genotypes Under Rainfed Conditions

Irfan Öztürk, Remzi Avcı, Banu Tülek, Turhan Kahraman, Adnan Tülek

Trakya Agriculture Research Institute Edirne, Türkiye

Barley is an essential crop in the Trakya region and it grows for feed and malting in the region. Due to changing environmental conditions, there are variations in yield, quality and leaf diseases depending on environmental factors in genotypes with 2 and 6 rows. In barley, cold damage may occur in alternative varieties due to the low temperature in early spring. In addition, biotic stress factors are also effective due to rainy and humidity conditions during the shooting and heading phase. The experiments were carried out in the 2016-207 growing cycle and composed of 36 two-rowed and 36 six-rowed barley genotypes in alpha-lattice blocks with three replications. In the study, grain yield, net blotch, scald, plant height, days of heading, 1000-kernel weight (TKW), test weight (TW) and protein ratio and relationship among these characters were investigated. The genotypes were screened for scald and net blotch under natural epidemic conditions. According to the results, there were significant differences among genotypes for the parameters investigated. The mean grain yield in two-rowed was 8576 kg ha-1 and in six-rowed genotypes was 8454 kg ha-1. In two-rowed genotypes mean 1000-kernel weight was 51.2 g, test weight 72.9 kg and protein ratio 11.6%. In six-rowed genotypes mean TKW was 37.0 g, TW 69.5 kg and protein ratio 10.8%. In two-rowed genotypes based on double-digit scores, a total of 11 barley genotypes highly tolerant to Net blotch (Prenophora teres) scored between 11 and 33. While 2 barley genotypes were highly tolerant to Scald leaf disease in 6-row genotypes, 22 barley genotypes were found to be very sensitive. In two-rowed genotypes, Net blotch negatively slightly affected grain yield, TKW, TW and protein ratio. Scald (Rhynchosporium secalis) is one of the important biotic stress factors in barley. Scald leaf disease negatively affected 1000-kernel weight (r=-0.391*) and test weight (r=-0.482**). Scald leaf disease also negatively affected grain yield. In the study, 5 genotypes from the 2-rowed experiments and 2 genotypes from a 6-rowed experiment were selected for breeding studies.

Keywords: Barley, genotype, grain yield, quality parameter, biotic stress

[PP-58]

Climate Change and Plant Breeding

Mustafa Demirel, Hakan Aktaş

Isparta University of Applied Sciences, Faculty of Agriculture, Horticulture Department, Isparta, Turkey

Climate change has become an important problem today by changing the characteristics of the atmosphere such as precipitation, humidity and temperature. Since the mid-1800s, humans have contributed to the release of carbon dioxide and other greenhouse gases into the air. Increased CO2 concentration has led to an increase in atmospheric temperature and global warming. Climate change; hot airwaves, drought, floods and many weather events can cause more power and frequency. For these reasons, changes in the water cycle and temperatures and possible seasonal shifts are expected to directly affect the agricultural sector under the control of these systems. Estimated climate changes will affect the production and production areas; It is thought that the severity, frequency, and increase of excessive weather events may cause a decrease in yield in agriculture. For example; with global warming, farmlands are dry for a long time, and some regions are flooded with the effect of heavy rains, causing agriculture to become unsuitable. In addition, due to climate change, it is thought that there may be serious changes in the disease and harmful population that we call biotic stress as well as events such as drought and floods. In many agricultural areas where this situation is felt, it is reported that there are many serious problems with growing. It is not possible for the cultivars in many species grown today to take place in the market if they are not tolerant to these adverse conditions. For this reason, it is thought that there is a need for gene sources that can be resistant or tolerant to these conditions. In this context, it is predicted that breeding programs to develop varieties that are resistant or tolerant to biotic and abiotic factors may be much more important. Therefore, it is thought that it is important for the public and private sectors to determine new strategies by testing their lines or varieties against stress factors as soon as possible. This review has been prepared especially for the problems that may be caused by abiotic stress factors and the opportunities for use in the subject of breeding.

Keywords: Abiotic, Biotic, Climate change, Global warming, Plant breeding

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[PP-59]

Study on Some Quality and Morpho-Physiological Traits of Durum Wheat (Triticum durum L. Desf.) Genotypes

Balkan, A.[1], Bilgin, O.[1], Başer, İ.[1] Göçmen, B. D.[1], Özcan, K.[2]

[1]Tekirdağ Namık Kemal University, Agricultural Faculty, Department of Field Crops, Turkey

[2]Tekirdağ Namık Kemal University, Thrace Seed Valley Appl. and Research Center, Turkey

The study was carried out in the experimental field of the Department of Field Crops, Faculty of Agriculture, Tekirdağ Namık Kemal University in 2020-2021. In the study, totally 25 durum wheat genotypes (6 cultivars, 12 advanced lines, and 7 landraces) were used as experimental material. The experiment was conducted in a randomized complete block design with 3 replications. In the study, the grain quality and morpho-physiological traits such as canopy temperature, chlorophyll content, leaf area index, and plant height were investigated in some durum wheat genotypes.

The canopy temperature ranged from 23.333-20.433 OC, chlorophyll content 52.533-43.167 SPAD, leaf area index 3.633-1.767, thousand-grain weight 34.667-41.833, protein content 14.233-16.333, test weight 78.933-87.033, semolina colour 14.880-15.627 and plant height 99.00-75.33 cm in investigated durum wheat genotypes. Genotypes Hacımestan and Sorgül for canopy temperature, genotypes Atkı 2, NZFM 1 and NZFM 7 for chlorophyll content, genotypes Atkı 2, NZFM 4 and NZFM 1 for leaf area index, genotypes Kıbrıs 2 and Ionia 3 for plant height, genotypes NZFM 1, NZFM 7 and Devedişi 2 for thousand-grain weight, genotypes Atkı 2 and Hacımestan 2 for protein rate, genotypes Japiga and Boğacak 2 for test weight and genotypes Japiga, Boğacak, Kızıltan 91 and NZFM 7 for semolina colour were determined as promising genotypes.

Keywords: Durum wheat, genotype, chlorophyll content, semolina colour, canopy temperature

[PP-60]

Breeding for Niche Specific Ideotypes in Commercial Agricultural Crops

Ajaz Ahmad Lone[1], Zahoor A Dar[1], Shabir H Wani[1], Faik Kantar[2], Audil Gul[1], Ozer Callis[2]

[1]Dryland Agriculture Research Station, Sher-e-Kashmir University of Agriculture Sciences & Technology of Kashmir INDIA
[2]Akdeniz University-Antalya Turkey

Plant breeding programmes across globe aim to improve the yielding adaptability, stable performance, uniformity in expression of traits, biotic and abiotic stress resilience and good harvest quality. Unravelling genetic diversity for the particular traits responsible directly or indirectly for grain yield as incorporation of genetic diversity for yield traits is a pivotal move towards ensuring food security in present as well as future. Ideotype breeding provides a way of bridging the gap between the utilization of unimproved germplasm (wild species and their relatives) with improved crop gene pool. Ideal plant architecture ensures ease in use of cultural practices, allow mechanized harvest at cheaper costs and ensures pods ability to avoid coming in contact with the ground soil, ensuring better seed quality. Plant growth and development is a results of multiple interactions and trade-offs among various vital biological processes like morphological, physiological and biochemical acting simultaneously at different scales and there is a competition for the same resources. These inter-linkages and trade-offs makes it difficult to decipher phenotype construction and improve crop performance in various agro-climatic conditions prevailing for plant growth. Clear cut understanding of interactions and trade-offs between traits or processes contributing to crop performance and their genetic bases becomes essential aspect of ideotype breeding. Phenotyping platforms supported by an ideal model characterizing a set of traits provides a phenotyping fingerprint to explore trait correlations in a target population. Advancements in Genetic Engineering, marker assisted breeding, high throughput phenotyping and molecular genetics tools have enhanced efficacy of breeding gains in cultivar development in major economic crops. Developing smart crops with efficient designs for maximizing returns under given set of cultivation practices like herbicide tolerant soybeans, transgenic for pest resistance in corn, biofortified golden rice etc. Breeding by design approach ensures expression of specific gens to control desired allelic variation for agronomically important traits. All these scientific breeding modules ultimately lead to what we call as a proper ideotype.

Keywords: Breeding, Ideotype, Agriculture crops

[PP-61]

The Effect of Gamma Irradiation on Groundnut (Arachis hypogaea L.)

Moin Qureshi, Bülent Uzun, Engin Yol

Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya, Turkey

Mutation is a heritable change in the genetic material and it can generate random genetic variations, resulting in a mutant line. It is one of the breeding methods to increase phenotypic variation and develop new cultivars as well as to enhance the yield, better nutritional quality, and wider adaptability of the world's most important crops such as wheat, rice, pulses, millets, and oilseeds. Mutations can be induced by several techniques, such as physical, chemical, and insertional mutagen treatments. Groundnut (*Arachis hypogaea* L.) is a major economic crop, has high oil and protein content, and is the world's fourth most produced oil crop. The aim of this study was to determine the effective gamma irradiation dose for inducing mutations in groundnut. Gamma radiation doses (200 and 300 Gy) were applied to the groundnut cultivar "NC7". Based on observed parameters, significant variations were found between treatments for the features of seed germination percentage, seedling survival, and pods per plant. The experiment results revealed that the increase in the gamma ray's dosage reduced the germination percentage of the seed. The results further revealed that the seed treated with 200 Gy and 300 Gy showed a germination percentage of 56% and 46%, respectively. The mean of number of capsules 11.1 for the dose of 200 Gy and 10.6 for the dose of 300 Gy.

Keywords: Peanut, variation, diversity, mutagen

[PP-62]

Determining TSWV Resistance Levels for Some Characteristics of Capia Pepper Lines

Nora Abdelfattah Nassar Allam[1], Gülbanu Kiymaci[1], Ünal Kal[2], Onder Turkmen[2]

[1]Selcuk University, Intitute of Science, Hoticulture Department, Konya
[2]Selcuk University, Faculty of Agriculture, Hoticulture Department, Konya

Tomato spotted wilt virus (TSWV) is a viral disease agent that limits pepper production and causes economic losses in the world. The gene controlling resistance to TSWV (Tsw) has been detected in many Capsicum chinense pepper genotypes ('PI 152225', 'PI 159236', 'CNPH 275''C00943', and '7204') and mapped on chromosome 10 it has been mapped to cultivars (Capsicum annum). Although the homolog of Sw-5 could not be mapped, phenotypically similar genes are present in tomatoes, with many Sw5 homologs found in similar regions in tomatoes and pepper. The relationship between Tsw and Sw5 has been studied through genetic studies of TSWV. The most effective and environmentally friendly way to combat this viral pathogen is to use resistant varieties. Our study investigated the resistance levels of 40 genotypes at S3 stage against tomato spotted wilt virus (tswv). investigated SCAR marker was used in molecular studies. Genotypes were determined as 5 homozygous resistant (RR), 15 sensitive (rr), and 20 heterozygous resistants (Rr).

Keywords: Pepper, TSWV, Molecular marker

[PP-63]

Mapping of Bacterial Wilt and Canker (Clavibacter michiganensis Subsp. michiganensis) Resistance in Tomato Mutant Lines Using Whole Genome Sequence Analysis

Mumin Ibrahim Tek[1], Ferhat Ozdemir[2], Halil Karakas[2], Deniz Karabulut[2], Shabir Hussain Wani[3], Ozer Calis[1]

[1]Akdeniz University Faculty of Agriculture Plant Protection Department, The Campus 07059 Konyaalti-Antalya/TURKIYE
[2]Tokat Gaziosmanpasa University Faculty of Agriculture Plant Protection Department, Tasliciftlik-Tokat/TURKIYE
[3]Genetics and Plant Breeding Mountain Research Centre for Field Crops, Khudwani, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar, Jammu and Kashmir, India

Bacterial wilt and canker disease caused by Clavibacter michiganensis subsp. michiganensis (Cmm), is one of the most serious diseases of tomato around the globe. Using Cmm-resistant cultivars for tomato production is eco-friendly and effective method to control the bacterial disease. However, Cmm resistance is still unclear and there is no report about Cmm-resistant commercial tomato cultivar within extensive studies. The mutant lines were generated by using 0.5% Ethyl methanesulfonate (EMS) chemical mutagen from susceptible NCEBR3 plant; M3-9 and M3-15 plants were determined as resistant against Cmm isolate 2 at M3 population previously. Individual mapping populations were established with M3-9 and M3-15 mutant line and a resistance locus was mapped at chromosome V of tomato. Resistance locus was linked with SL20210_883i SSR marker flanked by single nucleotide polymorphism markers. Therefore, we have focused on to reveal Cmm-resistance locus sequence with using Illumina HiSeq for determining and comparing genetic polymorphisms. The polymorphism between NCERBR3 susceptible and M3-9, M-15 resistant mutant lines is useful to generate specific marker for marker assisted selection (MAS) in tomato. Further molecular analyses could be performed to generate novel markers for Cmm-resistant cultivars using the next generation sequence system.

Keywords: Tomato, Bacterial Wilt, Canker, EMS, SSR, SNP, NGS

[PP-64]

Pomological and Phenological Characteristics of Promising Sweet Cherry (Prunus avium L.) Progeny

İsmail Demirtaş

Cherry is one of the leading fruit species that is consumed lovingly all over the world and that provides a high level of income to its producer. Changing consumer demands, climatic factors, production costs and biotic and abiotic stress conditions necessitate the development of new cherry varieties. However, there are important problems in the cultivation of old cherry varieties such as yield, quality and self-incompatibility.

In this context, cherry cultivar breeding has been started by hybridization by Eğirdir Fruit Research Institute (MAREM). In this study, promising cultivar candidates were obtained as a result of crossings (0900 Ziraat X self-compatible or incompatible cultivars) made in MAREM. Phenological and some fruit quality characteristics of 7 promising cherry genotypes were determined.

The phenological and pomological characteristics of the genotypes have varied over the years. Harvest times, fruit weights, seed weights, stem weights, fruit stem lengths, Soluble solids content (SSC) and pH values of the genotypes were determined.

Keywords: Sweet Cherry, Crossbreeding, Fruit, Pomology, Phenology

[PP-65]

Advances in Industrial Crops Breeding in Transitional Zone Agricultural Research Institute

Arzu Kose, Ferda Kosar, Ceyda Nur Yurdagul

Transitional Zone Agricultural Research Institue

Safflower and Opium Poppy are plants that stand out among industrial crops with their different aspects, but their value is overlooked. Safflower is one of humanity's oldest crops, first cultivated in Mesopotamia. It is cultivated in a wide range of ecological habitats predominantly in semiarid and temperate regions of the world. In the world, the earliest reference to the opium poppy growth and use in Southwest Asia, in 3,400 B.C. Turkey recognized as traditional cultivators of poppy, has the largest share of the opium poppy cultivation among the six countries in the world that legally produce the poppy under the supervision of the United Nations. Breeding research on these crops has been going on for many years in the Transitional Zone Agricultural Research Institute established in 1929. Safflower is a drought –resistant annual crop having different way of use. In Turkiye, research on this crop was initiated at Eskişehir Sazova Plant Breeding station in 1930. As a result of these studies, The first safflower variety Yenice was registrated with 25 % oil ratio. Dincer varieties were registered while the line no. 5-154 has been given seed production permit. Despite long years' research on breeding and agronomy of safflower, breeding program was ended in 1988 due to its failure to create the expected demand in Turkish agriculture. The Institute continued its efforts with genetic stock renewal and multiplication of breeder seed. Breeding research was re-started in 2000, considering the national demands, and line 5-154, which previously had seed production permit, was registered with the name Remzi Bey-05. The main objective of the safflower breeding research at Transitional Zone Agricultural Research Institute is to develop varieties meeting demands by producers, consumers and industrial end-users. Selection, crossing and mutation methods are being used in these breeding efforts. Thanks to the ongoing breeding program of the Institute, Balci (38-41 % oil ratio), and Yektay (37-39 % oil ratio) which is superior to existing varieties in terms of oil content and oil yield was registered in 2011 and 2019, respectively.

The main aim of poppy breeding programme is to develop opium poppy varieties with higher capsule and seed yields, higher morphine and thebaine contents, better resistance to insects and diseases and better tolerance. The research was started in 1985. Initially, a germplasm has been established with material collected from different national sources such as opium growing areas in Turkey the gene bank in Izmir and an international sources (mainly USA). In the name of the Institute, the first poppy varieties with a morphine content of over 0.5% were registered in 1995 as Kemerkaya-95 and Anayurt-95. Thanks to the ongoing breeding efforts Celikoglu, Hüseyinbey and Seyitgazi varieties with 1% morphine ratio were registered in 2019. These varieties are widely cultivated in poppy-producing area.

Keywords: safflower, opium poppy, breeding, variety

[PP-66]

Barley Breeding Studies in Eskisehir Transitional Zone Agricultural Research Institute

Soner Yüksel

Transitional Zone Agricultural Research Institute,
Eskisehir/Turkey

Transitional Zone Agricultural Research Institute is the first agricultural research institute that was founded in Turkey. The working areas of the institute are to develop the plants which are grown in the Middle Anatolia and Transitional Regions, to study growing techniques and controlling pests and diseases, and to produce original seeds of the registered varieties. Barley breeding studies started with the foundation of the institute in 1925 as parallel to wheat research. Early times of the institute barley breeding and agronomy studies were conducted in harmony. In the breeding studies, the crosses are made every year and the suitable material is selected in segregating populations. In the segregating material modified bulk method is applied. In this step selected material is transferred to screening nurseries and then evaluated in the yield trials in the following year. The yield trials are conducted in Hamidiye experimental fields of the institute. Regional Yield Trials (RYTs) are conducted in locations where winter barley is grown to see the performances of the advanced lines for several years. Promising lines from RYTs are submitted to the National Variety Testing Institute for final evaluation and registration as new cultivars. In this study, the characteristics of the malting barley variety SABRİBEY developed in 2019 and the forage barley variety YÜKSEL, which was accepted by the registration committee a year later, is given.

Keywords: Barley, Breeding, Variety, Yield, Registration

[PP-67]

Identification of Superior Winter Wheat Genotypes With High Grain Yield and Quality Combined With Stripe Rust Resistance in Uzbekistan

Zafarjon Ziyaev[1], Saidmurad Baboev[1], Ram Sharma[2]

[1]Institute of Plant Genetics and Experimental Biology, Cereal Genetics, breeding and seed production laboratory, Tashkent, Uzbekistan
[2]ICARDA, 6 Osiyo Street, Tashkent 100000, Uzbekistan

Winter wheat is the most important food crop in Central Asia. Even though the wheat varieties grown in Uzbekistan are mainly high yielding; their end-use quality is often low due to their exotic origin and diverse wheat growing environments of Uzbekistan. Many wheat varieties of foreign origin do not fully meet the requirements of the milling industry in terms of baking and other quality indicators. This results in imports high-quality grain and flour products from other countries. In addition, the climatic condition of the main irrigated wheat area in Uzbekistan is favourable for stripe rust epidemics. Observations in recent years have shown that stripe rust pathogen overwinters in wheat fields planted early in the fall, and this in turn leads to recurrence of stripe rust epidemics every 2-3 years. One of the main reasons for these outbreaks is cultivation of stripe rust susceptible wheat varieties. The area under cultivation of the available stripe rust resistant varieties is increasing but a few resistant varieties have become susceptible after a few years of cultivation due to variable nature of the stripe rust pathogen. Identification of wheat genotypes with diverse sources of stripe rust resistance and high grain and bread quality wheat cultivars are the most important tasks of the breeding activities in Uzbekistan. To attain this objective, Institute of Plant Genetics and Experimental Biology with funding support from Ministry of Innovative development of Uzbekistan started evaluation of germplasm developed by the International Winter Wheat Improvement Program (IWWIP), which is a joint wheat breeding program of the Government of Turkey, CIMMYT and ICARDA. In 2020, 610 advanced breeding lines obtained from IWWIP were tested for stripe rust resistance under artificial inoculation in the field. These lines were also evaluated for agronomic and quality traits. Based on stripe rust resistance, and superiority for agronomic and quality traits 86 genotypes were identified and further evaluated together with 14 released varieties

in 2021.Several promising genotypes with high grain protein content (>=14%), high gluten strength (sedimentation value >=60ml), high gluten content (>=28%), TKW (>=40gr) and test weight (>=760gr/l) were selected for further evaluation for varietal release. The superior genotypes identified in this study could be valuable for national, regional, and international wheat improvement programs.

Keywords: Grain yield, quality, resistance, stripe rust, winter wheat

[PP-68]

Yield and Yield Components of Newly Developed Safflower Lines

Oğuzhan Aydın[1], Dr. İllhan Subaşı[2], Dr. Fatma Kayaçetin[3], Dr. Muhittin Bağcı[1], Sefa Ünal[1]

[1]Oilseed Crops Breeding Unit, Central Research Institute for Field Crops, Ankara, Türkiye
[2]Seed Science & Technology Department, Faculty of Agriculture, Abant İzzet Baysal University, Bolu, Türkiye
[3]Medicinal & Aromatic Plants Department, Kalecik Vocational School, Ankara University, Ankara, Türkiye

Fats are one of the essential nutrients because they contain high energy and fat-soluble vitamins. Safflower (Carthamus tinctorius L.) is an important oilseed crop that contains 25-45% oil in its seeds, its oil is characterized by highly unsaturated fatty acids, safflower is also, resistant to drought, and has a wide adaptation capacity. The main objectives of breeding studies in oilseed crops are to develop cultivars with high seed yield, high oil content, and high oil yield per unit area. This study was conducted at the Central Research Institute for Field Crops (CRIFC), İkizce Research and Production Farm, within the scope of "Safflower Breeding Studies" in 2021. In the study, seed yield, oil content, and oil yield of 25 lines (developed by the CRIFC Oilseed Crops Breeding Unit with the selection breeding method) and 5 safflower cultivars were evaluated. As a result of the study, the seed yield varied between 1554.44 to 3279.63 kg/ha. The highest seed yield was obtained from Line119. When the oil content was analyzed, it was found to be between 27.32% to 36.48%. In the study, it was determined that 5 lines (Line80, Line39, Line8, Line61, and Line123) had a higher oil content than BALCI (35.24%), which had the highest oil content cultivar in this study. Oil yields were found between 542.46 to 1237.10 kg/ha. Three lines (Line119, Line123, and Line141) that surpassed the BALCI cultivar with the highest oil yield stood out. According to the findings obtained in this study, Line119 came to the fore as the most promising line for arid and semi-arid areas of Central Anatolia and transition regions in terms of seed yield and oil yield.

Keywords: Safflower, breeding, seed yield, oil content, oil yield

[PP-69]

Determination of the Seed Yield and Resistance to Broomrape Parasite of Some Hybrid Sunflower Varieties in Different Locations

Veli Pekcan[1], Mehmet Ibrahim Yılmaz[1], Bayram Serkan Cabar[1], Samet Sağlam[1], Ersan Çan[2]

[1]Trakya Agricultural Research Institute, Edirne, Türkiye
[2]Areo Seeds, Antalya, Türkiye

Sunflower is the most cultivated oil crops in Turkey and grows almost all part of Turkey. Broomrape parasitic weed (Orobanche cumana Wallr.) is the most reducing factor of production of sunflower, which, is the. Even if Orobansha genetically resistant sunflower seed yield in Turkey as well as in Eastern Europe. With developing of new races of Orobanche, the broomrape has started to be seen intensively in the Konya location where sunflower is planted the most after Trakya Region. This study was carried out in 2021 in order to determine the yield and resistance of broomrape of sunflower hybrids developed by Thrace Agricultural Research Institute in Edirne and Konya locations. Trials were set up in dry conditions in Edirne, in irrigated conditions in Konya, in RCBD design with 4 replications. Broomrape resistance tests were carried out by artificial inoculation method using a mixture of Orobanche collected from Thrace region in Edirne and under natural infested conditions in Konya location. In the study, TTAE 20-12, TTAE 20-13 and TTAE 20-44 in Edirne location, TTAE 20-32 and TTAE 20-70 hybrids in Konya location exhibited higher performances than other candidates in terms of yield and oil ratio among candidate cultivars. In terms of resistance to broomrape parasite. TTAE 20-12, TTAE 20-40 and TTAE 20-64 varieties were found to be resistant in both locations. However, some cultivars were found to be resistant in different locations. This result indicated that there are different races of broomrape in both locations.

Keywords: Sunflower, seed yield, resistance, broomrape, races

[PP-70]

Determination of the Performance and Quality of Rice (Orzya sativa L.) Genotypes in Samsun Conditions

Özgür Azapoğlu, Serkan Yılmaz, Melih Enginsu, Rasim Ünan

Black Sea Agricultural Research Institute

This research was carried out to determine the performance and quality of rice genotypes in Samsun ecological conditions. In the study, 10 rice genotypes (7 candidates, 3 standards) were used. regional yield trials of these genotypes conducted in Bafra and Tekkeköy districts in 2018 and 2019 in a randomized block design with 3 replications. In the study, paddy grain yield, 1000 grain weights of paddy and rice, and yield of broken and unbroken rice of genotypes were investigated. Significant differences were found between cultivars in terms of these characteristics. At the same time, environment and genotype x environment interactions were found to be important for these characters. In terms of rice grain yield, genotypes 200938- KA098 and KA1116 were in the same group with the standards. Although the Ilkeren cultivar is in the middle ranks in terms of yield and quality, since it is an early cultivar candidate among the registered cultivars in Türkiye, a registration application was made in 2020, and it was registered under the name of Ilkeren in 2022.

Keywords: Rice (Oryza sativa L.), rice genotype, cultivar environmental intraction, registration

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[PP-71]

Revealing Local Wild Plant Species Potential for Microgreens

Onur Karaağaç[1], Ahmet Balkaya[2], Fatih Öğütçü[1], Üzeyir Yiğit[1], Özge Kılıç Tosun[3]

[1]Seed Certification and Variety Test Station, Ministry of Agriculture and Forestry, Samsun, Türkiye
[2]Department of Horticulture, Faculty of Agriculture, Ondokuz Mayıs University, Samsun, Türkiye
[3]Yeşilyurt Demir Çelik Vocational High School of Samsun, Ondokuz Mayıs University, Samsun, Türkiye Türkiye

Microgreens are young and tender vegetables or herbs that provide attractive color, flavor, and nutrition. The concept of microgreens is generally less popular in many countries including Türkiye. The purpose of this study was to evaluate the yield and quality of microgreens grown by different led lights and from different vegetables or herbs genetic resources from Türkiye. Local populations of *Rumex acetosella* (Sheep's sorrel), *Chenopodium quinoa* (quinoa), *Brassica oleracea* (kale and cabbage), *Beta vulgaris* (red beet) and *Fagopyrum esculentum* (buckwheat) were used as microgreens. The led light treatments (red, blue, red+blue, and white) were provided by continuous (24-h) lighting at a photosynthetic photo flux density of around 150 μmol m^{-2} s^{-1}. The growth chamber was maintained at 25 °C/18 °C and 16/8 h light/dark. Highest color pigments in both leaf and hypocotyl parts of microgreens were detected under red plus blue (50R:50B) spectrum while the lowest were found under white spectrum. Blue light decreased hypocotyl length in all microgreens. However, red light resulted in significant hypocotyl elongation. White led caused an increases leaf area. Yield and taste values varied according to both light type and genotype. As a result, it was evaluated that especially some kale, red beet and buckwheat genotypes could be used for microgreen production in Türkiye. In addition, red plus blue (50R:50B) light is recommended for the production of quality microgreen.

Keywords: microgreen, genetic resource, sorrel, quinoa, beet, kale, buckwheat

[PP-72]

Population Improvement in Adapop 9e and 9f Sweet Corn (Zea mays saccharata) Gene Research

Mehmet Cavit Sezer, Mesut Esmeray, Ahmet Duman, Niyazi Akarken, Cem Serdar Cerit, Memis Bilgici, Ipek Koca Recber

Maize Research Institute, Sakarya, Türkiye

Plant genetic resources of the plant studied are essential for plant breeding studies. Because the "genetic resources" of that plant are of primary importance, since the desired "inbred lines" to be achieved in order to obtain hybrid varieties is to reveal a variety. From the point of view of maize plants, these genetic resources are called "populations". As stated in many publications, open pollinated materials, composites, synthetic materials, and F2 progeny of hybrid varieties are used in the creation of populations.

One of the sub-varieties of the maize plant is sweet corn. One of the sub-projects of the "Marmara Region Maize Breeding Research Project" carried out by Sakarya Maize Research Institute is the "Marmara Region Population Breeding Research". Our aforementioned sub-project continues only in our sweet corn materials called "Adapop 9". Our Adapop 9 sweet corn population has 7 subpopulations. In this study, the studies carried out in the "Adapop 9e" and "Adapop 9f" subpopulation in the years 2020-2022 are given.

In our project, "S1 Recurrent Selection Method" is used. Our Adapop 9e material; In 2020, 31 materials selected in previous years were transferred to the "sweet corn breeding program" and at the same time, "Adapop 9e (S1) C1" was obtained by creating a "Recombination Block". In 2021, the "Inbred Reproduction Block" was established and 36 Adapop 9e (S1) C1 materials selected, which deemed suitable. In 2022, "Recombination Block" was established and Adapop 9e (S1) C2 was obtained. Our Adapop 9f material; In 2021, the "Inbred Reproduction Block" was established and 41 Adapop 9f (S1) C0 materials were selected, which were deemed suitable. In 2022, "Recombination Block" was established and Adapop 9f (S1) C1 obtained.

Keywords: maize breeding, sweet corn, population improvement, S1 recurrent selection

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[PP-73]

Selection of Advanced Bread Wheat (Triticum aestivum L.) Lines in terms of Yellow Rust (Puccinia striiformis F. sp. tritici) and Grain Yield in Sakarya Conditions

Lütfü Demir, Şinasi Orhan, Sinan Bayram

Maize Research Institute, Sakarya, Türkiye

Yellow rust (Puccinia striiformis f. sp. tritici) is one of the most important fungal diseases of wheat in our country. Fungus threats wheat production of Turkey and causes serious yield losses in suitable years via epidemics. Advanced bread wheat lines were evaluated in terms of yellow rust disease under natural epidemic and grain yield in this research, which was carried out in an augmented experimental design in the 2021-2022 growing season, in Sakarya rainfall-based conditions. In the research were used as material 125 bread wheat lines and 5 control varieties (Tahirova-2000, Mirsa, Kaynarca, Nusrat, Halis) in the preliminary yield trial carried out within the scope of the "South Marmara Region Bread Wheat Breeding Research" project carried out by Sakarya Maize Research Institute. Five of the 125 bread wheat lines tested in this study were in the "Resistance" group in terms of yellow rust. Six of the lines are grouped as "Sensitive". It was determined that 82 lines used in the study were in the "Immune" group. Infection coefficient in bread wheat lines ranged from 2 to 100. The highest infection coefficient was determined as 100 in the 33 numbered bread wheat line. This line was followed by 6 and 22 bread wheat lines with an infection coefficient of 80. The lowest infection coefficient was determined as 2 in wheat lines 1 and 42. The grain yields of the bread wheat lines used in the research varied between 253.5-703.2 kg da-1. The lowest grain yield was determined in line 25, and the highest yield was determined in line 66. As a result of this study, 68 promising lines among 125 advanced bread wheat lines evaluated in terms of yellow rust and grain yield were selected to be taken to the next stage.

Keywords: Bread wheat, yellow rust, grain yield

[PP-74]

Use of SSR Molecular Markers to Develop Source Materials in Maize Breeding

Ipek Koca Recber, Mehmet Cavit Sezer, Ahmet Duman, Niyazi Akarken, Cem Serdar Cerit, Memis Bilgici, Mesut Esmeray

Maize Research Institute, Sakarya, Türkiye

The main aim of maize breeding is to create inbred lines. The selection of source materials to be used in creating these inbred lines is also important. Varieties, populations and inbred lines can be used as source materials. Selecting the lines in the same heterotic groups, especially in the source materials to be created by using inbred lines, will increase the probability of the lines to be created will be from the same heterotic groups.

In this study, genetic distance data to be used when crossbreeding between lines to create new source material with inbred lines in Sakarya Maize Research Institute were achieved by using SSR markers. 96 inbred lines were examined using 17 SSR markers and data to be used in future studies were obtained. Because of the study, it was seen that the lines were separated into 2 groups. The number of alleles obtained from SSR loci ranged from 3 to 6, with an average of 3.8 alleles. Genetic diversity varied between 0.30 and 0.70, with an average of 0.55.

The data achieved because of the study will be used in the breeding program in the next year. Inbred lines that are genetically close to each other will be crossed with each other to create narrow genetic-based beginning source materials. Crossbreeding within this group will also be made by considering the phenotypic characters of the inbred lines.

Keywords: maize inbred line, SSR marker, source materials, genetic distance

[PP-75]

Evaluation of Registered Tomato Varieties in Türkiye

Yıldırım Şamil Özden[1], Meltem Özbay Konca[2], Ertan Güney[2], Dilek Altınkaynak[2]

[1]The Union of Plant Breeders (BİSAB), Ankara, Türkiye
[2]Variety Registration and Seed Certification Center (VRSCC), Ankara, Türkiye

Tomato (Solanum lycopersicum L.) is the most significant vegetable grown in Türkiye and also around the world. Tomato is one of the most freshly and processing consumed vegetable in Türkiye, and it has also different fruit types due to the wide variation in other vegetable species. The climatic conditions are different and open field - greenhouse production also allows tomato cultivation throughout the year in Türkiye.

The Variety Registration System began in 1963 in Türkiye. Total 7353 vegetable varieties have been registered since 1963 in all species, the biggest share among them is tomato with 1922 number. The number of domestic breeding varieties is 637 as a percentage of %32; the number of foreign breeding varieties is 1305 as a percentage of %68.

According to the last 10 years in registration system, 1021 tomato varieties have been registered that domestic breeding varieties is 455 as a percentage of %45; foreign breeding varieties is 566 as a percentage of %55. Also, domestic hybrid varieties are exported to 80 countries.

As can be seen from the data, The Domestic Türkish Breeding Tomato Varieties are increasingly taking place in the market.

Keywords: tomato, variety registration, domestic breeding

[PP-76]

Morphological Characterization of Some Local Leek Genotypes Grown in Turkey

Osman Yasar Uslu, Meryem Ipek, Ahmet Ipek

Bursa Uludag University

Leek (*Allium ampeloprasum* var. *porrum* L.) is an important plant species for human health. Turkey is one of the important leek producing country in the world. Although leek cultivation in Turkey has been generally done with local varieties, use of hybrid cultivars has been increasing in recent years, which can lead to loss of the local cultivars and landraces. However, local genotypes are an important part of plant genetic resources. Detection of variations in local populations at the morphological level is important in terms of conservation of genetic resources and breeding studies. In this study, 16 local leek genotypes obtained from different regions of Turkey were characterized by using 12 morphological parameters. Although no significant morphological differences were observed among the plants within the genotype, statistically significant differences were found between the genotypes. Three genotypes obtained from the Marmara region were found to be with high shaft length, which is highly preferable characteristic in Turkey. In the measurements and observations, the shaft diameter of the genotypes varied between 4.56 cm and 6.52 cm, and the shaft length ranged between 9.80 cm and 42.52 cm. Five genotypes had no or very weak head formation at the base of the shaft while six genotypes had moderate and the remaining five genotypes had strong head formation. Significant variation among the genotypes in terms of leaf number, leaf length, leaf with, leaf-shaft angles, leaf color, plant weight, umbel diameter and flowering period characteristics were also detected. Sixteen local leek genotypes characterized with morphological features can be used as plant material for future breeding studies and the results obtained from this study can contribute to researchers and germplasm management.

Keywords: *Allium ampeloprasum* var. *porrum*, genetic diversity, germplasm, morphological characters

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[PP-77]

Determination of Genetic Relationships in Some Local Lettuce (*Lactuca sativa* L.) Populations by SSR Primers

Elif Yetilmezer, Mikail Çalışkan, Ülkü Selcen Haydaroğlu, Yusuf Coşkun

Department of Biotechnology, Field Crops Central Research Institute,Republic of Turkey Ministry of Agriculture and Forestry, Ankara, Türkiye

In this study, it was aimed to reveal the intra- and inter-population genetic relationships in 5 different local lettuce (*Lactuca sativa* L.) populations grown in Konya, Bartın and Samsun. 4 primer combinations (Li04, LSSA22, LSSB11 and LSSB37) were used in SSR-Fragment analysis. A total of 73 polymorphic and evaluable SSR fragments, 12, 6, 42 and 13, were obtained for primers Li04, LSSA22, LSSB11 and LSSB37, respectively. When the intra- and inter-population genetic similarity levels were examined among 48 genotypes, the lowest similarity index was determined as 0.562 and the highest similarity index as 0.986. In the dendrogram created using the similarity index, it is seen that the genotypes are gathered under 7 main groups. It has been determined that each of the populations taken from Konya, Bartın and Samsun contains different genotypes in itself. There are individuals with genetic affinity among the populations. In addition, it has been determined that some individuals belonging to a population taken from Konya contain genotypes far from all groups.

Keywords: Lattuce, SSR, DNA Fragment Anlyses

FULL TEXT PRESENTATIONS

Eggplant genome editing using CRISPR Cas9 technology

Vese PAKASHTICA[1], Nedim MUTLU[1], Hasan PINAR[2], Inanc SOYLU[3], Cansu BULBUL[4], Aidai MURATBEK KYZY[1], Selcen DOGAN[1], Alparslan KARABENIZ[1], Adem KABA, [1] Fatma AKCAKALE[1], Ahmet Barkan BOSTAN[1], Mamoudou ZONON[1]

[1]Akdeniz University, Department of Agricultural Biotechnology, Antalya,TURKEY
[2]Erciyes University, Department of Horticulture Kayseri,TURKEY
[3]University of Nebraska-Lincoln, Department of Plant Pathology, Lincoln-Nebraska, USA
[4]Areo Seed Company, Antalya,TURKEY

INTRODUCTION

Eggplant (*Solanum melongena* L.,) is one of the main used vegetables in many countries. It has a long growth period which makes as one of the vegetables that is more exposed to pests, disease infestation, environmental stresses and parasitic weeds.

Orobanche spp. known as broomrape is one of the parasitic weeds that can cause huge damages to yields of eggplant. It is a well- known fact that these parasite seeds for germination need to be exposed to specific chemicals called strigolactones [SLs], which are released by the host roots.

The CCD8 gene is involved in the synthesis of strigolactones and plays an important role in controlling growth and development. CRISPR-Cas9 has been applied to manipulate the SlCCD8 gene in eggplant (*Solanum melongena*).

Using the Agrobacterium-mediated plant transformation method gRNA and Cas9 were transferred to eggplant. As the material was used eggplant cotyledons. The successful editing of eggplant lines was confirmed by Sanger sequencing. The induced mutations were stably inherited in the T1 progeny. Our findings based using CRISPR-Cas9 technology opens the way to the development of eggplant genotype's resistance to parasitic weeds.

METHODOLOGY

Transformation

Agrobacterium tumefaciens strain EHA105 with plasmid pFGC-pcoCa9 was used for transformation of eggplant cultivar. Yamula was used as a material for this study.

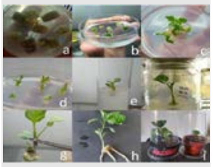


Figure 1. Plant transformation and regeneration: Initiation of callusing at the cut ends of cotyledon explants, followed by greenish compact callus and shoot proliferation (a,b, and c); strong shoot and shoot elongation after one month (d,e,f,g); 4-5 leaf stage shoots and their rooting (h); acclimation of rooted shoots (i).

METHODOLOGY

Mutant Screening

Genomic DNA was first isolated from the leaves of an eggplant using the CTAB method. In order to determine whether the mutation occurred in the target gene, investigation was carried out using primers that were unique to SlCCD8 gRNAs.

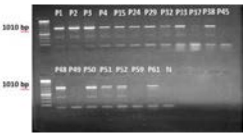


Figure 2. PCR analysis of T0 transgenic plants with specific primers showing positive amplification of expected bands.

After transformation of the CRISPR/Cas9 constructs in eggplant cotyledons and regeneration, eggplant T0 individuals were analyzed by Sanger sequencing. T1 population was generated by selfing of T0 plants. Plants were grown in controlled greenhouse conditions.

Figure 3. T1 population generated by selfing of T0 plants.

Hydroponic Root Screening System

Figure 4. In order to demonstrate that the CRISPR/Cas9-generated mutations in the CCD8 gene confer resistance to P. *aegyptiaca*, seeds of P. *aegyptiaca* were used to test eggplants from the T2 population.

RESULTS

After one month of being infested with P. *aegyptiaca* seeds, wild-type plants have a high number of parasites attached to their roots, but mutant plants have a significantly lower parasite infection rate.

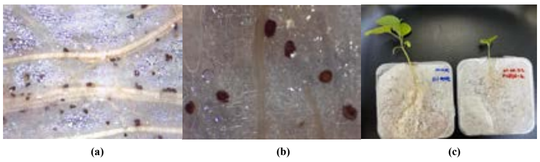
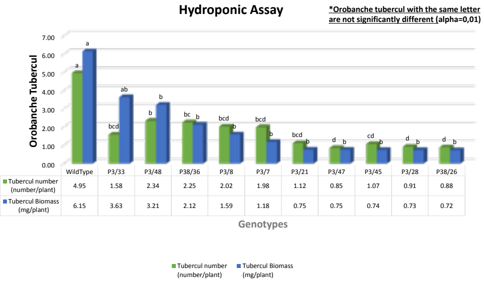

(a) (b) (c)

Figure 5. P. *aegyptiaca* seed attachment (a) to the wild-type root surface of the eggplant, (b) unattachment to the mutant, (c) whole plant image of wild type and P3-47 mutant.

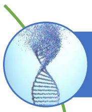
Figure 6. The number of attached parasitic tubercules of P. *aegyptiaca* to the roots of eggplant was significantly reduced in the CCD8 Cas9 mutated lines compared to the wild type.



	WildType	P3/33	P3/48	P38/36	P3/8	P3/7	P3/21	P3/47	P3/45	P3/28	P38/26
🟩 Tubercul number (number/plant)	4.95	1.58	2.34	2.25	2.02	1.98	1.12	0.85	1.07	0.91	0.88
🟦 Tubercul Biomass (mg/plant)	6.15	3.63	3.21	2.12	1.59	1.18	0.75	0.75	0.74	0.73	0.72

Table 1. Statistical significance difference between mutants and wild type was analyzed by SAS

CONCLUSIONS



We generated a significant mutation in eggplant using CRISPR/Cas9 that can be used in breeding programs to create resistance to parasitic weeds.

The P3/47, P3/28 AND P38/26 showed resistance to plant parasite to P. *aegyptiaca* compared to wild type.

Hydroponic root screening system established for screening mutants for resistance against P. *aegyptiaca*.

IV. International Plant Breeding Congress

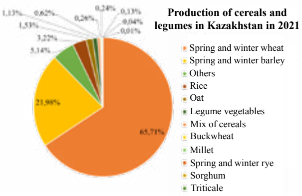
21 – 25 November 2022

Identification of SNP markers for grain quality traits in a barley collection (*Hordeum vulgare* L.) harvested in Kazakhstan

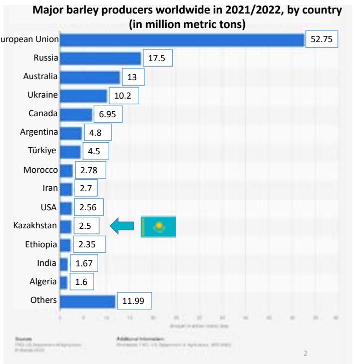
<u>Genievskaya Yuliya</u>, Almerekova Shyryn, Turuspekov Yerlan

Laboratory of Molecular Genetics
Institute of Plant Biology and Biotechnology
Almaty, Kazakhstan

- In Kazakhstan, barley is the second most important cereal after wheat;
- Currently, Kazakhstan provides 0.8 million metric tons of barley to the international market;
- The country is among the largest exporters of barley in the world.



Production of cereals and legumes in Kazakhstan in 2021



Major barley producers worldwide in 2021/2022, by country (in million metric tons)

Country	Production
European Union	52.75
Russia	17.5
Australia	13
Ukraine	10.2
Canada	6.95
Argentina	4.8
Türkiye	4.5
Morocco	2.78
Iran	2.7
USA	2.56
Kazakhstan	2.5
Ethiopia	2.35
India	1.67
Algeria	1.6
Others	11.99

Basic steps of the study

Phenotyping of barley collection for two years to assess grain quality traits in three regions of Kazakhstan.

Genome-wide association study (GWAS). Identification of significant associations between SNP markers alleles and phenotypic variations.

Selection of markers significantly associated with the traits of interest.

Transformation of SNP markers into KASP assays. Design of KASP primers.

Validation of KASP assays using previously non-genotyped material.

Materials and methods

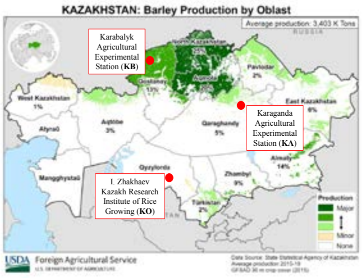


Figure 1 – Barley-producing regions of Kazakhstan and experimental fields used in the study.

- Spring barley collection, including 557 2-R and 6-R accessions from the USA and 104 2-R accessions from Kazakhstan (661 accessions in total) grown in tree regions of Kazakhstan – Kostanay (north), Karaganda (center), and Kyzylorda (south) regions in 2010 and 2011 (Fig. 1).
- Studied grain quality traits: content of raw <u>protein</u> (GPC, %), <u>starch</u> (GSC, %), <u>grain</u> <u>test weight</u> (TWL, g/L), and <u>extractivity</u> (GEX, %).
- The GPC, GSC, and EX were measured using the NIRS DS2500 Grain Analyzer (FOSS, Hillerød, Denmark), with the calibration supplied by the manufacturer. TWL was determined according to the guide provided by the Canadian Grain Commission (www.grainscanada.gc.ca).
- The collection was genotyped using barley iSelect 9K SNP array resulted in 2,344 polymorphic markers.
- GAPIT for R software package were used for GWAS analyses (MLM model).
- The collection of 34 promising spring barley lines was used for KASP genotyping and validation.

Step 1. Phenotyping of barley collection

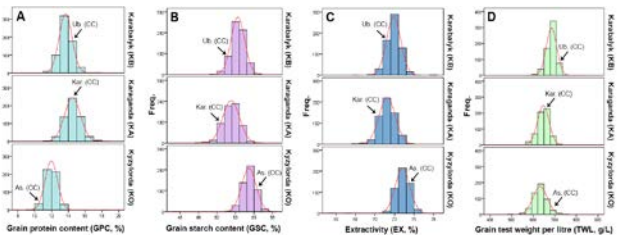


Figure 2. Average values over two years of grain quality traits of the collection harvested in three regions. (A) Grain protein content (GPC,%). (B) Grain starch content (GSC,%). (C) Extractivity (EX,%). (D) Grain test weight per liter (TWL, g/L). Freq.—frequency; CC—check cultivar; Ub.—Ubagan—check cultivar of KB; Kar.—Karagandinsky 5—check cultivar of KA; As.—Assem—check cultivar of KO

Step 2. Genome-wide association study (GWAS)

- As a result of the GWAS analysis, 76 associations between grain quality traits and SNP markers were detected on all seven chromosomes (p-values < 0.001).
- The linked MTAs (LD (r2) > 0.1) were grouped together, resulting in 30 QTLs in total (Fig. 3).

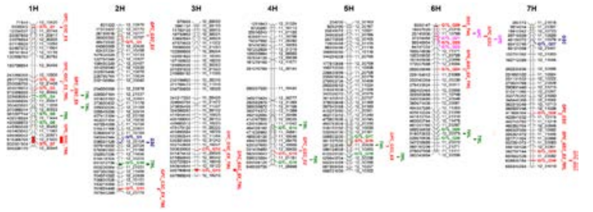


Figure 3. The positions of QTLs associated with barley grain quality traits on the genetic map. The names of SNPs and QTLs are shown on the right, and the positions of the loci are shown on the left of the linkage maps as base pairs (bp). The QTLs identified in this study are highlighted in blue for grain starch content, pink for grain protein content, green for grain test weight, and red for multi-trait QTLs. GPC—grain protein content; GSC—grain starch content; EX—extractivity; TWL—grain test weight.

Step 3. Selection of markers significantly associated with the traits of interest

- For 25 out of 30 QTLs, possible candidate genes and/or QTLs from literature were found. SNP markers with high significance were chosen for further validation (Table 1).

Table 1. List of the most significant marker–trait associations ($p < 2.6\times 10^{-5}$ and FDR-adjusted $p < 0.05$) for grain quality traits. Novel QTLs are indicated in bold.

# of MTA	QTL	KASP assay	Trait	SNP	Chr.	Pos. (bp)	*p*-Value	FDR Adjusted *p*-Value	R²	Allele	Effect
1	*QTL_Q2*	*ipbb_hv_116*	GPC	11_11336	1H	261,773,377	6.37×10^{-6}	0.0039	0.023	A	0.495
2			GSC				1.03×10^{-4}	0.0396	0.019	G	0.565
3	***QTL_Q8***	**-**	**GSC**	**11_10178**	**2H**	**48,475,931**	$\mathbf{7.64\times10^{-5}}$	**0.0367**	**0.020**	**G**	**0.455**
4	***QTL_Q12***	***ipbb_hv_6***	**GPC**	**11_21505**	**3H**	**580,635,994**	$\mathbf{2.14\times10^{-6}}$	**0.0021**	**0.026**	**A**	**0.590**
5			**TWL**				$\mathbf{1.15\times10^{-7}}$	**0.0002**	**0.035**	**A**	**20.275**
6			**GSC**				$\mathbf{6.01\times10^{-5}}$	**0.0367**	**0.021**	**G**	**0.647**
7	*QTL_Q13*	*ipbb_hv_119*	GPC	11_10935	3H	678,512,385	1.25×10^{-4}	0.0482	0.017	C	0.391
8			TWL				2.75×10^{-7}	0.0003	0.033	C	16.244
9	*QTL_Q20*	-	TWL	11_20886	6H	53,62,408	4.96×10^{-5}	0.0190	0.020	A	8.744
10	*QTL_Q24*	*ipbb_hv_7*	EX	12_31509	6H	203,509,034	7.21×10^{-6}	0.0138	0.027	A	0.656
11			GPC				9.10×10^{-8}	0.0002	0.033	G	0.664
12			TWL				3.53×10^{-6}	0.0017	0.027	G	17.627
13			GSC				2.40×10^{-6}	0.0046	0.029	A	0.759
14	***QTL_Q29***	***ipbb_hv_128***	**GPC**	**11_21103**	**7H**	**582,767,743**	$\mathbf{8.17\times10^{-6}}$	**0.0039**	**0.023**	**A**	**0.494**
15			**TWL**				$\mathbf{1.85\times10^{-6}}$	**0.0012**	**0.028**	**A**	**16.331**
16			**GSC**				$\mathbf{5.26\times10^{-5}}$	**0.0367**	**0.021**	**G**	**0.591**

Chr., chromosome; Pos., physical position on the chromosome; FDR, false discovery rate; R2, phenotypic variation explained by the MTA; GPC, grain protein content (%); GSC, grain starch content (%); EX, extractivity (%); TWL, grain test weight per liter (%).

Step 4. Transformation of SNP markers into KASP assays

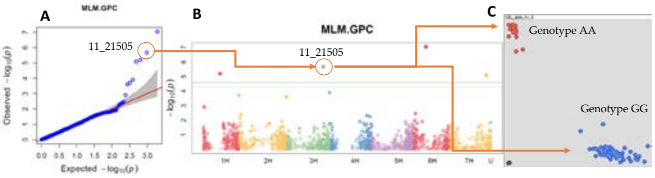


Figure 4. Flowchart of the development of KASP assay. (A) Quantile-quantile (QQ) plot of significantly associated SNPs from GWAS. (B) Manhattan plot of significantly associated SNPs. (C) KASP plot with the results of new material genotyping.

Table 2. The list of KASP assays for SNP markers associated grain quality traits.

SNP	KASP	Chr.	Allele 1	Allele 2	Allele 1 primer (forward)	Allele 2 primer (forward)	Common primer (reverse)
11_21505	*ipbb_hv_6*	3H	A	G	GAAGGTTGGACTGGCCCTGCGGA	GAAGGTTGGACTGGCCCTGCGGG	TCAGGCCATCCTTATCGGCCCATT
12_31509	*ipbb_hv_7*	6H	C	T	TTTGGTTGGGAGTTTTGCTTC	TTTGGTTGGGAGTTTTGCTTT	CAGCACCCTTTAGTACTCTCCCTCC
11_11336	*ipbb_hv_116*	1H	A	G	TCAGCTACGTAGTGTTACAATACA	TCAGCTACGTAGTGTTACAATACG	GGGAAATGCAAGAGAACAGTGT
11_10935	*ipbb_hv_119*	3H	A	C	TCCCAGATGGCCTGCACA	TCCCAGATGGCCTGCACC	ACGATGACGCCTCTCTTCAC
11_21103	*ipbb_hv_128*	7H	T	C	GTGGTTGCTGGTGGTGGT	GTGGTTGCTGGTGGTGGC	ACTCCGTCAAGAAGAGGCTC

Table 3. Effect of genotypes on grain quality traits in the 34 tested barley breeding lines

2020						
***ipbb_hv_6* (chromosome 3H)**	***p*-value**	**Genotype**	**N**	**Mean**	**SD**	**Effect**
Grain protein content (GPC,%)	3.47×10^{-4}	A:A	6	11.45	0.23	−1.15%
		G:G	28	12.60	1.44	+1.15%
Grain starch content (GSC,%)	1.23×10^{-5}	A:A	6	61.27	0.45	+1.71%
		G:G	28	59.56	1.19	−1.71%
Extractivity (EX,%)	2.88×10^{-4}	A:A	6	78.32	0.42	+1.10%
		G:G	28	77.22	0.84	−1.10%
***ipbb_hv_128* (chromosome 7H)**	***p*-value**	**Genotype**	**N**	**Mean**	**SD**	**Effect**
Grain protein content (GPC,%)	0.005	T:T	5	11.64	0.25	−0.89%
		C:C	29	12.53	1.45	+0.89%
Grain starch content (GSC,%)	0.016	T:T	5	60.95	0.76	+1.26%
		C:C	29	59.69	1.27	−1.26%
2021						
***ipbb_hv_6* (chromosome 3H)**	***p*-value**	**Genotype**	**N**	**Mean**	**SD**	**Effect**
Grain protein content (GPC,%)	9.16×10^{-5}	A:A	6	12.60	0.83	−2.60%
		G:G	28	15.20	1.10	+2.60%
Grain starch content (GSC,%)	5.89×10^{-5}	A:A	6	62.13	0.53	+2.05%
		G:G	28	60.08	0.78	−2.05%
Extractivity (EX,%)	1.14×10^{-5}	A:A	6	78.65	0.30	+0.93%
		A:A	28	77.72	0.69	−0.93%
MEAN						
***ipbb_hv_6* (chromosome 3H)**	***p*-value**	**Genotype**	**N**	**Mean**	**SD**	**Effect**
Grain protein content (GPC,%)	4.69×10^{-6}	A:A	6	12.03	19.80	−1.87%
		G:G	28	13.90	31.69	+1.87%
Grain starch content (GSC,%)	5.38×10^{-8}	A:A	6	61.70	0.36	+1.87%
		G:G	28	59.83	0.81	−1.87%
Extractivity (EX,%)	4.85×10^{-5}	A:A	6	78.48	0.33	+0.99%
		G:G	28	77.49	0.68	−0.99%
***ipbb_hv_128* (chromosome 7H)**	***p*-value**	**Genotype**	**N**	**Mean**	**SD**	**Effect**
Grain starch content (GSC,%)	0.037	T:T	5	61.24	0.96	+1.27%
		C:C	29	59.97	0.94	−1.27%

Step 5. Validation of KASP assays

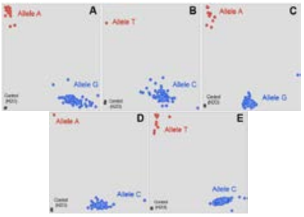


Figure 5. KASP plots of five SNPs associated with grain quality traits. (A) *ipbb_hv_6*. (B) *ipbb_hv_7*. (C) *ipbb_hv_116*. (D) *ipbb_hv_119*. (E) *ipbb_hv_128*. Red and blue dots denote genotypes and black dots are negative control (H2O)

Conclusions

- Generally, studied barley collection had demonstrated high levels of variation in grain protein and starch content, as well as highly variable extractivity and test weight in all three regions of Kazakhstan. Phenotypic data provided sufficient variability for the GWAS.
- Seventy-six MTAs were identified in the GWAS on all 7 barley chromosomes for all studied grain quality traits. They were unified in 30 significant QTLs, considering the pleiotropic effect and genetic linkage of several markers. Five of pleiotropic QTLs with the highest significance ($p < 2.6\times10^{-5}$ and FDR-adjusted $p < 0.05$) were selected for KASP assays development.
- Validation of 7 KASP assays, which were associated with grain protein content, starch content and grain test weight in the GWAS, confirmed associations of two assays – *ipbb_hv_6* (chromosome 3H) and *ipbb_hv_128* (chromosome 7H) .
- KASP assays associated with key barley grain quality traits may be used for rapid and relatively cheap identification of promising germplasm. While other QTLs detected in different regions of Kazakhstan have a potential usage for local barley breeding programs.

This study was supported by the grant AP08052804 "**Development and validation of KASP arrays efficiency for key productivity and grain quality traits in two-rowed spring barley**" from the Ministry of Education and Science of the Republic of Kazakhstan.

Results were reported in the "Agronomy" journal (Genievskaya Y., Almerekova S., Abugalieva S., Chudinov V., Blake T., Abugalieva A., Turuspekov Y. Identification of SNP markers associated with grain quality traits in a barley collection (*Hordeum vulgare* L.) harvested in Kazakhstan. Agronomy. 2022. V. 12. P. 2431).

Thank you for your attention!

Genome-wide association study for leaf rust and stem rust resistance in bread wheat growing in Kazakhstan

Alibek Zatybekov[1], Yuliya Genievskaya[1], Aralbek Rsaliyev[2], Akerke Amalova[1], Moldir Yermagambetova[1], Saule Abugalieva[1] and Yerlan Turuspekov[1*]

1 Laboratory of Molecular Genetics, Institute of Plant Biology and Biotechnology, Almaty 050040 Kazakhstan;
2 Laboratory of Phytosanitary Safety, Research Institute of Biological Safety Problems, Gvardeisky 080409, Zhambyl Region, Kazakhstan;
* Author for correspondence (yerlant@yahoo.com)

Common wheat (*Triticum aestivum* L.), is one of the main cereal crops cultivated around the world and is important for food security. Kazakhstan is among the ten largest exporters of wheat, with a volume of 11.4 thousand tons produced in 2019. According to the Bureau of National Statistics of Kazakhstan, the sown area under wheat was 12.2 million hectares in 2021, which represents about 76.7% of the total area used for cereal crops in the country. One of the largest problems in wheat production all over the world is foliar diseases, in particular *Puccinia graminis* f. sp. *tritici* (*Pgt*), causing stem rust (SR), and *Puccinia triticina* Eriks. (*Pt*), causing leaf rust (LR). One of the most effective ways to prevent wheat rust epidemics is the development of cultivars with durable resistance to pathogens. The development of new cultivars with high productivity and LR and SR disease resistance, including using marker-assisted selection, is becoming an important priority in local breeding projects. Therefore, the search for key genetic factors controlling resistance in all plant stages, including the seedling stage, is of great significance. LR and SR resistance is controlled by a diverse group of genes, designated as *Lr* and *Sr*, respectively. In the literature, approximately 80 *Lr* and about 60 *Sr* genes have been identified and described in bread wheat, durum wheat, and diploid wheat species. In this work, we applied a genome-wide association study (GWAS) approach using 212 local bread wheat accessions that were phenotyped for resistance to specific races of *Pt* and *Pgt* at the seedling stages. The collection was genotyped using a 20 K Illumina iSelect SNP assay, and 11,150 polymorphic SNP markers were selected for the association mapping. Using a mixed linear model, we identified 11 quantitative trait loci (QTLs) for five out of six specific races of *Pt* and *Pgt*. The comparison of the results from this GWAS with those from previously published work showed that nine out of eleven QTLs for LR and SR resistance had been previously reported in a GWAS study at the adult plant stages of wheat growth. Therefore, it was assumed that these nine common identified QTLs were effective for all-stage resistance to LR and SR, and the two other QTLs appear to be novel QTLs. In addition, five out of these nine QTLs that had been identified earlier were found to be associated with yield components, suggesting that they may directly influence the field performance of bread wheat. The identified QTLs, including novel QTLs found in this study, may play an essential role in the breeding process for improving wheat resistance to LR and SR. This research was funded by the Ministry of Agriculture of the Republic of Kazakhstan, grants number BR10765056, and by the Ministry of Education and Science of the Republic of Kazakhstan grant number AP08855387.

QTL mapping of agronomic traits in wheat using the Pamyati Azieva × Paragon mapping population tested in Kazakhstan

Akerke Amalova[1], Simon Griffiths[2] , Saule Abugalieva[1], Yerlan Turuspekov *[1].
[1] Laboratory of Molecular Genetics, Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan
[2] Department of Crop Genetics, John Innes Centre, Norwich, United Kingdom
*Corresponding author: yerlant@yahoo.com

INTRODUCTION

Wheat is one of the three most important food crops in the world. It is the staple food for about 40% of the world's population, as it is one of the most abundant sources of calories and protein in the diet, providing nearly 20% of the total dietary protein worldwide (Braun et al., 2010). Although genome-wide association studies (GWAS) are an increasingly informative tool in the mining of new quantitative trait loci (QTLs), a classical biparental mapping approach is still a widely used powerful method to search the unique genetic factors associated with important agronomic traits in bread wheat.

MATERIALS & METHODS

In this study, a newly constructed mapping population of Pamyati Azieva (Russian Federation) × Paragon (UK) consisting of 94 recombinant inbred lines (RILs) was tested in three different regions of Kazakhstan with the purpose of QTL identification for key agronomic traits. The RILs were tested in 11 environments of two northern breeding stations (NKAES, Petropavlovsk, North Kazakhstan region, and RPCGF, Shortandy, Aqmola region) and one southeastern station (KRIAPI, Almalybak, Almaty region).

The following eight agronomic traits were studied: heading days, seed maturation days, plant height, spike length, number of productive spikes, number of kernels per spike, thousand kernel weight, and yield per square meter. The 94 RILs of the PAxP cross were genotyped using Illumina's iSelect 20K single nucleotide polymorphism (SNP) array and resulted in the identification of 4595 polymorphic SNP markers.

RESULTS

The field experiments were conducted at three locations: 1) KRIAPI (2015–2020), 2) RPCGF (2018–2020), and 3) NKAES (2018–2019). RILs were studied at three locations, and the phenotypic trait variation indicated a large level of variability and significance among regions. Pearson's correlation results suggest that in RPCGF, HD was negatively correlated with YM2, while in NKAES and KRIAPI, this association was not observed (Figure 1, B). At all three testing sites, average values of NKAES, RPCGF, and KRIAPI, PH was positively correlated with YM2. NKS was significantly associated with the yield at all three sites, with the highest average values recorded in KRIAPI (0.47), followed by NKAES (0.34) and RPCGF (0.33) (Figure 1). In contrast, the average value of TKW over two years (2019-2020) was correlated with YM2 at the two northern stations but not in the southeastern region.

The total identified QTLs found in the three regions varied from 32 QTLs in Southeast Kazakhstan (KRIAPI), and 32 QTLs in (NKAES) and 16 QTLs (RPCGF) in Northern Kazakhstan (Figure 3). Only one common QTL (*Qhd-PAxP.ipbb-7A*) among the studied traits was identified in the three regions. Ten common QTLs identified in Shortandy (RPCGF) and Petropavlovsk (NKAES) were common between these regions, and five common QTLs were identified in the Almaty (KRIAPI) and Shortandy (RPCGF) regions (Figure 3). Three QTLs (*QYM2-PAxP.ipbb-2D.1, QYM2-PAxP.ipbb-4A*, and QYM2-PAxP.ipbb-5A.2) were detected only in Northern Kazakhstan (RPCGF and NKAES).

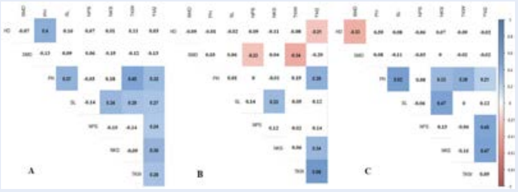


Figure 1. Pearson's correlation index based on multiple years' data in three regions: A) NKAES (Petropavlovsk); B) RPCGF (Shortandy); and C) KRIAPI (Almaty). Note: Correlations with $P < 0.05$ are highlighted in color. The color indicates either positive (blue) or negative (red) correlations.

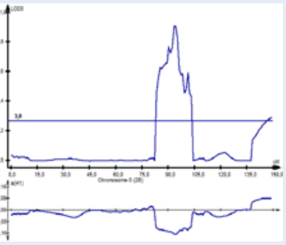


Figure 2. The quantitative trait locus *Qtkw-PAxP.ipbb-2B.2* for the trait "thousand kernel weight" on chromosome 2B.

Figure 3. The number of stable quantitative trait loci (QTLs) for eight studied traits identified in three regions (NKAES, Petropavlovsk, in blue; RPCGF, Shortandy, in brown; KRIAPI, Almaty, in blue circles).

The application of the QTL Cartographer statistical package allowed the identification of 53 stable QTLs for the studied traits. A survey of published studies related to common wheat QTL identification suggested that 28 of those 53 QTLs were presumably novel genetic factors. The SNP markers for the identified QTLs of the analyzed agronomic traits of common wheat can be efficiently applied in ongoing breeding activities in the wheat breeding community using a marker-assisted selection approach.

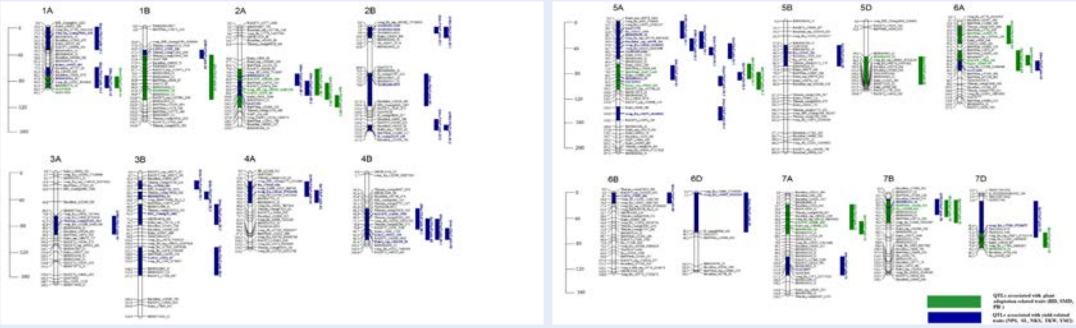


Figure 4. The genetic map of QTLs associated with plant adaptation and yield components and identified using the Pamyati Azieva x Paragon mapping population.

CONCLUSIONS

The RILs were tested in 11 environments in two northern and one southeastern region of Kazakhstan and showed a wide range in yield performance. In total, 39, 7, and 19 RILs were identified with a higher average YM2 than standard cultivars in NKAES, RPCGF, and KRIAPI, respectively. Two RILs, PAxP-05 and PAxP-01, showed high average TKW and YM2 values in all three regions.

The phenotypic data of RILs studied in 11 environments of the three regions were used for the identification of important QTLs associated with the studied agronomic traits. The application of the QTL Cartographer statistical package allowed for the identification of 53 stable QTLs out of a total of 296 QTLs for eight agronomic traits. A survey of published studies related to common wheat QTL identification suggested that 28 QTLs for the eight analyzed traits were presumably novel genetic factors, while 25 QTLs matched known associations.

The findings in this study can be very helpful for further validation of identified MTAs for their use in bread wheat breeding projects for the development of new competitive and highly productive cultivars.

ACKNOWLEDGMENTS: *The Ministry of Education and Science of the Republic of Kazakhstan grant number AP08855387, and by the Ministry of Agriculture of the Republic of Kazakhstan funded this research grants number BR10765056*

IV. INTERNATIONAL PLANT BREEDING CONGRESS 21-25 Nov 2022

Effects of Tray Conditions for Cucumber Cuttings

Nur Ülger[1] *, **Özlem Ertem** [2]
[1]Multi Tohum Tar. San. Tic. A.s. Antalya, Türkiye
[2] Multi Tohum Tar. San. Tic. A.s. Antalya, Türkiye
nulger@multitohum.com
oozer@multitohum.com

Introduction

Cucumber (*Cucumis sativus L.*) is one of the most economically important crops worldwide. Seedling quality has an important role in the production process of vegetables. Therefore, many researches have been done on the nursery conditions of various crops including the tray conditions of cucumber (de Mello et al., 2016). For research and development processes in production, plant cuttings are utilized. This study is performed to evaluate the effects of different tray soil contents for cucumber cuttings from different varieties. Bereket F1 and two different Multi Tohum F1 varieties were used to understand the effects of pearlite and peat-pearlite mixture (1:1) on rooting.

Results

Cucumber cuttings were obtained from hybrid cucumber plants which were located in the Multi Tohum greenhouse. After cuttings were collected from the plants, they were planted into trays that were prepared with pearlite and peat-pearlite mixture. The first rootings were observed on the seventh day (26.09.2021) after the cuttings planting into the trays. 9 out of 30 plants from the pearlite and 24 out of 30 plants survived from the peat-pearlite mixture. On the 23rd day, seedlings were ready for planting in the greenhouse. It observed that the plant growth rate of cuttings was slower than the standard growth of hybrids sown from seeds. The cavities only with pearlite have a more condensed structure compared with peat-pearlite mixtures.

As a result, cuttings planted in peat-pearlite mixture were better for cutting production for plant liveness and growth rate. For further research, hormone applications can be analyzed to improve plant vigor.

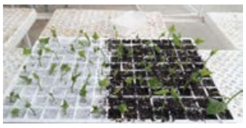


Figure 4. Planted cuttings in a tray at the nursery greenhouse conditions in the growth chamber

Figure 5. Storage of cuttings in controlled greenhouse conditions in the growth chamber

Figure 6. Transferred plantlets in the greenhouse

Figure 7. Cucumber plants in the greenhouse from plantlets

Materials & Methods

Table 1. Materials

Bereket F1
C1-F1 and C2-F1
150 cavity seedling nursery tray
Peat
Pearlite

Figure 1. Bereket F1

Table 2. Application dates

Steps	**Date**
Cutting and planting into trays	19.09.2021
Transfer into growth chamber	19.09.2021
Transfer into nursery transfer	24.09.2021
Planting into greenhouse (40cm)	11.10.2021

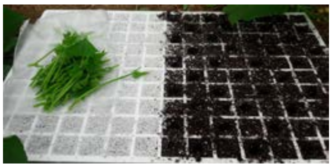


Figure 2. Tray prepared with pearlite(left) and peat-pearlite mix (1:1) (right)

Figure 3. Cutting sample (17cm)

1. Cuttings from 3 different cucumber hybrids were used.
2. Total of 9 trays were used for cuttings. For each hybrid, 3 separate trays were prepared with pearlite and pear-pearlite mixture (1:1) as replication.
3. Cuttings were collected from Multi Tohum greenhouses.
4. Total of 60 cuttings were planted into each tray by skipping one cavity.
5. Controlled greenhouse conditions were arranged in the growth chamber with a temperature of 24-25 ºC and humidity of 60-80%.
6. 5 days after planting, trays were transferred into the nursery.
7. 23 days after planting, plantlets were planted into the greenhouse.

REFERENCE;
de Mello, B. F. F. R., Trevisan, M. V., & Steiner, F. (2016). Quality of cucumber seedlings grown in different containers. *Revista de Agricultura Neotropical*, *3*(1), 33-38.

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A perspective on the chromosome properties of local bottle gourd landraces

Ahmet L. Tek

Department of Agricultural Genetic Engineering, Ayhan Şahenk Faculty of Agricultural Sciences and Technologies, Niğde Ömer Halisdemir University, 51240, Niğde, Turkey

IV. International Plant Breeding Congress, Antalya, November 21-25, 2022

Contents

Abstract

Ribosomal DNAs and various banding patterns are landmarks in molecular cytogenetics providing useful information for karyotyping and addressing individual chromosomes. **Bottle gourd** is the only cultivated species of the ***Lagenaria* genus** with high genetic diversity. After **CMA_3/DAPI** fluorochrome banding we investigated the GC- and AT-rich regions in interphase nuclei of five different local accessions. Fluorescence *in situ* hybridization (**FISH**) was conducted to determine the number and location of **45S** and **5S rDNAs** in bottle gourd. Our results showed four strong CMA_3 regions in interphase and on mitotic metaphase chromosomes. FISH revealed four strong signals of 45S rDNA at the termini of two metaphase chromosome pairs and terminal 5S rDNA signals at another pair of chromosomes. The presence of four positive CMA3 bands colocalizes with four 45S rDNA signals in all bottle gourd accessions. Our results allow distinguishing two out of eleven chromosome pairs of bottle gourd.

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Plant material / Bottle gourd / *Lagenaria siceraria*

❑ Bottle gourd, ***Lagenaria siceraria***, is a member of the **Cucurbitaceae family**, also known as calabash or white-flowered gourd.

❑ Bottle gourd is the **only cultivated species**.

❑ It is a diploid crop species with **$2n = 2× = 22$** chromosomes.

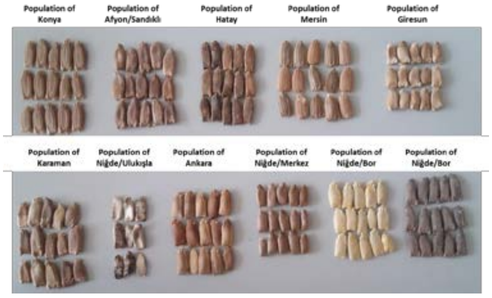
❑ The genome size of this plant is approximately **365 Mbp**.

❑ The Lagenaria genus consists of **six species**: *L. siceraria* (cultivated form), *L. sphaerica, L. rufa, L. breviflora, L. sphaerica,* and *L. guineensis*.

❑ All six species are naturally found in **Africa**, the supposed center of genetic diversity for *L. siceraria.*
❑ Turkey has bottle gourd genetic resources in different location.

(Beevy and Kuriachan 1996), (Achigan-Dako et al., 2008)

Different population of bottle gourd in Turkey



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Potential uses of bottle gourd

❑ Bottle gourd is cultivated for food, decoration, medicine, domestic utensils, musical instruments, containers, and fishing floats.

❑ Some bottle gourd varieties are grown for their seeds which are rich in oil and essential amino acids.

❑ Additionally, bottle gourd seedlings are used as a rootstock for watermelon against adverse effects in soil such as low temperature, high pH, salinity, excessive water as well as soil-borne diseases, such as Fusarium wilt.

❑ For seedless watermelon production, bottle gourd pollen has recently been utilized to pollinate watermelons.

Therefore, bottle gourd is a crop of great economic interest and a detailed characterization at the chromosome and genome level is desirable.

(Morimoto and Mvere, 2004, Xu et al., 2011), (Yetisir et al., 2007), (Achigan-Dako et al., 2008), (Sugiyama et al., 2014)

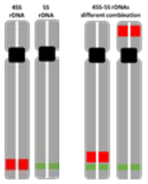
Ribosomal DNAs (rDNAs)

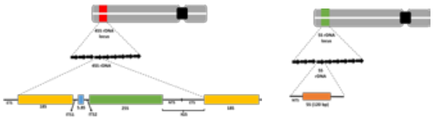
Ribosomal DNAs (rDNAs) encode the RNA components of ribosomes. **Two structurally distinct gene families of rDNAs exist in plant genomes**, specifically known as **45S** and **5S** rDNAs.

Non-transcribed spacers and tandem repeat units of the **18S-5.8S-26S** ribosomal genes are present in the 45S rDNA.

The 5S rDNA genes consist of a non-transcribed spacer and a conserved coding region of **120 bp**.

45S and 5S rDNA genes can be present at one or more positions within a set of chromosomes and be used as chromosomal markers.

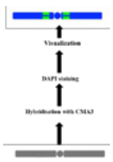




(Long and Dawid, 1980), (Long and Dawid, 1980; Lombello and Pinto-Maglio, 2007; Han et al., 2008; Heslop-Harrison and Schwarzacher, 2011; Li et al., 2016; Santos-Sanchês et al., 2019)

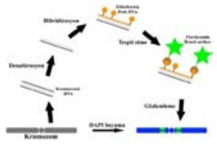
CMA$_3$ (chromomycin A$_3$)

CMA$_3$ a GC-rich specific fluorochrome, and DAPI, an AT-rich specific fluorochrome, banding techniques can also be useful to differentiate between chromosomes.



Fluorescence in situ hybridization (FISH)

FISH, has been widely used for constructing chromosomal maps, for chromosome identification, for studying the dynamic organization of chromatin in interphase nuclei as well as for studying chromosome homology and karyotype evolution.



(Kim et al. 2002), (Lysak et al., 2006; Probst, 2018; Santos et al., 2020)

Methods

Step 1

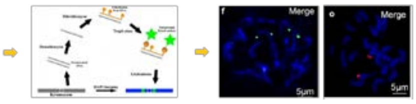
Germination of plant material

Step 2

Mitotic chromosome preparation

Step 3 - Step 4

CMA3/DAPI staining and Fluorescence in situ hybridization (FISH) and signal detection



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Results

IV. International Plant Breeding Congress, Antalya, November 21-25, 2022

Chromomycin A$_3$/DAPI (CMA$_3$/DAPI) staining in *Lagenaria siceraria* nuclei and mitotic chromosomes (2n = 2× = 22) from five different local accessions.

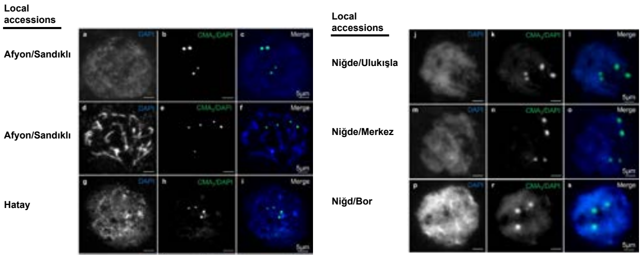

Figure 1. Interphase nuclei (**a-c, g-i, j-l, m-o, p-s**), prometaphase chromosomes (**d-f**), GC-rich loci stained with CMA$_3$ (**b, e, h, k, n, r**; green signals) and DAPI merge image (**c, f, i, l, o, s**) are shown on the chromosomes. Images are shown from the local accessions obtained from provinces of Sandıklı (**a-f**), Hatay (**g-i**), Niğde/Ulukışla (**j-l**), Niğde/Merkez (**m-o**), Niğde/Bor (**p-s**). Scale bar = 5μm

Localization of 45S and 5S rDNA in *Lagenaria siceraria* nuclei and mitotic chromosomes (2n = 2× = 22)

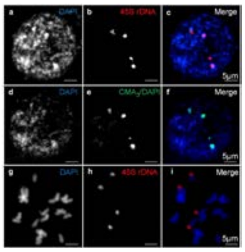

Figure 2. DAPI stained interphase chromosomes (**a-c**), metaphase chromosomes (**g-i**), 45S rDNA loci labeled with digoxigenin (**b, h**; red signals of rhodamine), 45S rDNA loci merge image (**c, i**) is shown on the chromosomes. Interphase nuclei (**d-f**), GC-rich loci staining with CMA$_3$ (**e**; green signal).

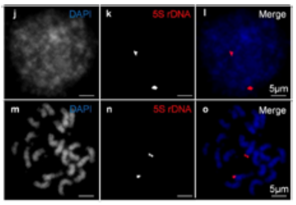

Figure 3. DAPI stained interphase chromosomes (**j-l**), metaphase chromosomes (**m-o**), 5S rDNA loci labeled with digoxigenin (**k, n**; red signals of rhodamine), 5S rDNA loci merge image (**l, o**) is shown on the chromosomes. Scale bar = 5μm

Discussion

When we investigate CMA$_3$ bands in terms of size and intensity, a pair of chromosomes have big and another pair of chromosomes consistently have small signals in both metaphase and interphase stages whereas we did not detect clear differences on 45S rDNA signals using FISH.

To detect the position and number of 45S and 5S rDNAs, FISH with digoxigenin-labeled (DIG) probes was applied. In interphase nuclei, four strong red signals of 45S rDNA were observed. The size and intensity of all four red signals were similar, which is in contrast to our findings from the CMA$_3$ bands. Four strong 45S rDNA signals were also detected on the short arm ends of two mitotic metaphase chromosome pairs. Two strong signals of 5S rDNA were observed in interphase nuclei as well as on metaphase chromosomes. There was no prominent difference in the size and intensity of 45S and 5S rDNA signals. The 5S rDNA signals appeared on the short arm of termini of a metaphase chromosome pair. The two rDNA families are usually not positioned on the same chromosomes, with some exceptions. In conclusion, rDNA loci and CMA$_3$ bands in accessions of *Lagenaria siceraria,* as in other species provide useful markers to distinguish at least two chromosome pairs individually.

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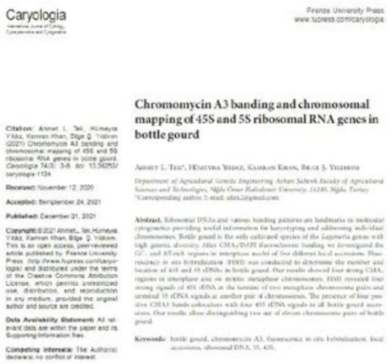
(Waminal and Kim, 2012; Li et al., 2016)



Caryologia

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Chromomycin A3 banding and chromosomal mapping of 45S and 5S ribosomal RNA genes in bottle gourd

Ahmet L. Tek*, Hümeyra Yıldız, Kamran Khan, Bilge Ş. Yıldırım

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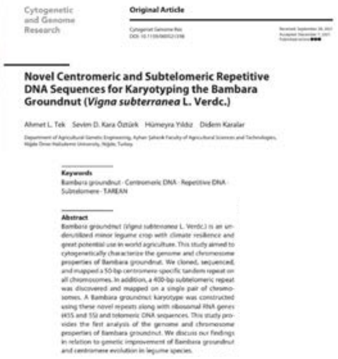
Competing Interests: The Author(s) declare(s) no conflict of interest.



Cytogenetic and Genome Research

Original Article

Novel Centromeric and Subtelomeric Repetitive DNA Sequences for Karyotyping the Bambara Groundnut (*Vigna subterranea* L. Verdc.)

Ahmet L. Tek Sevim D. Kara Öztürk Hümeyra Yıldız Didem Karalar

Keywords
Bambara groundnut · Centromeric DNA · Repetitive DNA · Subtelomere · TAREAN

Abstract
Bambara groundnut (Vigna subterranea L. Verdc.) is an underutilized minor legume crop with climate resilience and great potential use in world agriculture. This study aimed to cytogenetically characterize the genome and chromosome properties of Bambara groundnut. We cloned, sequenced, and mapped a 50-bp centromere-specific tandem repeat on all chromosomes. In addition, a 400-bp subtelomeric repeat was discovered and mapped on a single pair of chromosomes. A Bambara groundnut karyotype was constructed using these novel repeats along with ribosomal RNA genes (45S and 5S) and telomeric DNA sequences. This study provides the first analysis of the genome and chromosome properties of Bambara groundnut. We discuss our findings in relation to genetic improvement of Bambara groundnut and centromere evolution in legume species.

Plant chromosome lab team

teklab_chromo

TekLab Nohu

TEKLAB

Thanks for listening.

College of Food, Agricultural and Environmental Sciences/ Department of Horticulture and Crop Science

CFAES

Genomic selection to predict Fusarium Head Blight (FHB) resistance of wheat lines from the great plains using Ohio phenotypic data

Lenin Rodriguez, Carlos Ignacio, Nelly Argüello, Corinne Marfori and Clay Sneller

Introduction

Fusarium Head Blight (FHB)

- FHB is one of the most critical diseases on wheat, provoked by the fungus *Fusarium graminearum.*
- This disease directly affects the yield and quality; moreover, the mycotoxin produced by the fungus has adverse effects on human and animal consumption.
- Host resistance is the primary approach to decreasing the damage caused by this fungus.

Fig 1. Spike damaged by FHB (Photo: CIMMYT)

Fig 2. Visual damage seen in the field

Genomic Selection (GS)

- GS is a modification of marker-assisted selection (MAS) that, instead of using a few markers, considers the genetic worth of individuals based on the information of all the markers distributed across the genome.
- Phenotypic and genotypic data is collected in a training population (TP). That data is used to develop a GS model that is used to predict the value of other individuals that were not in the TP.

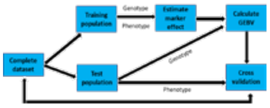


Fig 3. Diagram of genomic selection adapted from Robertsen, et al. (2019).

Rationale and significance

- Hard Red Winter Wheat (HRWW) in the Great Plains is affected by FHB. Phenotyping HRWW for FHB resistance in the Great Plain is difficult as low humidity, low rainfall, and high winds greatly decrease disease incidence and intensity. The Ohio State University's wheat breeding program routinely produces vary high FHB pressure in a FHB nursery. It maybe more effective to phenotype HRW on Ohio under high disease pressure and use that data to predict the value HRWW that to screen HRWW in the Great Plains.

Fig 4. US map showing selected states for the study.

Objective

- Assess the value of FHB data collected in SD, NE, and OH on HRWW lines to predict the FHB phenotype of these lines when grown in the Great Plains.

Hypothesis

- The use of Ohio's phenotypic data will increase the accuracy of predicting the FHB resistance of Great Plains HRWW.

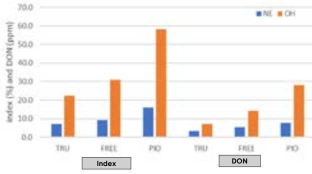


Fig 5. Comparison of disease pressure in FHB nurseries in Nebraska and Ohio using data from 2014 to 2021.

Materials and Methods

Two datasets, one from 2020 and one from2021

Training Population: 373 HRW lines from NE and SD in 2020(NE20, SD20) and 434 lines in 2021 (NE21, SD21)

FHB resistance assessed in Ohio, Nebraska and South Dakota in misted and inoculated nurseries

Collected data on Fusarium Index (IND), Fusarium damaged in the Kernel (FDK), and Deoxynivalenol (DON)

All lines genotyped using genotyping by sequencing (GBS)

Data Analysis

Training and Prediction Population

			NE20	NE20	NE21	NE21	SD20	SD20	SD21	SD21	NE NON-TP LINES	SD NON-TP LINES
Training population	Training population	TP Phenotype	OH20	NE20	OH21	NE21	OH20	SD20	OH21	SD21	NE, ANY YEAR	SD, ANY YEAR
	NE20	OH20	CV									
	NE20	NE20		CV								
	NE21	OH21			CV							
	NE21	NE21				CV						
	SD20	OH20					CV					
	SD20	SD20						CV				
	SD21	OH21							CV			
	SD21	SD21								CV		

Fig 6. Genomic selection matrix showing the possible combination among germplasm origin and training population phenotypes for cross-validation.

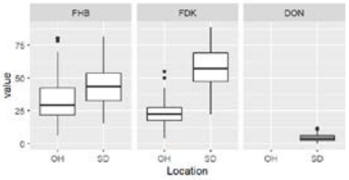


Fig 7. Boxplot of FHB index, FDK and DON evaluation of HRWW lines tested in South Dakota and Ohio.

Summary

Genomic Selection (GS) may complement or substitute phenotypic selection to shorten cycles of wheat evaluation.

We hypothesize that GS could predict the performance of wheat lines from the great planes using Ohio Phenotypic data.

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Meuwissen TH, Hayes BJ, Goddard ME (2001) Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819-1829.

Acknowledgments

U.S. Wheat & Barley Scab Initiative

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Questions? Contact Lenin
rodriguezbetancourth.1@osu.edu
https://hcs.osu.edu/our-people/lenin-rodriguez-betancourth

Effect of indole 3-butyric acid on the rooting of *Cinnamomum zeylanicum* by air layering

Danter Cachique [1], Héctor Guerra[1], Jane Correa[2]

1. Research Institute of the Peruvian Amazon: E-mail: dcachique@gmail.com

2. Hospital II-2 Minsa-Tarapoto

ABSTRACT

The present work was developed with the purpose of optimizing a methodology using indole 3-butyric acid in the rooting of *Cinnamomum zeylanicum* by means of air layering. The trial was conducted at the Research Institute of the Peruvian Amazon. IIAP-San Martin. Two types of branches and 4 doses of indole 3-butyric acid were tested. The rooting of cinnamon branches was achieved by air layering with the application of 0.6% IBA as a hormonal inducer and the use of primary branches. Vegetative propagation by air layering allows us to have seedlings with genetic uniformity and will contribute to the use of genotypes selected for their commercial interest.

Keywords: *Cinnamomum zeylanicum*, rooting, indole 3 butyric acid, air layering

1. Introduction

Cinnamon is a common spice used by different cultures around the world for several centuries. It is obtained from the inner bark of trees of the genus Cinnamomum, it is a species of tropical evergreen. In addition to culinary uses, cinnamon is also considered in native medicine as a remedy for respiratory, digestive and gynecological diseases (Shen Q, et al., 2002).

Vegetative propagation helps maintain genotype integrity and ensures the conservation of valuable genetic material, as well as multiplying superior genotypes and increasing genetic gain in a very short time using the additive and non-additive components of the total genetic variance (Zobel & Talbert, 1988). Indole-3-butyric acid (IBA) is an effective auxin to promote rooting of cuttings in a large number of species. The advantages of IBA are: it is non-toxic at various concentrations, it is not easily degraded by light or microorganisms, and it lasts longer on the application site, resulting in greater efficacy (Blazich, 1988).

The present investigation was carried out with the objective of optimizing a vegetative propagation methodology evaluating the effect of indole 3-butyric acid on the rooting of Cinnamomum zeylanicum by air layering.

2. Materials and methods

The trials of this study were carried out at the Research Institute of the Peruvian Amazon, in the city of Tarapoto, San Martín.

Branch rooting was performed by air layering on mother plants with desirable phenotypic characteristics. For this, the main and secondary branches were selected that had a thickness between 0.5 and 1.0 cm, which were cut 1 cm longitudinally, the solutions arranged in their respective concentrations of AIB hormone were adhered, they were immediately placed in substrate lightweight to keep moisture in; Finally, it was covered with black plastic and two ties were made at the ends of the plastic to give the encapsulation shape. This is how the prepared material remained during the time that the test remained.

A completely randomized design with a 2 x 4 factorial arrangement consisting of 8 treatments, 3 replications and 10 branches per experimental unit was used. Two types of branches (main and secondary) and 4 doses of indole-3-butyric acid (0.0; 0.2; 0.4; and 0.6%) were tested for rooting induction. The evaluation was carried out 40 days after the air layering, the data were analyzed by analysis of variance and submitted to Tukey's test ($p<0,05$) to determine the nature of the treatments. Prior to analysis, the percentage data were transformed using the formula arcsen $\sqrt{\%}$ and the count data transformed to $\sqrt{x+1}$ (Snedecor y Cochran 1980).

3. Results and discussion

Effects of IBA doce and type of branches

The purpose of treating branches with growth regulators is to increase the rooting percentage, reduce root initiation time and improve the quality of the root system formed. Indole-3-butyric acid is an effective auxin to promote rooting of cuttings in a large number of species (Hartmann et al., 1997). The rooting capacity of cinnamon sticks is greater by increasing the dose of indole-3-butyric acid until reaching an optimum of 0.6%. (Table 1). This behavior has been observed in other tropical species (Hartmann et al., 1997: Mesén, 1998) Likewise, in the species C. s*pruceanum*, 99% rooting was determined by applying IBA at an adequate dose (Vallejos et al., 2014).

In relation to the type of branches, it is observed that there is no significant difference in terms of the number of roots (Table 2). This behavior can be attributed to the fact that the two types of branches used have sufficient leaf area and that they continue their photosynthetic production in the leaves (Ruiz & Mesén, 2010).

In the rooting of cinnamon, the number and length of roots have a directly proportional relationship with the dose of indole butyric acid, obtaining the highest number and length of roots when using 0.6% of indole-3-butyric acid (Table 3). This behavior is due to the fact that the number of roots produced is highly influenced by the ability of the cutting to provide carbohydrates, either from reserves or produced through photosynthesis, to the area where the roots emerge (Lovell & White, 1986).

On the Fig. 1. The rooting of primary and secondary branches of Cinnamomum zeylanicum rooted with 0.6% AIB by air layering is shown, accelerating the rooting process in contrast to what was reported by Velastegui, V. (2011) who mentions that, at 102 days, the treatment of 6000 mg kg -1 of ANA showed the best results in number of roots (18); root length 16.68 cm and stem diameter with 1.22 cm.

Fig. 1. Ramas primarias (A) y secundarias (B) de *Cinnamomum zeylanicum* enraizadas con 0.6 % de AIB mediante acodo aéreo

Tabla 1. Effect of different doses of indole 3-butyric acid (IBA) on the rooting of *Cinnamomum zeylanicum* by air layering at 40 days

DOSE (%)	ROOTING (%)	ROOT (Nº)	ROOT LENGTH (cm)
0.6	85.00 **a**	17.03 **a**	7.33 **a**
0.4	70.00 **b**	5.43 **b**	2.11 **b**
0.2	53.33 **c**	1.37 **b**	0.54 **c**
0.0	25.00 **d**	0.55 **b**	0.13 **c**

* Means with different letters in the same column differ statistically according to Tukey's test (p<0,05)

Tabla 2. Effect of branch type on *Cinnamomum zeylanicum* rooting by air layering at 40 days

BRANCHES	ROOTING (%)	ROOT (Nº)	ROOT LENGTH (cm)
Primary	60.00 **a**	7.09 **a**	3.04 **a**
Secondarys	56.67 **b**	5.10 **a**	2.02 **b**

* Means with different letters in the same column differ statistically according to Tukey's test (p<0,05)

Tabla 3. Effect of Dose & Branch Type interactions on *Cinnamomum zeylanicum* rooting by air layering at 40 days

INTERACIÓN A x B	ENRAIZAMIENTO (%)	RAICES (Nº)	LONGITUD DE RAIZ (cm)
0.6 % x Primarias	90.00 **a**	20.60 **a**	9.37 **a**
0.4 % x Primarias	60.00 **c**	5.90 **c**	2.12 **c**
0.2 % x Primarias	70.00 **d**	1.40 **c**	0.58 **d**
0.0 % x Primarias	90.00 **g**	0.47 **c**	0.11 **d**
0.6 % x Secundarias	80.00 **b**	13.47 **ab**	5.29 **b**
0.4 % x Secundarias	70.00 **c**	4.96 **bc**	2.11 **c**
0.2 % x Secundarias	46.67 **e**	1.33 **c**	0.51 **d**
0.0 % x Secundarias	30.00 **f**	0.63 **c**	0.15 **d**

** Means with different letters in the same column differ statistically according to Tukey's test (p<0,05)

4. Conclusions

The vegetative propagation of Cinnamomum zeylanicum is possible and can be accelerated using a dose of 0.6% indole-3-butyric acid as a hormonal inducer and the use of primary branches by air layering.

Cknowledgements

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Development of Maize Varieties Suitable for Central Anatolian Conditions

Mehmet TEZEL[1*] Erdal GÖNÜLAL[1] Ramazan Çağatay ARICI[1] Gazi ÖZCAN[1]

Orcid:0000-0002-4632-3572, 0000-0002-1621-0892, 0000-0003-2317-0603, 0000-0001-7482-7770

[1] Bahri Dağdaş International Agricultural Research Institute – Konya/Türkiye

*Author e-mail: mehmettezel@gmail.com

Abstract

This study was obtained from the trials established in 2019 of maize breeding studies carried out in Central Anatolian conditions. In the study, 20 single hybrid maize combinations and 5 standard maize varieties (P0937, DKC5741, P0900, DKC5364, and P0573), which were crossed using inbred lines in 2018, were used. In the study carried out in the randomized blocks trial design in Konya Bahri Dağdaş International Agricultural Research Institute fields, grain yield, number of flowering days, grain moisture, plant height, and ear height observations, and measurements were taken.

The average grain yield was obtained as 11.90 t ha^{-1}, the average of the standards was 12.88 t ha^{-1}, while the average yield of single hybrid maize combinations was 11.66 t ha^{-1}. In the study, 5 single hybrid maize combinations (KTM 18.39, KTM 18.46, KTM 18.44, KTM 18.47, and KTM 18.68) reached higher yields than the other standard maize varieties. Number of flowering days was between 76.7 days (KTM18.45 and P0937) / 79.3 days (KTM 18.66), grain moisture at harvest was between 14.1% (DKC5364) / 23.2% (KTM 18.65) and plant height was 242 cm (KTM 18.67) / 294 cm (KTM 18.44).

With this study carried out in Central Anatolian conditions since 2008, it has been seen that productive varieties suitable for the region can be developed.

Key Words: Maize breeding, local variety, single hybrid, yield

Orta Anadolu Şartlarına Uygun Mısır Çeşitlerinin Geliştirilmesi

Özet

Bu çalışma Orta Anadolu şartlarında yürütülen yerli mısır ıslah çalışmalarının 2019 yılında kurulan denemelerden elde edilmiştir. Çalışmada 2018 yılında kendilenmiş hatlar kullanılarak melezlemeleri yapılan 20 adet tek melez mısır kombinasyonu ve 5 standart mısır çeşidi (P0937, DKC5741, P0900, DKC5364 ve P0573) kullanılmıştır. Konya Bahri Dağdaş uluslararası Tarımsal Araştırma Enstitüsü arazilerinde Tesadüf blokları deneme deseninde yürütülen çalışmada tane verimi, çiçeklenme gün sayısı, tane nemi, bitki boyu ve koçan yüksekliği gözlem ve ölçümleri alınmıştır.

Ortalama tane verimi 11.90 t ha^{-1} olarak elde edilmiş olup, standartların ortalaması 12.88 t ha^{-1} olurken tek melezlerin verim ortalaması 11.66 t ha^{-1} olmuştur. Çalışmada 5 adet tek melez (KTM 18.39, KTM 18.46, KTM 18.44, KTM 18.47 ve KTM 18.68) standartların verimlerinden daha yüksek değere ulaşmıştır. Çiçeklenme süresi 76.7 gün (KTM18.45 ve P0937)/79.3 gün (KTM 18.66) aralığında, hasatta tane nemi % 14.1 (DKC5364)/% 23.2 (KTM 18.65) aralığında ve bitki boyu 242 cm (KTM 18.67)/ 294 cm (KTM 18.44) aralığında elde edilmiştir.

Orta Anadolu şartlarında 2008 yılından itibaren yürütülen bu çalışma ile bölgeye uygun verimli çeşitlerin geliştirilebileceği görülmüştür.

Anahtar Kelimeler: Mısır ıslahı, yerli çeşit, tek melez, verim

Introduction

Maize is the most produced and consumed grain in the world after wheat, and it is used in many sectors, especially in human and animal nutrition. Maize trade has an important place in the world, and the USA, the largest maize exporter, has directed its investments and priorities regarding ethanol production towards maize. This will lead to an increase in maize prices in international markets in the future. In the near future, with the use of maize in bioethanol production by developed countries, twice as much maize as the current production will be needed (Üstün 2007).

Maize production and yield in Turkey have increased significantly in recent years, Konya and surrounding provinces supply approximately 20% of the country's production. In addition, it is at the forefront in terms of the presence of cattle and ovine animals and the number of poultry, and the need for maize is increasing. For this reason, since the importance and consumption of maize increases, the development of local varieties with good quality and low grain moisture at harvest and the creation of populations are among the important priorities of maize breeding studies in this region. For this purpose, The National Corn Breeding Project and the development of new varieties continue in 7 institutes under the General Directorate of Agricultural Research and Policies. The new hybrids obtained from the studies are put into trials in 10 different environments.

Material and Method

The study was carried out in Konya ecological conditions in 2019 in the fields of Bahri Dağdaş International Agricultural Research Institute. In 2018, 20 single hybrid maize combinations were crossed using inbred lines and 5 standard maize varieties (P0937, DKC5741, P0900, DKC5364, and P0573) were used. The experiment was carried out in three replications according to the Random Blocks Trial Design. The study area has a continental climate, that receives very little precipitation during summer and the precipitation regime is irregular. Some meteorological data of the study area are given in Table 1, and according to the table, the precipitation amount of the maize grown period (May-September) was 91.4 mm for long years, while it was 71 mm in 2019 (Anonymous 2019).

Table 1. Some meteorological data of the experimental area*.

Year	Data	May	June	July	August	September	Temp. Mean/Precip. Total.
		Months					
Long years	MeanTemp(°C)	15.4	19.6	22.6	22.2	17.5	19.5
	Max.Temp.(°C)	22.2	26.4	29.8	29.9	25.8	26.8
	Min.Temp.(°C)	8.4	12.2	15.4	15.0	10.5	12.3
	Precip. (mm)	43.3	24.5	6.9	5.5	11.2	91.4
2019	MeanTemp(°C)	15.8	20.2	22.9	23.2	17.6	19.9
	Max.Temp.(°C)	26.3	28.9	30.2	30.2	27.0	28.5
	Min.Temp.(°C)	8.0	14.0	15.3	16.1	10.4	12.8
	Precip. (mm)	10.2	45.6	7.6	1.2	6.4	71.0

* Meteorological data were taken from https://www.mgm.gov.tr.

When the soil properties of the study area are analyzed, it is seen that the organic matter ratio is sufficient (2.2%), there is no salt problem (0.86 mhos/cm), it is sufficient in terms of phosphorus and potassium, the pH value is 7.8, and the soil texture has a clayey structure. The first soil preparation was made with a plow, and just before planting, the second process was carried out with a rotavator. The pre-plant in the experiment was Hungarian vetch. Considering the results of soil analysis with planting, fertilization was made in a way that 100 kg of phosphorus and 400 kg of nitrogen per hectare were taken, and the remaining part of the nitrogen was applied in parts during the development period with drip irrigation, and it was completed to 250 kg ha^{-1}. In the study, which was designed to be 70 cm between rows and 18 cm above rows and 4 rows, the parcel length was 5 meters. The planting process was carried out on the 7th May of 2019, and the parcel width was 2.8 x 5 = 14 m^2 in planting and 1.4 x 5 = 7 m^2 after the edge effects were removed at harvest. After planting, 50 mm of irrigation water was given with a sprinkler irrigation system for equal germination and development in all plots. Afterward, when the soil moisture is monitored gravimetrically and 40% of the useful water is consumed, irrigation was carried out using the drip irrigation system so that the reduced moisture is completed to the field capacity (Özbahçe and Gönülal, 2019).

Weed control was done with Florasulam active ingredient herbicide and after mechanical weed control, laterals were laid one for each row.

Observations and measurements of other characteristics examined in the study (Plant height, number of flowering days, first ear height, ear/stalk ratio, and leaf/stalk ratio) were made according to the technical instruction used for grain maize (Anonymous, 2018). The harvest was done at the end of October in the form of harvesting the middle two rows. The yield was calculated by correcting the parcel yields obtained from the experiment according to 15% grain moisture at harvest. The variance analysis of the results obtained in the study was made with the JMP 11.2.1 package program according to the randomized blocks trial design, and the differences and groupings between the genotypes were made according to the LSD test (Anonymous, 2014).

Results and Discussion

The average values of the properties examined in the study are given in Table 2. It was determined that there were significant differences between the genotypes in all the traits examined in the study, except for the flowering period (Table 2).

When single hybrids and standard varieties are examined in terms of grain yield, the average yield of the experiment was 11.90 t ha^{-1}, grain yields of single hybrids ranged between 8.59 t ha^{-1}(KTM18.41) and 14.20 t ha^{-1}(KTM18.39) and the grain yields of standard varieties were It has been determined that it varies between 11.75 t ha^{-1}(P0573) and 14.02 t ha^{-1}(0937). In terms of grain yield, the KTM18.39 single hybrid had the highest grain yield, while 9 of the single hybrids were in the same group with P0937 variety (Table 2). Our results of grain yield were similar to that of Kılınç et al. (2018), Özata and Kapar (2014), Sayaslan et al. (2010), and Sakin et al. (2016). The results showed higher values of Atakul et al. (2014) and Idikut and Yıldız (2018). Alp and Kahraman (2017) showed lower values than the results of Aydın (2011) and Karaşahin and Sade (2012). It is thought that the differences with the previous studies are due to the variety, ecology, and growing conditions.

In the study, the average grain moisture values at harvest were 17.7%, while the grain moisture values of single hybrids were found between 14.4% (KTM18.45) - 23.2% (KTM18.65) at harvest, and between 14.2% (DKC5364) - 16.1% (P0900) for standard varieties (Tables). 2). Of the single crosses, ADA 8.2 and ADA 6.15 were genotypes with a grain moisture content of less than 15%. Grain moisture in maize is also affected by the variety, especially the last irrigation time (Gönülal et al., 2021), and the grain moisture results obtained from this study were similar to the results of Karaşahin and Sade (2012), and lower than the results of Özata and Kapar (2014) and higher than the results of Atakul et al. (2014) and Kılınç et al. (2018).

According to the results, the average flowering period in the experiment was 78.4 days, and single hybrids showed values between 76.7-79.3 days. Number of flowering days was found close to each other between standard varieties and single hybrids (Table 2). The results regarding number of flowering days were similar with the findings of Alp and Kahraman (2017), Sayaslan et al. (2010), and Idikut and Yıldız (2018). The results related to the number of flowering days were higher than the results of Atakul et al. (2014), Aydın (2011), Kılınç et al. (2018), and Özata and Kapar (2014). The relative humidity and temperature of the air affect pollination and fertilization (Emeklier 1997). Although the flowering period depends on the variety, it is affected by environmental conditions such as temperature and humidity in different places. Hot days following the emergence of maize shorten the flowering period of the plants. Appropriate temperatures in the days following the maize planting in Konya enable the plants to reach the total temperature required for flowering in a short time.

According to the results of the experiment, the average plant height was 265 cm, the plant height of single hybrids was changed between 242 cm (KTM18.67) and 294 cm (KTM18.44 and KTM18.69), and the height of the standard varieties was between 242 cm (DKC 5741) and 260 cm (P0573) (Table 2). In general, plant height of single hybrids was higher than the standard varieties. Plant height is an important vegetative trait that is largely standardized by genes and affects yield (Hallauer and Miranda 1987). The results were similar to the results of Karaşahin and Sade (2012), Alp and Kahraman (2017), and Kılınç et al. (2018) and higher than the results of Aydın (2011), Sakin et al. (2016) and Sayaslan et al. (2010) and lower than results of Atakul et al. (2014) showed. It is thought that the differences with the previous studies are due to the variety, ecology, and growing conditions.

In the experiment, the average first ear height was measured as 97.4 cm. The first ear heights of single hybrids were measured between 84.3 cm (KTM18.70) and 123 cm (KTM18.44), and the first ear heights of the standard varieties were measured between 71.7 cm (P0937) and 88.3 cm (0573) (Table 2). First ear height, like plant height, is largely under the influence of genes (Hallauer and Miranda 1987). However, it is affected by environmental conditions. This feature, which is important for machine harvesting, is generally requested not to fall below 1 m. The fact that the first ear heights of single hybrids were above 1 m indicates their suitability for machine harvesting. While the first ear height values obtained from the experiment were similar to the results of Öz and Kapar (2003) and Tezel and Aksoyak (2008), the results were lower than the values obtained by Atakul et al., (2014), and Aydın (2011).

Table 2. Observation and measurement values of the experiment

No	Variety	Yield (t ha^{-1})	Moisture (%)	Number of flowering days	Plant height (cm)	First ear height (cm)
1	KTM18.39	14.20 a	19,8 bc	79,0	280 af	115,7 ab
2	KTM18.46	13.54 ac	17,4 bh	79,0	289 ab	109,0 ae
3	KTM18.44	13.32 ac	20,3 ab	78,7	294 a	123,0 a
4	KTM18.47	13.23 ac	18,0 bf	78,3	246 g	109,7 ad
5	KTM18.68	12.94 ad	17,9 bf	79,3	269 ag	92,0 ci
6	KTM18.14	12.82 ae	16,9 ci	78,0	260 bg	93,0 ci
7	KTM18.69	12.49 ag	16,6 di	78,3	294 a	103,0 bh
8	KTM18.70	12.28 ai	19,8 bc	78,3	243 g	84,3 hk
9	KTM18.45	12.11 ai	14,4 hi	76,7	265 ag	86,7 gk
10	KTM18.67	11.62 ci	17,3 bh	79,0	242 g	89,0 fk
11	KTM18.65	11.53 ci	23,2 a	78,0	262 ag	105,3 ag
12	KTM18.66	11.27 ci	19,2 bd	79,3	247 g	91,7 dj
13	KTM18.43	10.77 dj	19,9 bc	79,0	282 ae	121,0 ab
14	KTM18.71	10.73 dj	19,1 be	79,0	265 ag	95,3 ci
15	KTM18.62	10.63 dej	18,7 be	77,7	289 ab	105,7 ag
16	KTM18.42	10.47 fj	17,8 bf	78,7	254 dg	111,3 ac
17	KTM18.40	10.38 gj	15,2 fi	78,7	256 cg	90,0 ek
18	KTM18.64	10.20 hj	19,7 bc	79,3	282 ad	103,0 bh
19	KTM18.63	10.10 ij	17,6 bg	79,7	268 ag	107,3 af
20	KTM18.41	8.59 j	17,8 bf	79,3	287 ac	107,0 af
21	P0937	14.02 ab	16,0 ei	76,7	249 fg	71,7 k
22	DKC5364	13.44 ab	14,1 i	77,3	250 eg	82,0 ik
23	DKC5741	12.75 af	16,0 ei	78,0	242 g	72,3 jk
24	P0900	12.45 ah	16,1 ei	78,0	255 dg	77,3 ik
25	P0573	11.75 bi	14,6 gi	77,7	260 bg	88,3 fk
	Average	11.90	17,7	78,4	265	97,4
	St. average	12.88	15,4	77,5	251	78,3
	F value	**	**	ÖD	**	**
	CV (%)	11,7	10,5	1,4	7,4	12,0
	LSD	2.28	3,0	ÖD	40	19,5

Conclusion

Due to the limited vegetation period in the Central Anatolian Region, varieties with high yield and low moisture content in the autumn harvest period are of great importance in maize farming. The existence of a large number of single hybrids in terms of grain yield and harvest grain moisture characteristics in the breeding material developed and examined within the scope of the maize breeding project in the region shows that new high yield and low harvested grain moisture domestic hybrid maize varieties suitable for Central Anatolian conditions may emerge.

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Effect of flour beetle's (*Tribolium confusum*) infestation of wheat flour's (Triticum durum) toxicological properties for human consumption

Noureddine Laadel[1]*, Abdelmalek Oulmi[2], Cyntia Mekideche[3], Zouhir Boulgueraguer[4], Sofiane Guettaf[5] ,Akram Kout[6], Nadia Benzidane[7]

[1]Laboratory of Improvement and development of plant and animal production, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

[2]Laboratory for the Valorization of Natural Biological Resources (LVNBR), Faculty of Nature and Life Science, Ferhat ABBAS University Sétif-1, 19000 Setif, Algeria

[3]Department of Biology and plant Ecology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

[4]Department of Geology, Laboratory of water resources and sustainable development REDD, , BADJI Mokhtar, Annaba University. Algeria

[5]Laboratory of Applied Microbiology, Faculty of Nature and Life Science , Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

[6]MISC Laboratory. Abdelhamid Mehri Constantine 2 University. Algeria

[7]Laboratory of Applied Biochemistry, Faculty of Nature and Life Science , Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

Corresponding Author: Noureddine LAADEL, Email: noor-bio@gmx.fr

Abstract:

Wheat is one of the most consumed cereals in the world. It comes from a type of grass (*Triticum*) that is grown in countless varieties around the world. large quantities of flour are stored in open shounas and/or blinds. Under these conditions, the flour is attacked by various biological factors including insects. Flour beetle (*Tribolium confusum*) attack stored grain products such as flour, cereals, meal, crackers, beans, spices, pasta, cake mix, dried pet food, dried flowers, chocolate, nuts, seeds, and even dried museum specimens.These beetles have chewing mouthparts, but do not bite or sting. The red flour beetle may elicit an allergic response. Over the past three decades, the presence and adverse effects of certain toxic compounds in flour as a result of insect pest infestation during storage has been of growing international concern. Previous studies have indicated that flour extracted from wheat that has suffered infestation by insect pests such as *Tribolium confusum* could be affected in its nutritional, chemical and rheological characteristics. Each change in these factors depends on many variables, such as wheat type, pest species, level of infestation and environmental conditions. previous studies have indicated that infestations by insect pests and their influence on the hygienic parameters of wheat flour. Fifty bowls, 1 kilogram, of flour were used filled with wheat flour 80 % extraction. A 50 larvae of *Tribolium confusum* were put into each bowl and 15 jars, for 2 months at 25 ^{0}C and 50% of relative humidity. At the end of this period, all samples were sieved to recover the insects and then analyzed. Mutagenic and Carcinogenic compounds, increased by the rate of 211.22 and 21.83% compared to 1.29 and 2.17% for the uninfected samples, respectively.

Keywords: wheat flour, insects' infestation, flour beetles, Mutagenic and Carcinogenic

Antioxidant Activity of Phenolic Compounds of *Pistacia lentiscus*

Nadia BENZIDANE1*, Sofiane GUETTAF2, Lekhmici ARRAR1, Chaima Djehiche,1 Noureddine LAADEL3 and Abdelmalek OULMI4

1* Laboratory of Applied Biochemistry, Department of Biochemistry, Faculty of Nature and Life Science, University Ferhat Abbas, Sétif, ALGERIA

2 Department of Natural Sciences, Faculty of Natural and Life Sciences Kouba High School 1University, Algiers-ALGERIA

3 Department of Biology and Plant Physiology, Faculty of Natural and Life Sciences, Ferhat Abbas Sétif-1University, Setif-ALGERIA

4 Department of Biology and Animal Physiology, Faculty of Natural and Life Sciences, Ferhat Abbas Sétif-1University, Setif-ALGERIA

Corresponding author: nadia19000@hotmail.fr

ABSTRACT

Objective: To investigate antioxydant activity, total phenolic and flavonoid content of methanol and aqueous extracts of ***Pistacia lentiscus*** root, stem and leaf parts selected from Ain Arnat Setif regions of Algeria. **Methods**: The antioxydant activity of different extracts (aqueous and Methanol fractions) from ***Pistacia lentiscus*** was evaluated by the DPPH scavenging test. The total phenolic and total flavonoid content of these extracts was determined according to the Folin-Ciocalteu procedure and Aluminum chloride colorimetric assay respectively. Total phenolic content was measured by Folin Ciocalteu reagent. **Results:** All the extracts showed significant antioxydant activities and contained important levels of phenols. The methanol extract from ***Pistacia lentiscus*** showed the greatest antioxydant capacity, which was probably due to its high content of polyphenols. Total flavonoid content was found equal for all extracts. **Conclusions**: Our results of antioxydant assays were justified and partially supported the popular usage of the tested plants. The high antioxydant activity found in the plant in this region suggested that ***Pistacia lentiscus*** is a good source of natural compounds which might have benefits for health.

Keywords: *Pistacia lentiscus*, Folk medicine, Flavonoids contents, Polyphenols, Antioxidant activity:

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CYTOPLASMIC GENOME PREDICTION IN CUCUMBER (*Cucumis sativus* L.) HYBRID VARIETY BREEDING AND IT'S USAGE IN BREEDING

Leyla ÖZTÜRK AKAR, Osman GÜLŞEN, Sinan ZENGİN,
G. Elif VURAL

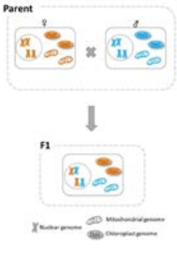
Cucumber (*Cucumis sativus* L.)

- Widely cultivated & economically important
- Worldwide production of >87 million tons in 2019 (http://www.fao.org/faostat/en/?#data/QC)
- Turkey ranks second after China w/1.9 million ton production.
- Develop domestic hybrid varieties
- Narrow genetic diversity, difficults breeding

- Doubled haploid technique + Marker asisted Selection ✓
- To get heterosis, reciprocal crosses can be made based on the cytoplasmic organelles (plastid and mitochondria) btw individuals are different from each other significantly increases the labor.

★ Plastid genome - maternal

★ Mitochondrial genome - paternal



Park et al.,2021 Inheritance of choloroplast and mitochondrial genomes in cucumber
revealed by four reciprocal F1 hybrid combinations

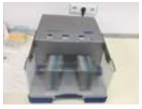
- Molecular-based Breeding w/ Cytoplasmic Genome Prediction

⇩

- If origins of individuals same, than need for reciprocal crosses will be eliminated, and a significant labor and time savings will be provided.
- Our aim was configure out our parental lines reciprocal cross need by Cytoplasmic Genome Prediction for accelarate breeding.

Materials and Methods

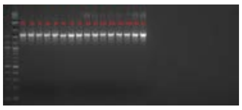
- 4 plastid genome regions **(rbcL, psb-trnS, trnHK, trnST)** of 50 donor genotypes were sequenced.
- These regions are assumed to be non-conserved due to their intergenic location
- DNA isolation of 50 genotypes by CTAB method.
- Region specific polymorphic universal primers (Gülşen and Ceylan, 2011) were used for PCR assays. (50 ul)



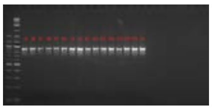
- 15 ul of PCR products were imaged and the resulting band sizes are approximately about 900, 1500, 3000 and 1400 base pairs.

TrnS-TrnT

TrnH-TrnK



30S-ribosomal



TrnK exon1-TrnK exon2

- 35 ul PCR products were sent to MASGEN Ar-Ge Ltd.Şti for sequencing.
- MEGA Genetic Analyses program was used for statistical analyses.
- Cucumber plastid region length w/150.501 bp
- 4 plastid regions length w/6.300 bp fully sequenced, alignment results were obtained.

↓

★ No nucleotide variation can be detected

Conclusion

- According to alignment results, no cytoplasmic genome difference among 50 genotypes, all have same maternal background.
- Reciprocal crosses are made based on the idea that the cytoplasmic organelles (plastid and mitochondria) between individuals are different from each other.
- So assumed that there was no cytoplasmic genome difference between the hundreds of inbred lines obtained using 50 genotypes, reciprocal crosses were excluded.

Conclusion

- We used only plastid specific primers, therefore our results indicate only maternal origins not paternal origins.
- Therefore combined use of plastid and mitochondria specific primers may produce more comprehensive results about need of reciprocal crosses.
- This analysis can provide rapidity and savings in breeding by eliminating unnecessary reciprocal test crosses.

Agromar Plant Molecular Genetics Laboratory

Tübitak 1501 / Project Number; 3190673

‘Development of DH and Molecular-based Variety by using Cucumber Ovarian Culture and Irradiated Pollen Techniques’

Thank You!

Short Palms for Improved Harvesting Efficiency

Siti Khadijah Mohd Rais[1], Wan Rusydiah Wan Rusik[1], Teh Chee Keng[2] and Harikrishna Kulaveraasingam[1]
[1] Sime Darby Research Sdn Bhd, KM10, Jalan Banting-Kelanang, PO Box 207, 42700, Banting, Selangor, Malaysia
[2] Sime Darby Plantation Technology Centre, 1st Floor, Block B, UPM-MTDC Technology Centre III Malaysia, Lebuh Silikon, Putra Square, 43400 Serdang, Selangor, Malaysia

The most crucial operation in oil palm plantation is harvesting of fresh fruit bunches that known to be a labour and energy intensive process. The economic life of the oil palm is mainly determined by the height of the palms, when the palm is too tall it becomes uneconomical to harvest either due to unavailability of skilled harvesters, cost or duration taken to harvest the bunches and safety to the harvesters. Shorter palms may help to address these four issues. In breeding, progeny and individual palms selection are the most suitable approach for improvement of secondary traits in oil palm because their phenotypic expression strongly influenced by environment factors. Short palms were 28% shorter than normal height but it's compensated by higher bunch weight in short population without sacrifice the overall fresh fruit bunch yield. This short palms material also produced higher oil to dry mesocarp (O/DM) and oil to bunch (O/B) ratio compared to normal DxP which contribute to higher oil extraction rate (OER). OER is important parameter that is directly related to the profitability of an oil palm plantation.

Objective : To produce short oil palms for improved harvestability and productivity
Benefits:

- Short height can make harvesting easier, faster and cheaper
- Harvesting times per palm are reduced for short palms, and hence this increases harvesting efficiency
- Bunches are more visible in shorter palms making identification of optimal ripeness easier
- Harvesting can be done by unskilled workers

TABLE 1 : HARVESTING TIME & WORKERS PRODUCTIVITY(2 WORKERS PER GANG BASED ON PALM'S HEIGHT)

Operation	Age in Years After Planting	Trunk Height (m)	Harvesting Time (min/palm)	Productivity (bunches/day)
Cutting FFB	2-4	1.00	0.7	400-1000
	8	3.00	1.8	150-250
	>8	>3.00	2.6	50-90

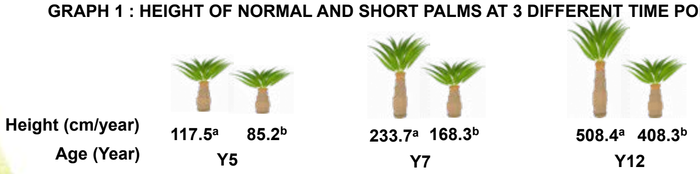
Note: Based on 50 centimeters height increment per year. Source: Turner and Gillbank (1982), Jelani (1997)

TABLE 2 : YIELD , OIL YIELD AND HEIGHT PERFORMANCE OF NORMAL AND SHORT PALMS

GROUP	No. of Palms	FFB (mt/h/y)	FFB (kg/p/y)	BNo (no/p/y)	BWt (kg/p/y)	O/DM (%)	O/WM (%)	O/B (%)	T. Ht. (cm)	Ht. Inc. (cm)
Kulai-Nigerian X AVROS (Normal DxP)	120	39.52^{a}	219.57^{a}	28.16^{a}	7.82^{b}	71.5^{a}	49.7^{a}	22.5^{b}	233.7^{a}	46.7^{a}
Kulai-Nigerian X URT-Calabar (Short DxP)	108	35.79^{b}	198.86^{b}	22.06^{b}	9.16^{a}	73.4^{a}	50.6^{a}	26.0^{a}	168.3^{b}	33.6^{b}

Note: Means that do not share a letter within columns are significantly different according to Tukey at $p<0.05$
Abbreviation : FFB (mt/h/y) = Fresh Fruit Bunch (metric tonne/hectare/year), FFB (kg/p/y) = Fresh Fruit Bunch (kilogram/palm/year), BNo (no/p/y) = Bunch Number (number/palm/year) , BWt (kg/p/y) = Bunch Weight (kilogram/palm/year), ODM (%) = Oil to Dry Mesocarp (%), O/B (%) = Oil to Bunch (%), T.Ht (cm) = Trunk Height (centimetre) and Ht. Inc. (cm) = Height Increment (centimetre) – Trunk Height at 7 years old
Source: Trial BO/PT/29 in Seri Intan Estate

GRAPH 1 : HEIGHT OF NORMAL AND SHORT PALMS AT 3 DIFFERENT TIME POINT



Note: Slow height increment identified based on 3 time point measurements. Short palms have 40.8 cm/year height compared to normal palms which was 50.8 cm/year at 12 years old.

SHORT VERSUS NORMAL DXP

Short DXP

Normal DXP

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DETERMINATION OF RESISTANCE LEVELS OF QUALIFIED TOMATO GENOTYPES TO *Meloidogyne incognita*, TOMATO YELLOW LEAF CURL VIRUS, TOMATO SPOTTED WILT VIRUS, TOMATO MOSAIC VIRUS

Selcan EROĞLU[1*], Ali Tevfik UNCU[2], Ayşe Özgür UNCU[2], Neslihan ISSI[1], Banu Çiçek ARI[1], Gülbanu KIYMACI[1], Önder TÜRKMEN[1,3]

[1]Selcuk University, Faculty of Agriculture, Department of Horticulture, Konya/Turkey

[2]Necmettin Erbakan University, Faculty of Science, Department of Molecular Biology and Genetics, Konya/Turkey

[3]Necmettin Erbakan University, Eregli Faculty of Agriculture, Konya/Turkey

*Author for correspondence (selcan930@gmail.com)

Abstract

Tomato (*Solanum lycopersicum* L.), one of the vegetable species, is one of the vegetables that covers an important area in terms of reproduction both in Turkey and in the world. Although Turkey is not among the gene centers, it ranks 4th in the world in terms of production after China, India and the USA. According to consumer demands, tomato varieties such as pink, beef, bunch, cocktail are grown. In recent years, an important production potential of pink tomatoes has started to emerge in Turkey, and breeding programs are carried out in this context. The main goals in breeding are high yield, quality and resistance to stress factors, and molecular assisted selection is a fast and reliable method, especially in determining the levels of resistance to biotic stress factors. In this study, the determination of the resistance levels of 339 tomato genotypes, which have the potential to become parent lines due to their agromorphological characteristics, against *Meloidogyne incognita* (Nematode), Tomato Yellow Leaf Curl Virus (TYLCV), Tomato Spotted Wilt Virus(TSWV), Tomato Mosaic Virus (ToMV) in the S6 stage was the subject of this study. When the results of the study were examined, 235 resistant lines to *Meloidogyne incognita*, 175 resistant to TYLCV, 201 resistant to TSWV and 211 resistant to ToMV lines were determined among 339 genotypes and they were included in the breeding process in order to develop resistant varieties against these biotic stress factors.

Keywords: *Meloidogyne incognita*, Tomatoes, ToMV, TSWV, TYLCV.

Toxicological properties of flour beetle's (*Tribolium confusum*) infestation on *Hordeum vulgare* consumption

Abdelmalek OULMI[1*], Noureddine LAADEL[2], Cyntia MEKIDECHE[3], Zouhir BOULGUERAGUER[4], Sofiane GUETTAF[5] ,Akram KOUT[6], Nadia BENZIDANE[7]

[1]Laboratory for the Valorization of Natural Biological Resources (LVNBR), Faculty of Nature and Life Science, Ferhat ABBAS University Sétif-1, 19000 Setif, Algeria

[2]Laboratory of Improvement and development of plant and animal production, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

[3]Department of Biology and plant Ecology, Faculty of Nature and Life Science, Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

[4]Department of Geology, Laboratory of water resources and sustainable development REDD, , BADJI Mokhtar, Annaba University. Algeria

[5]Laboratory of Applied Microbiology, Faculty of Nature and Life Science , Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

[6]MISC Laboratory. Abdelhamid Mehri Constantine 2 University. Algeria

[7]Laboratory of Applied Biochemistry, Faculty of Nature and Life Science , Ferhat Abbas University Sétif-1, Sétif 19000, Algeria

Corresponding Author: Abdelmalek OULMI, Email: oulmi@yahoo.fr

Abstract:

Barley (Hordeum vulgare), a member of the grass family, is a major cereal grain grown in temperate climates globally. It was one of the first cultivated grains, particularly in Eurasia as early as 10,000 years ago. In 2020, world production of barley was 157 million tonnes, led by Russia producing 13% of the world total. Spain, Germany, Canada, and France were major producers. It can be susceptible to many diseases, but plant breeders have been working hard to incorporate resistance. The devastation caused by any one disease will depend upon the susceptibility of the variety being grown and the environmental conditions during disease development. Serious diseases of barley include powdery mildew caused by Flour beetle (*Tribolium confusum*). The presence and adverse effects of certain toxic compounds in flour as a result of insect pest infestation during storage has been of growing international concern. Previous studies have indicated that flour extracted from wheat that has suffered infestation by insect pests such as *Tribolium confusum* could be affected in its nutritional, chemical and rheological characteristics.. Fifty bowls, 1 kilogram, of flour were used filled with wheat flour 80 % extraction. A 50 larvae of *Tribolium confusum* were put into each bowl and 15 jars, for 2 months at 25 ^{0}C and 50% of relative humidity. At the end of this period, all samples were sieved to recover the insects and then analyzed. Mutagenic and Carcinogenic compounds, increased by the rate of 231.87 and 23.55% compared to 1.87 and 2.99% for the uninfected samples, respectively.

Keywords: *Hordeum vulgare*, Insects' infestation, Flour beetles, Mutagenic and Carcinogenic

Evaluation of Advanced Barley Lines for Yield and Yield-Related Traits in Aegean Region Conditions

Aydin Imamoglu[1], Seda Uces[1], Mustafa Cerit[1]

[1] Aegean Agricultural Research Institute, Izmir / Turkey

TAGEM
R&D AND INNOVATION

INTRODUCTION

Barley (*Hordeum Vulgare* L.) is known as 4th important crop after wheat, maize, and rice. It is mostly used for animal feeding, the malting industry, and human consumption. Global barley production is 156,7 million tons with 51,4 million hectares of harvesting area (TEPGE 2020). Barley has wide adaptation due to outstanding salt, frost, and dry conditions which makes barley a suitable crop for unfavorable conditions (Giorgi et al. 2008). Türkiye is an important barley producer in the Mediterranean area. With climate change, the region would be affected and climate could be unpredictable. Therefore, barley can take over other plants in cultivation areas.

OBJECTIVES

☆The objective of this study was to evaluate superior barley lines with high quality and yield potential.

☆Register enhanced genotypes for farmer use in the region.

MATERIALS AND METHODS

☆The experiment was conducted at the Aegean Agricultural Research Institute Station in Izmir and Balıkesir using a randomized completely block design (RCBD) with four replication under rain-fed conditions.

☆In this study, 20 advanced barley lines developed in the barley breeding program and 5 check varieties (Sancak, Bayrak, İmbat, Aybar, and Hilal) were used.

☆Data were recorded for grain yield, thousand kernel weight, ≥2,5 mm particle size, and hectoliter weight.

RESULTS

ANOVA	H^2	σ^2Gen	σ^2 G X E	Mean	LSD	CV
Yield	0,43	1124,53	3283.93**	51,43	72,50	12,88
Hectoliter	0,69	2.12**	0,33	63,98	2,33	3,82
TKW	0,91	20.38**	3.35*	42,17	4,53	7,75
Sieve	0,81	43,98**	21,75**	79,99	8,82	6,89

Table 1: Analysis of variance and broad-sense heritability and mean performance of corresponding traits. σ^2Gen: Genotypic Variance, σ^2G X E: Genotype-by-Environment Variance, H^2 : Broad Sense Heritability, LSD: Least Significant Difference for genotype effect CV: Coefficient of Variation, TKW: Thousand Kernel Weight.

Traits	Yield	Hectoliter	TKW
Hectoliter	-0,018		
TKW	-0.58**	0,12	
Sieve (2,5 <)	-0,48*	0,035	0,85**

Table 2: Correlation coefficients among traits collected. TKW: Thousand Kernel Weight.

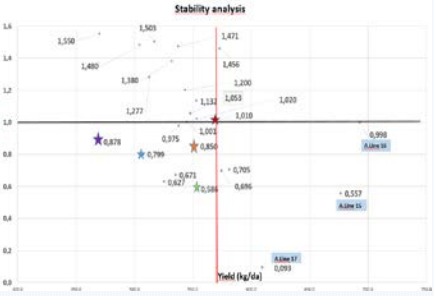

Figure 1: stability analysis of yield across environments.
★imbat ★sancak ★bayrak ★ hilal ★ aybar

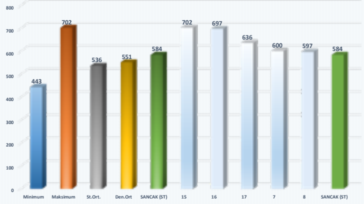

Figure 2: stability analysis of yield across environments.

Çeşit/Hat No	Verim (kg/da)	Grup.
15	702	A
16	697	A
17	636	AB
7	600	BC
8	597	BC
SANCAK (ST)	584	BD
BAYRAK (ST)	576	BE
12	554	CF
İMBAT (ST)	551	CF
6	551	CF
21	543	CG
19	541	CG
18	541	CG
24	540	CG
14	540	CG
11	535	CG
22	534	CG
9	531	CH
25	520	DH
23	507	EI
AYBAR (ST)	507	EI
13	498	FI
20	477	GI
HİLAL (ST)	459	HI
10	443	I
DEN.ORT.	551	
F	5,7297**	
DK(%)	12,46	
AÖF (%5)	72,58	

Table 2: LSD test for yield.

CONCLUSION

➢Based on stability analysis grain yield was significantly influenced by GbyE, however, some of the lines showed high stability.

➢Over all lines 15, 16, and 17 out yielded the standards (536 kg/da), with 702, 697, and 637 kg/da respectively.

➢Two lines could be registered as new varieties or used in barley breeding programs to improve grain yield.

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Advances in *Climate-Resilient* Temperate Tree Breeding: A Case Study in Peach

Omer Atagul[1], Alejandro Calle[2] and Ksenija Gasic[2]

[1]East Mediterranean Transitional Zone Agricultural Research Institute, 46060 Kahramanmaras, Turkey
[2]Department of Plant and Environmental Sciences, Clemson University, 105 Collings St., Clemson, SC 29634

Overview

- Background
- Challenges
- Objective of Project
- Plant Material
- Method
- Results

Background - peach

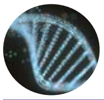
Peach
is originated in China ~3300 – 2500 BC and belongs to the Rosaceae family, genus *Prunus* (L.). It is the third most-produced temperate tree fruit species.

Production
Annually ~ 25 M tons worldwide, 750,000 tons in the U.S
South Carolina is #2 in the nation in peach production ~ 84,000 tons

Consumption
Peaches are often used for fresh consumption, although a significant portion of peach production is processed by canning industry (jelly, jam, fruit juice, yogurt pulp, and liquor)

Background - peach

Peach is genetically best characterized *Prunus* species, with many genes controlling essential traits and under Mendelian behavior (Monet et al., 1996).



Peach has a relatively simple genome: diploid (2n = 2x = 16), small (230 Mb), and naturally self-pollinating (Verde et al., 2013).

Peach genome was the first tree fruit genome sequenced in Rosaceae and has been used as a model in modern genetic studies to investigate the inheritance of desired traits, including climate resilience.

Challenges

Climate change can cause a risk for fruit tree production manufacture in numerous areas of the world.

In 2007, 2017 and 2022 after warm winter, southeastern peach growers lost most of their crop due to late spring frost

- Early bloom
- Late Spring Freeze destroyed the crop
- Low chill varieties got enough chilling

SOUTHEAST FarmPress

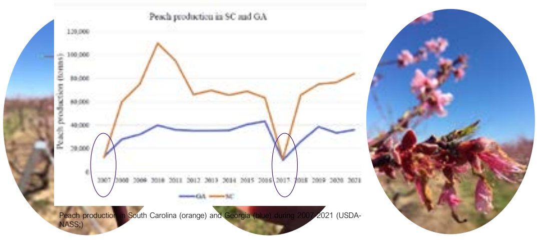
CROPS > ORCHARD CROPS

90 percent of South Carolina's peach crop destroyed

Challenges - climate change

Global climate change has a major influence on the phenology of dormancy and blooming and presents an increasing risk for crop loss due to spring frost.

In 2022,



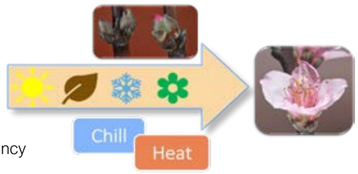
Peach production in South Carolina (orange) and Georgia (blue) during 2007-2021 (USDA-NASS;)

Dormancy

Three phases/stages of dormancy period classified by Lang (1987) in temperate trees;

- para-dormancy
- endo-dormancy
- eco-dormancy

Essential for overcoming endodormancy for bud break.



Chilling and heat requirements play a key role in bloom date

Chill requirement (CR)

Chill requirement is defined as the minimum duration of low temperatures that are required for the release from endodormancy (Fadón et al., 2020)

Chilling Hours Model	Utah Chilling Unit Model	Dynamic Model

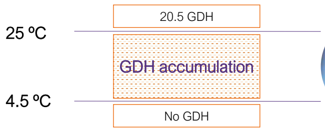
Heat requirement (HR)

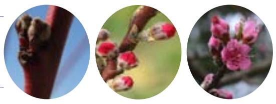
Heat requirement
is a thermal time that must be accumulated for peach trees to reach blooming

Growing degree hour
Richardson et al. (1975) proposed the growing degree hour (GDH) model that counts the heat accumulation from endo-dormancy release to full bloom and further improved by Anderson et al. (1986)

Heat requirement

Growing degree hour (GDH)
characterizes the thermal temperature necessary for growth during eco-dormancy based on the critical threshold base temperature (Tb).

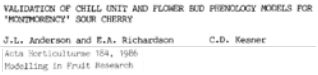




Previous research

How do we know the threshold base temperatures (Tb) of peach cultivars?

- Attempts to determine GDH have generally assumed a Tb of 4.4 °C in common across all *Prunus* sp. (Anderson et al., 1986)



VALIDATION OF CHILL UNIT AND FLOWER BUD PHENOLOGY MODELS FOR 'MONTMORENCY' SOUR CHERRY

J.L. Anderson and E.A. Richardson C.D. Kesner

Acta Horticulturae 184, 1986
Modelling in Fruit Research

- Bielenberg and Gasic (2022) reported base temperatures of -1.85, -0.5, 0.9 and 4.34 ºC in four peach cultivars, Elberta, Hakuho, Junegold and UFGold, respectively, as well as Tb range from -1.15 to 8.68 ºC in segregating progeny.

Peach [*Prunus persica* (L.) Batsch] Cultivars Differ in Apparent Base Temperature and Growing Degree Hour Requirement for Floral Bud Break

Douglas G. Bielenberg[1] and Ksenija Gasic[2]*

[1]Department of Biological Sciences, Clemson University, Clemson, SC, United States
[2]Plant and Environmental Sciences, Clemson University, Clemson, SC, United States

Objective Of Project

Hypothesis: Peach germplasm differs in base temperature (Tb) and total heat accumulation and provides an opportunity for breeding for climate resilience

- Evaluate variability of heat requirement in peach germplasm in relationship with the chilling requirement.
- Detect genomic regions associated with heat requirement in peach to facilitate development and application of DNA test(s) in breeding for high heat requirement

Significance of the work

In this study, we estimated HR diversity in a large set of U.S. peach germplasm to test hypothesis if observed diversity could be used in breeding to counter climate change.

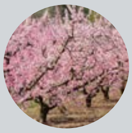
To do that:

We investigated HR in peach germplasm, the interaction of CR and HR in relation to BD, and the influence of different climatic conditions to these traits in the U.S. peach germplasm, over eight different climatic years (2014-2021).

Plant material – phenotypic data

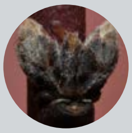
Musser Fruit
Research Center

Peach germplasm
(N=136)
F2 peach progeny
N=269)



Weather data
(2014-2021)

Chill hours
(Okie,1998)



Methods – phenotypic data

Bloom Date	Recorded when 90% of flowers buds were fully open and data expressed as Julian Days (JD; days from January 1st).
Chill requirement satisfaction	The day of the year that each accession completed its CR, estimated by calculating the sum of chill hours (CHs) using the model developed by Weinberger (1950).
Heat requirement	Under three base temperatures (Tb): standard, (4.5 ºC), lower (2.5 ºC) and higher (6.5 ºC)
Statistical analyses	➢ Descriptive statistics ➢ The best linear unbiased prediction (BLUP) – Mixed effect model ➢ Pearson correlation coefficient (*p* < 0.001) ➢ The effect of CR and HR on BD (ANOVA, t-test (*p* < 0.05)

Results

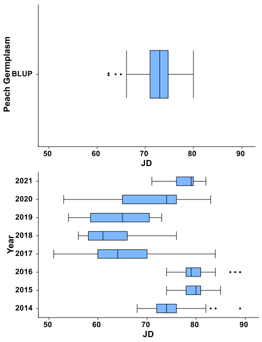
Bloom date (BD)

BD BLUP ranged from 62 (SC-2 and SC-10) to 80 (Sweet September and Tra-Zee) Julian days (JD)

Earliest BD recorded in 2017 (Galaxy; 51 JD) and the latest in 2014 and 2016 (Raritan Rose; 89 JD)

BD skewed to mid- and late-season blooming;

4 (3%) very early (60 to 65 JD; March 1st – 6th)
22 (16%) early
85 (62.5%) mid-season
19 (14%) late
6 (4.5%) very late (79 to 80 JD; March 20th – 21st)



Eight-year BLUP (top) and annual (bottom) bloom date, expressed as Julian Days (JD) in the U.S. peach germplasm

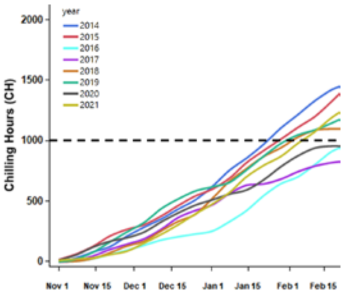
Chill requirement (CR)

CR of the peach germplasm ranged from 516 to 1116 CHs.

18 low	(501 - 650 CH)
6 low-medium	(651 - 700 CH)
57 medium	(701 - 800 CH)
24 medium-high	(801 - 850 CH)
24 high	(851 - 1000 CH)
7 very high	(>1000 CH)

Annual differences in the CR fulfillment:

low chill accumulation, <1000 CH fulfillment by February 15th in three seasons: 2015/16, 2016/17, and 2019/20



Season evolution of chill hours (CH) accumulation from November 1st until February 15th using Weinberger (1950) model.

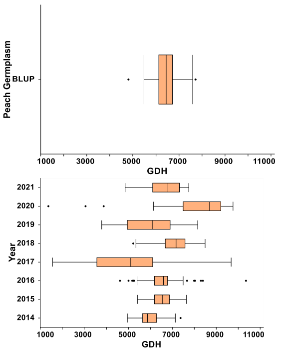
Heat requirement (HR)

Overall BLUP HR ranged from 4808 (SC-7) to 7721 (Glowingstar) GDH.

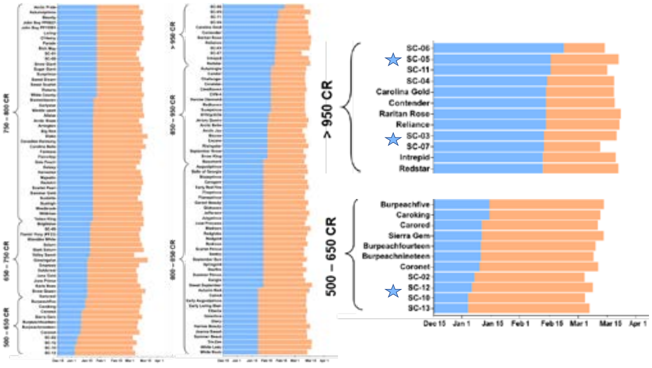
Most accessions (N=104) accumulated 6000 - 7000 GDH, and only breeding line SC-7 exhibited a BLUP HR < 5000 GDH.

Annual heat accumulation ranged from 1362 (SC-7) to 10,348 (Snowqueen) GDH in 2020 and 2016, respectively.

~5000 – 8500 GDH HR intervals observed in most years, except in 2017 and 2020, wide interval was observed ~1500 to 9500 GDH.



Eight-year BLUP (top) and annual (bottom) heat requirement, expressed as growing degree hours (GDH) in the U.S. peach germplasm



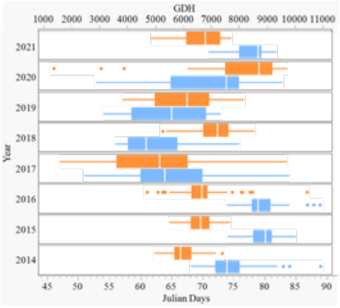
Temperature, BD and HR

Temperature increase from 2017 to 2020 resulted in earlier blooming and lower GDH, particularly for early blooming cultivars.

HR accumulation variation of up to 5500 GDH for the same accessions (e.g., 'Redglobe', 'September Sun', 'Sunprince' and 'Julyprince') observed in different years.

An 8 days advance of the end of bloom observed within the last four years (2018 - 2021).

BD intervals >20 days (2014, 2017, 2018, and 2020) and <11 days (2015 and 2021) recorded



Bloom date (blue) and Heat requirement (orange) for the U.S. peach germplasm in seven years.

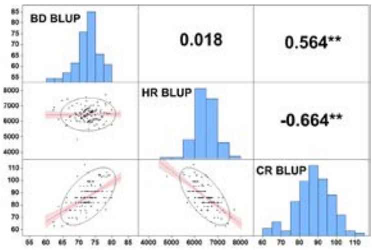
Trait correlations

Regarding annual interaction between traits;

- BD and CR (r = 0.476 to 0.720)
- HR and CR (r = - 0.195 to - 0.787)
- BD and HR (positive and negative correlation was reported)

Significance of CR and HR on BD;

- HR and CR significantly affecting BD in all years (p < 0.0001)
- 2017 – (HR)
- 2016 – (CR; based on transformed data)



Pearson correlation ($p < 0.001$) between bloom date **(BD)**, heat requirement **(HR)**, and chill requirement **(CR)** in the U.S. peach germplasm using the best linear unbiased prediction (BLUP) values of eight analyzed years (2014-2021).

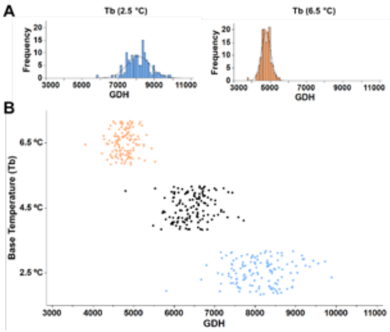
HR and Tb

BLUP;

Tb = 2.5 °C (5811 – 9891 GDH)
Tb = 4.5 °C (4808 – 7721 GDH)
Tb = 6.5 °C (3814 – 5539 GDH)

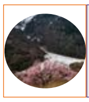
~1670 GDH increase (Tb = 2.5 ºC) or reduction in HR predicted (Tb = 6.5 ºC)

The rate of change in GDH was not the same in low and high HR accessions.

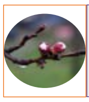


Frequency distributions of heat requirements **(A)** and comparison of heat requirement accumulation for each accession **(B)** in the U.S. peach germplasm under 2.5 (orange), 4.5 (black) and 6.5 (blue) °C base temperature (Tb) in Richardson's model.

Conclusions



Peach breeding germplasm has variable heat requirement and provides and opportunity to breed for targeted heat requirement.



- Threshold base temperatures (Tb) should be revisited to allow precise determination of HR.

Information provided in this study establishes foundation for further understanding of genetic background and inheritance of heat requirement in peach that could lead to development of molecular tools for breeding for adaptive plasticity to environmental change.

Acknowledgement- Special thanks to

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Research Associate : John Mark Lawton and Trey Burrell
Graduate students : Ufuk Caglar, Gizem Demirel

Musser Fruit Research Farm Crew

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THANK YOU!

&

QUESTIONS

QTL mapping of yield and yield-related traits in winter wheat TAM 113 and Gallagher

Mustafa Cerit [1,2], Zhen Wang [2,3], Shuhao Yu [2], Smit Dhakal [2], Jorge L. Valenzuela-Antelo [2,3], Mehmet Dogan [2,3], Chenggen Chu [2], Xiaoxiao Liu [2], Keke Hui [2],
Jaqueline A. Avila [2], Brittany M. Ehrlich [2], Shichen Wang [4], Paul St Amand [5], Qingwu Xue [2], Jackie C. Rudd [2], Amir M. H. Ibrahim [3], Guihua Bai [5],
Geraldine B. Opena [3], Bryan E. Simoneaux [3], Jason Baker [2], Shannon Baker [2], Ravindra N. Devkota [2], Kirk Jessup [2], Shuyu Liu [2]

[1] Aegean Agricultural Research Institute, Menemen-İzmir/TÜRKİYE
[2] Texas A&M AgriLife Research and Extension Center, Amarillo, TX;
[3] Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas
[4] Genomics and Bioinformatic Service Center, College Station;
[5] USDA, Hard Winter Wheat Genetics Research Unit, 4008 Throckmorton Hall, Manhattan, KS 66506, USA.

INTRODUCTION

- Wheat (*Triticum aestivum* L.) is one of the largely grown cereals in the world and a primary source of human consumption, livestock, and industry (Grote et al., 2021).
- Increasing grain yield is closely linked with some traits; plant height (PH), thousand kernel weight (TKW), grain number per spike, total biomass (BM), number of tillers, and grain weight per spike.
- Quantitative trait loci (QTL) mapping identifies the genomic regions that linked with quantitative traits and it can also help us to understand the genomic structure and how many genes importantly contribute to the trait.
- Understanding the genetic structure of yield and yield components in dryland and irrigated conditions could help to develop better germplasm or cultivars.

OBJECTIVES

- The objective of this research is to identify quantitative trait loci (QTL) associated with yield and its components a using recombinant inbreed line (RIL) in different Texas Environments.

MATERIAL AND METHODS

- 191 RILs and parents were genotyped in Texas A&M AgriLife Genomics and Bioinformatics Service at College Station using the ddRADseq genotyping protocol in Illumina Novaseq 6000 sequencing system (Yang et al., 2020).
- Agronomical data were collected on plant height(PH), heading date, spike per meter (SPM), biomass, thousand kernel weight, and grain yield (GYLD) were collected in three environments.
- Joinmap 4.0 (Van Ooijen JW., 2006) were used the create 25 linkage group and inclusive composite interval mapping (ICIM) was performed using ICImapping 4.2 (Meng et al. 2015).
- A set of 8075 single nucleotide polymorphisms (SNPs) were used to construct a high-density genetic map and QTL analyses.

RESULTS AND DISCUSSION

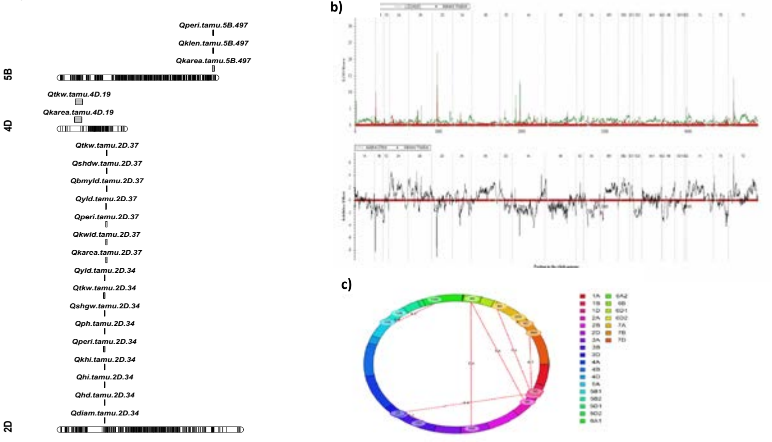

Fig. 1. **a)** QTLs associated with yield and components, **b)** whole genome scan with additive effect, **c)** epistatic interactions

QTL name	Peak Mbp	Trait	ANALYSIS	LOD	PVE	Add
Qhd.tamu.2D.34	34.43	HD	MET, 19BSP, 19CS, 19MCG, 20CS, 20MCG, 21BD	21.89-179.84	34.82-57.45	1.5-4.86
Qph.tamu.2D.34	34.43	PH	19BSP, 20MCG	11.35-19.84	15.46-28.78	2.11-3.48
Qkarea.tamu.2D.37	36.9	KAREA	MET, 19BSP, 20EMN	8.67-17.54	14.89-18.15	(-0.29) -(-0.18)
Qperi.tamu.2D.37	36.9	KPERI	20EMN	4.45	8.81	-0.1652
Qyld.tamu.2D.37	36.9	YLD	MET, 20CS, 20MCG	9.13-33.40	11.72-26.14	(-37.64) -(-8.99)
Qkwid.tamu.2D.37	37.25	KWID	MET, 20EMN, 19BSP	5.29-18.58	12.68-17.48	(-0.04) -(-0.02)
Qtkw.tamu.2D.37	37.25	TKW	MET, 20MCG, 20EMN	5.62-8.40	10.09-12.55	(-1.01) -(-0.37)
Qklen.tamu.5B.497	496.62	KLEN	MET, 19BSP, 20EMN	3.92-8.34	4.91-7.71	0.04-0.05
Qtkw.tamu.6A.573	573.37	TKW	20MCG, 20EMN, 21BD	4.20-8.36	8.37-12.97	(-1.03) -(-0.74)
Qperi.tamu.6A.98	98.34	KPERI	MET, 19BSP, 20EMN	5.42-12.40	11.06-12.52	(-0.18) -(-0.12)
Qklen.tamu.6A.113	113.23	KLEN	MET, 19BSP, 21BD	5.38-11.21	10.99-11.48	(-0.07) -(-0.04)
Qkwid.tamu.7D.65	65.22	KWID	MET 19BSP, 20MCG,	5.55-9.23	6.99-12.64	0.015-0.037
Qhd.tamu.7D.70	70.03	HD	MET, 19BSP, 20CS	3.78-16.11	1.81-5.10	(-0.96) -(-0.58)

Table 1. Consistent QTL for kernel length and kernel width from three mapping populations

CONCLUSIONS

- A total of 153 QTL region were found out of 119 genetic location for 20 different traits.
- 16 QTL were consistent at least two individual envirnments.
- Three cluster QTL region were identified on 2B, 2D, and 7D.
- QTL on 2D was located in the flanking region of *Ppd-D1*, a major gene that regulated photoperiodism

ACKNOWLEDGMENT

We thank Texas A&M wheat breeding teams and genetic program, Texas A&M AgriLife Research, USDA- Central Small Grain Genotypic Lab. and Ministry of Education of Turkey Republic.

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The Heritability for Flower Productivity and Defoliation in Diploid Roses

Seza Noyan[1,2], David H. Byrne[2],Ellen Young, Oscar Riera-Lizarazu[2], Stella Kang[2],Ellen Young[2], Jeekin Lau[2],Stella Kang[2], Natalie Anderson[2], and Pam Hornby[2]
[1]Aegean Agricultural Research Institute, Menemen-İzmir/Turkey
[2]Deparment of Horticultural Sciences, Texas A&M University, College Station, Texas

Introduction

- Roses are one of the most valuable garden plants in the world. Roses (n=7, 2x to 10x), a woody perennial plant of genus Rosa (Rosaceae family) was first cultivated more than 5000 years ago in China, Western Asia, and Northern Africa. The major classes of modern roses for ornamental use (garden roses, pot roses, and cut roses) were developed via hybridization among Chinese, European, and Middle Eastern roses. Although flower characteristics such as fragrance, size, color, and form are important, consumers demand two essential traits that well adaptation and more flower productivity. The focus of this study was to calculate the heritability of defoliation as measured by monthly assessments and flower productivity as measured by weekly ratings of flower intensity of 10 inter-related diploid rose families created by using a combination of 11 parents.

Objectives

- The objective of this study is to estimate the heritability associated with flower intensity and defoliation by evaluating the percentage of the canopy covered or affected by the trait among 10 inter- related diploid rose families in College Station, Texas.

Material and Methods

- Ten diploid rose families (330 seedlings) derived from well-adapted breeding lines with *Rosa wichuriana*, 'Old Blush' and 'Ducher' parentage (M4-4, J06-30-3-3, J06-14-20-3) crossed with commercial rose cultivars ('Sweet Chariot', 'Vineyard Song', 'Little Chief', 'Old Blush', 'Red Fairy') were used.
- Diploid rose plants were planted in a randomized complete block design with two replications in October 2018 at the Texas A&M University Horticulture Teaching Research and Extension Center in Somerville, TX.
- Flower productivity was measured by rating the plants for flower intensity weekly. A 0 to 9 scale was used to estimate flower intensity based on the percent of the canopy covered with flowers.
- Plants were evaluated for defoliation on 0-9 scale monthly from April to November. Ratings are based on percentage of foliage missing from an optimally full plant canopy.

April week 1 April week 2 April week 3

Importance of weekly flower intensity evaluation among the 10 diploid rose families in College Station, Texas, in 2019.

Rating=2 Rating=4

Rating=6 Rating=9

Example of flower intensity ratings in roses in College Station, Texas, in 2019.

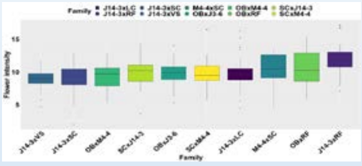
Rating	Description
0	No defoliation, optimally full canopy.
3	~30 percent of the leaves missing
5	~50 percent of the leaves missing
7	~70 percent of leaves missing
9	~90 percent or more of leaves fallen

Defoliation scale used to evaluate defoliation of 10 diploid rose families

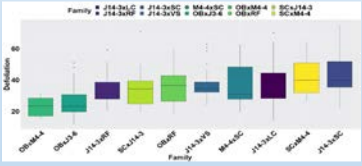
Results

- J14-3 x RF was the most productive family and J14 x VS had the lowest flower intensity
- Flower intensity peaked in May and September and had the lowest levels in July and August
- $V_{gxe}/V_g < 1$, Low narrow sense heritability, High broad sense heritability

- J14-3xSC and SC x M4-4 less foliage and OBxM4-4 and OBxJ3-6 more foliage
- Defoliation was low in June and Increased to a peak level in November
- $V_{gxe}/V_g < 1$, Moderate narrow sense heritability, High broad sense heritability



	Genetic variance		Genetic variance
V_{gxe}	4.1	h^2 (V_A/V_P)	0.10
V_{gxe}/V_g	0.63	H^2 $(V_A+V_D)/V_P)$	0.81



	Genetic variance		Genetic variance
V_{gxe}	128.7	h^2 (V_A/V_P)	0.44
V_{gxe}/V_g	0.62	H^2 $(V_A+V_D)/V_P)$	0.90

Further Research

- This study uses only one year of data, additional data needs to be collected to verify and strengthen the conclusions
- The next step would be to combine this phenotypic data with genotypic data to do QTL (quantitative trait loci) analysis.
- Our ultimate purpose is to select plants that have continuously flowering and healthy (low disease and defoliation) throughout the season.

Acknowledgements

- Thank you to my advisor Dr. Byrne and his lab and Texas A&M AgriLife Research

Evaluation of seedling and adult-plant stripe, leaf, and stem rust resistance in the A-genome diploid relatives of wheat

Buket Şahin[1,2,3], Duane Wilson[2,3], John Raupp[2,3], Robert Bowden[2,4], Jesse Poland[2,3,5], and Bernd Friebe[2,3]

1.Regional Cereal Rust Research Center, Aegean Agricultural Research Institute, 35660 Menemen, Izmir, Turkiye. 2.Department of Plant Pathology, Kansas State University, Manhattan, Kansas 66502, USA. 3.Wheat Genetics Resource Center (WGRC), Kansas State University, Manhattan, Kansas 66502, USA. 4.USDA/ARS/Hard Winter Wheat Genetics Research Unit, Kansas State University, Manhattan, KS 66506, USA. 5.Center for Desert Agriculture, King Abdullah University of Science and Technology, Thuwal 23955, Saudi Arabia

INTRODUCTION

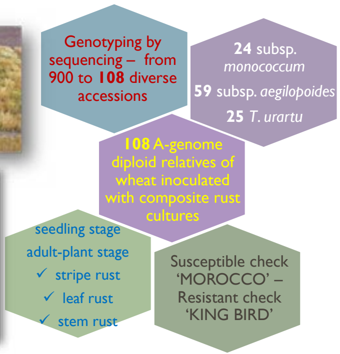
- Einkorn wheat, which was domesticated approximately 10,000 years ago, has long been seen as a possible source of important genetic diversity for wheat breeding.
- The three rust diseases, stripe, leaf, and stem are among the most serious biotic threats to wheat production in the world. Rust diseases cause significant losses in yield and quality. The most effective strategy to control rust diseases is the development of the resistant cultivars.

Figure 1 – Geographic distribution of A-genome wheat species in the WGRC gene bank.

OBJECTIVES

- The A-genome mini core set of the Wheat Genetics Research Center (WGRC) was selected using different selection parameters, such as genetic diversity, geographical distribution, phenotypic variation, and population structure. This study is aimed at
- Identifying stripe, leaf, and stem rust seedling and adult-plant resistance in a set of A-genome wheat species.

MATERIALS & METHODS



Genotyping by sequencing – from 900 to **108** diverse accessions

24 subsp. *monococcum*
59 subsp. *aegilopoides*
25 *T. urartu*

108 A-genome diploid relatives of wheat inoculated with composite rust cultures

seedling stage
adult-plant stage
✓ stripe rust
✓ leaf rust
✓ stem rust

Susceptible check 'MOROCCO' – Resistant check 'KING BIRD'

RESULTS

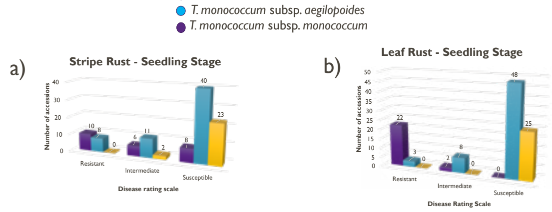


Figure 2 – Distribution of infection types of 108 accessions evaluated for seedling resistance stripe rust (a) and leaf rust (b) under greenhouse conditions. Stakman scale (0-4 infection type) was used for seedling evaluations and Resistant: from ; to 1+, Intermediate: from 2- to 2+, Susceptible: from 3- to 4.

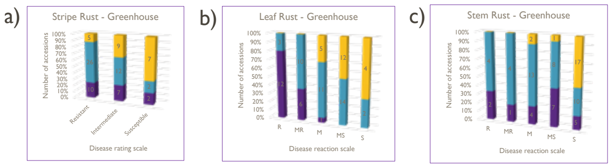


Figure 3 – Frequency of distribution of 80 accessions evaluated for stripe rust (a), leaf rust (b), and stem rust (c) at the adult-plant stage under greenhouse conditions.

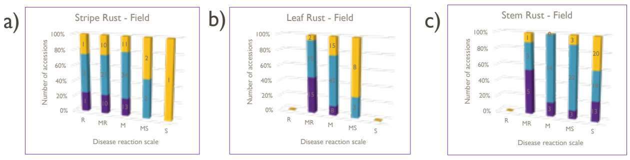


Figure 4 – Frequency of distribution of 108 accessions evaluated for stripe rust (a), leaf rust (b), and stem rust (c) at the adult-plant stage under field conditions. Cobb scale was used for adult plant evaluations in the field and R: Resistant, MR: Moderately Resistant, M: Moderate, MS: Moderately Susceptible, S: Susceptible.

CONCLUSION

- The diploid A-genome wheat species have been identified as an important and valuable genetic resource. We evaluated a diverse set of A-genome accessions, and several accessions with single and multiple resistance to different rusts were identified, which can be the starting point of using these genes in wheat improvement.

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buket.sahin@tarimorman.gov.tr
https://arastirma.tarimorman.gov.tr/etae/Personel
@RegionalRust

THE EFFECTS OF OPEN SUN DRYING AND OVEN DRYING ON DRIED FRUIT QUALITY CHARACTERISTICS IN PURE LINES DEVELOPED FOR DRIED PEPPER BREEDING

G. Elif Vural[1] Cafer Doğanlar[1] Ali Kün[1] Sinan Zengin[1] Özge Meral[1] Ş. Şebnem Ellialtıoğlu[2]

[1]Antalya Tarım Hybrid Seeds Co. Antalya, Türkiye
[2]Ankara University Technopolis, Doqutech Academy Llc. Co., Ankara, Türkiye

ABSTRACT

Pepper (*Capsicum annuum* L.), which originates from the Americas and is grown in every region of the world, has great commercial importance, both fresh and processed (spices, tomato paste and pickles). Türkiye is the fourth largest producer country in world pepper production with a share of 7.3%. 8.17% of this production is dry pepper and 91.83% is fresh pepper production. Although dried pepper has a unique and important place in traditional Turkish cuisine, our high quality commercial F1 hybrid varieties developed for this purpose are almost non-existent. For this reason, variety development studies have been accelerated in recent years. It is also common to dry pepper as a whole, in addition to processing it as powdered pepper and chili pepper. Developing varieties suitable for all these uses will fill an important deficiency in the pepper seed market in our country and especially in other countries where the culinary culture is similar.

For this purpose, as a result of the studies carried out for the collection of local dried pepper genotypes in our country and the development of pure lines with the folded haploidy (Doubled Haploid : DH) technique, more than 200 pure lines were examined. 20 pepper lines selected from among them formed the plant material of this research. For 20 DH dried pepper lines, trials were set up in 3 different locations, Adana / Tuzla, Antalya / Serik and Manisa / Turgutlu, and three harvests were made during the growing period. Harvest time was determined by measuring the amount of water-soluble dry matter during harvest periods. Conventional drying method (under 50% shade net in sunny weather) and drying method in tunnel type ovens were used to determine the drying performance of DH pepper lines whose pre-washing and filtration processes were completed. Drying processes were carried out in İzmir / Kemalpaşa location. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. Fruit samples obtained in each harvest were taken to drying tests. In these tests, the values of parameters such as moisture, ash, oil, pH, processing efficiency, sensory evaluations (color, juiciness, crispness, flavor, general acceptability) and dry product shelf life were calculated separately for both sun drying and oven drying methods. In dry product shelf life studies, the samples dried in the sun and in the oven were stored at room conditions (24°C). On the 32nd, 48th and 64th days, the weights, color parameters (L*(brightness), a*(redness), b*(blueness)), shape and taste characteristics of the products were evaluated as packed in vacuum and normal bags. As a result of the evaluations, prominent pure lines were determined in order to develop hybrid varieties for drying.

***Figure 1.** Examples of DH varieties used in the study.*

***Figure 2.** Sun drying process*

MATERIAL AND METHODS

PREWASH PROCESS

Pepper samples were immersed in 50 ppm sodium hypochlorite, 1% citric acid, 1.5% salt solutions and distilled water for 10 minutes.

SUN DRYING METHOD

After the pre-washing processes were applied, the peppers were both cut into longitudinal strips and taken on a rope as a whole, and hung in the bunk bed system to dry in the sun under 50% shade tulle.

OVEN DRYING METHOD

Pepper samples, which were pre-washed, were dried using a tunnel-type drying oven. The products are taken into trays specially produced for the use of the drying oven and after placing them on the carriage with shelves, the process is carried out in the drying room. There are special equipment in the system to circulate the air in the tray and the dryer. In this type of dryer, the air is heated by the heater in the device, no hot air is taken from outside. The products are left to dry for 6-8 hours at 60-70°C. With the hot air flow that is continuously heated and introduced into the system, moisture formation is prevented and the problems that may occur in the quality of the products are minimized.

QUALITY ANALYSIS, DRY PRODUCT SHELF LIFE AND SENSORY EVALUATION

Before drying, the amount of water-soluble dry matter in fresh fruits was determined using the "Milwaukee MA871" digital refractometer device. Moisture, ash (TS EN ISO 2171, 2010), oil (TS EN ISO 11085, 2016), pH and process efficiency analyzes were made and calculated as % values. The moisture determination of the samples weighing 3-5 g from the dried products was made using the "Sartorius MA 45" device.

In the dry product shelf life analyzes, the samples dried both in the oven and in the sun were also evaluated according to their storage status in vacuum packages and non-vacuum packages. Color values were measured using a "Spektropen" hand-held colorimeter according to the CIE (International Commission on Illumination) color system .

In the dried and stored samples, on the 32nd, 48th and 64th days, analyzes such as shape and taste for the evaluation of the shelf life of the dry product, color, juiciness, crispness, flavor and general acceptability were performed for sensory evaluation. 10 trained panelists were used to evaluate these features. Scoring from 1 to 9 was made. 1 point was used as the worst value and 9 points as the best value

***Figure 3.** Oven and sun dried samples. Products stored in vacuum and non-vacuum packages were used in dry product shelf life analyses.*

***Figure 4**. Prewash process*

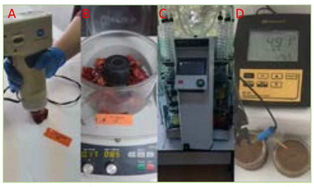

***Figure 5.** Equipment for analysis. A. Spectropen colorimeter; B. Blender: for grinding products; C. used for oil determination; D. pH meter*

ORIGIN	Open Field Code	Moisture (%)		Ash (%)		Oil (%)		Water-soluble dry matter (%)		pH		Process efficiency (%)	
		Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying
Azatlı Biberi/M.Kemalpaşa	1A	4,92	5,95	6,62	7,52	5,24	5,32	5,9	1,1	5,2	5,4	10,0	11,1
Azatlı Biberi/M.Kemalpaşa	1B	4,87	5,91	5,55	7,55	6,01	6,09	4,4	1,8	5,1	5,3	9,7	10,3
Azatlı Biberi/M.Kemalpaşa	1C	4,98	6,01	6,32	8,23	5,83	6,12	6,5	1,2	5,3	5,5	11,0	12,4
Yerel genotip/Bozdoğan	3	5,62	6,65	5,78	6,68	5,16	5,23	2,8	1,6	5,4	6,0	9,4	10,1
Çukurören Biberi/Bilecik	6	5,34	6,37	7,96	8,52	6,62	6,71	5,4	3,4	5,2	5,7	13,7	15,3
Çorum kurutmalık/Çorum	17B	5,89	6,92	7,85	8,97	6,13	6,24	6,8	1,9	5,6	6,3	9,8	11,2
Maraş Biberi/Maraş	26A	3,64	4,99	8,84	10,05	5,87	5,91	7,3	3,2	5,2	5,2	15,3	16,6
Acı Dolmalık Biber/Maraş	28	6,39	7,42	7,91	9,81	7,36	7,43	5,2	2,5	5,5	5,9	14,9	16,0
Tatlı Üçburun/Manisa	31	4,56	5,59	5,46	6,23	5,21	5,25	3,5	1,5	5,1	5,3	6,4	9,8
Kale Biberi/Denizli	45	3,91	4,92	6,04	7,03	5,92	6,01	3,4	1,6	5,2	5,4	8,6	9,3
Dolmalık/Oğuzeli	46	3,98	4,67	5,63	7,56	5,63	5,73	5,6	2,7	6,1	6,7	9,1	9,1
Sivaslı Biberi/Uşak	67	4,88	5,91	6,52	7,82	4,98	5,04	5,4	1,2	5,9	6,5	9,8	10,1
Tokat İstek Tip/Tokat	74B	6,37	7,42	8,01	8,51	5,45	5,56	3,1	2,2	5,7	5,8	10,7	12,3
Elazığ Biberi/Elazığ	76	6,23	7,88	7,99	8,46	6,78	6,82	4,2	1,0	5,2	5,2	12,0	13,7
Urfa/Harran	Erkenci Urfa	5,76	7,27	8,79	9,14	6,92	7,02	3,6	3,3	5,3	5,4	12,3	14,7
Urfa/Harran	Geçci Urfa	5,23	6,26	8,36	9,56	6,68	6,73	4,6	1,6	5,2	5,3	11,3	13,3
Hatay/Samandağ	Samandağ Tip I	3,96	5,95	8,91	9,91	6,16	6,27	7,7	4,3	5,3	5,7	14,0	15,3
Hatay/Samandağ	Samandağ Tip II	4,67	5,71	8,62	9,65	6,37	6,41	6,8	3,8	5,4	5,8	10,5	12,5
Hatay/Samandağ	Samandağ Tip III	4,58	5,64	8,73	9,74	6,54	6,61	6,9	3,3	5,5	5,5	11,7	13,9
Tokat	Tokat Dolma	6,73	7,76	7,36	9,78	6,67	6,64	6,0	1,1	5,9	6,3	13,5	14,6

***Table 1.** Post-Drying SÇKM, Moisture, Ash, Oil, pH and Process Efficiency Parameters*

RESULTS

In the moisture, ash and process efficiency evaluations, higher values were observed in the samples dried by oven drying method. The amount of water-soluble dry matter in oven-dried samples has an average of 60% lower values compared to sun-dried samples. No significant difference was observed in oil measurements.

There were no significant differences in dry product shelf-life weight measurements for any variation of sun-dried and oven-dried samples. There is a partial high value in the oven drying method, based on the vacuum packages only at the end of the 64th day in the figure values.

In the first measurements, the taste values were close to each other, but the taste values of the samples dried in the oven on the 64th day were higher than those dried in the sun.

In color analysis, the L* and a* values of the samples dried by oven drying method and stored in vacuum and non-vacuum packages are higher than sun drying. A low L* value represents the black color of the product. b* values show a certain increase according to the measurement dates.

ORIGIN	Open Field Code	Colour		Juiciness		Crispness		Taste		General Acceptability	
		Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying
Azatlı Biberi/M.Kemalpaşa	1A	7	8	6	7	9	8	8	8	8	8
Azatlı Biberi/M.Kemalpaşa	1B	7	7	6	7	9	8	8	8	8	8
Azatlı Biberi/M.Kemalpaşa	1C	8	9	7	8	9	7	7	8	7	7
Yerel genotip/Bozdoğan	3	8	9	6	7	6	6	7	7	7	8
Çukurören Biberi/Bilecik	6	8	9	8	9	9	8	9	9	9	9
Çorum kurutmalık/Çorum	17B	5	6	7	7	6	6	8	7	8	8
Maraş Biberi/Maraş	26A	8	8	8	8	7	7	8	8	9	7
Acı Dolmalık Biber/Maraş	28	9	9	9	8	8	7	9	9	9	9
Tatlı Üçburun/Manisa	31	7	8	7	7	6	6	8	8	7	7
Kale Biberi/Denizli	45	6	7	6	6	7	7	6	7	7	7
Dolmalık/Oğuzeli	46	7	7	7	7	6	6	8	8	7	7
Sivaslı Biberi/Uşak	67	8	8	8	9	7	7	7	7	8	8
Tokat İstek Tip/Tokat	74B	9	9	9	9	8	8	7	7	8	8
Elazığ Biberi/Elazığ	76	8	8	8	8	7	7	8	8	8	8
Urfa/Harran	Erkenci Urfa	8	7	8	8	9	8	9	9	9	9
Urfa/Harran	Geçci Urfa	7	7	8	8	8	7	7	7	8	7
Hatay/Samandağ	Samandağ Tip I	7	8	7	7	9	8	9	9	9	9
Hatay/Samandağ	Samandağ Tip II	7	7	7	8	9	8	8	7	8	8
Hatay/Samandağ	Samandağ Tip III	6	7	6	6	9	8	9	9	9	8
Tokat	Tokat Dolma	8	8	9	8	7	7	8	8	9	9

***Table 2**. Sensory evaluations. (Scored from 1 to 9; 1: lowest score, 9: highest score*

ORIGIN	Open Field Code	Dry Product Shelf Life											
		Colour											
		32nd Day											
		L*				a*				b*			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed
Azatlı Biberi/M.Kemalpaşa	1A	19,83	19,81	21,35	21,34	16,31	16,29	17,31	17,29	11,44	11,45	13,08	13,05
Azatlı Biberi/M.Kemalpaşa	1B	13,69	13,68	15,89	15,87	15,52	15,49	16,34	16,33	10,34	10,32	11,89	11,87
Azatlı Biberi/M.Kemalpaşa	1C	14,30	14,27	19,38	19,36	9,07	9,03	9,19	9,12	11,67	11,68	12,85	12,84
Yerel genotip/Bozdoğan	3	12,81	12,80	15,85	15,84	16,30	16,29	17,56	17,54	13,42	13,38	15,61	15,62
Çukurören Biberi/Bilecik	6	66,01	66,02	68,26	68,23	35,40	35,41	36,57	36,58	49,64	49,63	52,33	52,37
Çorum kurutmalık/Çorum	17B	29,40	29,36	33,14	33,12	18,15	18,14	19,64	19,62	5,97	7,93	9,26	19,24
Maraş Biberi/Maraş	26A	31,94	31,97	35,46	35,42	17,41	17,39	18,31	18,32	16,41	16,44	18,78	18,75
Acı Dolmalık Biber/Maraş	28	49,87	49,85	51,63	51,62	41,19	41,23	42,43	42,41	39,86	39,87	40,14	40,12
Tatlı Üçburun/Manisa	31	22,38	22,37	23,76	23,74	18,34	18,32	19,36	19,35	11,29	11,27	13,46	13,45
Kale Biberi/Denizli	45	34,64	34,61	36,74	36,72	28,51	28,48	29,89	29,88	19,65	19,66	21,31	21,32
Dolmalık/Oğuzeli	46	23,59	23,58	27,64	27,63	16,58	16,54	18,86	18,84	12,07	12,03	13,31	13,35
Sivaslı Biberi/Uşak	67	44,90	44,91	48,94	48,91	36,53	36,52	37,54	37,55	29,65	29,64	31,1	31,08
Tokat İstek Tip/Tokat	74B	39,10	39,06	44,05	44,03	29,82	29,83	30,31	30,29	20,12	20,08	21,4	21,37
Elazığ Biberi/Elazığ	76	23,76	23,79	28,41	28,37	24,2	24,19	26,46	26,47	24,58	24,61	25,32	25,30
Urfa/Harran	Erkenci Urfa	55,74	55,72	60,15	60,14	47,63	47,61	48,66	48,34	41,75	40,78	43,65	43,64
Urfa/Harran	Geçci Urfa	36,54	36,53	39,67	39,65	28,84	28,88	29,32	29,31	27,38	27,36	28,14	28,15
Hatay/Samandağ	Samandağ Tip I	33,65	33,62	37,61	37,59	33,78	33,76	35,13	35,12	23,93	23,94	26,3	26,34
Hatay/Samandağ	Samandağ Tip II	32,85	32,84	35,67	35,66	30,17	30,14	32,51	32,49	20,87	20,83	21,65	21,63
Hatay/Samandağ	Samandağ Tip III	37,47	37,48	43,81	43,78	29,91	29,87	31,87	31,88	17,64	17,63	19,23	19,21
Tokat	Tokat Dolma	28,81	28,77	37,28	37,26	21,50	21,49	24,75	24,73	19,15	19,11	20,46	20,44

ORIGIN	Open Field Code	48th Day											
		L*				a*				b*			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed
Azatlı Biberi/M.Kemalpaşa	1A	20,12	20,13	23,63	23,61	17,35	17,32	18,35	18,32	13,43	13,45	14,81	14,79
Azatlı Biberi/M.Kemalpaşa	1B	14,01	13,99	16,05	16,03	17,03	16,98	17,75	17,74	11,42	11,37	13,65	13,64
Azatlı Biberi/M.Kemalpaşa	1C	15,2	15,21	20,27	20,24	11,25	11,23	12,33	12,34	14,34	14,30	14,40	14,38
Yerel genotip/Bozdoğan	3	13,13	13,09	17,61	17,62	18,42	18,41	19,25	19,23	15,63	15,66	16,83	16,84
Çukurören Biberi/Bilecik	6	67,23	67,22	69,04	69,03	36,38	36,44	37,01	37,02	50,32	50,39	53,65	53,61
Çorum kurutmalık/Çorum	17B	30,12	30,08	34,22	34,24	19,45	19,38	21,51	21,54	10,05	10,02	10,67	10,69
Maraş Biberi/Maraş	26A	32,01	32,04	36,52	36,51	19,43	19,44	19,58	19,55	19,71	19,63	20,19	20,18
Acı Dolmalık Biber/Maraş	28	50,15	50,16	52,56	52,54	43,09	43,06	43,04	43,01	42,65	42,67	42,41	42,39
Tatlı Üçburun/Manisa	31	23,88	23,86	24,13	24,11	20,21	20,16	19,69	19,68	13,61	13,56	15,63	15,62
Kale Biberi/Denizli	45	35,22	35,23	37,75	37,72	29,49	29,47	32,86	32,87	22,64	22,60	23,57	23,55
Dolmalık/Oğuzeli	46	24,15	24,11	28,44	28,45	18,40	18,39	21,17	21,15	14,49	14,52	16,47	16,48
Sivaslı Biberi/Uşak	67	45,1	45,09	49,33	49,32	37,50	37,56	39,63	39,64	30,97	31,04	33,11	33,07
Tokat İstek Tip/Tokat	74B	40,28	40,24	45,31	45,33	32,21	32,14	33,75	33,78	22,9	22,87	22,83	22,85
Elazığ Biberi/Elazığ	76	24,29	24,32	29,42	29,41	28,95	28,96	28,68	28,65	27,41	27,33	26,31	26,30
Urfa/Harran	Erkenci Urfa	56,02	56,03	61,39	61,37	49,35	49,32	49,37	49,34	42,92	42,94	44,84	44,82
Urfa/Harran	Geçci Urfa	37,13	37,11	40,16	40,14	31,19	31,14	31,44	31,43	30,01	29,96	30,25	30,24
Hatay/Samandağ	Samandağ Tip I	34,55	34,56	38,25	38,22	57,80	37,78	36,75	36,76	25,13	25,09	27,98	27,96
Hatay/Samandağ	Samandağ Tip II	35,91	35,87	36,77	36,78	32,07	32,06	33,23	33,21	24,13	24,16	24,36	24,37
Hatay/Samandağ	Samandağ Tip III	39,43	39,42	44,3	44,29	31,46	31,52	32,10	32,11	19,61	19,68	22,77	22,73
Tokat	Tokat Dolma	29,07	29,03	38,64	38,66	23,54	23,47	26,40	26,43	20,87	20,84	21,59	21,61

ORIGIN	Open Field Code	64th Day											
		L*				a*				b*			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed
Azatlı Biberi/M.Kemalpaşa	1A	19,24	20,73	23,60	23,62	16,32	17,97	19,95	19,94	11,21	14,15	15,41	15,38
Azatlı Biberi/M.Kemalpaşa	1B	11,35	14,59	18,63	17,42	14,32	17,63	18,34	18,32	10,34	12,07	14,50	14,49
Azatlı Biberi/M.Kemalpaşa	1C	16,87	15,81	20,51	20,49	16,37	11,88	15,24	15,23	16,49	15,01	15,89	15,87
Yerel genotip/Bozdoğan	3	16,47	13,69	18,62	18,64	17,46	19,06	21,04	21,05	19,34	16,36	18,36	18,32
Çukurören Biberi/Bilecik	6	56,00	67,82	69,48	69,44	29,35	37,09	39,66	39,63	32,62	51,09	55,69	55,71
Çorum kurutmalık/Çorum	17B	29,04	30,68	35,03	35,02	19,00	20,03	25,44	25,40	19,31	9,72	11,25	11,23
Maraş Biberi/Maraş	26A	29,34	32,64	38,15	38,16	20,78	20,09	21,31	21,33	20,75	20,33	22,34	22,36
Acı Dolmalık Biber/Maraş	28	46,31	50,76	52,99	53,01	39,56	43,71	46,54	46,53	39,65	43,37	44,66	44,63
Tatlı Üçburun/Manisa	31	23,45	24,46	26,48	26,47	17,56	20,81	22,08	22,06	12,57	14,26	16,46	16,45
Kale Biberi/Denizli	45	33,74	35,83	38,94	38,92	29,37	30,12	34,69	34,68	11,42	23,30	5,65	25,63
Dolmalık/Oğuzeli	46	21,01	24,71	29,30	29,32	11,32	19,04	24,33	24,34	18,76	15,22	18,15	18,11
Sivaslı Biberi/Uşak	67	40,32	45,69	50,09	50,05	24,59	38,21	43,31	43,28	38,43	31,74	33,87	33,89
Tokat İstek Tip/Tokat	74B	35,98	40,84	46,13	46,12	23,65	32,79	35,93	35,89	28,74	23,57	23,33	23,31
Elazığ Biberi/Elazığ	76	22,78	24,92	34,82	34,83	30,48	29,61	30,19	30,21	29,65	28,03	28,20	28,22
Urfa/Harran	Erkenci Urfa	49,36	56,63	61,87	61,89	34,23	49,97	51,70	51,69	42,11	43,64	46,62	46,59
Urfa/Harran	Geçci Urfa	24,68	37,71	42,24	42,23	30,26	31,79	33,77	33,75	24,63	30,66	32,69	32,68
Hatay/Samandağ	Samandağ Tip I	27,85	35,16	39,21	39,19	31,43	38,43	38,94	38,93	21,07	25,79	29,65	29,63
Hatay/Samandağ	Samandağ Tip II	37,67	36,47	37,06	37,08	30,74	32,71	36,49	36,50	22,08	24,86	25,95	25,91
Hatay/Samandağ	Samandağ Tip III	34,78	40,02	45,35	45,31	31,10	32,17	33,49	33,46	19,98	20,38	23,97	23,99
Tokat	Tokat Dolma	22,16	29,63	39,48	39,47	22,63	24,12	29,95	29,91	14,37	21,54	22,50	22,48

***Table 3**. 32, 48 and 64. Day Dry Product Shelf Life Evaluations (Color; L*, a*, b*)*

ORIGIN	Open Field Code	Dry Product Shelf Life											
		32nd Day											
		Weight (kg)				Shape				Taste			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed
Azatlı Biberi/M.Kemalpaşa	1A	0,098	0,101	0,129	0,131	8	8	8	8	7	9	8	8
Azatlı Biberi/M.Kemalpaşa	1B	0,092	0,094	0,109	0,110	8	8	7	8	8	8	7	6
Azatlı Biberi/M.Kemalpaşa	1C	0,098	0,099	0,112	0,115	7	8	8	8	8	9	7	7
Yerel genotip/Bozdoğan	3	0,041	0,042	0,063	0,065	7	5	7	7	8	7	7	7
Çukurören Biberi/Bilecik	6	0,172	0,176	0,195	0,199	9	9	9	9	8	9	8	8
Çorum kurutmalık/Çorum	17B	0,066	0,068	0,086	0,087	8	7	7	7	9	8	8	7
Maraş Biberi/Maraş	26A	0,038	0,041	0,059	0,061	7	6	7	7	7	6	8	9
Acı Dolmalık Biber/Maraş	28	0,287	0,289	0,320	0,321	8	9	7	8	8	8	7	7
Tatlı Üçburun/Manisa	31	0,083	0,084	0,099	0,102	8	6	6	5	7	6	4	5
Kale Biberi/Denizli	45	0,095	0,096	0,121	0,123	8	7	7	7	6	6	5	5
Dolmalık/Oğuzeli	46	0,104	0,108	0,131	0,135	7	6	7	6	8	7	7	6
Sivaslı Biberi/Uşak	67	0,232	0,234	0,256	0,257	9	8	7	7	7	8	8	8
Tokat İstek Tip/Tokat	74B	0,243	0,246	0,264	0,266	8	7	8	8	9	8	7	7
Elazığ Biberi/Elazığ	76	0,185	0,187	0,206	0,207	8	8	7	8	9	8	6	7
Urfa/Harran	Erkenci Urfa	0,193	0,194	0,213	0,216	8	8	9	9	9	9	7	7
Urfa/Harran	Geçci Urfa	0,121	0,122	0,014	0,142	7	7	7	8	7	8	6	7
Hatay/Samandağ	Samandağ Tip I	0,150	0,154	0,017	0,174	8	8	8	8	8	9	8	8
Hatay/Samandağ	Samandağ Tip II	0,100	0,102	0,131	0,132	6	6	7	6	9	8	7	7
Hatay/Samandağ	Samandağ Tip III	0,112	0,113	0,137	0,138	8	7	8	8	8	9	7	7
Tokat	Tokat Dolma	0,264	0,268	0,297	0,298	9	8	8	8	8	9	7	6

ORIGIN	Open Field Code	48th Day											
		Weight (kg)				Shape				Taste			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed
Azatlı Biberi/M.Kemalpaşa	1A	0,094	0,099	0,123	0,122	8	8	7	7	7	8	7	7
Azatlı Biberi/M.Kemalpaşa	1B	0,090	0,092	0,102	0,099	8	7	7	6	7	8	7	6
Azatlı Biberi/M.Kemalpaşa	1C	0,089	0,097	0,113	0,112	9	8	8	8	6	7	8	7
Yerel genotip/Bozdoğan	3	0,082	0,083	0,064	0,062	6	5	6	6	6	6	6	5
Çukurören Biberi/Bilecik	6	0,165	0,174	0,181	0,178	8	9	7	8	6	8	8	8
Çorum kurutmalık/Çorum	17B	0,062	0,066	0,071	0,069	8	7	7	6	7	8	6	5
Maraş Biberi/Maraş	26A	0,035	0,039	0,057	0,055	7	6	8	7	5	6	8	8
Acı Dolmalık Biber/Maraş	28	0,282	0,287	0,3	0,299	9	9	8	8	4	8	7	7
Tatlı Üçburun/Manisa	31	0,080	0,082	0,098	0,095	6	5	6	5	5	6	3	4
Kale Biberi/Denizli	45	0,086	0,094	0,119	0,118	8	7	6	7	6	6	6	5
Dolmalık/Oğuzeli	46	0,105	0,106	0,123	0,121	7	6	7	5	7	7	7	6
Sivaslı Biberi/Uşak	67	0,223	0,232	0,25	0,247	8	8	7	7	7	8	8	7
Tokat İstek Tip/Tokat	74B	0,240	0,244	0,252	0,250	7	7	8	8	6	7	5	6
Elazığ Biberi/Elazığ	76	0,181	0,185	0,194	0,192	8	8	9	8	7	7	8	7
Urfa/Harran	Erkenci Urfa	0,187	0,192	0,198	0,197	9	8	9	9	7	8	8	7
Urfa/Harran	Geçci Urfa	0,118	0,120	0,141	0,138	8	7	8	8	8	8	8	6
Hatay/Samandağ	Samandağ Tip I	0,144	0,152	0,162	0,161	7	8	9	8	7	8	7	8
Hatay/Samandağ	Samandağ Tip II	0,099	0,100	0,114	0,112	6	5	7	5	6	7	6	6
Hatay/Samandağ	Samandağ Tip III	0,102	0,111	0,12	0,117	8	7	7	7	7	8	8	8
Tokat	Tokat Dolma	0,262	0,266	0,276	0,274	8	8	8	8	8	8	7	7

ORIGIN	Open Field Code	64th Day											
		Weight (kg)				Shape				Taste			
		Sun Drying		Oven Drying		Sun Drying		Oven Drying		Sun Drying		Oven Drying	
		Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed	Vacuum Packed	Non Vacuum Packed
Azatlı Biberi/M.Kemalpaşa	1A	0,092	0,095	0,117	0,118	5	7	8	7	5	6	6	7
Azatlı Biberi/M.Kemalpaşa	1B	0,089	0,088	0,097	0,095	6	7	7	6	4	6	6	5
Azatlı Biberi/M.Kemalpaşa	1C	0,102	0,093	0,109	0,108	5	4	8	7	4	5	7	6
Yerel genotip/Bozdoğan	3	0,098	0,079	0,062	0,058	4	5	6	5	2	4	5	4
Çukurören Biberi/Bilecik	6	0,189	0,170	0,172	0,174	7	8	6	6	4	7	8	8
Çorum kurutmalık/Çorum	17B	0,102	0,062	0,066	0,065	5	7	7	6	5	6	4	4
Maraş Biberi/Maraş	26A	0,076	0,035	0,065	0,051	6	6	8	7	3	4	7	7
Acı Dolmalık Biber/Maraş	28	0,299	0,283	0,273	0,295	5	8	7	7	6	7	7	7
Tatlı Üçburun/Manisa	31	0,053	0,078	0,093	0,092	2	4	5	4	2	4	5	4
Kale Biberi/Denizli	45	0,072	0,090	0,119	0,115	5	6	6	6	5	4	4	4
Dolmalık/Oğuzeli	46	0,143	0,102	0,114	0,116	4	5	5	5	4	5	4	5
Sivaslı Biberi/Uşak	67	0,345	0,228	0,241	0,240	7	8	7	6	5	6	6	6
Tokat İstek Tip/Tokat	74B	0,256	0,240	0,245	0,246	8	7	8	7	4	5	6	6
Elazığ Biberi/Elazığ	76	0,257	0,181	0,190	0,188	7	7	7	7	6	6	7	7
Urfa/Harran	Erkenci Urfa	0,118	0,188	0,192	0,191	7	8	8	8	6	7	8	7
Urfa/Harran	Geçci Urfa	0,124	0,116	0,138	0,134	6	7	7	7	5	6	7	6
Hatay/Samandağ	Samandağ Tip I	0,165	0,148	0,152	0,154	8	7	7	7	6	7	6	8
Hatay/Samandağ	Samandağ Tip II	0,089	0,096	0,109	0,108	4	5	5	4	5	5	4	5
Hatay/Samandağ	Samandağ Tip III	0,090	0,107	0,115	0,114	3	6	6	6	5	6	7	6
Tokat	Tokat Dolma	0,275	0,262	0,273	0,271	6	7	8	7	5	6	7	6

***Table 4.** Dry Product Shelf Life Evaluations of 32, 48 and 64 Days (Weight. Shape, Taste)*

DISCUSSION

It has been observed that the oven-dried samples have a certain superiority in shape, flavor, weight, moisture, pH, process efficiency and color evaluations. In both drying methods, it is seen that the products stored in vacuum packages are not affected by the quality losses that occur in the products over time, or are relatively less affected.
In the traditional drying method, adverse conditions such as toxic risks due to air pollution, the inability to dry the product uniformly and the direct contact of the sun's rays with the dried product may occur. These negativities cause both the prolongation of the drying process and the loss of quality in the product (Ayhan, A., 2005). As the temperature increases during the drying process, the drying time of the samples becomes shorter (6-8 hours). The reason for this is that as the temperature increases, the existing moisture in the pepper samples is removed faster. **Products dried in a controlled environment are cleaner than products dried under the sun, and there is less change in natural color, taste, odor and nutrients at the end of drying.** With controlled drying, the product is protected from adverse environmental conditions (Ertekin et al., 2001; Yaldız, 2001).

In this study, ideal genotypes were determined on the basis of plant and fruit observations and analysis results after drying (high dry matter amount in pepper, low moisture, high ash, low oil, ideal dry product shelf life). **Tokat Dolma and genotypes number 28 were determined as suitable for stuffing and drying studies. 6, 26A, Erkenci Urfa and Samandağ type I genotypes were determined as suitable for slicing and drying studies.**

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COMPARISON OF PURE LINES DEVELOPED FOR DRIED EGGPLANT BREEDING IN TERMS OF QUALITY CHARACTERISTICS

Cafer Doğanlar[1] **Gülsün Elif Vural**[1] **Sinan Zengin**[1] **Tuncay Karakuş**[1] **Ş. Şebnem Ellialtıoğlu**[2]

[1]Antalya Tarım Hybrid Seeds Co. Antalya, Türkiye
[2]Ankara University Technopolis, Doqutech Academy Llc. Co., Ankara, Türkiye

ABSTRACT

Türkiye ranks fourth in world vegetable production. According to the 2021 data of the Turkish Statistical Institute (TUIK), Türkiye produced approximately 32 million tons of vegetables. Eggplant constitutes 2.6% of vegetable production. Türkiye is the fourth largest producer country in world eggplant production after China, India and Egypt. Although eggplant is mostly used for fresh consumption, its use takes its place in Turkish cuisine with different recipes thanks to processing techniques such as canning and drying. Especially in the gastronomic culture of certain geographical regions such as Southeastern Anatolia, the position of eggplant, both fresh and dried, is very important. Dried eggplant production is common in provinces such as Adana and Gaziantep, and the drying process is traditionally done outdoors and under the sun. However, there are technologically developed technical drying methods as an alternative to this traditional method.

In the studies populations were collected from the regions in Türkiye where the local dried eggplant genotypes were grown, and doubled haploid (DH) pure lines were obtained from them by anther culture. By examining criteria such as yield, fruit characteristics and growth strengths, 44 eggplant pure lines were selected among more than 200. The material of the study presented here consists of 44 selected DH eggplant lines. Harvesting was done three times during the growing period in 3 different locations, Adana / Tuzla, Antalya / Serik and Manisa / Turgutlu. Before drying, the amount of water-soluble dry matter in the fruits was determined with a refractometer device. Conventional drying method (under 50% shade net in sunny weather) and drying method in tunnel type ovens were used to determine the drying performance of DH eggplant lines whose pre-washing and filtration processes were completed. Drying processes were carried out in İzmir / Kemalpaşa location. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. In the oven drying process, the samples were laid on the baking tray and kept at 65°C for 6 hours, and the drying processes were completed. Various drying tests were applied to dried fruit samples. In these tests, the values of parameters such as moisture, ash, oil, pH, processing efficiency, sensory evaluations (color, juiciness, crispness, flavor, general acceptability) and dry product shelf life were calculated separately for both sun drying and oven drying methods. In dry product shelf-life studies, the samples dried in the sun and in the oven were stored at room conditions (24°C). On the 32nd, 48th and 64th days, the weights, color parameters (L*(brightness), a*(redness), b*(blueness)), shape and taste characteristics of the products were evaluated as packed in vacuum and normal bags. At the end of the study, prominent dried eggplant DH lines were determined to be used for test hybridizations.

Figure 1. *Prewash process*

Figure 2. *Sun drying process*

MATERIAL AND METHODS

PREWASH PROCESS

Eggplant samples were immersed in 50 ppm sodium hypochlorite, 1% citric acid, 1.5% salt solutions and distilled water for 10 minutes.

SUN DRYING METHOD

After the pre-washing processes were applied, the eggplants were both cut into longitudinal strips and taken on a rope as a whole, and hung in the bunk bed system to dry in the sun under 50% shade tulle.

OVEN DRYING METHOD

Eggplant samples, which were pre-washed, were dried using a drying oven. The products are taken into trays specially produced for the use of the drying oven and after placing them on the carriage with shelves, the process is carried out in the drying room. There are special equipment in the system to circulate the air in the tray and the dryer. In this type of dryer, the air is heated by the heater in the device, no hot air is taken from outside. The products are left to dry for 6-8 hours at 60-70°C. With the hot air flow that is continuously heated and introduced into the system, moisture formation is prevented and the problems that may occur in the quality of the products are minimized.

QUALITY ANALYSIS, DRY PRODUCT SHELF LIFE AND SENSORY EVALUATION

Before drying, the amount of water-soluble dry matter in fresh fruits was determined using the "Milwaukee MA871" digital refractometer device. Moisture, ash (TS EN ISO 2171, 2010), oil (TS EN ISO 11085, 2016), pH and process efficiency analyzes were made and calculated as % values. The moisture determination of the samples weighing 3-5 g from the dried products was made using the "Sartorius MA 45" device. In the dry product shelf life analyzes, the samples dried both in the oven and in the sun were also evaluated according to their storage status in vacuum packages and non-vacuum packages. Color values were measured using a "Spektropen" hand-held colorimeter according to the CIE (International Commission on Illumination) color system .

In the dried and stored samples, on the 32nd, 48th and 64th days, analyzes such as shape and taste for the evaluation of the shelf life of the dry product, color, juiciness, crispness, flavor and general acceptability were performed for sensory evaluation. 10 trained panelists were used to evaluate these features. Scoring from 1 to 9 was made. 1 point was used as the worst value and 9 points as the best value.

ORIGIN LOCATION	Open Field Code	Water Soluble Dry Matter %	Moisture %		Ash %		Oil %		pH %		Process efficiency %	
			Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying
O.P. Variety	Adana dolmalık	3,3	4,93	5,93	6,25	7,95	0,35	0,43	4,75	4,99	1,9	3,0
O.P. Variety	Topan 374	3,5	4,83	6,03	6,35	7,87	0,26	0,33	4,68	4,94	2,0	3,5
O.P. Variety	Antep Dolmalık	4,1	5,03	6,33	6,55	7,25	0,37	0,44	4,95	5,29	1,7	4,7
Manisa / Turgutlu	D-048	3,2	5,63	7,13	5,48	8,05	0,25	0,31	5,01	5,26	2,9	5,8
Manisa / Turgutlu	D-051	3,5	5,43	6,53	6,35	7,45	0,16	0,29	5,15	5,38	2,7	7,1
Manisa / Turgutlu	D-057	3,4	4,93	6,13	5,85	7,05	0,47	0,54	4,65	4,86	2,1	5,1
Manisa / Turgutlu	D-0146	3,9	5,93	7,13	6,85	8,05	0,35	0,41	4,58	4,84	2,9	6,5
Adana Topan Patlıcan	D-055A	3,7	5,43	6,93	6,35	7,85	0,36	0,46	4,89	5,13	2,5	6,0
Adana Topan Patlıcan	D-074A	4,2	5,63	6,53	6,55	7,45	0,37	0,49	4,52	4,77	2,9	6,7
Adana Topan Patlıcan	D-079A	4,3	5,23	6,23	6,15	7,25	0,45	0,46	5,14	5,37	2,7	6,1
Adana Topan Patlıcan	D-A89	4,5	5,43	6,63	6,35	7,55	0,36	0,38	4,78	4,92	2,2	4,3
Adana Topan Patlıcan	D-A90	3,5	6,03	7,33	6,95	8,25	0,37	0,45	4,69	4,93	2,7	4,5
Aydın / Nazilli	D-114	4,2	6,13	7,63	7,05	8,55	0,35	0,42	4,85	5,07	1,8	3,6
Aydın / Nazilli	D-234	4,5	6,53	7,63	7,45	8,55	0,46	0,53	4,79	5,00	5,7	7,3
Aydın / Nazilli	D-235	4,1	5,73	6,93	6,65	7,85	0,37	0,43	5,10	5,32	2,0	4,0
Manisa / Salihli	D-570	4,6	7,41	8,61	7,85	9,05	0,45	0,50	5,14	5,42	6,9	8,8
Manisa / Salihli	D-571	4,5	7,63	9,13	8,55	10,05	0,46	0,53	4,75	4,99	6,6	9,1
Manisa / Salihli	D-576	4,2	7,03	7,93	7,95	8,85	0,37	0,43	4,98	5,24	1,6	4,7
Burdur / Merkez	D-580	3,2	7,93	8,93	8,85	9,95	1,74	1,69	5,15	5,41	6,5	8,2
Burdur / Merkez	D-581	4,8	5,12	6,98	8,55	9,75	1,73	1,75	5,11	5,36	2,8	6,7
Gaziantep / Oğuzeli	D-582	3,6	7,63	8,93	8,55	9,85	0,37	0,38	4,78	5,12	1,7	4,4
Gaziantep / Oğuzeli	D-584	3,4	5,63	7,13	6,55	8,05	0,45	0,47	4,85	5,06	1,6	6,5
Gaziantep / Oğuzeli	D-586	4,2	5,63	6,73	6,55	7,65	1,62	1,74	4,47	4,73	4,5	6,9
Gaziantep / Oğuzeli	D-587	4,3	5,43	6,63	6,35	7,55	0,37	0,44	4,58	4,82	1,6	3,7
Gaziantep / Oğuzeli	D-588	4,1	5,73	6,93	6,65	7,85	0,35	0,42	4,67	4,92	1,8	3,0
Gaziantep / Oğuzeli	D-590	4,2	7,83	9,33	8,75	9,25	1,67	1,71	4,85	5,08	7,2	8,4
Artvin / Hopa	D-628	3,6	6,33	7,23	7,25	8,15	0,37	0,42	5,01	5,15	1,3	2,4
Artvin / Hopa	D-630	4,1	6,43	7,43	7,35	8,45	0,25	0,32	4,95	5,19	4,8	6,3
Adana / Akkapı	D-632	4,6	5,33	6,53	6,25	7,45	0,36	0,42	4,87	5,09	2,2	3,7
Adana / Akkapı	D-634	4,6	5,63	6,93	6,55	7,85	0,47	0,57	4,52	4,73	2,2	3,5
Doğal Topan Patlıcan	D-635	4,4	5,43	6,93	6,35	7,85	0,35	0,47	4,73	4,95	2,3	3,9
Doğal Topan Patlıcan	D-637	4,5	5,03	6,13	5,95	7,05	0,46	0,47	4,52	4,80	1,7	3,2
Doğal Topan Patlıcan	D-638	4,1	5,43	6,63	6,35	7,55	0,47	0,49	5,12	5,36	2,3	3,8
Doğal Topan Patlıcan	D-639	4,2	5,23	6,43	6,15	7,35	0,35	0,43	4,83	5,09	2,4	4,9
Adana / Sarıçam	D-640	4,6	5,33	6,83	6,25	7,75	0,21	0,28	4,76	5,10	1,7	3,5
Adana / Sarıçam	D-641	4,5	6,33	7,23	7,25	8,15	0,27	0,34	4,98	5,23	2,2	4,1
Adana / Sarıçam	D-644	4,2	5,33	6,33	6,25	7,35	0,35	0,41	4,91	5,25	2,0	2,8
Adana / Sarıçam	D-645	4,1	5,43	6,63	6,35	7,55	0,46	0,51	4,81	5,02	2,3	3,9
Adana / Sarıçam	D-646	3,7	5,83	7,13	6,75	8,05	0,37	0,44	4,76	5,02	2,3	4,1
Adana / Sarıçam	D-647	4,6	5,73	7,23	6,65	8,15	0,35	0,41	4,65	4,89	2,4	4,2
Adana / Sarıçam	D-648	4,8	5,63	6,73	6,55	7,65	0,36	0,46	4,66	4,91	2,3	4,2
Balıkesir / Bandırma	D-650	4,9	5,43	6,63	6,35	7,55	0,37	0,49	4,68	4,91	1,7	4,3
Urfa / Mezra	D-654	4,5	5,86	7,85	7,65	8,85	1,76	1,69	4,71	4,85	7,2	9,8
Urfa / Mezra	D-655	4,7	5,98	8,14	7,85	9,35	1,65	1,78	4,69	4,93	7,7	10,4

Table 1. *Post-Drying SÇKM, Moisture, Ash, Oil, pH and Process Efficiency Parameters*

Figure 3. Oven and sun dried samples. Products stored in vacuum and non-vacuum packages were used in dry product shelf life analyses.

ORIGIN LOCATION	Open Field Code	Sensory Evaluation (1-9) points									
		Colour		Juiciness		Crispness		Taste		General Acceptability	
		Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying	Sun Drying	Oven Drying
O.P. Variety	Adana dolmalık	7	8	7	8	7	8	8	8	7	8
O.P. Variety	Topan 374	9	8	8	9	9	9	9	8	9	9
O.P. Variety	Antep Dolmalık	6	7	7	8	7	8	7	7	7	8
Manisa / Turgutlu	D-048	7	8	7	9	8	8	8	8	8	8
Manisa / Turgutlu	D-051	8	8	8	8	8	8	8	8	8	8
Manisa / Turgutlu	D-057	7	7	7	7	8	9	8	7	8	8
Manisa / Turgutlu	D-0146	8	8	7	8	9	9	9	8	8	8
Adana Topan Patlıcan	D-055A	8	9	8	9	7	8	7	9	8	9
Adana Topan Patlıcan	D-074A	7	8	7	8	6	8	6	8	7	8
Adana Topan Patlıcan	D-079A	6	8	7	7	7	9	7	8	7	8
Adana Topan Patlıcan	D-A89	9	8	8	8	8	8	8	8	8	8
Adana Topan Patlıcan	D-A90	6	7	7	9	7	9	7	7	7	8
Aydın / Nazilli	D-114	9	8	9	8	9	9	9	8	9	8
Aydın / Nazilli	D-234	8	9	8	7	8	8	8	9	8	8
Aydın / Nazilli	D-235	7	8	7	8	8	8	8	8	8	8
Manisa / Salihli	D-570	8	7	7	9	7	9	8	7	8	8
Manisa / Salihli	D-571	7	9	8	8	8	8	8	9	8	9
Manisa / Salihli	D-576	6	8	6	7	7	9	7	8	7	8
Burdur / Merkez	D-580	6	7	8	8	8	8	8	7	8	8
Burdur / Merkez	D-581	7	8	8	9	9	9	9	8	8	9
Gaziantep / Oğuzeli	D-582	5	7	6	8	6	8	7	7	6	8
Gaziantep / Oğuzeli	D-584	5	6	5	8	6	7	6	6	6	7
Gaziantep / Oğuzeli	D-586	6	7	7	9	7	9	8	7	7	8
Gaziantep / Oğuzeli	D-587	6	7	7	9	8	8	8	7	7	8
Gaziantep / Oğuzeli	D-588	6	8	7	9	7	7	7	8	7	8
Gaziantep / Oğuzeli	D-590	7	7	8	8	8	8	8	7	8	8
Artvin / Hopa	D-628	6	4	7	7	7	9	8	4	7	6
Artvin / Hopa	D-630	8	7	8	8	9	8	9	7	9	8
Adana / Akkapı	D-632	7	8	7	9	7	7	7	8	7	8
Adana / Akkapı	D-634	6	7	7	8	8	8	8	7	7	8
Doğal Topan Patlıcan	D-635	7	9	8	7	7	7	8	9	8	8
Doğal Topan Patlıcan	D-637	8	9	8	8	9	8	9	9	9	9
Doğal Topan Patlıcan	D-638	6	8	7	9	8	8	8	8	7	8
Doğal Topan Patlıcan	D-639	6	8	7	8	7	8	7	8	7	8
Adana / Sarıçam	D-640	8	7	8	7	9	7	8	7	8	7
Adana / Sarıçam	D-641	6	8	6	9	7	8	7	8	7	8
Adana / Sarıçam	D-644	8	7	8	8	9	7	9	7	9	7
Adana / Sarıçam	D-645	8	8	8	7	8	9	8	8	8	8
Adana / Sarıçam	D-646	9	9	8	8	9	8	9	9	9	9
Adana / Sarıçam	D-647	8	8	8	9	9	7	9	8	9	8
Adana / Sarıçam	D-648	7	7	8	8	7	8	8	7	8	8
Balıkesir / Bandırma	D-650	6	8	8	7	7	9	8	8	7	8
Urfa / Mezra	D-654	8	7	8	8	9	8	9	7	9	8
Urfa / Mezra	D-655	8	8	8	9	9	9	9	8	9	9

Table 4*. Sensory evaluations. (Scored from 1 to 9; 1: lowest score, 9: highest score*

RESULTS

The highest dry matter content of 4.9% was obtained from the genotype D-650. The lowest dry matter amount was determined as 3.2% in genotypes D-048 and D-580.

Genotype D-048, which has the lowest ash ratio in the sun drying method, showed a 46% difference in the oven drying method and the ash ratio was determined at the level of 8.05%. These results show that the products dried with the oven drying method are represented with higher ash values than the sun drying method.

The average pH value of eggplant samples was 4.82 in the sun drying method, and this value was determined as 5.06 with an increase of 5% in the oven drying method. The highest pH value was 5.15 (D-580) and the lowest pH value was 4.47 (D-586) in the sun-dried samples. Cakir, I. (2000) reported the pH value of eggplant as 4.5 in his study and this value supports our study data.

The average oil content of sun-dried products is 0.5%. On average, 17% higher oil levels were detected in the oven-dried samples. On the other hand, Nisa et al. (2009) found the oil values in different samples as 0.88%, 0.66%, 0.50% and 0.72% in their study. Our results seem consistent with Nisa's reports.

To determine the processing efficiency (Total dried fruit (kg) / Total fresh fruit (kg) x100) formulation was used and calculated as a % value. The most significant difference between the post-drying processes examined in sun and oven drying methods was observed in the process efficiency. It was determined that the processing efficiency of the samples dried with the oven drying method was 93% higher on average compared to the sun drying method.

In the evaluations of the 32nd day, the weight values of the samples stored in non-vacuum packages were 80-90% higher in the oven drying method compared to the sun drying method. Although this difference decreased relatively in the 48th and 64th day evaluations, it was determined that the samples dried in the oven had higher values.

The samples dried in the sun and stored in vacuum packs scored higher than the samples in non-vacuum packs. High values were observed in both variations of the oven drying method.

The L* values of the sun-dried samples were lower than the oven-dried samples in all three different evaluation stages. The decrease in the L* value is important as it indicates that the color of the product changes towards black. Bayraktaroğlu Urun, G. (2015) reported that the L values of the samples dried by the convective and infrared-convective combined method were higher than the sun drying method. Bayraktaroğlu's study and the data of this study support each other.

Figure 4. *Examples of DH varieties used in the study.*

Figure 5. *Equipment for analysis. A. used for oil determination; B. Spectropen colorimeter; C. Milwaukee MA871 refractometer device; D. Etüv; E. pH meter.*

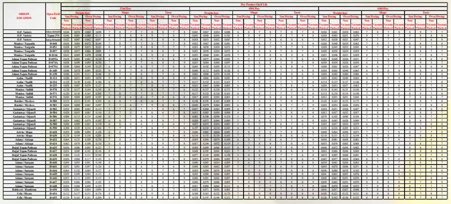

Table 2. *Shelf Life Evaluations of 32, 48 and 64 Days (Weight. Shape, Taste)*

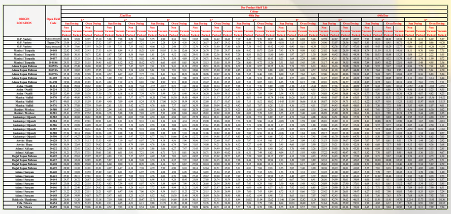

Table 3. *32, 48 and 64. Day Dry Product Shelf Life Evaluations (Color; L*, a*, b*)*

DISCUSSION

It was determined that the oven drying method represented higher values compared to the sun drying method in the evaluations of oil, ash, pH and process efficiency from the post-drying processes. The samples, which were dried in the oven and in the sun, were evaluated separately according to their preservation in vacuum and non-vacuum packages. In the dry product shelf life (Weight, Taste, Shape and Color) evaluations, it was determined that the samples stored in vacuum packages had higher values than the samples stored in non-vacuum packages in both drying methods. In sensory evaluations, the scores made by the panelists are partially higher in the samples dried with the oven drying method, although there is no big difference.

In the traditional drying method, adverse conditions such as toxic risks due to air pollution, the inability to dry the product uniformly and the direct contact of the sun's rays with the dried product may occur. These negativities cause both the prolongation of the drying process and the loss of quality in the product (Ayhan, A., 2005). As the temperature increases during the drying process, the drying time of the samples becomes shorter (6-8 hours). The reason for this is that as the temperature increases, the existing moisture in the eggplant samples is removed faster. In the oven drying method, it is applied with higher temperatures than the sun drying method. With the oven drying method, the environmental problems encountered in the sun drying method have been eliminated and a drying process in which factors such as temperature and hygiene are under the control of the applicator has been provided.

In this study, ideal genotypes were determined on the basis of plant and fruit observations and analysis results after drying (high dry matter amount in eggplant, low moisture, high ash, low oil, ideal dry product shelf life). D-644 and D-632 coded genotypes were found to be suitable for slicing drying studies, and D-654 and D-581 coded genotypes were found to be suitable for slicing drying studies.

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School of Agriculture, Policy and Development

Use of Convolutional Neural Network Model for Detection Of *Puccinia striiformis* f. sp. *tritici* and Comparing Disease Severity Monitoring Methods on Scanned Images

[1]Aegean Agricultural Research Institute, Menemen-Izmir/TÜRKİYE
[2]School of Agriculture, Policy and Development, University of Reading, Reading-United Kingdom

Turan Gökberk ÇON[1], Alexey Mikaberidze[2]

INTRODUCTION

- In the management of *Puccinia striiformis* f. sp. *tritici* measurement of conditional severity is necessary for breeding research. In addition, the detection of the disease is necessary to determine the time and method of management.
- This study enlights two parts. In the first part, a Convolutional Neural Network (CNN) model that can detect the yellow rust (YR) disease is created and tested. The second part focuses on the use of ImageJ software-based ZymoMacro, and the HSB color space method to measure disease severity on scanned images.

OBJECTIVES.

- What is the success of the CNN-based detection model in distinguishing between yellow rust and infected leaf images in theory and in test plants?
- Is it possible to detect yellow rust disease by using Zymomacro_Scanner_V2.1.1 macro or HSB color space adjustment on ImageJ software? Is it possible to increase the success of the macro by changing settings?

MATERIALS & METHODS

- **Study one: Convolutional Neural Network based YR detection model**

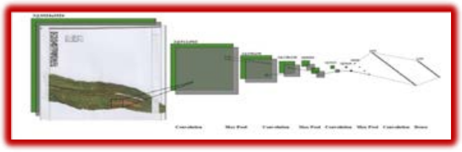
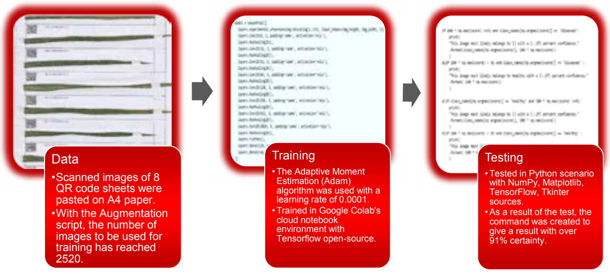


Figure 1. LeNet style diagram of CNN Rust Detection model



Data
- Scanned images of 8 QR code sheets were pasted on A4 paper.
- With the Augmentation script, the number of images to be used for training has reached 2520.

Training
- The Adaptive Moment Estimation (Adam) algorithm was used with a learning rate of 0.0001.
- Trained in Google Colab's cloud notebook environment with Tensorflow open-source.

Testing
- Tested in Python scenario with NumPy, Matplotlib, TensorFlow, Tkinter sources.
- As a result of the test, the command was created to give a result with over 91% certainty.

- **Study two: comparison of severity measurement methods**

Ground Truth

*The areas with pustules were selected with the ImageJ selection tool.

*The area size of the pustules, the number of pustules, and the rate of pustules on the leaf were determined.Compared with other methods

Zymomacro Scanner

*The severity of yellow rust was measured in the macro with the CIE LAB color space without making any changes.

*Background noise reduction is aimed by changing CIE LAB values. It is aimed to make the selection of pustules easier by increasing the selection size.

HSB Colour Space Adjustments

*Hue, saturation and Brightness have been selected at the value where pustules can be selected most easily.

*The ImageJ process settings are set to remove background noises less than 3 pixels.

RESULTS.

- **Study one: CNN Model training**

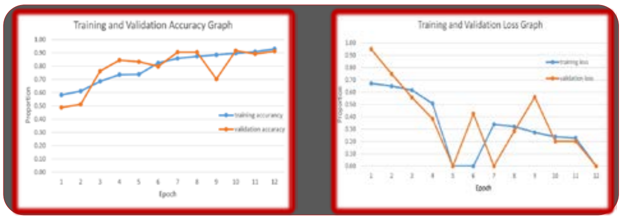


Figure 2. Training validation accuracy and validation loss graphs

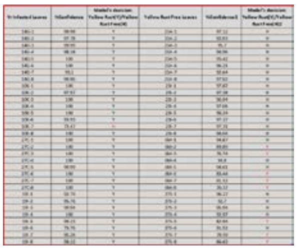


Table 1. CNN model test results

* The model performed 86% correct prediction success in 64 leaf images in which it was tested.

* While it is on average 96% sure in his correct predictions, it is on average 79% sure in his incorrect predictions.

* When it checked the leaves without yellow rust disease, it was estimated correctly with an average of 95% accuracy.

- **Study two: HSB Colour Space Adjustments**

* Correlation ratio was determined for the measurement of pustule number (0.77) and the ratio of pustule areas to leaf (0.72).

* HSB color space measurement method found more and larger pustules than actual values. Figure 3 compares the number and area of pustules on a single leaf.

Figure 3. Comparison of ground truth and colour threshold adjustments

ZymoMacro Scanner

* While the macro scanner measuring with the default macro settings showed a correlation of 0.69, this rate was increased to 0.85 with the edited macro settings.

CONCLUSIONS

The YR detection model's accuracy rate rose up to 91% validation at the end of the training. The model performed a promising prediction success on the test materials.

HSB color space measurements were found to be unsuccessful in measuring the severity of yellow rust disease. The ZymoMacro Scanner, which normally defaulted to Septoria tritici Blotch disease, did not give good results when used for yellow rust, but the changes made to the macro settings that increased the correlation rate are promising to create a specific macro for yellow rust.

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For more information contact with
turangokberk.con@gmail.com

Infected with ToBRFV (Tomato Brown Rugose Fruit Virus) Disinfectant Efficacy Trial on Tomato Plants

Özlem Demir, Damla Ulusoy
Anamas Seed Company, Serik, Antalya

Infected with ToBRFV (Tomato Brown Rugose Fruit Virus) Disinfectant Efficacy Trial on Tomato Plants

Özlem DEMİR, Damla ULUSOY
Anamas Seed Company, Antalya-Turkey
Auothor for correspondence: ozsimdem@gmail.com

In this study, it was aimed to determine the effectiveness of disinfectants against ToBRFV under controlled and farmer conditions. A trial of 184 plants was established using the Samyeli F1 cultivar of Anamas company with the randomized blocks trial design. Planting was done according to a random block design, one infected plant per block. To ensure that these plants are infected with ToBRFV; When the tomatoes reached the true two-leaf stage, mechanical inoculation was applied 3 times with the "soft sponge pad" method at regular intervals with the "ToBRFV-Ant-Tom: MT107885" isolates we have. In the evaluation of the effectiveness of disinfectants in farmer conditions against ToBRFV; Disinfectants with active substances such as 0.5-1% HCl, 11.2% Hydrogen peroxide and silver-containing (300 cc/100 lt) were found to be effective. It has been observed that these disinfectants, which are applied from above with hand sprayers, have a preventive effect on the spread of the virus in an uncontaminated greenhouse as a result of regular use once a week. It has been observed that these disinfectants, which are applied from above with hand sprayers, have a preventive effect on the spread of the virus in the greenhouse as a result of regular use once a week. At the end of the experiment, the plants in the greenhouse were subjected to molecular tests. The bands seen in the gel electrophoresis show that the disinfectants are not effective on the related virus agent and the plants are 100% infected with ToBRFV. In addition to the early diagnosis of the presence of virus diseases and the removal of diseased plants from the greenhouse, routine hygiene procedures in the greenhouse are also very important. For this reason, disinfectant studies to prevent ToBRFV from infecting tomato production areas come to the fore. As a result, it has been observed that disinfectants, which are effective in controlled conditions, delay the epidemic in the greenhouse but do not prevent ToBRFV infection in studies conducted under farmer conditions.

Keywords: Disinfectant, Tomato, ToBRFV, Virus infection

Increasing Breeding Studies Efficiency by Supporting Plant Breeding Software with Data

Canseri Bozkuş, Prof. Dr. M. Ziya Fırat, Prof.Dr. Deniz Ümit Uluşar, Prof.Dr. Nedim MUTLU

Beautifulmind Yazılım ARGE, Plant Breeding Software, ANTALYA TEKNOKENT

Biometri and Genetics /Zootechny Department-Agricultural Engineering, Akdeniz University, Antalya

Software Engineering, Akdeniz University, Antalya

Agricultural Biotechnology, Akdeniz University, Antalya

Author for correspondence (canseri@beautifulmind.com.tr)

Abstract (kısaltılmış)

Plant breeding is the art and science of improving important agricultural plants for the benefit of humankind. Breeders work to make our food, fiber, forage, and industrial crops more productive, nutritious, more resistant to diseases, better phenotype and better genotype. Breeders reduce the pesticide use and they protect the environment by developing resistant varieties. The most important thing that breeders do is developing crops which has good yield to be able to feed expanding human population in the world.

In today agricultural business plant breeding have become quite difficult. One of important reason is companies not pay enough attention to data management, storing and analysis by software. Using software determines and shows whether the breeding strategies are effective or not. It can be obtain more succesfull hybrids than usual by using the plant observation, resistance and genetic information datas. Plant breeding software is important to make plant breeders work easier and make seed busines sustainable.

Evaluation of Genetic Relationship among Different Soybean Cultivars in Two Regions of Mazandaran and Alborz Provinces

Parastoo Majidian[1], Bahram Masoudi[2]

[1]Crop and Horticultural Science Research Department, Mazandaran Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO), Sari, Iran.

[2]Seed and Plant Improvement Department, Seed and Plant Improvement Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

Abstract

In order to determine genetic diversity among new soybean germplasm, 119 and 124 new soybean imported genotypes with four control samples (Saman, Katol, Kosar and Sahar) in Alborz province and (Telar, Sari, Wiliams and Sahar) in Mazandaran province were investigated based on augmented design project respectively. The genotypes studied were assessed according to different agronomical and morphological traits such as days to flowering, days to maturation, plant height, number of node, number of secondary branch, number of null pod, number of pod in whole plant/secondary branch, number of seed per plant, seed yield per plant, plant biological yield, seed oil and protein percentage. The results showed that the highest amount of phenotypic variation coefficient were related to seed yield (84.23), number of null/infertile pod (75.8) and number of seed in plant (75.28) and the lowest amount of phenotypic variation coefficient belonged to protein percentage (3.96), oil percentage (4.27) and days to full maturation (9.33) in Alborz province. In Mazandaran province, the highest amount of phenotypic variation coefficient were belonged to seed yield (89.93), number of null pod (85.9), number of pod in secondary branch (74.3) and the lowest one was considered as oil percentage (2.99), protein percentage (3.25) and days to full maturation (14.01). The mean comparison of seed yield indicated that the genotypes of Clark curly pubesce, GH 66-6-14, Seedmakers 1-E, Delmar and Valder had the highest seed yield in Alborz province. In addition, the genotypes of Alaric, Mediachev, Chico, Telar and Dakota No. 3338 exhibited the most seed yield per plant in Mazandaran province. Thus, it could be suggested that the superior genotypes compared to control samples had capability to make use of them in further breeding programs.

Keywords:

New soybean genotypes, morphological and agronomical traits, genetic relationships

Introduction

One of plant breeding method is to import cultivar from foreign countries as cultivar introduction approach if they are compatible with the climate cultivated and have superiority than control sample, they will choose for plantation in a wide area. The basic elements of any breeding program are to find out diversity and selection, which can be achieved by choosing the right traits in terms of genetic diversity in the population. Scientific studies and investigations in breeding programs in the field of genetic diversity provide the possibility to increase our knowledge of the studied species, prevent genetic erosion and finally help to collect and protect plant species.

Soybean is considered as valuable source of oil and protein. Its seed contain 20-25% of oil and 30-45% protein which have influenced by environmental parameters and type of plant genotype (Malek et al., 2014). Although the Soybean varieties availability in our country has optimum diversity in terms of qualitative and quantitative traits, it is significant to have acknowledge about the existence soybean cultivars′ genetic potential for expansion its cultivation and production in consideration to economic status of soybean throughout Iran. In fact, it is possible to perform more breeding programs in order to breed soybean with the assessment of agronomical traits, especially the traits have important role in soybean yield (Carter et al., 2004).

Numerous studies have been carried out in relation to soybean genetic diversity by various researchers throughout the World. For example, the morphological variation of 205 soybean genotypes were evaluated in China based on morphological parameters (Zhang et al., 2006). In addition, all genotypes studied were grouped in three clusters as the first group contained 149 genotypes with less growth period and height, as well as less node number and secondary branch. The second group consisted of 54 genotypes with more growth period and high height, less 1000 seed weight and more pod and seed per pod. And the third group contained two genotypes with maturity group of four and with the highest growth period, plant height and 1000 seed weight. In other study, 54 cultivars and pure imported soybean lines were investigated according to augmented design method with three control samples of Williams, Kosar and Sahar (Majidian et al., 2019). The result of cluster analysis grouped samples into two main clusters and four sub-cluster based on resistance of cultivars to phythophthora disease following by introduction of cultivars Amcor 98, Beeson 80, Winchester, Graham and Colfax as superior in seed yield and phothophthora resistance.

In the other research, the soybean genetic diversity was evaluated based on morphological molecular markers showing that the significant difference between the genotypes studied. Moreover, three out of 14 markers of microsatellite markers amplified 42 alleles and PIC ranged from 0.55 to 0.88 (Khatab et al., 2016). Considering to the importance of soybean plant, the aim of this study was to evaluate the genetic diversity of different soybean genotypes in accordance with morphological traits in two regions of Mazandaran and Alborz provinces.

Materials and methods

In this study, 119 genotypes (collected from plant gene bank of Australia) in Alborz province with control samples of Saman, Kosar and Sahar and 124 genotypes (collected from plant gene bank of Germany) in Mazandaran province with control samples of Telar, Sari, Williams, and Sahar were evaluated based on augmented design with six blocks. Each genotype was cultivated on a two meter line with block height of 15 meter. The morphological traits studied contained number of days to flowering and maturation, node number, secondary branch number, pod number, seed number per pod, oil and protein percentage, seed yield and biological yield. In order to estimate the traits studied, five plants were selected from middle of each line randomly. The variance analysis of seed yield of control samples were calculated based on blocks design and mean comparison through LSR method using SAS version 15. The cluster analysis of the genotypes studied was performed using ward method to recognize genetic relationships following by determination of appropriate parental cultivars for further breeding programs.

Results and discussion

Based on the obtained results, the highest phenotypic variation related to seed yield per plant (84.23), infertile pod number (75.8) and seed number per plant (75.28), and the less phenotypic variation related to protein percentage (3.96), oil percentage (4.27) and days to full maturation (9.33) in Alborz province (Table 1). In Mazandaran province, the highest phenotypic variation belonged to seed yield (89.93), infertile pod (85.9), pod number in secondary branch (74.3), and the less phenotypic variation were observed in oil percentage (2.99), protein percentage (3.25), and days to full maturity (14.01) (Table 1).

Table 1. The statistical parameters of different traits among the studied genotypes in Alborz and Mazandaran provinces

CV%	Mean	Maximum	Minimum	Region	The studied trait
19.61	63.51	89	25	Alborz	Days to flowering
23.15	27.11	48.00	20.00	Mazandaran	
17.76	77.59	99	39	Alborz	Days to pod production
18.04	47.98	74.00	37.00	Mazandaran	
14.57	92.03	115	55	Alborz	Days to start seed filling
17.90	60.71	88.00	42.00	Mazandaran	
11.31	116.95	147	83	Alborz	Days to full seed filling
15.09	76.52	113.00	57.00	Mazandaran	
10.72	124.45	155	88	Alborz	days to start maturation
15.66	92.47	136.00	63.00	Mazandaran	
9.33	135.75	165	101	Alborz	Days to full maturation
14.01	117.54	149.00	65.00	Mazandaran	
22.65	98.67	189.8	42.8	Alborz	Height (cm)
32.85	67.95	125	20.67	Mazandaran	
18.73	17.69	26.6	10.75	Alborz	Node number
35.39	8.80	21	3.67	Mazandaran	
48.94	7.80	17.4	2.08	Alborz	Secondary branch number
44.60	2.82	5.67	0.00	Mazandaran	
38.63	24.84	62	6.8	Alborz	Pod number in secondary branch
74.30	22.98	102.00	0.00	Mazandaran	
39.92	38.24	95.6	14.6	Alborz	Pod number per plant
50.98	48.07	180.11	7.00	Mazandaran	
75.80	2.03	13.2	0	Alborz	Infertile pod number
85.9	2.29	9.67	0.00	Mazandaran	
75.28	93.66	350.4	11.8	Alborz	Seed number per plant
46.87	136.97	312.00	18.67	Mazandaran	
48.59	96.15	250	30.34	Alborz	Biological yield per plant (gr)
42.42	46.81	150	21	Mazandaran	
84.23	12.69	57.28	0.42	Alborz	Seed yield per plant (gr)
89.93	12.64	87	3.82	Mazandaran	
4.27	21.29	23.5	19.52	Alborz	Oil percentage
2.99	21.47	22.9	20.15	Mazandaran	
3.96	32.85	35.37	30.2	Alborz	Protein percentage
3.25	37.56	39.94	34.82	Mazandaran	

Among 119 genotypes studied in Alborz province, 89 genotypes reached to maturity stage and grouped in four clusters. Based on cluster analysis of Alborz province, the first, second, third and fourth clusters had 23, 49, 8 and 9 genotypes, respectively (Table 2, Figure 1). In Mazandaran province, the cluster analysis grouped the studied genotypes in four clusters which contained 56, 30, 25, 13 genotypes from the first and fourth clusters respectively (Table 3, Figure 2). The results of clustering showed that the genotypes of GH66-6-14 (29), Valder (78), GH66-6-6 (30), Seedmakers 1-E (66), Lee late (43) and Clark curly pubesce (8) were superior in consideration to yield and its parameters in Alborz province. In Mazandaran province, the superior genotypes were considered as Mediachev (18), Dornburger Stamm 106 (85), ISz 11 (111), Dakota No. 3338 (88).

Introduction of new superior germplasm to expand soybean cultivation needs to discover the characteristics of soybean parents by aim of transferring new gene to next generation. In similar study, the morphological traits and genotype variation of soybean were evaluated based on frequency of phenotypic and genotypic variation resulting the creation of eight clusters which the cluster number one and eight had the highest genetic variation. The cluster number eight had two genotypes of GM-6 and GM-27 with high seed yield that could be used in further breeding programs (Shilpasshree et al., 2021. In the other research, the new superior soybean varieties were found based on diverse morphological characters such as pod height, pod thickness, and pod wide. The result indicated that the longest young and mature pod was found in MLGG 0582 and the thickest young pod was observed in MLGG 0583, while the widest was reported by MLGG 0617 (Ningsih et al., 2019). The other research reported on characterization of morphological traits and estimation of genetic relationships for intermediate soybean collected from South Korea based on cluster analysis (Vu et al., 2013). In accordance with 11 agronomical traits, three clusters were created as cluster I included 20 *G. max*, cluster II included 12 intermediate, and cluster III included 22 *G. soja* and four intermediate lines. These phenotypic and genetic data suggest that the intermediate type lines could be distinguished between *G. max* and *G. soja* lines. However, the intermediate type could not be classified as a new species (Vu et al., 2013). Since soybean has self-fertility higher than 98% and low genetic diversity among its cultivars, it is of great importance to determine various soybean genotypes with different maturity groups to estimate their potential for further crossing programs and their cultivation compatibility and stability in different regions

Table 2. The agronomical parameters of soybean genotypes studied in Alborz province

Cluster no.	Genotype name	Seed yield	Plant height	Oil%	Protein%	Days to flowering	Days to maturity	Cluster no.	Genotype name	Seed yield	Plant height	Oil%	Protein%	Days to flowering	Days to maturity
1	Bienville	26.49	113.2	20.51	33.21	81	158	2	Nessen	7.61	87.67	20.08	32.17	68	140
1	Bossier	0.42	95	20.76	33.46	80	165	4	Noir 1	12.04	42.8	20.69	33.16	25	104
2	Bragg	22.52	103.2	21.57	32.19	61	133	2	Ogden	12.29	92.6	21.55	33.81	60	129
1	Braxton	6.23	110.2	20.31	32.55	74	141	2	Palooka	4.91	130	20.07	33.26	70	131
2	Cajeme	8	114.6	21.51	31.24	68	139	1	Parana	2.71	96.2	20.05	33.27	70	147
2	Centennial	5.25	102.8	21.28	32.56	65	140	4	Pella	28.93	91.2	22.8	31.69	30	113
1	CES 414	7.75	111.4	19.58	35.37	81	161	2	Pershing	2.26	53.2	21.25	34.46	58	131
3	Clark curly pubesce	57.28	97.2	21.3	34.72	44	139	2	PF 72-317	13.38	94.4	21.87	30.54	62	132
2	Clark EE	16.58	95.2	22.6	32.28	61	139	2	Pickett	9.99	90.8	22.37	33.84	60	141
4	Clarke Ete	19.86	96.6	20.28	34.8	52	116	4	Pomona	15.49	74.8	22.24	30.79	46	113
3	Coker 338	33.19	92.5	22.92	30.9	61	124	4	Provar	18	83	21.63	34.31	30	111
2	Curtis	8.29	81.4	20.96	33.51	67	128	1	R-315	1.14	110.2	21.94	32.69	68	145
2	Dare	7.2	79.8	22.41	31.38	59	139	2	Ransom	9.86	101.4	21.16	33.57	62	132
1	DEH 124234	1.2	132.67	19.52	34.29	83	145	2	RH69-3	7.31	95.8	21.79	31.84	68	128
2	DEH 124242	4.89	122.2	21.48	33.61	69	140	2	Rillito	2.68	103.2	22.12	31.66	70	135
3	Delmar	37.07	95.8	22.52	30.43	52	113	1	Roanoke	4.94	118.8	21.14	33.66	70	147
1	Delsta	9.51	104.2	20.05	33.28	89	140	2	Rokusun LFP	10.09	108	22.27	32.53	61	140
2	Deltapine 345	4.8	89.2	20.58	33.02	58	131	2	Rokusun NP	9.76	83.4	21.19	33.79	74	139
2	Dickie	4.87	88.8	21.7	30.2	66	130	1	Sanalona-77	8.67	104	20.46	32.42	78	147
4	Disoy	6.55	50.2	21.33	33.79	37	101	3	Seedmakers 1-E	43.6	97.5	21.53	34.86	35	113
2	Douglas	11.22	63.2	22.89	32.73	51	116	1	Seln 13	10.92	128.8	20.06	33.24	69	152
1	Dowling	4.82	92.83	20.07	32.34	82	149	1	Semgreen	9.02	94.6	20.02	33.78	68	145
2	Dyer	6.09	92.2	21.71	30.62	60	129	1	Semgreen No.2	8.83	62.33	20.43	34.26	74	155
2	Dyer A	7.04	87.6	21.01	32.04	61	127	2	SHW 17	12.42	80	21.96	33.74	73	145
1	Eyre	7.42	106.6	20.3	34.41	87	147	1	Sojo 4	24.66	111	20.29	34.6	76	143
1	Florida	2.49	152.2	20.55	31.63	77	147	2	Stonewall	6.24	97	21.28	33.5	70	132
2	Foster	5.02	107	21.24	31.89	68	147	2	Tamazula S-80	11.2	106.8	21.09	30.94	69	137
2	Gail	9.58	87.8	21.55	32.38	64	140	2	Tracy	13.43	79.2	21.65	33.84	72	154
3	GH 66-6-14	51.28	189.8	20.35	34.86	62	117	2	Triton	12.58	105	22.34	30.61	59	130
3	GH 66-6-6	33.14	128.6	20.98	34.61	61	132	2	UQ 19	3.12	112.4	21.01	32.1	70	142
1	Gordon	6.78	103.5	20.66	34.04	67	147	2	UQ 36	10.4	117	22.19	32.47	69	137
2	HGH 1311	14.84	86	21.13	30.7	72	135	3	Valder	36.84	119.2	20.8	34.4	53	127
2	Hill	10.83	85.8	23.01	30.91	61	146	1	Walters	3.05	89.4	22.18	30.91	61	164
2	Hood 75	6.94	96.6	21.34	33.35	60	140	4	Wayne	16.75	114.4	22.74	33.16	53	122
2	Hutcheson	19.35	77	23.28	30.49	60	138	2	Wic 35	14.22	97.6	22.54	32.74	44	128
2	Improved hood	4.84	57.8	21.89	32.67	70	134	1	Wills	2.54	154	20.71	33.59	87	145
1	Jackson	22.14	99.8	20.56	33.48	65	146	1	Wright	8.17	103	19.8	33.86	76	149
2	Jeff	8.42	100.8	20.85	32.14	65	140	4	Wye	17.13	50.2	23.5	30.95	44	109
1	John alford	8.35	109	20.86	31.71	71	145	2	Yaqui 80	12.95	109	20.94	33.69	64	133
2	Kino	8.74	86.4	21.72	33.07	59	140	2	Saman	10.33	137.5	21.61	33.41	58.33	133.83
2	Lancer	12.54	83	20.27	32.85	69	132	2	Sahar	8.20	79.93	22.51	30.92	56.83	135.16
2	Lee	11.93	75.33	21.9	32.55	60	139	2	Katol	9.85	129.7	20.93	34.83	61.5	141.66
3	Lee late	26.41	85.5	19.74	34.58	69	135	4	Kosar	7.71	106.57	21.78	34.29	38.16	117.16
2	McNair 600	21.41	108.6	20.86	33.18	69	135								
2	Nathan	6.14	105.6	20.96	33.8	60	130								
2	Nautilus	13.79	100.4	21.38	31.61	63	140								
LSI 5%		4.33	26.05			5.29	8.9			4.33	26.05			5.29	8.9

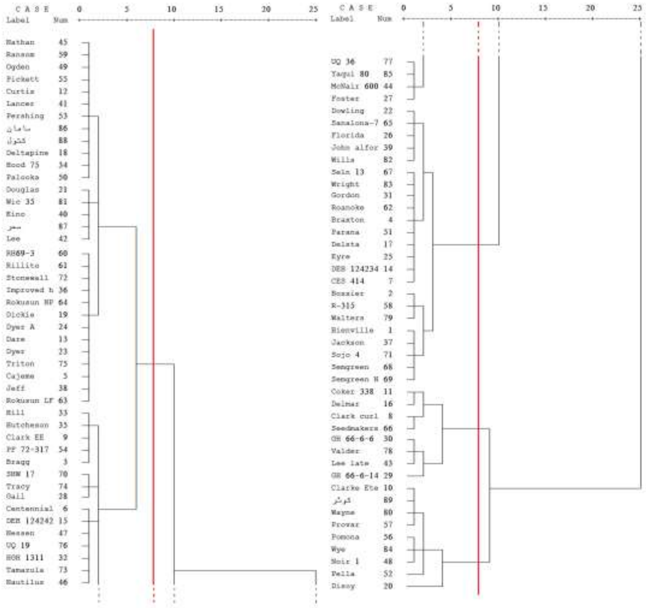

Figure 1. Dendrogram obtained from cluster analysis using Ward method in order to grouping genotypes in Alborz province

Table 3. The agronomical parameters of soybean genotypes studied in Mazandaran province

Cluster no.	Genotype name	Seed yield	Plant height	Oil%	Protein%	Days to flowering	Days to maturity	Cluster no.	Genotype name	Seed yield	Plant height	Oil%	Protein%	Days to flowering	Days to maturity
1	Cayuga	5.1	65	21.65	36.78	23	114	2	Troll	6.32	65	22.38	38.02	33	113
1	Heimkraft I (Samenfarbe)	4.04	58.33	22.16	39.78	22	116	3	T288	7.36	75	21.47	36.47	33	142
1	Vilnensis	5.23	78.33	22.52	39.43	24	82	4	DT97-4290	19.89	93.33	22.1	36.29	37	147
1	Altonagaarden	5.43	91.67	22.23	39.91	21	96	4	Forrest	5.97	100	22.9	34.82	45	138
1	Lilablüte	4.56	72.67	22.17	38.58	22	138	4	OSAGE	13.53	87.67	20.94	36.02	48	138
1	Locala 11	4.25	83.33	22.15	39.76	20	113	4	Smith Super	6.81	109.67	21.04	37.03	44	137
1	Juhomoravska drobnozrna Zltá	5.58	79	21.65	36.78	21	114	1	Hisoy-1651	6.41	63.33	21.28	36.15	25	93
1	Ruská Zltá	9.59	78.33	20.73	39.58	22	94	1	Grant (REP)	7	56	21.24	36.08	26	118
1	Cina 5202	5.61	68.33	22.38	38.02	23	95	1	Rampage	8.74	34.33	22.41	39.00	24	119
2	Slovenská Drobnozruná	19.29	61.67	20.45	36.71	22	116	1	Ti Lin No 9	7	29.33	21.34	36.25	27	111
1	Chico	50	48.33	21.65	38.41	23	138	1	Precoce 90 (REP)	12	40.33	20.98	36.09	24	109
1	Pagoda	6.22	76.67	20.88	39.05	24	94	1	Semu 8008	5	30.67	22.26	38.74	23	88
3	Reatz	10.91	75.33	21.39	36.79	23	137	1	" Flora"	10	20.67	21.69	37.31	27	119
3	Simpson	6.19	76.67	22.36	38.40	22	116	1	Semu 8001	20.29	55	20.41	36.64	23	88
2	Hodoninska Zluta	5.56	63.33	21.88	37.17	23	115	2	Uo7-90	10	58.33	21.56	37.09	22	110
2	Izj hua	4.59	45	22.07	37.43	22	102	4	Alaric	87	51.67	20.48	39.02	31	147
1	Mandurska 2	6.77	83.33	22.36	38.91	23	100	2	Protana	20.47	63.33	20.65	37.07	23	143
1	Mediachev	55	69.33	20.15	36.17	24	88	2	Prastsja	15.5	55	20.74	37.23	24	114
1	OAC Dorado	8.03	101	21.97	39.44	23	115	2	Amurskaja 57	6.43	110	21.23	36.07	26	137
3	OAC Shire	16.02	63.67	20.47	39.94	22	116	1	SOJA 698	8.73	98.33	21.26	36.57	25	104
2	Rampage	4.5	76	22.2	37.65	31	115	1	Morsoy	6.4	80	21.17	35.96	24	117
1	Sibley	4.53	64.33	22.17	39.80	22	114	1	BORA	7.33	78.33	21.36	36.29	27	115

2	Stride	8.32	90	22.73	37.29	23	115	3	Mazowiecka II	10.5	50.33	21.22	36.50	22	138
1	PI 475822 A	8.32	78.33	20.66	39.22	27	118	3	Brillmeyer	16.93	56.67	20.9	39.66	24	124
3	Apollo	7.75	83.33	21.28	36.15	31	116	2	Zarja	17.58	76.67	20.16	36.19	27	119
2	Beeson	6.21	104.67	21.5	36.53	30	113	2	Erfurt	5.62	103.33	21.47	36.47	24	106
3	Beeson 80	6.19	110.67	22.31	39.05	31	119	3	Ke-si 283	5	51.67	21.82	37.07	24	126
3	Colfax	6.5	78.33	21.62	39.31	30	119	3	SOJA 690	11.67	80	21.36	36.74	23	121
1	Hack (REP2)	7.9	90.67	22.07	38.41	27	115	2	SOJA 838	10.8	67.67	21.33	36.69	24	119
1	Provar	7.34	90	21.45	39.68	27	116	3	SOJA 1539	5.14	66.67	21.55	36.61	33	135
1	RCAT Alliance	7	83.33	21.2	36.02	26	115	1	Kirowogradskaja 5	18.75	61.67	20.79	37.32	26	119
1	Sandusky	5.79	105	22.12	38.04	25	114	3	KG 31	8	61.67	21.48	36.49	24	129
2	Vertex	4.5	85	22.03	37.36	24	116	3	Toshidai 7910	14.83	41.67	20.74	35.68	26	143
3	T295H	8	93.67	21.46	38.87	32	119	3	Giesseler	14.85	39.67	21.08	38.93	25	139
1	APEX	5.44	64	21.45	36.44	31	117	3	Chi Sha	5.5	40	21.59	36.68	29	131
3	Pella	4.63	104	22.3	37.82	30	149	1	Noir des Freres Dippe	8.33	47.67	21.4	36.81	24	120
3	Yale	5.66	106.67	22.65	38.46	31	114	3	Brun Hatif Rouest	6.12	36	21.3	36.19	24	129
3	L75-3735	5.48	125	20.32	39.05	34	143	1	Grignon 39	14	43.33	22.46	39.32	22	65
3	S39-99	4.37	91.67	21.29	38.22	33	142	1	Dornburger Stamm 106	28.67	34.33	20.45	36.71	31	94
2	PI 475822 B	6.05	105	21.19	37.78	34	144	1	Flambean	6.47	57.67	21.2	36.02	24	119
4	Columbus	20.28	82	22.03	38.76	34	119	2	Len-Sin-pin-din	15.53	75	21.81	38.36	24	119
4	Crawford	22.27	86.67	20.44	36.69	33	124	1	Dakota No. 3338	38.33	62.67	20.4	39.65	25	91
3	Perry	10.94	75	21.58	37.12	32	148	1	SOJA 1535	8.72	76.67	21.5	36.98	24	118
4	Pershing	18.11	71.33	21.93	37.70	45	149	1	Iregi Sz. 1	16.29	71.67	20.57	39.43	26	89
3	Pixie	10.21	48.33	22.25	38.68	31	138	2	SOJA 1088	9	61.67	21.45	36.90	24	109
4	Spry	18.33	73.33	22.4	37.08	48	147	1	Saljut 216	14.06	66.67	20.65	39.85	23	105
LSI 5%		17.12	23.92			8.90	5.58			17.12	23.92			8.90	5.58

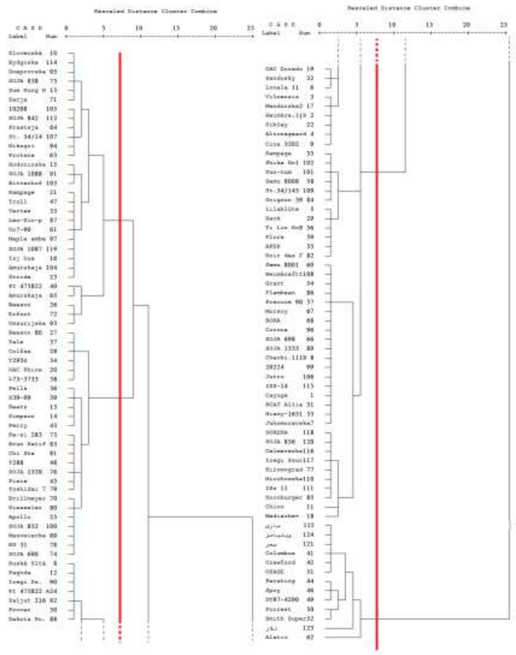

Figure 2. Dendrogram obtained from cluster analysis using Ward method in order to grouping genotypes in Mazandaran province

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Effect Of Parental Lines On Germination Of Avsar F1

Nur Ülger[1] *, Zehra Nur Arda[2]
[1]Multi Tohum Tar. San. Tic. A.s. Antalya, Türkiye
[2] Multi Tohum Tar. San. Tic. A.s. Antalya, Türkiye
nulger@multitohum.com
zarda@multitohum.com

Introduction

Pepper (*Capsicum spp.)* is one of the most important crops for production worldwide due to its consumption as a vegetable and spice (Crosby, 2008). Seeds quality has an important role in the production process of crops. Therefore, many researches has been done to analyze germination (Tu K. et al., 2022) and its improvement on vegetable seeds (Goobkin, 1988) throughout the years. For pepper seeds production, seed quality is one of the major properties considered during the breeding process. This study is performed to evaluate the effects of parental lines seeds quality property affect on the hybrid. Avsar F1 (Multi Tohum Tar. San. Tic. A.s.) and its parental lines were used to understand parental effects on the germination of the hybrid.

Results

In this experiment, a capia pepper hybrid was used as the hybrid material. All pepper seeds were produced in Multi Tohum greenhouses which is located in Turkey. 100 cavity trays were prepared with peat-pearlite (1:1) mixture. Seeds were sown in the laminar flow cabinet which is located in Multi Tohum R&D Center. Distilled water (dH_2O) was used for all samples during the experiment. Seeds were counted three times, on the 7th, 10th, and 14th days. Average countings from 4 repetitive trays were recorded. On average, on the 7th day, 57 seeds from Avsar F1, 61 seeds from the female line, and 72 seeds from the male line were counted. On the 10th day, 89 seeds from Avsar F1, 88 seeds from the female line, and 80 seeds from the male line were counted. Finally, on the 14th day, from Avsar F1 female line and male line, 91, 86, and 95 seeds were counted respectively. It was observed that the germination level of the Avsar F1 hybrid was high at 91% and there is a parental line property effect present for the hybrid according to 86% and 95% germination levels of the parents.

Consequently, growth vigor and growth rate are high for hybrid and its parental lines. According to that, the hybrid is suitable for commercial production and sale in germination aspects. Moreover, hybrid germination quality is between parental lines with 91%. Due to the data, it is observed that parental line germination levels affect the hybrid. For further research, several different hybrids and their parental lines can be observed by their germination, and comparisons can be done.

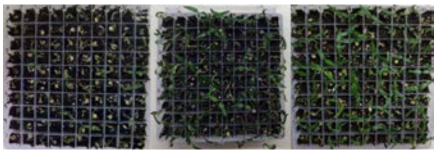
(a) (b) (c)

Figure 2. F pure line first day counting(a), second day counting(b), third day counting(c)

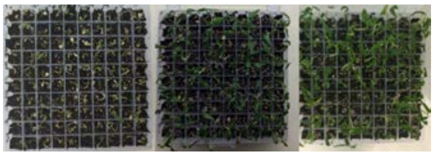
(a) (b) (c)

Figure 3. M pure line first day counting(a), second day counting(b), third day counting(c)

Materials & Methods

Table 1. Materials

Avsar F1
M and F pure lines
100 cavity seeds tray
Peat and pearlite mixture (1:1)
Laminar flow cabinet
seeds germination incubator
Disstilled water (dH_2O)

Figure 1. Avsar F1

Table 2. Application dates

Steps	Date
Sowing	24.01.2021
First counting	30.01.2021
Second counting	02.02.2021
Third counting	06.02.2021

1. Seeds from one hybrid and two of its parental lines were used.
2. A total of 12 trays were used for the germination test. For each line, 4 seperate trays were prepared with pearlite and pear-pearlit mixuture (1:1) as replication.
3. Total 100 seeds were chosen randomly and were sown into each tray in laminar flow cabinet under sterile conditions.
4. Prepared trays were stored in the seeds germination incubator under controlled environmental conditions, which is 65% humidity, 8h light 16h dark photoperiods and the temperature is between 20 C to 30 C.
5. 7, 10 and 14 days countings of the germinations were done inside the laminar flow cabinet.

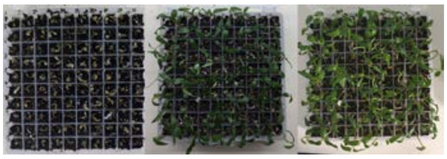
(a) (b) (c)

Figure 4. Avsar F1 first day counting(a), second day counting(b), third day counting(c)

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Sort-clones of *Malus sieversii* (Ledeb.) M. Roem. of Dzungarian population in the Main Botanical Garden

L.Sh. Shadmanova[1, 2], G.T. Sitpayeva[1], G.S. Mukanova[1]

[1] *Institute of botany and phytointroduction, Timiryazev str. 36 d, Almaty, 050040, Republic of Kazakhstan. E-mail:* sitpaeva@mail.ru

[2] *Al-Farabi Kazakh National University, Timiryazev str.71, 050038, Almaty, Republic of Kazakhstan. Author for correspondence:* laura_shadmanova@mail.ru

Keywords: Biochemical composition, *Malus sieversii*, sort-clones of Sievers apple tree.

Summary. One of the important tasks of FAO today is the conservation and sustainable use of biodiversity for food security. The richness of the flora of Kazakhstan, especially mountain fruit variety is a vital strategic resource that ensures sustainable economic development of the country. In this regard, the bred clone varieties of the Sievers apple tree become an attractive object for use in breeding.

Introduction

Kazakhstan possesses a unique genetic resource of a wild apple species *Malus sieversii*, which is the main ancestor of the cultivated apple tree [1; 2].

Natural populations are found in the mountainous regions of Kazakhstan, Kyrgyzstan, Uzbekistan and Western China [3; 4]. The largest natural populations of "*M. sieversii*" were found in the Zhungar Alatau, which is also a unique place for the concentration of agrobiodiversity, which is of significant interest for ensuring world food security [5].

In the 1960s, academician A. Dzhangaliyev created a unique collection fund of wild *M. sieversii* (more than 200 forms and sort-clones) in the Main Botanical Garden of Almaty [6]. To create this collection, valuable forms of *M. sieversii* were selected as a stock according to the phenotype, and brought to the sort-clones by means of occultation method on the stock of *M. sieversii*. Studying this collection made it possible to give a selection assessment and identify sort-clones with the greatest manifestation of valuable features [7].

It is known that consumers generally prefer juicy, fresh and sweet fruits. However, there are other factors that determine fruit quality, some of which are responsible for disease resistance. For example, total phenols, i.e. P-active substances, increase the preservation of the apple and the tolerance of the fruit tree to disease, adverse conditions and stress. In resistant varieties, P-active substances accumulate in larger quantities than in susceptible varieties [8-11]. At present, selection programs related to apples are aimed at obtaining ecologically clean products of apple fruit with hard, fertile, therapeutic and preventive properties. In this regard, determining the biochemical and technological characteristics of fruits along with their nutritional and taste properties is of great importance for the food industry and agriculture. The chemical composition of apples varies under the influence of various factors.

The aim of our study was to determine the biochemical and technological characteristics of new sort-clones of M. sieversii of the Dzungar Alatau population under the conditions of the Main Botanical Garden, to select clones of high value with biologically active substances that can be used in breeding and fruit production.

Materials and Methods

The average weight of the fruit was measured using a technochemical scale. Dry matter of fruits was determined out by drying to constant weight; water-soluble pectins and proto-pectins – by the carbazole method; the content of monosaccharides and total sugars – by decolorizing Felling liquid (Bertrand method) and by titration using titratable acid-alkali (0.1 n NaOH); juice yield – by squeezing the fruit [12]; P-active substances (catechins, leucoanthocyanins, anthocyanins) were determined by the colorimeric method using butyl alcohol and vanillin reagents in L.I. Vigorov's modification [13]. Each analysis was repeated 3 times for objective assessment.

Results and discussion

The introduction test and pre-breeding of *M. sieversii* sort-clones in the conditions of the Main Botanical Garden testifies to their high frost resistance; *M. sieversii* sort-clones are distinguished by uniform long-term growth of shoots and active leaf formation.

As a result of breeding-genetic analysis, we selected 10 promising sort-clones according to economic and valuable features for use in breeding:

TM1: 5-6 m of height, spherical crown, light green leaves, small; small fruits, 24 g, sweet-sour; ripening on the 1st decade of August.

TM2: 5 m of height, spreading crown, marquee-shaped; small fruits, 39 g, green; ripening on the 1st decade of August.

TM7: 4 m of height, spreading crown, narrow leaves; small fruits, 18 g, fresh-sweet, ripening on the 2nd decade of August.

TP19: 4 m of height, spreading crown, large fruits, 83 g, yellow with raspberry blurred cover colour, ripening in early of September.

TP20: 5 m of height, marquee-shaped crown, small fruits, 55 g, ripening in the 1st decade of August.

TP21: 5 m of height, spreading crown, large elongated leaves; large fruits, 90 g, green with a cover raspberry colour, sweet, ripening in the 1st decade of August.

TP25: 6 m of height, spherical crown, large fruits, 165 g, rounded, smooth, green with a cover blurry red colour, sweet-sour, ripening in the late of September.

TP22: 4 m of height, spherical crown, medium-thick leaves, narrow-leaved; small, acidic fruits, 26 g, ripening in the end of July.

TP23: 4 m of height, spherical crown, large leaves, medium elongated; acidic, 27 g, ripening in the 2nd decade of August.

TP24: 5 m of height, spherical crown, narrow leaves, medium thickness, small fruits, 23 g, acidic, ripening in the 1st decade of August.

The studied *Malus sieversii* new sort – clones were divided into the following groups according to the size of their fruits: very small (16...40 g) – TM-7, ТП-24, TM-1, ТП-22, ТП-23, TM-2, fine (41...70 g) – TM-5, below average (71...110 g) - TP-19, TP-21 and medium weight (111...150 g) – TP-25

Biochemical evaluation of *Malus sieversii* sort-clones revealed sorts with a high content of nutrients and biologically active substances. The studied sort-clones are distinguished by a high content of sugars, total acids, dry matter and pectins in fruits (Table 1).

Most of the studied clones of *M. sieversii* were small and highly acidic. High total organic acids from 1.11 to 2.29% was observed in TM-2, TP-24, TM-1, TP-25, TP-23, TM-5, TP-22 variety clones. TM-7 (0.49%) and TP-21 (0.71%) sort-clones were distinguished by low acidity.

Most of the investigated varieties-clones were distinguished by a high amount of water-soluble pectins of fruits from 1.04 to 2.5%: TP-22, TM-7, TP-24, TP-19, TP-25, TP-21, TM-2, TM-5, TM-1 (Table 1). The abundance of water-soluble pectins of the wild apple fruit allows to obtain various unadulterated jelly, marmalade and jam-like consistency products in confectionery and fruit production.

Malus sieversii sort-clones, which contain in fruits more than 600 mg/100 g of leukoantocyanins are of particular interest. Followings are among them: TP-22 (611 mg per 100 g), TP-24 (651 mg per 100 g); and P-active substances more than 400 mg/100 g, they are TP-22, TP-19 and TP-24 sort-clones (Fig. 1).

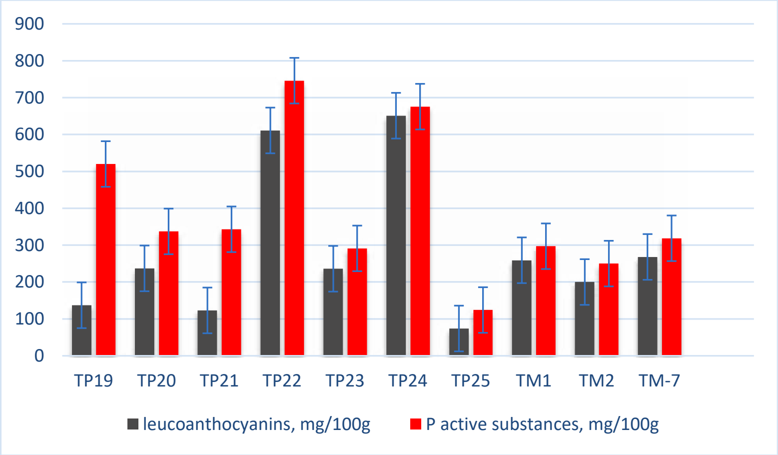

Figure 1. Content of leukoantocyanins and P-active substances in M. sieversii sort-clones

Conclusion

Thus, in the collection fund of the Main Botanical Garden (Almaty), more than 40 sort-clones of the Malus sieversii from the Zhungar Alatau were successfully introduced. The 10 most promising sort-clones in terms of breeding were identified. TP-21, TP-19, TP-23 and TP-25 sort-clones with complex valuable biochemical indicators deserve special attention. Their composition: in TP-21 sort-clone – 14% sugars, 123g/100g leukoantocyanins, 1.39% pectins; TP-19 sort-clone – 13% sugars, 137mg/100g leukoantocyanins, 520mg/100g P-active substances, 1.25% pectins; TP-23 sort-clone – 12% sugars, 236 mg/100g leukoantocyanins; TP-25 sort-clone – 11% sugars, 1.28% pectins.

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Comparison of yield potentials of some triticale lines and cultivars under different climatic conditions.

ÖZER E*, KELEŞ R*, ÇERİ S*, TÜRKÖZ M*, CERİT S.İ *, YAŞAR M*, TAŞ M.N*, KARA İ*, ESER C*, YILDIRIM T, KAYITMAZBATIR B*, YILDIRIM Y**, DEMİR L***, AKÇACIK A.G*, ŞAHİN M*, AYDOĞAN S*, HAMZAOĞLU S* DEMİR B*, GÜÇBİLMEZ C.M*, GÜR S*

* BAHRİ DAGDAS IARI-KONYA, **TRANSITIONAL ZONE ARI-ESKISEHIR,*** MAIZE RESEARCH INSTITUTE-SAKARYA

Author for correspondence (emel.ozer@tarimorman.gov.tr)

Abstract

Rising agricultural supply and increasing demand for arable land heighten the occurrence of abiotic stresses. Drought is one of the most important factors limiting crop production all over the world compared to other abiotic stresses. Drought as an abiotic stress reduces food production in the world and in our country as well. Drought stress occurring in any period of grow has negative effects on morphological, physiological and biochemical activities and ultimately leads to low yields(Coste *et al.*, 2001).

Triticale is a strong plant with efficient growth and adaptability to various environmental conditions. Triticale production in our country is increasing every year. It is used in animal feed such as poultry feed, silage, as well as in human nutrition, in making blended flour and in biscuit flour mixtures.

Triticale varieties, which are known for their compatibility with marginal conditions, need to receive the necessary precipitation in order to obtain optimum yield, which corresponds to an average seasonal precipitation of 230-250 mm. Even though triticale is below this precipitation average, sufficient grain yield cannot be reached as a cereal type. In recent years, where the impact of climate change has increased, it is one of the main subjects of Research Institutes to develop varieties that are compatible with climate change and have high tolerance to abiotic-biotic stresses.

This study was carried out in 20 lines and 4 varieties (TATLICAK-97, ALPERBEY, ÖZER & MİKHAM-2002) in a randomized block trial design with 4 replications in 6 different locations; Konya and its Konuklar district, Kayseri, Eskişehir & Sakarya provinces in 2020-2021. The precipitation of each planted location during the season was determined as Konya: 214.7 mm, Konuklar: 200 mm, Kayseri: 564 mm Eskişehir: 347,0 mm; Sakarya: 826.4 mm. (MGM-2021). Plant growth is not achieved due to poor soil conditions as well as insufficient rainfall in Karapınar location has been cancelled.

The average grain yield of the trial was determined as 3.494 t/ha. As a result of the variation analysis, the variance between locations and lines was found to be statistically significant. ($p<0.01$). Among the locations, Sakarya location gave the

highest grain yield (6.214 t/ha), while Konya location gave the lowest grain yield (1.446 t/ha). Among the lines, line 16 gave the highest grain yield.
According to the quality analyzes made on the samples taken from Konya, Kayseri and Konuklar locations, the thousand grain average of the trial was 34.35 g; Hectoliter: 71.81 kg; Protein content: 13.36%; SDS; 20.37 mm & Cellulose: 2.97%.
When all results are analyzed together, according to yield and quality; despite different climatic data, lines 1, 7,8,11,12,21 & 24 have been determined to give high quality values as well as high yield, and it is recommended to work on these lines for Central Anatolia and Transition Regions in cultivar breeding studies.

Key Words: Triticale, breeding, quality, climate change

Bazı tritikale hatlarının ve çeşitlerin farklı iklim koşullarında verim potansiyellerinin karşılaştırılması.

Özet

Artan tarımsal arz ve ekilebilir arazi için artan talep, abiyotik streslerin oluşumunu artırmaktadır. Kuraklık, diğer abiyotik streslere kıyasla tüm dünyada bitkisel üretimi sınırlayan en önemli faktörlerden biridir. Abiyotik bir stres olarak kuraklık, dünyada ve ülkemizde de gıda üretimini azaltmaktadır. Büyümenin herhangi bir döneminde meydana gelen kuraklık stresi, morfolojik, fizyolojik ve biyokimyasal aktiviteler üzerinde olumsuz etkilere neden olmakta ve sonuçta düşük verimlere yol açmaktadır.

Tritikale, verimli büyüme ve çeşitli çevre koşullarına uyum sağlama yeteneği olan güçlü bir bitkidir. Ülkemizde tritikale üretimi her yıl artmaktadır. Kanatlı yemi, silaj gibi hayvan yemlerinde olduğu gibi insan beslenmesinde, karışımlı un yapımında ve bisküvi unu karışımlarında kullanılmaktadır.

Marjinal koşullara uygunluğu ile bilinen tritikale çeşitlerinin mevsimsel ortalama 230-250 mm yağışa tekabül eden optimum verimi alabilmesi için gerekli yağışı alması gerekmektedir. Tritikale bu yağış ortalamasının altında olmasına rağmen bir tahıl türü olarak yeterli tane verimine ulaşılamamaktadır. İklim değişikliğinin etkisinin arttığı son yıllarda iklim değişikliğine uyumlu ve abiyotik-biyotik streslere toleransı yüksek çeşitler geliştirmek Araştırma Enstitülerinin ana konularından biridir.

Bu çalışma 20 hat ve 4 çeşitte (TATLICAK-97, ALPERBEY, ÖZER & MİKHAM-2002) tesadüf blokları deneme deseninde 6 farklı lokasyonda 4 tekerrürlü olarak yürütülmüştür; 2020-2021 yıllarında Konya ve Konuklar ilçesi, Kayseri, Eskişehir ve Sakarya illeri. Mevsim boyunca ekim yapılan her yerin yağış miktarı Konya: 214.7 mm, Konuklar: 200 mm, Eskişehir: 347,0 mm; Sakarya: 826,4 mm. (MGM-2021). Karapınar mevkiinde yetersiz toprak koşullarının yanı sıra yetersiz yağış nedeniyle bitki gelişimi sağlanamamaktadır.

Denemenin ortalama tane verimi 3.494 t/ha olarak belirlenmiştir. Varyasyon analizi sonucunda lokasyonlar ve hatlar arasındaki varyans istatistiksel olarak

anlamlı bulunmuştur. ($p<0.01$). Lokasyonlar arasında en yüksek tane verimini Sakarya lokasyonu (6.214 t/ha) verirken, en düşük tane verimini (1.446 t/ha) Konya lokasyonu vermiştir. Hatlar arasında en yüksek tane verimini hat 16 vermiştir.

Konya, Kayseri ve Konuklar lokasyonlarından alınan numuneler üzerinde yapılan kalite analizlerine göre denemenin bin dane ortalaması 34,35 gr; Hektolitre: 71.81 kg; Protein içeriği: %13,36; GBF; 20,37 mm & Selüloz: %2,97.

Verim ve kaliteye göre tüm sonuçlar birlikte analiz edildiğinde; 1, 7,8,11,12,21 ve 24 nolu hatların farklı iklim verilerine rağmen yüksek verim ve kalite değerleri verdiği belirlenmiş olup, çeşitte İç Anadolu ve Geçiş Bölgeleri için bu hatlarda çalışılması önerilmektedir. üreme çalışmaları.

Anahtar Kelimeler: Tritikale, ıslah, kalite, iklim değişikliği

Introduction

Triticale is a hardy plant with efficient growth and adaptability to various environmental conditions. High grain yield and nutritional qualities of wheat. In addition to climate changes, the effect and severity of drought, our soils are becoming more and more barren due to improper agricultural practices. The prevalence of triticale, which can be grown in such areas and has better resistance to different environmental stresses than wheat and barley, is increasing in our country.

Along with the feed consumption with the new varieties, the use of flour as a blend has caused the cultivation areas to become more widespread. For this reason, it is of great importance to expand and develop existing triticale studies and to register new varieties that can adapt to different ecologies. Due to the drought problem that has manifested itself from time to time in recent years, there is a need for high yielding, high quality, tolerant/resistant to the diseases and pests present in the region, tolerant to nutrient problems and environmental factors such as cold and arid, for dry areas.

Triticale is grown on 3.7 million hectares of land in the world and 13.7 million tons of triticale is produced, with an average yield of 3.703 kg/ha (Anonymous, 2020). According to FAO-STAT-2020 data, production is carried out in 39 different countries in the world. Poland, Germany, Belarus, France and Hungary are the countries that produce the most triticale, respectively. Triticale, which tends to increase in grain growing areas both in the world and in our country; With the effect of biotic and abiotic plant growth factors, it is in a more advantageous position compared to other cereals in marginal areas.

Global warming, which has begun to make itself felt seriously all over the world, and the resulting climate changes have begun to significantly affect plant production in many countries. Especially frequent droughts and excessive and unexpected rainfall disrupt the usual systems and balances in agriculture of many countries. Changes in the ecological system make it necessary to make changes in the existing plant production pattern and to develop products that can adapt to new conditions.

A significant part of the lands described as agricultural areas are not suitable for the production of many plant species. Therefore, there is a significant gap in both the balanced diet of humans and the supply of feed for livestock. If the suitable part of the unused agricultural lands in Turkey and the lands with low yield from wheat are utilized by planting triticale, an additional income source will be provided to the farmers of the region. At the same time, global climate changes cause low yields in many plant species and grains.

In this 2-year study carried out within the scope of the National Triticale Breeding Studies carried out at Konya Bahri Dağdaş International Agricultural Research Institute (BDUTAEM), 20 genotypes and 4 standard varieties in 5 different climate locations (Konya & Konya-Konuklar, Kayseri, Eskişehir and Sakarya) in terms of grain yield and some quality criteria. performances were compared and the effects of climate change over the years in terms of yield and quality were tested.

Material and Method

This study was carried out with 4 replications, consisting of some triticale lines and cultivars (20 lines and 4 cultivars (Tatlıcak-97, MİKHAM-2002, Alperbey& Özer), according to the randomized blocks trial design. In this study, a comparison was made according to the yield and quality of the materials planted under rain-based conditions in the experimental fields of Konya province Karatay Bahri Dağdaş UTAEM, TİGEM Konya/Konuklar, Kayseri/Yahyalı location, Sakarya Maize Research Institute and Eskişehir Transition Zone Agricultural Research Institutes in the 2020-2021 and 2021-2022 planting seasons.

Table 1: Varieties & Lines Used as Trial Material

No	Lines
1	**MELEZ-2001/ HAWKEYE-AUST**
	BDMT 13 00 05 TF5 5/19 OBD OBD OBD OBD OBD OBD OBD
2	**MELEZ-2001/ HAWKEYE-AUST**
	BDMT 13 00 05 TF5 5/24 OBD OBD OBD OBD OBD OBD OBD
3	**BDMT 98/8S/ÜMRANHANIM**
	BDMT 13 00 11 TF5 11/14 OBD OBD OBD OBD OBD OBD OBD
4	**BDMT 98/8S/10-11 TF4-1**
	BDMT 13 00 12 TF5 12/11 OBD OBD OBD OBD OBD OBD OBD
5	**BDMT 98/8S/10-11 TF4-1**

	BDMT 13 00 12 TF5 12/23 OBD OBD OBD OBD OBD OBD OBD
6	PRESTO/10-11 TBVD-24
	BDMT 13 00 17 TF5 17/8 OBD OBD OBD OBD OBD OBD OBD
7	PRESTO/10-11 TBVD-24
	BDMT 13 00 17 TF5 17/17 OBD OBD OBD OBD OBD OBD OBD
8	CIMMYT-1/10-11 TBVD-24
	BDMT 13 00 22 TF5 22/14 OBD OBD OBD OBD OBD OBD OBD
9	BDMT 98/8S/10-11 TF4-1
	BDMT 13 00 12 TF5 12/22 OBD OBD OBD OBD OBD OBD OBD
10	CIMMYT-1/10-11 TBVD-24
	BDMT 13 00 22 TF5 22/20 OBD OBD OBD OBD OBD OBD OBD
11	6TB219/3/6TA876//6TB163/6TB164/4/2* ...../4/RES-1409-16M5/MAH 17637.1//DAGRO
	BDMT 13 00 31 TF5 31/6 OBD OBD OBD OBD OBD OBD OBD
12	LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/MANATI_1/7/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9
	BDMT 13 00 10 TF5 15/7 OBD OBD OBD OBD OBD OBD OBD OBD
13	LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/MANATI_1/7/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9
	BDMT 13 00 10 TF5 15/10 OBD OBD OBD OBD OBD OBD OBD OBD
14	LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/MANATI_1/7/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9
	BDMT 13 00 10 TF5 15/14 OBD OBD OBD OBD OBD OBD OBD OBD
15	LIRON_2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/BULL_10/MANATI_1/7/DAHBI_6/3/ARDI_1/TOPO 1419//ERIZO_9
	BDMT 13 00 11 TF5 16/23 OBD OBD OBD OBD OBD OBD OBD OBD
16	FAHAD_5/JAYWICK-AUST
	BDMT 10 00 28 TF5 29/24 OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD
17	ANOAS_3/TATU_4//SUSI_2/3/ TATLICAK-97
	BDMT 10 00 31 TF5 32/17 OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD
18	6TB219/3/6TA876//6TB163/6TB164/4/2* ...../5/TMB-II-3/11…
	BDMT 09 00 03 TF5 3/22 OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD
19	CMH77A.1024/2*YOGUI_1//CIVET#2/3/JLO 97/…/4/BAGAL_3/FARAS_1/3/ARDI_TOPO1419//ERIZO_9
	BDMT 08 00 71 F5 25/8 OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD
20	ARDI/GNU//2*FAHAD_1/4/ERIZO_6/NIMIR_4//…
	BDMT 09 00 45 C OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD OBD
	Varieties
1	TATLICAK-97
2	MİKHAM-2002
3	ALPERBEY
4	ÖZER

Quality analysis methods

The methods used in quality analysis are as follows:
Thousand-grain Weight (g): The thousand-grain weight (g) in grams will be determined by randomly counting four hundred grains from each grain product of each material and weighing it (Elgün et al., 2014).
Hectoliter Weight (kg): Hectoliter Weight: The weight of 100 liters of wheat in kilograms will be determined by the hectoliter measuring device. From the filling pipe of the discharge container filled with the wheat sample, the wheat falls into the measuring cylinder. The wheat in the filled hopper is weighed. Hectoliter weight is calculated as kg by using a 1-liter scale and multiplying the result by 100 (Elgün et al., 2014).
Protein Ratio (%): In homogeneously ground grain samples, the protein ratio (nitrogen ratio* factor 5.70 will be used) will be determined by the AOAC 992.23 method with the LECO FP 528 device (Anonymous, 2009).
SDS sedimentation (%): SDS (sodium dodecyl sulfate) sedimentation values will be analyzed according to AACC 56-70 (Anonymous, 2000). 50 ml of bromophenol blue is added to 3 g of flour, shaken at a rate of 12 times in 5 seconds, and immediately placed in a mechanical shaker and shaken for a total of 5 minutes. Then, 50 ml of sodium dodecyl sulfate sedimentation solution will be added to it and shaken for another 5 minutes, and the SDS sedimentation value will be determined by reading the sedimentation amount after 5 minutes by placing it on a flat surface.
Crude Cellulose (%): It will be determined with a calibrated NIR (Foss DS2500 F) device according to the method of Van Soest et al. (1991).

Meteorological Data:

In Table 2-3 & 4 given the locations meteorological data. The precipitation of each planted location during the season was determined as Konya: 214.7 mm, Konuklar: 200 mm, Kayseri: 564 mm Eskişehir: 347,0 mm; Sakarya: 826.4 mm. (MGM-2021). Plant growth is not achieved due to poor soil conditions as well as insufficient rainfall in Karapınar location for this reason trials has been cancelled.

Table2. Meteorological Data Of Konya/Karatay

		Sep.	Oct.	Nov.	Dec.	Jan	Feb.	Mar.	Apr.	May	June	July.	Agus.	Total
LTY(1990-2020)	Mean Temp (ºC)*	19,4	13,4	6,2	1,5	-0,3	1,3	6,0	10,9	15,9	20,5	24,1	24,0	11,9
	Max. Temp. (ºC)	38,8	31,6	25,4	21,8	17,6	23,8	28,9	30,9	34,4	36,7	40,6	39,0	40,6
	Min. Temp. (ºC)	-3,0	-8,4	-20,0	-26,0	-28,2	-26,5	-16,4	-8,6	-1,2	1,8	6,0	5,3	-28,2
	Precp (mm)	15,9	29,7	34,5	45,6	35,9	23,1	27,4	34,2	38,2	27,8	6,5	6,5	325,3
2020-2021	Mean Temp (ºC)*	21,3	15,8	5,4	4,2	2,2	2,4	4,4	11,6	18,3	19,0	24,1	23,2	12,7
	Max. Temp. (ºC)	39,3	31,8	17,6	14,7	20,6	20,1	22,1	29,5	33,4	31,9	38,2	36,4	39,3
	Min. Temp. (ºC)	7,4	1,7	-1,0	-8,3	-12,7	-17,3	-9,7	-2,3	0,7	4,0	9,1	8,5	-17,3

	Precp (mm)	3,3	2,3	14,5	7,1	24,0	0,3	32,6	16,6	0,7	19,5	0,1	3,0	124
2021-2022	Mean Temp (ºC)*	17,2	11,7	7,7	0,7	-2,4	1,0	0,6	12,9	14,6	20,4	22,5	26,0	11,1
	Max. Temp. (ºC)	33,0	26,6	22,2	18,3	14,8	15,4	19,5	29,3	32,5	32,5	36,3	36,2	36,3
	Min. Temp. (ºC)	-1,1	-2,9	-9,6	-24,2	-25,9	-12,7	-10,2	-6,2	2,0	8,4	9,9	14,4	-25,9
	Precp (mm)	20,1	0	11,1	52,8	34,6	24,4	20,3	0,9	30,6	14,5	3,8	2,6	215,7

Table 3. Konya/Karapınar & Konya Konuklar Seasonal Precipitation(mm)

YEARS	KARAPINAR	KONUKLAR
2020 SEP	4,8	14,2
2020 OCT	6,40	25,00
2020 NOV	23,80	12,20
2020 DEC	31,60	22,20
2021 JAN	41,60	27,00
2021 FEB	5,00	0,80
2021 MAR	32,80	42,40
2021 APR	18,20	10,40
2021 MAY	0,20	9,40
2021 JUNE	27,20	36,80
2021 JULY	0,60	0,00
TOTAL	192,20	200,40

Table 4. Meteorolgical Data of Sakarya Location

Year	*Month*	*Temperature (^{o}C)*			*Precipitatiom (mm)*
		Max	*Min.*	*Mean*	
2020	***Oct***	***27,9***	***17,1***	***21,4***	***68,4***
	Nov	***18,0***	***9,3***	***13,0***	***35,3***
	Dec	***16,6***	***10,1***	***12,9***	***56,9***
2021	***Jan***	***14,1***	***7,4***	***10,2***	***139,0***
	Feb	***12,9***	***4,0***	***8,1***	***79,8***
	Mar	***13,0***	***4,2***	***7,9***	***101,4***
	Apr	***18,0***	***8,4***	***12,6***	***80,6***
	May	***26,0***	***13,3***	***19,0***	***74,4***
	June	***26,6***	***16,1***	***21,0***	***88,1***
	July	***30,8***	***20,6***	***25,2***	***101,5***
	Total				*826,4*

Results and Discussion

The yield was calculated by correcting the parcel yields obtained from the experiment at harvest. The variance analysis of the results obtained in the study was made with the JMP 11.2.1 package program according to the randomized blocks trial design, and the differences and groupings between the genotypes were made according to the LSD test (Anonymous, 2014).

Table 5. Grain Yield Results Obtained According to the Average of Locations

Line/Variety	2020-2021	Location	2020-201
16	415.6	**Konya**	144.6
14	401.0	**Konya/Konuklar**	286.9
17	390.1	**Kayseri**	242.3
21	380.5	**Eskişehir**	451.7
8	377.1	**Sakarya**	621.5
9	371.9	**LSD**	43.82
19	371.2	**Std of Mean**	349.6
11	365.3		
7	361.2		
24	359.0		
22	356.3		
1	355.6		
23	352.8		
12	348.8		
TATLICAK-97	303.5		
MİKHAM-2002	290.4		
ALPERBEY	341.8		
ÖZER	287.9		
CV	20.7		
LSD	45.02		
Mean	349.4		

According to the quality analyzes made on the samples taken from Konya, Kayseri and Konuklar locations, the thousand grain average of the trial was 34.35 g; Hectoliter: 71.81 kg; Protein content: 13.36%; SDS; 20.37 mm & Cellulose: 2.97%.

Table 6. Quality Results of Konya-Konuklar and Kayseri ()

Line &Variety	1000 KW (g)	Hectolıter(Kg)	Protein(%)	SDS(ml)	Cellulose(%)
16	35,35	71,29	12,91	19,17	2,98
14	34,28	74.06	13.13	18,00	3,03
17	34,66	71,23	13,46	19,67	3,03
21	33,63	72,16	13,50	19,00	3,13
8	36,79	72,02	13,29	22,00	2,95
9	33,15	72,89	12,95	17,00	2,87
19	34,61	70,92	13,17	20,67	3,01
11	38,41	72,24	13,27	21,33	2,98
7	34,04	71,83	13,59	23,33	2,90
24	31,62	72,06	13,56	21,17	3,11
22	33,88	70,71	13,11	22,83	2,90
1	35,17	69,91	13,51	19,50	3,04
23	37,75	72,34	13,33	22,50	2,84
12	30,04	72,50	13,69	21,67	2,87
TATLICAK-97	30,27	72,06	13,53	20,17	2,94
MİKHAM-2002	28,36	71,77	13,33	20,67	2,92
ALPERBEY	34,52	72,03	13,87	22,00	2,90
ÖZER	32,39	70,57	13,60	19,17	3,00

Conclusion

All results are analyzed together, according to yield and quality; despite different climatic data, lines 1, 7,8,11,12,21 & 24 have been determined to give high quality values as well as high yield, and it is recommended to work on these lines for Central Anatolia and Transition Regions in cultivar breeding studies.

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Evaluation of Wheat (*T. aestivum* L.) Germplasm under Temperate Conditions and Identification of Sources of Yellow Rust Resistance Genes (yr) using Molecular Markers

Basharat Ul Islam[1], Shabir H. Wani[2,4]*, Gazala H. Khan[2], Saba Mir[2], M. Saleem Dar[2], Najeeb ul Rehman Sofi[2]. Asif B. Shikari[1], Fayaz Mohiddin[2], M. Anwar Khan[1], R.R. Mir[1], Ajaz A. Lone[3,4], Z. A. Dar[4], Mumin Ibrahim Tek[3], Ozer Calis[3], G. P. Singh[5]

1. Division of GPB, Faculty of Agriculture, Wadura, Sopore, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu and Kashmir, India

2. Mountain Research Centre for Field Crops, Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology, Srinagar, Jammu and Kashmir, India

3. Department of Molecular Plant Pathology, Faculty of Agriculture, Akdeniz University, 07070 Campus-Antalya/Turkey.

4. DARS Rangreth, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu and Kashmir, India

5. ICAR-Indian Institute of Wheat and Barley Research, Karnal India

Corresponding author email: shabirhwani@skuastkashmir.ac.in

Presenting author: Shabir H Wani

Abstract

Wheat is highly affected by yellow rust disease particularly under cooler environments and the losses can reach up to 100 percent depending on the severity of infection and susceptibility of genotype. The utmost effective tactic to manage this disease is the use of resistant varieties. To identify potential resistant genotypes that could be used in yellow rust resistance breeding programs the present study was conducted with the aim of screening 192 wheat genotypes, including 6 released varieties as check genotypes, for resistance against yellow rust disease at Mountain Research Centre for Field Crops (MRCFC) Khudwani, SKUAST-Kashmir, India. Under field conditions, 57 genotypes, including those cultivars whose resistance reaction towards the pathogen was already established, showed resistance reaction. Similarly, 29 genotypes of wheat were moderately resistant and remaining all were either moderately susceptible or susceptible against yellow rust. Further a subset of 111 wheat genotypes was tested against the six most virulent races viz., 7S0, 23S119, 110S119,110S84, 47S119(T), 46S119, of yellow rust pathogen under controlled epiphytotic conditions. It was found that 12 wheat genotypes exhibited resistance against all these six virulent races. Further, a subset of ninety-seven wheat genotypes were characterized at the molecular level for the presence of four effective yellow rust resistance genes viz., *Yr5*, *Yr10*, *Yr15*, *and* Yr17 by using their respective linked gene-based markers *STS7/8, XPSP3000, Xbarc-8 and VENTRIUP /* LN2 respectively. After molecular validation of wheat genotypes, it was found that *Yr5* gene was present in 9 genotypes, *Yr10* gene was found in 16 entries and *Yr15* gene was found in 14 entries. Similarly, *Yr17* gene was found in 32 genotypes of wheat and in rest of the remaining 65 genotypes, the yellow rust resistance gene was absent. The yellow rust resistance (*Yr*) genes studied in the current research program are effective in conferring resistance against the yellow rust disease. The genotypes identified as resistant both under field and controlled conditions and possessing *Yr* genes shall be used in yellow rust resistance breeding programs as effective donors for gene deployment.

Keywords: Molecular markers, *Puccinia striformis*, Stripe rust, Wheat, Yr genes

Possibilities to develop Dry Pea varieties for sustainable agriculture

Ahmet Ustaoğlu (ustaolu.a@gmail.com),
Selçuk Üniversitesi, Bitki Islahı ve Genetik Ana Bilim Dalı

Abstract

With the rapidly increasing world population, it is predicted that there may be problems in meeting the food need in the coming years. The importance of plant-based proteins instead of animal proteins is increasing for the nutrition of the human population. For this, it becomes a necessity to change agricultural production patterns. The need for protein in human nutrition can be met directly with legume plants (soybean, chickpea, pea, lentil and beans), as well as by the inclusion of these plants in other food products as industrial additives. Considering these problems, dry peas increase soil fertility in our improvement studies and reduce the fertilizer cost of the crops planted after it. It is necessary to develop large and high yielding varieties from dry pea and forage pea genotypes suitable for human consumption. According to the study we carried out in two different locations in Konya in 2017 growing seasons, the grain yields of 7 different pea genotypes (*Pisum sativum ssp.*) were determined as line and culture varieties selected from the population. According to the averages of the two locations; Grain yield in pea genotypes were obtained from *Pisum sativum cv* Salamanca, *Pisum sativum cv* Astronaute, *Pisum sativum cv* Guiduro, *Pisum sativum cv* Green Wood, *Pisum sativum cv* Whero, *Pisum sativum cv* PS306, *Pisum sativum cv* PS317. According to results in the trials, the yield ranking was as follows 5328 kg/ha, 4953 kg/ha 4744 kg/ha, 4161 kg/ha, 4113 kg/ha, 3773 kg/ha, 3437 kg/ha. It has been determined that line and pea varieties with high grain yield can be used as genetic soutce in breeding studies in the development of edible dry pea types. With breeding new dry pea varieties adaptable to central Anatolia and transition regions, and to increse their production in the future in those regions, we believe that the foreign dependency of the food and livestock sectors will decrease.

Keywords: dry pea, breeding, sustainable agriculture, vegetable protein.

Materials

Seven dry pea cultivars (Whero and Green Wood were obtained from Canterbury Seed Company Limited, 1 Range Street, Ashburton, 7700 New Zealand), (Salamanca and Astronaute were obtained from Norddeutsche Pflanzenzucht, Hans Georg Lembke GmbH, Hohenlieth, Germany) and (Guiduro were obtained from Semillas Batlle S.A., 1 Carrer de Santiago Rusinol, 4, 08750 Molins de Rei, Barcelona, Spain) in 2016. PS306 and PS317 was lines of local selection (Figure 1).

Figure 1: The seeds of Dry Pea cultivars

Methods

Trials were carried in 2 locations out in winter on 15'th October 2016. Seed sowing were planted in Konya Meram district and Konya Kadınhanı district.Trials were set up with 4 replications according to random blocks. 6 rows were planted with a plot length of 5 m, row spacing of 0.25 m and a row up of 4 cm. The edge effect between plots was left as 0.5 m. With the sowing, 60 kg of Diammoniumphosphate (DAP 18-46-0) fertilizer was applied per hektar.The experiment was carried out under aqueous conditions. The healthy development of the plants was ensured (Figure 2).

Figure 2: Location trial Image of Konya Meram district

Purpose / Authentic Value

Peas production in Turkey increased by 17%, with 1,538 tons in 2020 and 1,805 tons in 2021 (TUİK, 2022). However, in 2021, our total pea import was 173.908 tons and our export was 129.754 tons. Most of our exports have been to our neighboring country, Iraq, with 69,798 tons of dry peas (Chart 1). It is seen that it cannot meet the demands of dry peas with production and the solution is provided by imports.

Considering the changing climatic conditions and the food and protein needs of the increasing human population, there is an increasing trend towards vegetable proteins, which are cheaper than animal products. Cultivation of dry peas for spring is not common in our country and is not preferred.

Conclusion

Dried pea varieties that are suitable for local conditions, resistant to cold, early maturing, having high grain size and grain yield should be developed in accordance with edible consumption and animal feed.

Aim of study is to develop high yielding dry pea varieties suitable for winter conditions in Turkey. This research was carried out to determine the grain yield of dry peas lines and cultivars (PS306 and PS317 lines and Salamanca, Astronaute, Guiduro, Green Wood, Whero cultivars) sown in winter under the ecological conditions of Konya Meram and Konya Kadınhanı during the 2016-2017 vegetation period.

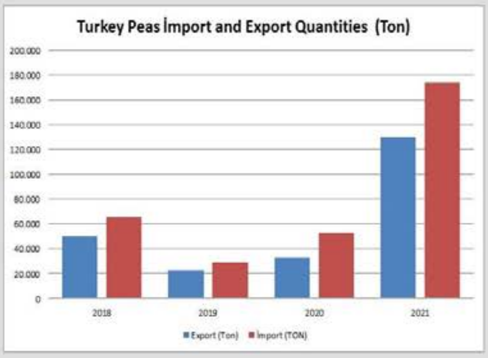

Chart 1. Turkey's pea import and export quantities ton (TUIK, 2022).

Result

Varieties and lines with a shorter vegetation period had higher yields in terms of grain size and yield. Cold tolerance has emerged as a common problem in trials. It has been observed that the local P306 and P317 line is more tolerant to cold than foreign varieties. The cultivars with the highest 1000 grain weight were Astronaute and Salamanca, while the lowest ones were Guiduro and PS317. Guduro was the tallest and Greenwood was the shortest variety in the trials. Seed production and regional yield trials of the selected lines continue in comparison with different varieties and lines.

Figure 3. Dry pea parcel and pod view

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Registration of "ATMACA" Pinto Bean

Dr. Evren ATMACA[1], Abdullah Taner KILINÇ, Ramazan AKIN, Dr. Sabri ÇAKIR, Mesut TOPAL

Transitional Zone Agricultural Research Institute, Tepebası, Eskisehir, Türkiye
*Responsible Author, e-posta: evren.atmaca@tarimorman.gov.tr

Among the aims of the Dry Bean breeding program carried out in our institute, it is aimed to develop varieties that can be resistant to diseases which are problematic in the production areas of barbuna and which can be cultivated in large grains, early and large production areas. In line with the improvement studies carried out for these purposes, our Istanbul-coded kidney bean genotype is obtained as a result of cross-linking to our genus of halo blight (*Pseudomonas syringae* pv.) In the form of a dwarf plant. Modified Bulk Method was brought up to F5 and Pinto bean line was obtained from the single plants selected from the selected parcels.

Registration Year: 2020

Breeding method: Hybridization

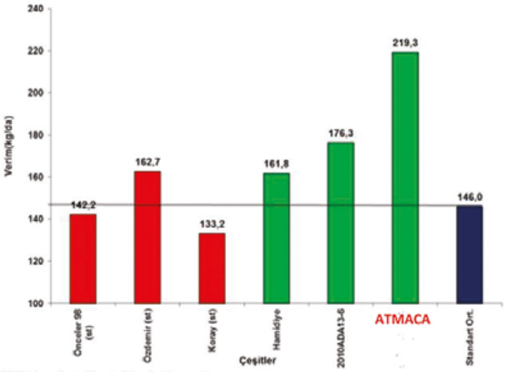
Morphological Features:

Growth habit: Semi climbing
Plant height: 65-85 cm
Flower color: Pink
Seed number per pod: 3-5
Seed type: Pinto bean
100 seed weight: 58,9-66,5 g.

Seed view of Atmaca

Agricultural properties:

Days to maturity: 111-116 days, It is a middle earliness variety.
Pod opening: None
Ability to harvest: Good
Seed Yield: Seed yield level varies between 183,9 and 337,7 kg/da. Most suitable sowing time for Central Anatolia Region is early May. If the maintenance is made with tractor drawn machinery Row spacing should be 70 cm, row distance 12-15 cm and the amount of seeds per unit area 8-10 kg/da for our variety cultivars.



TTSM registration trials yield results

Kalite Özellikleri/Quality features:

Cooking quality of seeds: Cooking time by soaking with water is 33-35 minutes. No more scattered after cooking. Variety can be used for canned features and its taste is very delicious. In addition to our variety is eaten as unripe pod.

Diseases and Pests:
The most important feature of variety is tolerant to root rot. It is tolerant to bacteria and virus diseases.

Recommended areas:
It is recommended for all large areas of pinto bean production.

Pod view of Atmaca

Field view of Atmaca

Registration of "BAHCIVAN" Runner Bean

Dr. Evren ATMACA[1], Abdullah Taner KILINÇ, Ramazan AKIN, Dr. Sabri ÇAKIR, Mesut TOPAL

[1]Transitional Zone Agricultural Research Institute, Tepebası, Eskisehir, Türkiye
*Responsible Author, e-posta: evren.atmaca@tarimorman.gov.tr

Runner bean occurs wild from Mexico to Panama. It was probably domesticated in Mexico. Nowadays runner bean is cultivated in temperate countries and occasionally in highland areas of Central and South America, Africa (e.g. Ethiopia, Kenya, Uganda, South Africa) and Asia. Runner bean is a crop for temperate climates. In the tropics it is most successful at altitudes of 1500–2000 m. Runner bean is more tolerant of cool conditions than other Phaseolus species, but damage occurs at temperatures below 5°C. At temperatures above 25°C fruit development is inhibited. Runner bean is extremely susceptible to drought and requires a well-distributed rainfall throughout the growing period. It needs a high relative humidity for seed set. Runner bean comprises short-day and day-neutral types. runner bean is adapted to a wide range of soils, but it prefers deep, well-drained, loamy, light- to medium-textured soils, with pH 6–7. Waterlogging is not tolerated. Runner bean's immature and mature seeds are consumed. In temperate regions the immature pods are most commonly eaten, sliced and cooked, as a vegetable. The young shoots, leaves and inflorescences are sometimes used (boiled or boiled and fried) as a vegetable while the tuberous roots are consumed boiled or chewed as candy. A root decoction is taken against malaria or applied to swollen eyes. In Central America runner bean is grazed by livestock and dried into hay. It is grown as an ornamental (Anonymous 2015).

Breeding efforts for runner bean have been directed to improvement of culinary quality (stringlessness) and disease resistance. Selection to improve cooking quality is promising since seed proteins of runner bean are more polymorphic than those of common bean. For dry seed production, improvement of plant habit and shorter pods are appropriate objectives of selection. Moderate levels of resistance to common bacterial blight (*Xanthomonas campestris* pv. *phaseoli*), Fusarium root rot (*Fusarium solani* f.sp. *phaseoli*) and white mould (*Sclerotinia sclero*tiorum) have been transferred from runner bean to common bean. Runner bean is also considered as a potential source of resistance against other diseases of common bean, including anthracnose, Ascochyta blight (*Phoma exigua*), angular leaf spot (*Phaeoisariopsis griseola*), powdery mildew (*Erysiphe polygoni*) and rust (*Uromyces appendiculatus*). Considerable tolerance to bean flies (*Ophiomyia* spp.) has been detected in runner bean, and tolerance has been transferred into common bean (Anonymous 2015).

In the study carried out for the purpose of evaluating the breeding programs in the local varieties in the scope of Dried Bean breeding programs conducted in our institute, the seeds obtained from this population named as "BOMBA" which is cultivated in the central villages of Erzurum province, were grown in the trial and application area of the Our Institute and the line was developed with pure-line selection breeding method.

Registration Year: 2020
Breeding method: Selection
Morphological Features:

Growth habit: Semi climbing

Plant height: 79-112 cm
Flower color: White
Seed number per pod: 3-4
Seed type: Bomba/Dermason
100 seed weight: 82,0-107,6 g.

Pods, seeds and flowers view of Bahçıvan

Agricultural properties:

Days to maturity: 120-130 gün/days, It is a middle late variety.
Pod opening: None
Ability to harvest: Good
Seed Yield: Seed yield level varies between 90 and 191 kg/da. Most suitable sowing time for Central Anatolia Region is early May. If the maintenance is made with tractor drawn machinery Row spacing should be 70 cm, row distance 12-15 cm and the amount of seeds per unit area 10-12 kg/da for our variety cultivars.

Field view of Bahçıvan

Quality features:
Cooking quality of seeds: Variety can be used for bean salad and its taste is very delicious. No more scattered after cooking.

Diseases and Pests:
The most important feature of variety is tolerant to root rot. İt is tolerant to bacteria and virus diseases.

Recommended areas:
It is recommended for all large areas of dry bean production.

Pods and seeds view of Bahçıvan

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MARKER-ASSISTED SELECTION: AN APPROACH FOR IMPROVING THE MAIZE QUALITY

Marija Kostadinović (kmarija@mrizp.rs), Danijela Ristić, Jovan Pavlov, Zoran Čamdžija, Dragana Ignjatović-Micić, Jelena Vančetović,

Maize Research Institute Zemun Polje, Belgrade, Serbia

INTRODUCTION

Marker assisted selection has gained considerable importance as it increases efficiency, reduces time and costs taken to obtain desirable genotypes. Molecular markers can aid selection of all target alleles that are difficult to assay phenotypically, in less time and with minimum linkage drag. Simple sequence repeats (SSR) are being used efficiently for introgressing a target allele, without any intermediate field selection. These markers can be used for direct selection of the target gene (foreground selection), as well as for fast recovery of recurrent parent's genome (background selection).

Maize Research Institute Zemun Polje (MRIZP) has a breeding program aimed at conversion of standard quality maize to quality protein maize (QPM), as well as to β-carotene (BC) rich maize, for growing in temperate regions.

The results presented here relate to foreground and background selection for improving the protein quality (tryptophan and lysine content) and β-carotene content of the maize inbred lines.

MATERIAL AND METHODS

Plant material MRIZP commercial inbred lines were used for marker assisted conversion to QPM and β-carotene rich maize (Figure 1). These lines, used as the recurrent parents, are components of the leading MRIZP hybrids. As donors of the favorable allele of *crtRB1* gene for BC and *opaque2* for QPM, lines from the International Maize and Wheat Improvement Center were used.

Foreground selection As gene-specific SSR markers, phi057 and umc1066 were used for QPM lines, while crtRB1-3′TE marker was used for BC lines.

Background selection SSR markers evenly distributed throughout the genome were used for identification of the genotypes with the highest proportion of recurrent parent's genome (RPG).

Trait	Gene	Primer	Sequence
High β-carotene content	*crtRB1*	crtRB1-3′TE-F	5′-ACACCACATGGACAAGTTCG-3′
		crtRB1-3′TE-R_1	5′-ACACTCTGGCCCATGAACAC-3′
		crtRB1-3′TE-R_2	5′-ACAGCAATACAGGGGACCAG-3′
High protein quality	*opaque2*	phi057-F	5’-CTCATCAGTGCCGTCGTCCAT-3’
		phi057-R	5’-CAGTCGCAAGAAACCGTTGCC-3’
		umc1066-F	5’-ATGGAGCACGTCATCTCAATGG-3’
		umc1066-R	5’-AGCAGCAGCAACGTCTATGACACT-3’

Table 1. The set of primers used as foreground selection markers for the *crtRB1* ans *opaque2* gene

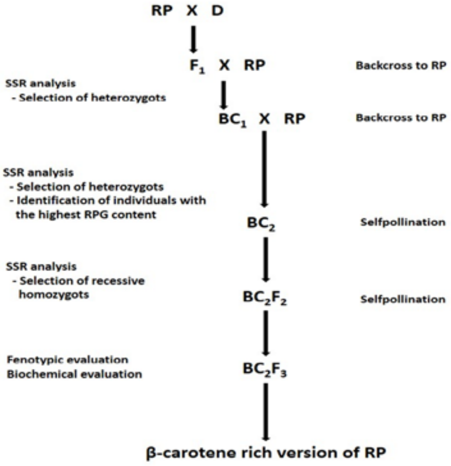

Figure 1. Schematic presentation of marker assisted conversion of standard maize to β-carotene rich maize line (RP-recurrent parent, D-donor line, RPG-recurrent parent's genome)

RESULTS AND DISCUSSION

Foreground selection Being the codominant markers, they successfully detected homozygous dominant, heterozygous and homozygous recessive plants separately (Figure 2). Percentage of heterozygous plants identified in BC_1 and BC_2 generations and homozygous recessive in BC_2F_2 was in accordance with the expected Mendelian ratio in backcross generations.

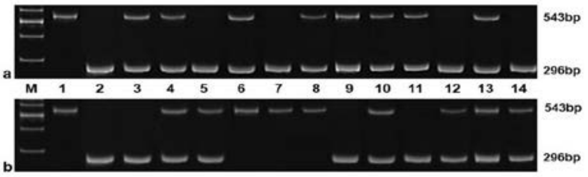

Figure 2. SSR profile of BC_2 (a) and BC_2F_2 (b) individual plants detected with the *crtRB1* gene specific marker.
M: 100bp DNA ladder, 1: donor parent, 2: recurrent parent, 3-14: BC_2 (a) or BC_2F_2 (b) individuals
a) 3, 4, 6, 8, 9, 10, 11 and 13 - heterozygotes
b) 6, 7 and 8 - recessive homozygotes

Background selection SSR markers evenly distributed throughout the genome were efficiently used for identification of BC_2 heterozygous plants with the highest proportion of recurrent parent's genome (RPG). The recovery of the recipient genome in our best lines varied from 93% to 99% for QPM and from 85% to 99% for BC.

Homozygous recessive genotypes with the highest RPG content were screened for biochemical and phenotypic traits to verify their nutritional and agronomical superiority. These newly developed lines are being used for developing high-yielding maize hybrids with improved nutritional benefit adapted to temperate regions.

THE BIOCHEMICAL COMPOSITION OF MAIZE HYBRIDS UNDER THE DIFFERENT CROP PROTECTION STRATEGIES FOR ECB ATTACK

Danijela Ristić[1], Snežana Gošić Dondo[1], Dragan Grčak[2], Marija Kostadinović[1], Jovan Pavlov[1],
Zoran Čamdžija[1]
[1]Maize Research Institute „ZemunPolje", 11185 Beograd, Serbia
[2]University of Priština, Faculty of Agriculture, Kosovska Mitrovica–Lešak, Serbia
dristic@mrizp.rs

INTRODUCTION

Maize is one of the three most economically important cereal grains exposed to abiotic stress which affects the occurrence and intensity of ECB attacks. *Ostrinia nubilalis* Hübn. may attack the maize plants causing the characteristic symptoms of elongated tunnels and circular holes, that can promote the progression of stalk rot. The most common strategy to control *Ostrinia nubilalis* is direct foliar application of insecticides. The aim of this work was to evaluate the whole grain biochemical composition of three maize hybrids belonging to different FAO maturity groups under two different insecticides and one bioinsecticide treatment.

MATERIALS AND METHODS

During 2021 three maize hybrids, belonging to different FAO maturity groups (H1 – 400, H2 – 500 and H3 - 600) were sown in the experimental field of the Maize Institute "Zemun Polje" (Belgrade, Serbia). Plants were treated with two insecticides chlorantraniliprole (Coragen, Du Pont, concentrated suspension 100 ml ha^{-1}) and deltametrin (Decis 2.5 EC, Bayer, concentrated emulsion in a quantity of 400 ml ha^{-1}) and bioinsecticide T4- *Bacillus thuringiensis* ssp. kurstaki (Lepinox Plus, 32000 IUTni /mg, CBC, wettable powder formulation, concentration 750 ml ha^{-1}). In the experimental field, maize ears were sampled at a moisture content of 14%. Phytochemical characterization was conducted for total protein and amino acid content, as well as for the sugar content (e.g. sucrose, fructose, glucose, lactose and maltose). According to Kjeldahl method the amount of total nitrogen was multiplied with conversion factor of 6.25 in order to determine total protein content. Sugar (fructose, lactose, maltose, glucose and sucrose) and amino acids content were validated by Ion Chromatography (IC) method.

RESULTS AND DISCUSSION

Obtained results for tested hybrids are presented in Figure 1, Figure 2 and Figure 3. The lowest level of protein content (from 7.06 to 7.77%) was observed in untreated control across all tested hybrids, compered to insecticides and bioinsecticide tretmant. Protein content was the highest in hybrids H2 (9.43%) and H3 (9.31%), treated with bioinsecticide Lepinox. In contrast, the sugar content was higher (from 2.46 to 3.02 g/100g) in untreated control for H1 and H3 hybrids, while H2 showed the highest sugar content with insecticide treatment (Decis). Reduced level of leucine (from 0.43 to 0.54%) and cystine (0.03 to 0.07%) content was observed in untreated control for all hybrids. Oppositely, increased level of leucine content was detected for all hybrids with Lepinox tretment. Total amino acid content was lowest in untreated control in all analyzed hybrids, while highest was with Lepinox for all tested hybrids.

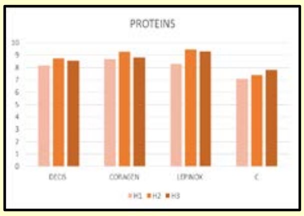

Figure 1. Effect of the applied treatment on protein content (%) in maize grain

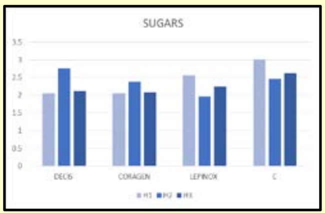

Figure 2. Effect of the applied treatment on sugar content (g/100g) in maize grain

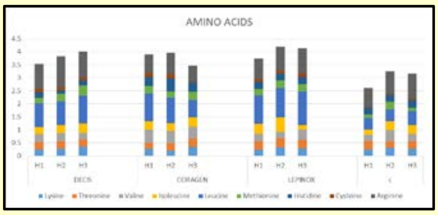

Figure 3. Effect of the applied treatment on amino acid (%) content in maize grain

CONCLUSIONS

- Maize hybrids showed a wide range of variation in phytochemicals in kernel after the different crop protection strategies for ECB control
- This variability observed in kernel quality among the different ECB control strategies can provide valuable information for choosing a sustainable pest control

Grain yield predictions of ZP maize hybrids

Zoran Čamdžija*, Milomir Filipović, Nenad Delić, Jovan Pavlov, Nikola Grčić, Danijela Ristić and Marija Kostadinović
Maize Research Institute, Slobodana Bajića 11185, Zemun Polje, Serbia
Author for correspondence (zcamdzija@mrizp.rs)

Introduction

According to the official FAOSTAT data Serbia ranks 19th when it comes to the maize grain production of 7.9 million tonnes per year.

Around 40% percent of maize grain production comes from mid-early maturing hybrids FAO 400, putting them at highest importance. Maize production in Serbia takes place with almost no irrigation (only 2-3%) at all, leaving production to the climatic conditions and natural rainfall. Mid-early hybrids spend longer period in more humid and more favorable conditions, flower earlier (late June-early July) thusly escaping the risk of higher temperatures covered with less or no rainfall at all in critical moments.

Considering the fact that maize hybrids are created by crossing inbred lines of opposite heterotic groups, the discovery of genetic distances (GD) is of great significance. With the presence of modern breeding tools for discovering heterotic pairs and GDs between used material an efficiency can be increased by reducing needed time for obtaining promising hybrids through more precisely planned field work. Single Nucleotid Polymorphism (SNP) markers proved to be highly accurate in discovering heterotic pairs through GDs.

Materials and methods

For this study 11 crosses were evaluated in order to compare the prediction of data obtained by GDs between crossed inbred lines with the results of same hybrids from field testing. 10 hybrids were new experimental hybrids, while ZP 457 was used as a check. 25k SNP Ilumina Infinium Array for maize was used to determine GD values between used inbreds to suggest the highest hybrid vigor in F1.

Crosses were done in 2020 following GD suggestions which ranged from 0.386 to 0.465 between crossed material (Table 1) to check out is it possible to predict specific superior hybrid performance before the field results itself. As a check ZP 457-market accepted hybrid (registered in 2018 in Republic of Serbia) was used together with 10 other hybrids. All 11 hybrids shared the same female component (Lancaster Sure Crop heterotic group), while male components from opposite heterotic groups (BSSS and Iowa dent) were used.

Table 1. Genetic distances between used maize inbred lines

INBRED LINE	L73B048	L-27/1-2-2	(ZPL-155/18-4/1 x L 325/75-2)	L-707-14-5	L-795-9-1	L-812-13-1	L-143-9-2	L-707-18-2	L-521-5-1	AKO-10-6	L-708-3-2	L-667-11-1
L73B048		0.211	0.457	0.235	0.220	0.287	0.315	0.294	0.270	0.412	0.293	0.266
L74B049	0.211		0.456	0.303	0.234	0.279	0.330	0.353	0.289	0.386	0.323	0.280
(ZPL-155/18-4/1 x L 325/75-2)	0.457	0.458		0.461	0.465	0.456	0.439	0.435	0.455	0.440	0.386	0.441
L-707-14-5	0.235	0.303	0.455		0.271	0.270	0.248	0.190	0.265	0.400	0.358	0.274
L-795-9-1	0.220	0.234	0.469	0.271		0.242	0.270	0.306	0.237	0.387	0.319	0.274
L-812-13-1	0.287	0.279	0.453	0.270	0.242		0.278	0.315	0.244	0.388	0.327	0.278
L-143-9-2	0.315	0.330	0.442	0.248	0.270	0.278		0.259	0.267	0.364	0.352	0.328
L-707-18-2	0.294	0.353	0.430	0.190	0.306	0.315	0.259		0.285	0.390	0.332	0.313
L-521-5-1	0.270	0.289	0.455	0.265	0.237	0.244	0.267	0.285		0.380	0.340	0.267
AKO-10-6	0.412	0.386	0.438	0.400	0.387	0.388	0.364	0.390	0.380		0.349	0.351
L-708-3-2	0.293	0.323	0.386	0.358	0.319	0.327	0.352	0.332	0.340	0.349		0.299
L-667-11-1	0.266	0.280	0.447	0.274	0.274	0.278	0.328	0.313	0.267	0.351	0.299	

GD values of used males ranged from 0.190 to 0.412 clearly stating one broad heterotic group. The most famous heterotic pair B-73 x Mo-17 as well as two Institute's top selling hybrids (ZP 434 and ZP 606) were also included for GD comparison with test hybrids with the GD values of 0.488, 0.466 and 0.462 respectively.

The trial was conducted in 2021 on two locations in Serbia Zemun Polje (ZP) and Kukujevci (KK), where grain yield and moisture were measured.

Results and discussion

Review of B-73 x Mo-17 through ZP 434 and ZP 606 to the newly created hybrids suggests GD values are decreasing with every new cycle of selection between crossed material. Results from field testing compared to GD values show somewhat positive correlation as for ZP 3 exp which ranked 2nd highest GD value and 3rd rank in grain yield outyielding ZP 457 significantly, but ZP 457 GD value of 0.458 (ranking third in GD) suggests higher yielder should be though to find (Table 2). Grain yield results proved the same hybrid ZP 457 to be one of the lowest yielders being superior only to ZP 4123 despite high GD value. In top three yielders GD values were in great correspondence for only one mentioned combination ZP 3 exp, but for the ZP 4 exp and ZP 457 taking first and third position according to the GD rank proved to be good only for 5th and 10th rank within obtained field results, while the lowest yielder ZP 4123 took 4th position according to GD values, having very high value of 0.457.

Table 2. Trial results of tested hybrids with GD values of crossed parents

No	Hybrid	Female		Moisture %*			Grain yield (GY) t/ha*			GY rank	GD**	GD Rank
			Male	ZP	KK	Average	ZP	KK	Average			
1	ZP 457	(ZPL-155/18-4/1 x L 325/75-2)	L74B049	17.6	17.6	17.6	8.2	9.4	8.8	10	0.458	3
2	ZP 1 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-143-9-2	19.7	18.3	19.0	8.3	11.0	9.7	7	0.439	9
3	ZP 2 exp	(ZPL-155/18-4/1 x L 325/75-2)	AKO-10-6	22.5	20.7	21.6	9.5	13.0	11.3	2	0.440	8
4	ZP 3 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-707-14-5	20.5	17.5	19.0	10.3	11.8	11.1	3	0.461	2
5	ZP 4 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-795-9-1	20.3	18.0	19.2	9.8	10.6	10.2	5	0.465	1
6	ZP 5 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-812-13-1	19.1	15.9	17.5	7.8	10.2	8.9	9	0.456	5
7	ZP 6 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-707-18-2	21.1	18.4	19.8	9.9	9.9	9.9	6	0.435	10
8	ZP 7 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-521-5-1	22.7	18.6	20.6	10.0	10.8	10.4	4	0.455	6
9	ZP 8 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-708-3-2	21.9	17.7	19.8	10.4	8.9	9.6	8	0.386	11
10	ZP 9 exp	(ZPL-155/18-4/1 x L 325/75-2)	L-667-11-1	21.2	17.8	19.5	10.8	12.6	11.7	1	0.441	7
11	ZP 4123	(ZPL-155/18-4/1 x L 325/75-2)	L73B048	15.9	13.7	14.8	6.6	10.0	8.3	11	0.457	4

* Locations: Zemun Polje (ZP) and Kukujevci (KK)
** Genetic distances between crossed parents

Conclusion

Today's plant breeding can not be conducted without application of modern technics provided by multidisciplinary approach. This result proves SNP to be very powerful tool in predicting heterotic pairs in ZP maize material and must be considered for more precise planned field work. Such approach is especially needed in case when large germplasm needs to be tested or attached to certain heterotic groups. But, despite the fact GD values being so informative on one side they do not specifically imply to the solution for detecting the most superior hybrid combination therefore leaving field observations to confirm start assumptions.

Stability analysis of different maize hybrids grown in Serbia

Jovan Pavlov*, Nenad Delić, Srboljub Živanov, Zoran Čamdžija, Nikola Grčić, Danijela Ristić, Marija Kostadinović
Maize Research Institute, Slobodana Bajića 11185, Zemun Polje, Serbia
Author for correspondence (jpavlov@mrizp.rs)

Introduction

Maize is the most important field crop in Serbia. The total surface area under maize production is in range from 800.000 to 900.000 hectares annually, which encompasses 25% of the total agricultural land area. The majority of the production is without irrigation, therefore there is a high variation in total annual production, depending on the amount and distribution of precipitations.

The main challenge for maize breeders in Serbia is to develop high yielding and stable hybrids for diverse environmental and climate conditions. Different response of genotypes to diverse environmental conditions is a result of genotype x environment (G x E) interaction. Several statistical methods have been developed for testing G x E interaction. Parametric methods are based on variance components and regression, while non-parametric methods are based on the ranks of genotypes in each environment.

Materials and methods

Seven commercial ZP maize hybrids within maturity range FAO 400-700 were tested at nine different locations across the Serbia for two years period. Selected locations represent the main growing regions in Serbia. Three parametric (Eberhart and Russel model (bi), Shukla's stability variance (ri^2), Francis and Kanneberg coefficient of variation, (CV) and two non-parametric approaches (Huhn rank stability measures Si^1 and Si^2) were used for the evaluation of the hybrids based on their stability.

Results and discussion

The highest yielding hybrid during two years of testing was ZP 5601 (9434 kg/ha) and this hybrid showed above average stability measured by different parameters. Hybrids ZP 606 and ZP 6263 were also high yielding and both good stability according to the majority of used parameters. Hybrids from FAO 400 maturity group had lower yield than the hybrids from other maturity groups and also performed less stable compared to late maturity hybrids.

Significant positive rank correlations were found between grain yield and CV (0.93*), grain yield and ri^2 (0,75*), as well as between CV and ri^2 (0,75*). For all other pairs of parameters positive non-significant correlation was observed, except between bi and Si^1 and bi and and Si^2.

Table 1: Grain yield and stability parameters of ZP maize hybrids tested at nine different environments during 2020-2021

Hybrid	Yield (kg/ha)	Rank	CV(%)	Rank	bi	Rank	ri2	Rank	Si(1)	Rank	Si(2)	Rank
ZP 427	8115	7	34.61	6	0.934	7	678879	7	0.22	5-6	3.06	5-6
ZP 457	8556	6	36.08	7	1.039	6	478248	5	0.18	2-3	2.59	3
ZP 555	8675	5	33.40	4	0.983	3	229299	4	0.14	1	3.06	5-6
ZP 5601	9434	1	31.78	1	1.021	4	151758	3	0.20	4	2.00	2
ZP 606	8962	3	32.76	3	1.002	1	77891	1	0.22	5-6	2.65	4
ZP 6263	9280	2	32.55	2	1.030	5	132134	2	0.18	2-3	1.65	1
ZP 707	8790	4	33.71	5	0.992	2	556084	6	0.29	7	3.94	7

Table 2: Spearmen's rank correlation coefficients between different stability parameters

	Yield	CV(%)	bi	ri2	Si(1)	Si(2)
Yield	x	0.93**	0.46	0.75*	0.02	0.58
CV(%)	0.93**	x	0.39	0.75*	0.13	0.54
bi	0.46	0.39	x	0.50	-0.25	-0.28
ri2	0.75*	0.75*	0.50	x	0.29	0.63
Si(1)	0.02	0.13	-0.25	0.29	x	0.48
Si(2)	0.58	0.54	-0.28	0.63	0.48	x

Conclusion

Based on the results obtained in this study, application of both parametric and non-parametric methods is useful for stability analysis in maize. In our study the highest yielding hybrids performed stable over different seasons and environments, but in some different studies the top yielding hybrids didn't perform stable. Therefore, it is of great importance to evaluate both, grain yield and their stability in order to detect the best adapted hybrids for wider area of production.

BREEDING OF WINTER FEED BARLEY GENOTYPES WITH HIGH DIGESTIBILTY UNDER TURKISH HIGHLANDS

Aytekin AKSOY[1], Gulizar MANAV[1], Fatma UYGUNSOY[1], Fatih DEMIRKUTLU, Ismet AYKOL[1], Serdar URAL[1], Mehmet TEKIN[2], Taner AKAR[2]

[1] TASACO Seed Company, Antalya, Turkey,
[2] Akdeniz University Faculty of Agriculture, Antalya, Turkey
Author for correspondence: tanerakar@akdeniz.edu.tr

This research was carried out to develop new winter type feed barley cultivars with high digestibility during the last six years under highland condition of Turkey. For this aim, 1100 single spike from 110 Turkish landraces were selected in the first year. Then, 130 line based on their cold tolerance, disease resistance, earliness and lodging resistance were determined in the second year. These lines together with for common checks such as Tarm, 92, Aydanhanım, Burakbey and Tosunpasa were experimented under Augmented design in 2019-20 season and they were characterized both genetically by using 21 diverse SSR markers and phenotypically by using 1000 kernel weight , volume weight, grading, starch, crude cellulose and protein, ADF, NDF so totally, 20 advanced lines were selected further evaluation in 2020-21 season. These genotypes were experimented under RBCD at two locations of Konya province and 11 candidate cultivars were selected based on yield and advanced feed quality parameters for regional yield trials in 2021-2022. These together with the four common checks under RCBD at 4 locations of Konya, Ankara and Eskisehir provinces and three candidate lines were nominated for registration trial. There was great variation in terms of digestibility parameters and grain yield among candidate lines compared to common checks. Among these, candidate line 148 with reasonable physical parameters such as 54,2 1000 kernel and 61,2 volume weights and 1,5 g under sieve and superior advanced feed quality parameters compared to the common checks such as 49,8 % starch, 2,8 % crude cellulose, 12,2 % crude protein, 3,5% ADF, 15,0% NDF was one of the most promising genotypes. This study showed importance of Turkish barley landraces and these candidate cultivars can be used parental lines as progenitors for further breeding studies.

Keywords: feed barley, digestibility, crude cellulose and protein, ADF, NDF

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Overview of Zucchini Yellow Mosaic Virus (ZYMV)

Emre ÖZTÜRK[1], Akife DALDA ŞEKERCİ[2]*

1 Alata Horticultural Research Institute, Erdemli, Mersin, Turkiye

2 Agriculture Faculty, Department of Horticulture, Erciyes University, Kayseri, Turkiye

E-mail:emre.ozturk2812@gmail.com

Abstract

The *Cucurbitaceae* family, which has more than 800 species, members have long been cultivated to be used as food, medicinal and also ornamental purposes. However, many plant diseases and pests cause losses of yield and quality in cucurbits and one of them is viral diseases. Zucchini Yellow Mosaic Virus (ZYMV) which causes serious yield losses in cucurbits production worldwide is a viral disease. It is often non-persistently transmitted by aphids and is also transmitted by seed in cucurbits, which may contribute to its rapid spread around the world. Zucchini Yellow Mosaic Virus shows symptoms such as mosaics, yellowing, clogs, curling at the leaf edges, deformation, vein opening, fragmentation of leaves, threading, shortening and thickening of the internodes, and also may result to loss of yield, quality and plant death. As it is known, there is no effective chemical control of virus diseases and the use of resistant/tolerant varieties is the most effective solution. For this reason, it is a very important criterion that the developed cucurbits F1 hybrid varieties are resistant/tolerant to ZYMV. In this study, about ZYMV is given, which is very common in cucurbit cultivation in our country and in the world and causes serious production and quality losses also, awareness is aimed to provide an overview of ZYMV resistant cucurbit breeding practices.

Key words: *Cucurbitaceae,* ZYMV, breeding

1. Introduction

The *Cucurbitaceae* family, commonly identified as cucurbits, consists of several economically and nutritionally important vegetable crops cultivated worldwide, such as cucumber, melon, watermelon, pumpkins, gourds and squashes. Pumpkins which belonging to the *Cucurbitaceae* family and cultivated in our country, also it classified as *Cucurbita moschata*, *Cucurbita pepo* and *Cucurbita maxima* (Yanmaz and Düzeltir, 2003). Fruit and seeds of pumpkin is evaluated as product. The fruit is used in fresh, ready-to-eat, canned food and confectionery industries. Its seeds are used as snacks, oil, cosmetics, medicine and animal feed, as well as in the bread and pastry industry (Kurtar et al., 2018). *Cucurbitaceae* have a very important place in human nutrition due to the high nutritional elements they contain. Pumpkin has high vitamins, mineral, water and protein contents. Turkiye provides production opportunities for many different plant species thanks to having different ecological conditions. In the world, 22,900.826 million tons of pumpkin production is made on 1.539,023 million hectares (FAO, 2019). Our country ranks 8th in world pumpkin production with 590,414 tons, contributing 2.58% to the total world production (FAO, 2019). Cucurbits which can be grown commercially, mostly greenhouse, is produced throughout the year in all regions of our country, especially in the Mediterranean and Aegean regions.

As with all cultivated plants, there are diseases and pests that affect the pumpkin negatively. More than 20 viruses have been characterized as infecting cucurbit crops in the major production areas. Among them, cucumber mosaic cucumovirus (CMV), watermelon mosaic potyvirus 2 (WMV2), squash mosaic comovirus (SqMV), melon necrotic spot carmovirus (MNSV) and papaya ringspot potyvirus (WMV1) are the most common (Lovisolo, 1980). One of the most important of these is the Zucchini yellow mosaic potyvirus (ZYMV).

ZYMV which was first isolated in Italy in 1973, identified in 1981, and later identified in all continents, is one of the most important cucurbit viruses that cause high economic damage. ZYMV is common in almost all countries where cucurbits are grown in temperate, subtropical, and tropical conditions. The virus is very harmful in highly mechanized production areas and in more traditional agro-ecosystems. It is often non-persistently transmitted by aphids and is also transmitted by seed in zucchini, which may contribute to its rapid spread around the world.

Due to viruses, losses of quality and product occur every year. Unfortunately, an effective method of combating viruses has not yet been found and the losses are increasing day by day. More than 59 active viruses have been detected in zucchini production areas in the world. One of the most harmful of these viruses is Zucchini Yellow Mosaic Virus (ZYMV). Mosaic symptoms, deformity and fruit spoilage were detected in leaves infected by ZYMV. This virus that are transmitted from plant to plant because of Aphididae pests and non-persistent ways (Çat et al., 2016).

The process of changing the genetic structure of plant species with economic value in line with the wishes of the consumers by benefiting from cytogenetic and genetic principles is called plant breeding (Tosun and Sağsöz, 2005). The main purpose of plant breeding is to create variation with the differences in the genetic structure and to produce individuals with higher quality, productive, more resistant to diseases and pests and with high adaptability (Tosun and Sağsöz, 2005). In 1973, a vigorous viral disease firstly appeared in zucchini plants in Northern Italy (Lisa et al., 1981). Infected these plants showed intense stunting of plants and yellowing symptoms in leaf and fruit. Lisa et al. (1981) identified this virus which named zucchini yellow mosaic virus (ZYMV). Also, in 1983 this virus was observed in Türkiye (Davis and Yilmaz, 1984). The result of studies, some cucurbits species were found tolerant/resistant to ZYMV. The most suitable solution to control viral diseases is the use of resistant species (Desbiez and Lecoq, 1997).

In this study, it is aimed to provide an overview of ZYMV resistant zucchini breeding practices.

2. Effects of ZYMV on Zucchini

Symptoms of ZYMV on cultivated crops are often very severe and cause significant yield losses. In addition, serious deformations, deterioration in fruit shape and color changes are seen in fruits obtained from diseased plants, which makes them unmarketable. The product losses can be varied between 50-100% because of the virus (Blua and Perring, 1992). Different symptoms are observed according to the type or variety. In *Cucurbita pepo* leaves develop a yellow mosaic and become severely blistered. Fruits are distorted with prominent lumps (Lisa and Lecoq, 1984). In other squash types such as *C. moschata*, *C. maxima*, symptoms may vary from mottle to severe mosaic with occasional recovery and fruits may also be severely distorted. In melon (*Cucumis melo*) early symptoms on leaves are vein clearing and yellow mosaic. Leaves are subsequently reduced in size, deformed, frequently with serrated edges and dark green blisters. Severe mosaic and deformations are seen on leaves, shoot tips and fruits of cucumber (*Cucumis sativus*). Spots and mosaicism are common in watermelon (*Citrullus lanatus*). Irregular coloration and deformities can be seen in fruits.

ZYMV has some fatal effect on plants, which were investigeted. According to studies, virus-infected zucchini leaves (*C. pepo* Eskandarani) showed violent symptoms on new leaves 2 weeks after inoculation. These symptoms were observed severe mosaicism, green blisters, size reduction and deformation (Radwan et. Al., 2007).

Photosynthetic pigment content of leaves (Chl a, Chl b and carotenoids) is significantly reduced in ZYMV infection. It was stated that Chl a, Chl b and carotenoid contents decreased under ZYMV infection (Radwan et al., 2007). In addition, a decrease of approximately 48% in the total pigment content was determined under ZYMV infection, while studies reported that leaf protein, carbohydrate and proline content increased in infected plants (Radwan et al., 2007).

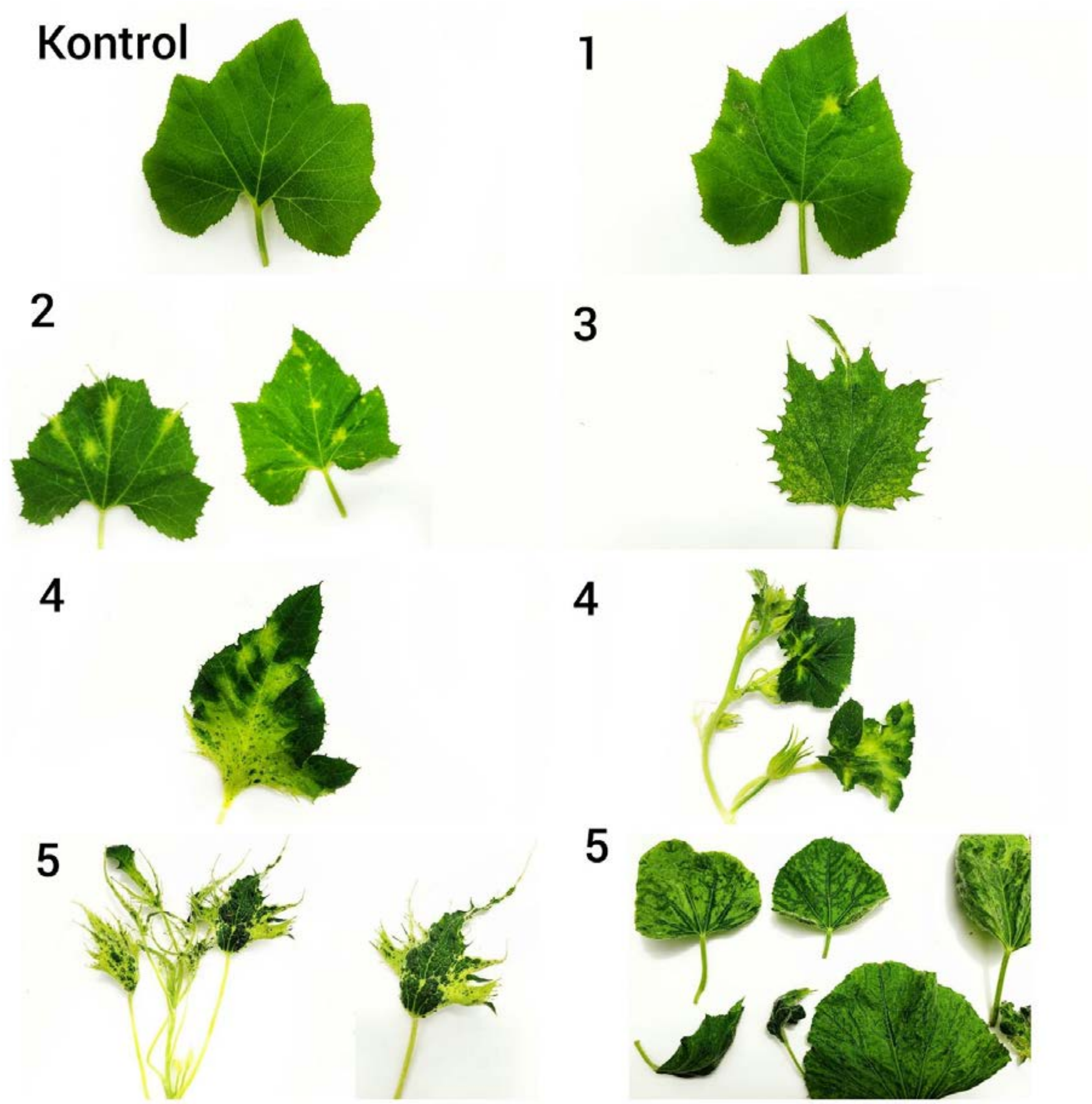

Fig. 1. Scale of damage caused by ZYMV in *Cucurbita pepo* (original: Dalda-Şekerci A., 2020)

3. Identification And Detection Methods

Assay on the indicator host ZYMV in a single infection is easily distinguishable from other common cucurbit-infecting viruses (Lisa and Lecoq, 1984). However, precise identification of the virus in field samples is difficult due to frequent mixed infections with other viruses. For this reason, laboratory tests are very important for an accurate diagnosis.

3.1. Serological Techniques

Polyclonal antisera provide rapid and practical detection of ZYMV (Lisa et al., 1981; Lecoq et al., 1983; Greber et al., 1987). Also, SDS-ID is useful for detecting mosaic viruses in cucurbits (Purcifull et al., 1988) and is therefore well suited for diagnosis in a limited number of samples. However, it is not suitable for multi-sample studies.

The enzyme-linked immunosorbent assay (ELISA) is now widely used method for more accurate and large-scale detection of ZYMV (Clark and Adams, 1977; (Desbiez and Lecoq, 1997). Double antibody sandwich (DAS)-ELISA is the most widely used variant of this technique due to its specificity and reproducibility. Menassa et al. (1986) described the detection of ZYMV in intact leaf discs by direct or indirect ELISA tests. In addition, serological tests using nitrocellulose membranes are used as an alternative to ELISA tests

3.2.Molecular Techniques

Polymerase chain reaction (PCR) has been used as an effective diagnostic tool. In the case of ZYMV, reverse-transcription (RT)-PCR has been used to amplify viral fragments of the 3’ terminal part of the genome, from extracted total plant RNA (Thomson et al., 1995).

In the use of molecular techniques, total RNA is isolated by using young leaves taken from plants determined to be infected with ZYMV by ELISA method, and then cDNAs are obtained by RT (Reverse transcription) process with RT-PCR method. In the second step, PCR is performed using these cDNAs. At the end of the RT-PCR processes, the preparations obtained in the virion analysis studies with the amplified nucleic acid material of ZYMV are stained with bromophenol blue and subjected to 1% agarose gel electrophoresis method.

The amplified fragment can be used for further molecular analysis. Immunostaining of virus from crude plant extracts following RT-PCR avoids the time-consuming step of RNA isolation.

Different molecular techniques have been used to distinguish serologically indistinguishable isolates of ZYMV. Barbara et al. (1995) used the restriction fragment length polymorphism (RFLP) molecular marker technique.

Studies About Resistance Breeding to ZYMV

The importance of viral diseases is in terms of plant health increasing since no chemical has yet been used in the fight against plant virus diseases. Since ZYMV is a disease transmitted by aphids, although some insecticides can be used, the applications only prevent the direct effect

of the pest and indirectly delay the spread of the disease. As a result, chemical control is not effective in the control of ZYMV. The use of resistant species is a very important factor in the fight against virus diseases (Çalışkan, 2007). Resistance genes to ZYMV have been identified for generally cultivated cucurbit species. The most of resistances are observed in wild species and breeding programs are required to transfer them into cultivated species.

Also, many studies have been carried out to develop new varieties resistant to ZYMV and to reveal the genetic structure of the disease, and studies are still continuing on this subject. Many researchers have tried to analyze the inheritance of ZYMV resistance and identify markers associated with resistance genes (Zraidi et al., 2006; Harris et al., 2009; Pachner et al., 2014; Capuozzo et al., 2017). The resistances are controlled by single genes (Desbiez and Lecoq, 1997). Ling and Levi (2007) conducted a study to find ZYMV resistant genotypes in gourd. Of these 190 genotypes, 36 were found to be fully resistant, 64 genotypes were partially resistant (some of the tested plants were resistant while others were susceptible), and 90 genotypes were found to be susceptible. Levi et al. (2009) investigated 56 gourd genotypes and important cucurbit species (*C. maxima* Duch., *C. pepo* L., *Citrullus* spp., *Cucumis melo* L., *Cucumis sativus* L.) using 236 SRAP markers. While all gourd genotypes were infected by whitefly, less affected genotypes were observed. Resistant genotypes to ZYMV virus were collected.

In studies conducted in different regions of Turkiye, it has been determined that ZYMV is observed in areas where cucurbits are grown and causes serious damage (Özalp, 1964). In the studies carried out that the presence of ZYMV was found in Adana, İçel, İzmir, Manisa, Afyon and Konya provinces in 1991, Ankara province in 1992, Amasya, Çorum, Samsun and Tokat provinces in 1995, Antalya in 1998 and Isparta in 2000, and Erzurum, Artvin in 2002 (Topkaya and Ertunç, 2015). All of the CP genes were cloned on the genomic RNAs of two strong ZYMV Turkiye isolates isolated from pumpkin and melon and determined their nucleotide sequences and amino acid sequences. At the end of the study, they determined that the CP gene of both ZYMV isolates consisted of 837 nucleotides and encoded CP with a size of 31.2 kDa, and they reached a phylogenetic analysis and found a high (97%) similarity between the nucleic acids of the two Turkiye isolates (Özer et al., 2012).

Result

Plant breeding: increasing population, increasing abnormal natural events due to climate change, drought, salinity etc. and is very important in the fight against pests. Breeding studies resistant to ZYMV are of great importance for pumpkin cultivation. Studies carried out to date, great progress has been made in breeding studies resistant to ZYMV, resistant and tolerant lines have been obtained, and plant genes in which the virus is effective have been investigated.

ZYMV, first observed in Italy in 1973, was difined worldwide within the last 25 years. Otherwise, ZYMV could have been an endemic virus in geographically restricted areas for a long term. ZYMV is now present worldwide and is responsible for important losses in cucurbits. The new strategies have been improved, and resistant plants (obtained by conventional breeding programs, biotechnological and molecular breeding technics, or pathogen-derived strategies) should be accessible within a few years for all of the cultivated species. On the other hand, the significant potential of versatility of the virus reveals that some resistances might be rapidly accomplish by ZYMV isolates, and that control programs will have to combine several techniques to remain efficient.

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Improvement of cotton varieties using modern genetic and biotechnological methods on the basis of biodiversity of the genus *Gossypium* L.

Fakhriddin N. Kushanov[1,2], **Ozod S. Turaev**[1,2], **Dilrabo K. Ernazarova**[1], **Ziroatkhon A. Ernazarova**[1]

[1]Institute of Genetics and Plant Experimental Biology, Academy of Sciences of the Republic of Uzbekistan, Qibray QFY, Yuqori-Yuz, Qibray district, Tashkent region, 111226 Uzbekistan

[2]Department of Biology, National University of Uzbekistan, University Street-4, Olmazor district, Tashkent, 100174 Uzbekistan

Author for correspondence (fakhriddinkushanov@gmail.com)

Abstract

Plant genetic diversity and resources are one of the most important resources for food security and agriculture. Many crop species especially their wild ancestors are responsible for the genetic variation associated with world food production. Creating a new variety using traditional breeding methods requires some hard work and a long time. Modern, marker-based selection (MAS) technology is somewhat more efficient than conventional selection methods in terms of resource efficiency and less time required for creating a new variety.

Keywords: Cotton, *Gossypium* L., genetic diversity, marker-assisted selection.

Review of the Abstracts

Cotton (*Gossypium*) is the main cash crop that supplies the world's textile industry with natural fiber. The genus *Gossypium* L. belongs to the small taxonomic tribe (*Gossypieae*) with nine genera in total, eight of which are classically recognized. The haploid set of cotton chromosomes is 13, and in nature, they occur as diploid (2n=26) and tetraploid (2n=52) species. At present, the genus *Gossypium* includes seven allotetraploid and 50 diploid species distributed among eight genome groups (A-G and K genomes).

The natural biodiversity of cotton - its wild relatives - is the richest source of genetic resources, the smallest part of which is used in breeding programs. Much of the gene pool is still waiting to be recognized. The rich potential of the Old-World species has been used extremely little; they are used mainly in the countries of Asia and India. In breeding terms, many forms of subspecies of these species, as well as New World species (*G. herbaceum* L ., *G. arboreum* L.), are of great practical interest, possessing a number of very valuable economic traits: high early maturity, resistance to water deficiency, disease, good fiber quality, fiber hygroscopicity.

The reasons for the extremely low use of the available intraspecific diversity are, first of all, the insufficiently high level of development of theoretical issues of taxonomy and phylogeny, as well as a number of objective problems that arise during hybridization, biotechnology, genetic engineering and other attempts to involve and transfer valuable germplasm into the genome of cultivated varieties.

The involvement of new alleles of genes of wild-growing relatives in the selection process greatly increases the prospect of creating unique source materials with useful properties and with a new gen-immune system of potential resistance to agricultural diseases and pests.

However, due to the difference in the number of chromosomes, the possibility of obtaining hybrids based on cross-breeding of diploid species and tetraploid species, in particular *G. hirsutum*, is limited. Since, under the influence of colchicine it is possible to double the number of chromosomes of diploid species and crossbreed with *G. hirsutum* varieties and thereby create starting materials for cotton breeding research.

One of the modern approaches to the study of plant genomes is the technology of molecular markers, which make it possible to fully assess phylogenetic relationships and relationships, identify varieties, and identify DNA markers associated with economically valuable traits. Once identified, these molecular markers allow faster and more efficient plant breeding with a significant reduction in financial costs.

Determination of heat and drought tolerant lines in segregating populations produced by interspecific crosses in eggplant

Esra Cebeci[1*], H.Filiz Boyaci[2], Yıldız Dogan[1], Laura Toppino[3], Giuseppe L. Rottino[3]

[1]: Batı Akdeniz Agricultural Research Institute, (BATEM), PK: 35, 07100, Antalya, Türkiye
[2]: Food Control Laboratory Directorate, 07260, Antalya, Türkiye
[3]: Council for Agricultural Research and Agricultural Economy Analysis, Montanaso, Lombardo, Italy

*Author for correspondence (esrac3@hotmail.com- Phone number: 0532 5833701)

Abstract

Nowadays abiotic stresses originated by climate change are one of the main factors causing reductions to the agricultural production. Heat and drought are the most prominent abiotic stress factors effecting both eggplant production worldwide and food security. Although eggplant is known as more tolerant to these stresses compared to other vegetables and solanaceous crops, its quality and yield suffers from severe stress conditions. In this research, 256 F2 plants developed from the interspecific cross between the wild relative of *Solanum insanum* L. and the pure line (BATEM-TDC47) from BATEM eggplant genepool were used as plant materials. Seedlings at 3-4 true leaves stage bred in three-liter pots filled with a 1:1 mixture of peat and perlite were subjected to drought stress test to this end, a 75% deficit irrigation was applied to the plants, while control plants were watered with the required amount to recover the 100% of ETp as appropriate management strategy. The stress symptoms of plants were determined by morphological and chemical analyses. Plant heights were measured on the 25th day of the experiment and visual evaluation stress symptoms was observed according to the 0-5 scale. Morphological observations, MDA (malondialdehyde) and proline content of selected plants were performed to confirm their tolerance levels to heat and drought. Following the drought test, the plants were transferred to the greenhouse for the determination of heat tolerant individuals.

Keywords: abiotic stress, drought, eggplant, heat, MDA, proline

Introduction

Eggplant (*Solanum melongena* L.) is a crop species belonging to the family of *Solanaceae* but unlike the other solanaceous crops tomato, potato and pepper it has an old world origin as it is originated from both Southeast Asia and India (Barchi et al., submitted). It is widely grown in Southern and Southeast Asia, where great part of the world's population is located so and is included in the International Treaty on Plant Genetic Resources for Food and Agriculture's list of the most important 35 food crops substantial for global food security (Fowler et al., 2003). The most important factors limiting eggplant production are biotic and abiotic stresses (Rotino et al., 2014). For a sufficient yield and good quality of fruits, eggplant needs to be irrigated regularly, with an optimal temperature ranging between 22 and 30 °C (Li et al., 2011).

Nowadays climate change is affecting the many parts of the world. Extreme weather events like Floods after heavy rains, heat waves or low temperature shocks, increased soil salinity and prolonged water scarcity (drought) are the main results of the climate change, and are the cause of great losses in agricultural production and fruit quality in recent years worldwide (Wakchaure et al., 2020). Due to Climate change and global warming, crops started to encounter more and more frequently drought and heat stresses during their vegetation and harvesting period in arid as also in semiarid regions especially with Mediterranean climate (Fahad et al., 2017). Although results of previous studies suggested that eggplant has tolerance to the principal abiotic stresses (including Drought, heat, salinity) compared to the other vegetables (Behboudian, 1977; Sarker et al., 2004; Díaz-Pérez and Eaton, 2015), it has been demonstrated in recent research that it suffers from extreme water stress deficit in terms of fruit quality and yield (Plazas et al., 2019; Wakchaure et. al., 2020: Singh et. al., 2021; Toppino et al., 2021). According to Karam et al. (2012) water deficiency application increasing from 20% to 40% of the optimal watering amount causes a yield decrease of nearly 60% with respect to the control; moreover, high temperatures above 38°C can seriously inhibit the growth of seedling, flower development, and eventually impact the fruit quality and yield of eggplant (Zong et al., 2018). Eggplant is among the top five vegetables constituting the diet of people living in drought-affected regions of the world (Wakchaure et al., 2020), as a consequence yield losses due to abiotic stresses could severely affect the daily diet and food supply chain in these regions. Adapting eggplant production to altered climatic conditions requires the development of tolerant cultivars. Crop wild relatives of eggplant display a wide genetic diversity and some of them possess tolerance traits against the principal biotic or abiotic stresses (Knapp et al., 2013; Fita et al., 2015; Plazas et al., 2019). Therefore, interspecific hybridization and introgression of useful traits from allied species into the eggplant genetic background may play a prominent role in increasing heat and drought tolerance of this crop species (Kouassi et al., 2016; Plazas et al., 2016). Evaluation of the response of segregating populations derived from inter-specific hybridization to heat and drought stresses and the selection of best performing progenies would reveal as an useful tool for the development of breeding lines with improved tolerance to stress (Espanani et al., 2019).

In this study, an interspecific hybridization was performed between *Solanum melongnena* L. and *Solanum insanum* L. and the response of the F2 segregating population to heat and drought was assessed aimed at the selection of best performing lines and development of tolerant lines to stressed conditions.

Material and Method

Material

256 individual F2 seedlings derived from the selfing of the interspecific F1 hybrid between the *S. melongena* L. BATEM-TDC47 pure line (sensitive parent) and the crop wild relative *Solanum insanum* L (tolerant parent) were used as a plant material. The Pure line "BATEM-TDC47" was developed in Bati Akdeniz Agricultural Research Institute under the project "Development of Qualified Genitors (Halfway Material) for Eggplant Breeding Programs and Seed Technology" (Project number: TAGEM/BBAD/10/A09/P01/12). The *Solanum insanum* L. accession employed as donor of tolerance trait was provided from INRAE, France. In addition, 60 seedlings of the F1 hybrid plus 60 seedlings of each parent line were tested for drought stress in a trial planned according to randomized block design with three replications to be compared with the F2 individuals.

Method

Seeds were sown in March 2021 and germinated in viols containing mixed peat moss and perlite (1:1) medium. Seedlings were equally watered with Hoagland solution (Hoagland and Arnon, 1950) until the 2th-3rd true leaves stage and then they were transferred to the pots. Two seedlings were planted per each pot and they were normally watered with Hoagland solution until proper root development for two weeks. The application of the water deficit treatment started on April 30, 2021; the entire F2 population and 10 plants for each of the three replications of F1 and parent plants were subjected to stress by applying 75% deficit water compared to the control. To determine the water amount to be supplied in both control and stressed irrigation, all pots from control group were weighed daily and then the control group was watered up to full recover the ETp difference (the amount of weight lost each day due to evapotranspiration); a media performed on this value was considered as 100% control supply therefore deficit water supply was calculated as the 25% of the average control value and applied to the drought stressed group (Kıran et al., 2019).

On the 25th day of the drought application all plant heights were measured with a ruler and all F2 plants were singularly evaluated according to the modified 0-5 visual scale already used by Banik et al. (2016) and Sseremba et al. (2018) where 0: No symptoms (control plants), 1: slow growth, 2: 25% yellowing and curling, 3: 25-50 %

yellowing and curling, dropping leaves, 4: 50–75% wilting and curling, drying, 5: more than 75% wilting and curling, dried plants. According to this scale, the 100 F2 plants displaying "slow growth" (Scale = 1) were selected as "tolerant to drought" and transferred to the greenhouse for the heat tolerance study and further morphologic characterization. Before the transfer, leaf samples were taken from each drought tolerant F2 plant together with the F1 and parents' both control and stressed plants to analyse the malondialdehyde (MDA) and proline leaf content. MDA was analysed according to Luts et al. (1996), while proline content was evaluated according to the Bates et al. (1973) method. Temperature and humidity were recorded during both the pot and greenhouse experiments and are presented in Figure 1 and 3.

Figure 1. Temperature (°C) and Humidity (%) recorded during the drought stress pot experiment

Temperature and humidity ranged between 15 °C – 45 °C and 23% - 65%, respectively during the drought experiment in pots. Figure 2 shows general view from the compartment in which the experiment was established and the responses of F2 population at the 25th day of drought application. Selected drought tolerant plants were transferred to the greenhouse where their tolerance to heat was evaluated using the morphologic descriptors modified from Boyaci et al. (2015) and detailed In Table 1. While the F2 best performing plants were morphologically characterized in greenhouse for heat stress, they were also selfed to generate the F3 generation.

Figure 2. A- General view from the compartment in which the drought experiment was established, B- The responses of F2 population on the 25th day of drought application

Table 1. The phenotypic descriptors and observation methods used in the study

Greenhouse climatic conditions were also recorded and shown in Figure 3. Characterized plants were self-pollinated by hand individually in greenhouse conditions to obtain F3 progenies. In greenhouse temperature ranged between 25 – 49 ^{0}C and the average temperature was recorded as 36 ^{0}C, humidity ranged between, 13%-- 99 and the average humidity was assessed as 76%.

Figure 3. Temperature (°C) and Humidity (%) recorded during the heat stress period

Results and Discussion

In terms of plant height, significant differences were observed between the drought-stressed groups of tolerant (*S. insanum* L.), sensitive (BATEM-TDC47) parents, and F1 hybrid plants measured on 25th day of the drought experiment with respect to their corresponding control group. The average plant height of the drought stressed group of *Solanum insanum* L. plants was 13,4 cm, while the average plant height of its control group was 17,6 cm. Drought stress accounted for 25,6% variation between the two groups. The average plant height of the sensitive genotype BATEM-TDC47 was 17,3 cm in the drought stressed group while 24,2 cm in the control group, with variation between the two groups of 28,5%. In F1 plants, the mean values ranged 19,4 cm in the control group, while being 15,9 cm in the stressed group, and the change rate was 18%. Simultaneously, wide variation was observed also among the F2 population in terms of plant heights under drought effect (Table 2).

Table 2. The effect of 75% water deficit on the plant height applied during the seedling period

Similarly, Semida et al. (2021) reported that water deficit in eggplant significantly affected and reduced plant height, stem diameter and number of leaves, as well as Fita et al. (2015) reported that plant height and fresh weight were the most distinctive morphological characters to determine drought tolerance in eggplant.

In the current study, morphologic damage level of the plants from F2 population was observed on the 25th day of the drought experiment using a 0-5 scale. 100 plants showed the lowest levels of damage as they displayed only a slow growth therefore they got "1" as scale value, being therefore evaluated as drought tolerant according to Kiran et al (2015) and transferred to the greenhouse for being further tested against heat tolerance. Additionally, in terms of the scale evaluation, 150 F2 showed symptoms as 25% yellowing and curling on plants and got "2" from the scale, being therefore noted as sensitive. Six among the 256 F2 plants got "3" as a scale value as they showed symptoms 25%-50% yellowing and curling on plants and dropping leaves and were also noted as sensitive. In addition, studies on melon (Kusvuran, 2010), pea (Ajayi et al., 2018), and kiwifruit (Zhong et al., 2018) revealed that the 0-5 scale is an effective tool in determining to drought tolerance.

Leaf samples harvested from 50 among the 100 tolerant F2 plants which also displayed desired morphological features were then analyzed for MDA and proline accumulations. MDA is the most frequently used biomarker of oxidative stress in plants, while proline is an amino acid which protects the plants from various stresses. An increase of proline levels under drought is related to a higher degree of adaptability to the plants to the stress; on the contrary an increase of the MDA values is linked to an higher sensitiveness While the MDA values ranged between 9,87 - 15,97 nmol/g FW, proline content was determined between 2,40 -16,70 µg g^{-1} and figure 4 showed the results of F2 plants. MDA and proline values detected in Parents and F1 plants' both under control and drought tested conditions are also presented in Table 3.

Table 3. MDA and proline amounts showing different degrees of increases under drought compared to the control plants

In this study, both MDA and proline amounts of F1 and parents showed increases under the effect of drought with respect to their respective control plants (Table 3). However, as expected, the sensitive parent has high MDA variation and low proline variation under drought stress with respect to the tolerant parent, which, on the contrary, displayed lower MDA and higher proline variation. Previously, Kıran et al. (2015) reported that there is an effective direct correlation between the scale value describing the level of symptoms and the levels of MDA, so that under drought stress conditions MDA levels display the lowest level of variation as the scale value decreases. Likewise previous studies conducted on beans (Kandemir et al., 2018) and tomatoes (Yekbun and Kabay, 2017), reported that MDA content increases according to the degree of damage to the cell membrane in plants subjected to stress therefore, as the MDA content increases, the range scale increases as the drought tolerance of plant decreases.

Figure 4. Graphic shows MDA and proline alteration in selected F2 plants

In a study on tomatoes, it was determined that dehydrated plants accumulate osmolytes such as proline in their leaves and protect themselves from the stress accordingly (Noori et al., 2018). In another panel study aiming at determining the drought effect among different cultivar of rice, which is a semi-aquatic species requiring consistent irrigation prolonged during all season to grow, it was established that the higher levels of proline were accumulated in those cultivars which also displayed the higher tolerance to water deficiency (Lum et al., 2014).

A panel of 100 F2 plants were selected as drought tolerant according to their overall good performance regarding plant height, symptoms scale value, MDA and proline content, and were therefore transferred to the greenhouse to be kept during the summer period, where their heat tolerance was assessed under normal irrigation conditions. For this purpose, the fruiting capacity of each plant was examined and the genotypes that could not set fruit under high temperature conditions were recorded as more sensitive to heat.

The results of phenotypic characterization with regard of many qualitative traits is detailed in Table 4. F2 average plant height, fruit length, fruit width and fruit weight were 106,4 cm, 14,0 cm, 6,8 cm and 55 g respectively.

Table 4. Data of some phenotypic traits scored among the 100 F2 plants determined as drought tolerant

Among the selected lines, significant differences were observed for all traits related to plant architecture, leaf prickles, leaf hairiness and fruit characteristics. The growth habit of the plants was neither upright nor widespread, the number of lobes in the leaf was average, and the plants were usually slightly spiny and hairy. Anthocyanin distribution in plant and leaves were also noted as mostly absent or low. The fruits were of various sizes, preferentially round but also oval or elongated.

Table 5. Some phenotypic characteristics of 100 lines selected as drought tolerant

The morphologic parameters revealed a wide range of phenotypic combination in the F2 population; Similarly, a wide segregation and variability, is usually expected in a segregant population obtained from a cross between cultivated eggplant and its wild relatives as reported in previous studies (Prohens et. al., 2013; Frary et al., 2014; Boyaci, 2020). Interspecific hybridization is a strategy which extremely helps to transfer many useful features from wild species to cultivated eggplant, leading to increase the genetic diversity of the latter (Kouassi et al., 2016; Plazas et al., 2019). Meanwhile, due to the wide variability that usually is generated in a progeny when two different species are combined, before taking part in any breeding program the best performing progenies selected for a desired trait need to be submitted to a deep phenotypic characterization to better assess their combination ability and avoid selection of also negative traits. (Gaufichon et al., 2010). With this study, the F2 plants determined as heat and drought tolerant were also morphologically characterized with a sufficient number of descriptors created for eggplant, and only the progenies of the plants with the best traits combination will be considered for future employment in breeding programs to develop new eggplant breeding lines with improved adaptability to stress.

Conclusion

Studies have been carried out for many years on tolerance to biotic stresses in eggplant. Thanks to many successful breeding programs, resistant cultivars to biotic stresses have been developed and are now available. As studies are mostly focused on the determination of resistance sources, the resilience to abiotic stresses is quite a new topic of discussion. This research is aiming to develop heat and drought tolerant lines in eggplant. 100 F2 lines Selected as the most drought and heat tolerant were morphologically characterized, selfed and progressed to the F3 generation. Drought tests and selfing of inbred lines in next generations will be continued to provide their durability and to be fixed at homozygous level, so that new eggplant hybrids with improved features as heat and drought tolerance will be developed in the future. In this respect, this study, which deals with the beginning of breeding studies for heat and drought stress, can be suggested as a model for breeding programs not only for eggplant but also for other species.

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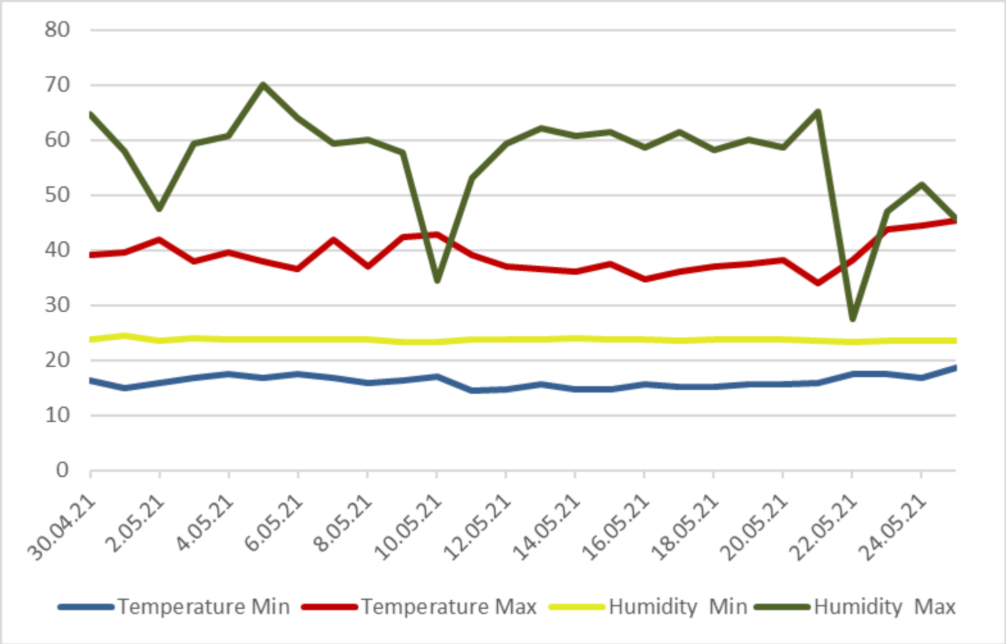

Figure 1. Temperature (°C) and Humidity (%) recorded during the drought stress pot experiment

Figure 2. A- General view from the compartment in which the drought experiment was established, B- The responses of F2 population on the 25th day of drought application

Table 1. The phenotypic descriptors and observation methods used in the study

No	Descriptors	Explanation
1	Growth habit	1= very upright 3= upright 5= intermediate 7= prostrate
2	Leaf blade lobs	1= very weak 3= weak 5= intermediate 7=strong 9= very strong
3	Anthocyanin distribution in plant	1=absent 3= low 5= intermediate 7= high
4	Anthocyanin distribution in leaves	1=absent 3= low 5= intermediate 7= high
5	Leaf prickliness	1= None 3=Very few (1-2) 5= Few (3-5) 7= Intermediate (6-10) 9=Many (11-20) 11= Very many (>20)
6	Leaf hairiness	1=absent 3= low 5= intermediate 7= high
7	Number of flowers/ inflorescence	number
8	Fruit load	1= very low 3= low 5= intermediate 7=high 9= very high
9	Leaf blade width	Measured in cm with ruler (Average of the best 3 leaves for each plant)
10	Leaf blade length	Measured in cm with ruler (average of the best 3 leaves for each plant.)
11	Total plant height	Measured in cm as the distance from the soil surface to the tip.
12	Varietal type	1=long 3=oval 5=round 7=striped
13	Predominant fruit colour	1=dark green 3=green 5=lilac 7=dark lilac 9=purple 11=dark purple 13=black
14	Secondary fruit colour	1=dark green 3=green 5=lilac 7=dark lilac 9=purple 11=dark purple 13=black
15	Fruit glossiness	1=opaque 3=intermediate 5=bright peel colour
16	Fruit curvature	1=round 3=no curvature 5=slightly curved 7=curved 9=S shaped 11= U shaped
17	Presence of grooves	1=absent 3=few 5=intermediate 7=many
18	Calyx fruit coverage	1= less than 10% 3=10-20% 5=20-30% 7=30-40% 9=50% and more
19	Fruit firmness	1=spongy 3=intermediate 5= tight
20	Fruit weight	Measured in g (average of 2-3 fruits from each plant)
21	Fruit length	Measured in cm (average of 2-3 fruits from each plant)
22	Fruit maximum diameter	Measured in cm (average of 2-3 fruits from each plant)
23	Fruit length/breadth ratio	Calculated
24	Peduncle length	Measured in cm (average of 2-3 fruits from each plant)
25	Fruit calyx prickliness	1= none 3= very few (1-2) 5= few (3-5) 7= intermediate (6-10) 9= many (11-20) 11= very many (>20)
26	Petiole length	Measured in cm
27	Fruit end button size	1=small 3=intermediate 5= large
28	Presence of chlorophyll on the pistil scar	1=absent 3= present
29	Fruit color distribution	1=uniform 3=mottled 5=netted 7=striped

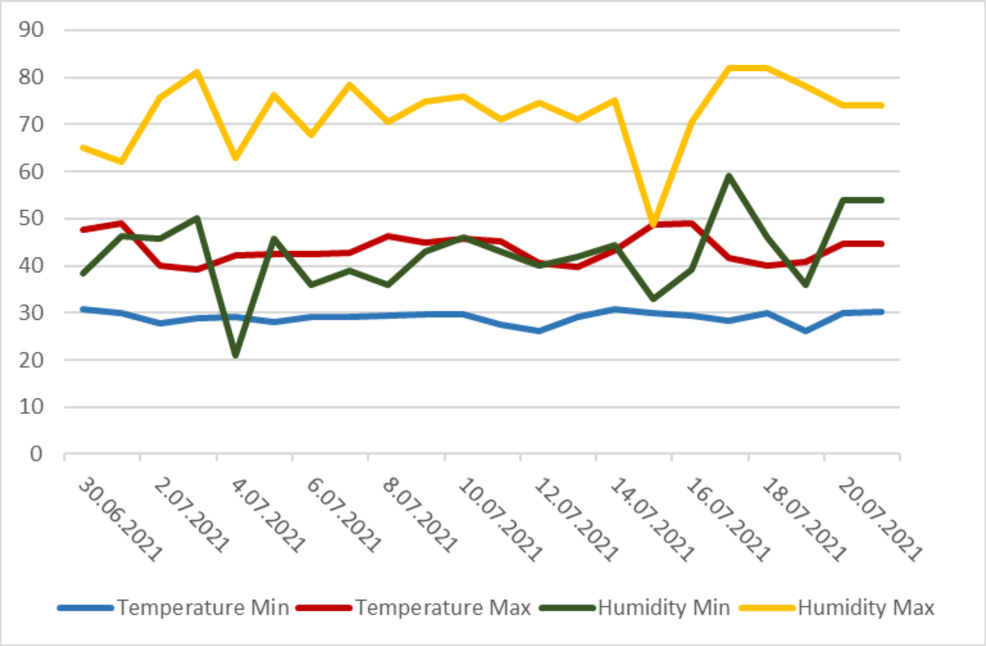

Figure 3. Temperature (°C) and Humidity (%) recorded during the heat stress period

Table 2. The effect of 75% water deficit on the plant height applied during the seedling period

	S. insanum		TDC47		TDC47 × *S. insanum*		F2**
	Control	**%75 WD**	**Control**	**%75 WD**	**Control**	**%75 WD**	**%75 WD**
Shortest plant height (cm)	12,0	10,0	18,5	14,0	15,0	11,0	10,0
Longest plant height (cm)	22,0	19	28,0	20,0	23,0	18,0	24,0
Average plant height (cm)	17,6	13,4	24,2	17,3	19,4	15,9	19,4
Standard deviation	3,1	2,7	3,1	2,2	2,8	1,9	3,1
% Variation	%25,6		%28,5		%18,0		-

WD: Water deficit **:max., min. and average values of 256 F2 individual seedlings

Table 3. MDA and proline amounts showing different degrees of increases under drought compared to the control plants

	S. insanum		**TDÇ47**		**TDÇ47 × *S. insanum***	
	Control	**Application**	**Control**	**Application**	**Control**	**Application**
MDA	11,1	12,5	7,5	9,0	14,1	15,6
% Variation	12,75%		19,20%		10,81%	
Proline	10,0	12,0	5,3	5,5	18,2	22,8
% Variation	20%		3,7%		25%	

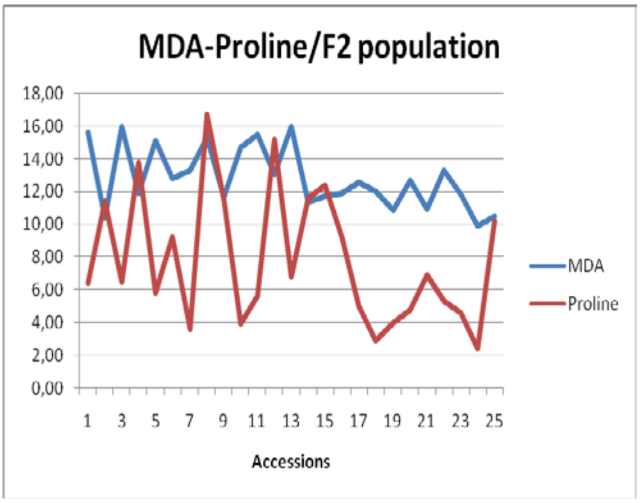

Figure 4. Graphic shows MDA and proline alteration in selected F2 plants

Table 4. Data of some phenotypic traits scored among the 100 F2 plants determined as drought tolerant

Trait	**Minimum**	**Maximum**	**Average**	**Standard Deviation**
Plant height (cm)	50,0	142,0	106,4	15,6
Leaf blade length (cm)	11,7	26,3	20,1	2,4
Leaf blade width (cm)	7,0	17,0	11,8	1,9
Petiole Length (cm)	3,0	15,5	7,3	1,5
Fruit length (cm)	3,0	14,0	8,4	1,7
Fruit width (mm)	28,0	68,0	48,9	6,8
Fruit weight (g)	26,0	140,0	55,0	20,9
Fruit length/breadth ratio (cm)	1,0	2,8	1,7	0,3
Peduncle length (cm)	3,0	15,5	7,3	1,1

Table 5. Some phenotypic characteristics of 100 lines selected as drought tolerant

No	**Descriptors**	**Results (*the numbers show how many plants are in which feature)**
1	Growth habit	2- very upright, 42- upright, 50- intermediate, 7- prostrate
2	Leaf blade lobs	1-very weak, 12- weak, 67- intermediate, 20- strong
3	Anthocyanin distribution in plant	30- absent, 65- low 5- intermediate
4	Anthocyanin distribution in leaves	68- absent, 30- low. 2- intermediate
5	Leaf prickliness	37- none, 14- very few. 35- few, 14- intermediate
6	Leaf hairiness	2- absent, 51- low, 46- intermediate, 2- high
7	Number of flowers/inflorescence	2- 1/2, 78- 1/3, 20- 3/4
8	Fruit load	10- low, 56- intermediate, 24- high, 10- very high
9	Varietal type	12- long, 20- oval, 68- round
10	Predominant fruit color	15- dark green, 9- green, 19- lilac, 15- dark lilac, 22-purple, 20-dark purple
11	Secondary fruit color	3- dark green, 52- green, 6- lilac, 5- dark lilac, 18- purple, 16- dark purple
12	Fruit glossiness	30- opaque, 46- intermediate, 24- bright peel color
13	Fruit curvature	1- round, 66- no curvature, 33-slightly curvature
14	Presence of grooves	100- absent
15	Calyx fruit coverage	20- less than 10%, 55- 10-20%, 24-20-30%, 1-30-40%
16	Fruit calyx prickliness	36- none, 7-Very few (<3), 33-Few (~5), 24-Intermediate
17	Fruit firmness	2- spongy, 43- intermediate, 55- tight
18	Fruit end button size	25- small, 36-intermediate, 39- large
19	Presence of chlorophyll on the pistil scar	70- absent, 30- present
20	Fruit color distribution	52- uniform, 28- mottled, 1- netted, 19- striped

Protoplast isolation from leaf mesophylls of haploid *Solanum sisymbriifolium* Lam. produced via anther culture

Buse Özdemir Çelik[1*], Hatice Filiz Boyacı[2], Esra Cebeci[3], Metin Tuna[4], Ahmet Naci Onus[5]

[1]: Elmalı Vocational School, Akdeniz University, Antalya, Türkiye

[2]: Republic of Türkiye Ministry of Agriculture and Forestry Antalya Food Control Laboratory Directorate, Antalya, Türkiye

[3]: Bati Akdeniz Agricultural Research Institute, Department of Vegetable Crops and Ornamentals, Antalya, Türkiye

[4]: Department of Field Crops, Faculty of Agriculture, Namik Kemal University, Tekirdag, Türkiye

[5]: Department of Horticulture, Faculty of Agriculture, Akdeniz University, Antalya, Türkiye

[*] Corresponding author e-mail (buse@akdeniz.edu.tr, Phone number: 0545 6015650)

Abstract

While the cultivated eggplant genotypes are susceptible to many biotic and abiotic stress factors the wild relatives of eggplant can be resistant to more than one factor. Nevertheless, the success in interspecific cross between cultivated form and wild relatives of eggplant is very limited because of incompatibility. Hence, using biotechnological approaches such as somatic hybridization can be useful tool to overcome this problem. This study aimed to achieve protoplast isolation, which is the first step for an alternative method for creating hybrid plants using haploid protoplasts for fusion that results directly with creation of a diploid plant. The use of haploid plants as a source of protoplasts is of great importance in terms of the ploidy level of the hybrids to be obtained in somatic hybridization, and no study has been found in eggplant on using haploid cells as a source of protoplasts and isolating them. The present study reports the isolation of viable protoplast from anther-derived haploid leaves of *Solanum sisymbriifolium*, which is the wild species, a useful material in eggplant plant improvement. Haploid plant leaves obtained by culturing anthers of *Solanum sisymbriifolium* Lam. yielded quality protoplasts after isolation and found to be useful as a protoplast source for further somatic hybridization studies.

Keywords: *Solanum sisymbriifolium*, protoplast isolation, haploid protoplast, eggplant.

Introduction

Eggplant (*Solanum melongena* L.) is one of the few cultivated *Solanaceous* species originating from India where it was first domesticated and where the greatest diversity is found (Daunay 2008). At first while it was mostly cultivated in temperate zones, tropical Asian countries and also in the Middle East and around the Mediterranean basin, today it is grewworldwide. Because of it has important source of nutrients in the diets of low-income consumers who lived around the most eggplant produced areas, its production has increased rapidly (Hanson et al. 2006). Additionally, it is a good source of antioxidants, which are beneficial to human health therefore interest in this plant is growing worldwide (Gürbüz et al. 2018).

Eggplant cultivation areas have been threatened by various diseases and insect pests especially bacterial wilt, phomopsis blight, little leaf, root-knot nematode (*Meloidogyne* spp.), fruit and shoot borer (Sharma et al. 2020; Toppino et al. 2022). Cultivated varieties of eggplant are susceptible to a wide array of pests and disease beside this, various abiotic stress conditions effects eggplant production every year but crop wild relatives of eggplant has economically important genes (Kashyap et al. 2003). These useful genes can transfer to the culture eggplant via different conventional and biotechnological techniques to the development of high yielding and horticulturally superior varieties with resistance to biotic and abiotic stresses (Sharma et al. 2020). One of this technique is interspecific hybridization to improve fruit quality, increase yield and introduce pest and disease resistances from wild relatives (Rotino et al. 2014).

Solanum sisymbriifolium Lam. is from the tertiary gene pool of eggplant known as resistant to multiple diseases (Bletsos et al. 2003; Gousset et al. 2005), for instance bacterial (*Ralstonia solanacearum*) and fungal (*Verticillium dahliae*) wilts (Collonnier et al. 2003) but it is sexually incompatible and doesn't cross with culture eggplant. Although sexual incompatibilities are a major barrier in crossing eggplant with the wild relatives, good ability to regenerate plants from various cultured explants of eggplant has provided opportunities for the application of a wide range of techniques in plant biotechnology including molecular and cellular methods for gene transfer (Hasan and Lester 1990; Devi et al. 2015; Saini and Kaushik 2019).

Plant protoplasts are cells from which the cell wall has been enzymatically removed and are attractive being used in basic research and plant improvement (Wang et al. 2017). Protoplast fusion is advantageous in overcoming the pre- and post fertilization obstacles faced in conventional breeding methods and is a different technique for developing interspecific hybrids of cultivated and wild eggplant and has enabled the easy transfer of desirable agronomic characters that are sexually incompatible in eggplants. While hybrids developed via this method usually express the desired trait, it is not uncommon for them to show the tendency to become sterile. While research has shown that there are exceptions, the inclusion of somatic hybrids into breeding activities is usually limited by their tetraploid characteristic. In all studies, diploid cells were used as a source of eggplant protoplasts (Gleddie et al. 1985, 1986; Sihachakr et al. 1989, 1993; Collonier et al. 2001; Rizza et al. 2002).

In suitable culture environments, protoplast sources remain the main factor to improve culture success. Several studies have reported on the physiological conditions required for isolation and culture of wild and cultivated eggplant leaf mesophyll protoplasts and their regeneration into plants (Bhatt and Fussuliotis 1981; Saxena et al. 1981; Gleddie et al. 1985). Although protoplasts can be isolated from different kinds of tissues, in most cases, mesophyll tissues have become the primary choice because of the ease in obtaining a high yield of protoplasts including eggplant (Sihachakr and Ducreux 1987a; Gleddie et al. 1985; Collonier et al. 2001).

This study aimed to achieve protoplast isolation, which is the first step for an alternative method for creating hybrid plants using haploid protoplasts for fusion that results directly with creation of a diploid plant.

Materials and methods

Plant Material

Anthers of a wild eggplant genotype (*Solanum sisymbriifolium* Lam) were cultured (unpublished). After 6 weeks of anther culture, the anther-derived embryos (Figure 1) were transferred to a semi-solid MS medium (Murashige and Skoog 1962) and cultured for obtaining haploid plantlets (Figure 2). The ploidy of all the new individuals was checked by flow cytometry. Samples were analysed using a Partec CyFlow Space flow cytometer (Munster, Germany) (Tuna 2015). All plantlets which obtained from anther culture were identified as haploid. Haploids produced under appropriate *in vitro* conditions by androgenesis were used as plant material.

Protoplasts were isolated from haploid plantlets of *Solanum sisymbriifolium* according to Sihachakr and Ducreux (1987a). Briefly, haploid leaves were cut into strips 2 mm wide and placed in 60 x 15mm petri dishes containing 6 ml enzyme solution: $CaCI_2$ (6mM), KH_2PO_4 (1mM), sucrose (0.5M), 1.5% (w/v) Cellulase R-10, 0.5% (w/v) Macerozyme R-10 and 0.05% (w/v) 2-(N-morpholino) ethanesulfonic acid (MES) buffer; pH was adjusted to 5.5. Enzyme solutions were sterilized by filtration through a 0.2-µm filter. Enzymatic digestions were performed in the dark at 27°C overnight. After digestion, the preparations were passed through a 40-µm nylon mesh filter to remove any undigested cell clumps and debris from broken cells. Following filtration and centrifugation, the haploid plants leaf protoplasts were purified using CPW solutions (27.2 mg/L of KH_2PO_4, 100 mg/L of KNO_3, 150 mg/L of $CaCl_2$, 250 mg/L of $MgSO_4$, and 0.16 mg/L of KI, 0.00025 of $CuSO_4$, pH 5.8) containing 25% sucrose and 13% mannitol gradient centrifugation. The viable protoplasts at the interface between the 2 layers were then carefully collected and washed 2 times by centrifugation at 850 rpm for 6 min in protoplast washing solution (0.8 M of Mannitol + 0.5 mM of $CaCl_2$) (Çimen 2020). Protoplast were observed microscopically using an inverse microscope.

Results and Discussion

Based on previous studies about isolation of leaves protoplasts from wild and cultivated eggplant, the aim of this study was to establish the first step for a reproducible method for the isolation of a large population of viable haploid leaf mesophyll protoplasts of *Solanum sisymbriifolium* Lam. The large numbers of androgenic haploid plants leaf mesophylls cells were used to generate haploid protoplast.

Results strongly showed the viable and culturable mesophyll protoplasts from haploid plantlets could be obtained successfully. The viable protoplasts were produced in an enzyme solution containing $CaCI_2$ (6mM), KH_2PO_4 (1mM), sucrose (0.5M), 1.5% (w/v) Cellulase R-10, 0.5% (w/v) Macerozyme R-10 and 0.05% (w/v) 2-(N-morpholino) ethanesulfonic acid (MES) buffer. The pH was adjusted to 5.5. In Figure 3, isolated protoplast cell are presented. The healthy protoplasts exhibited strongly green fluorescence. The current standard eggplant mesophyll protoplast isolation protocol is well-established, and has also been used in various modified forms for specific needs. In any case, in vitro cultures were found to be a suitable source for the isolation of viable protoplasts of eggplant (Saxena et al. 1981; Sihachakr and Ducreux 1987a).

Although there are several studies on the isolation of protoplasts from *S. sisymbriifolium* to obtain interspecific somatic hybrid plants, they are related to protoplasts isolated from diploid leaf tissues (Gleddiei et al. 1986; Kallo 1993, Kim et al. 2006). The present study is the first report of the isolation of viable protoplast from anther-derived haploid leaves of *Solanum sisymbriifolium*, which is the wild species, a useful material in eggplant plant improvement. In this work, a standard enzyme solution was used which reported for the isolation of protoplasts from mesophyll tissue of eggplant and its wild relatives (Sihachakr and Ducreux 1987a; Sihachakr et al. 1988, 1989).

In protoplast culture, genotype (Binding et al. 1981) and organ (Sihachakr and Ducreux 1987a) are well known to influence protoplast yield and division as well as further plant regeneration. In vitro conditions provided juvenile and homogeneous materials from which results were obtained from haploid leaves from *Solanum sisymbriifolium* Lam. Studies on the isolation of protoplasts from *Solanum rnelongena* leaves indicated that the environment and nutritional milieu of the donor plant were critical factors for the recovery of viable protoplasts. Similar observations were reported by Saxena et al. (1981) and Sihachakr and Ducreux (1987b) respectively for Solanum melongena and S. nigrum mesophyll protoplasts. In this study, high and fresh protoplast yields were obtained from mesophyll of haploid plantlets grown *in vitro* condition. These protoplasts found to be useful as a protoplast source for further somatic hybridization studies.

Identification of generate adequate yields of intact and viable protoplasts of haploid plants is important for somatic hybridization. Haploid leaves yielded quality protoplasts after isolation and could be useful as a protoplast source for further somatic hybridization studies.

Conclusion

Haploid protoplasts provide attractive system for somatic hybridization studies used in plant improvement. In comparison with diploid protoplasts, haploid protoplasts provide an original system for somatic hybridization studies which diploid somatic hybrids could be obtained after protoplast fusion. Recently, we succeeded, in regenerating haploid plants from wild eggplant (*Solanum sisymbriifolium* Lam.) anther-derived embryos and regenerate haploid plants from these embryos. We believe it is of great interest to know whether diploid somatic hybrids could be obtained after protoplast fusion from wild and cultivated haploid plants.

To serve this purpose, plant protoplasts have been prepared from somatic cells from which the cell wall was enzymatically removed have great significance in somatic hybridization. The use of haploid plants as a source of protoplasts is of great importance in terms of the ploidy level of the hybrids to be obtained in somatic hybridization, and no study has been found in eggplant on using haploid cells as a source of protoplasts and isolating them. The present study reports the isolation of viable protoplast from anther-derived haploid leaves of *Solanum sisymbriifolium*, which is the wild species, a useful material in eggplant plant improvement. Our results are very promising because they provides a solution to obtain diploid somatic hybrid directly. Interspecies dihaploid lines to be produced from *Solanum sisymbriifolium* will be able to be included in breeding programs in near future.

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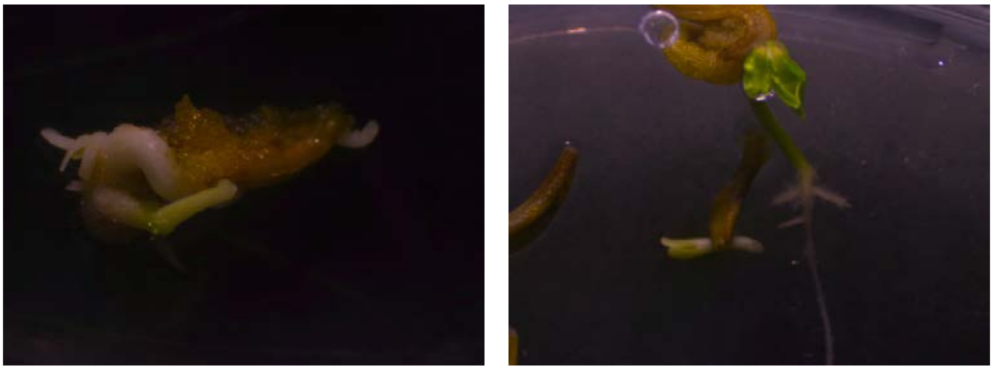

Figure 1. Anther-derived embryos from *Solanum sisymbriifolium* Lam.

Figure 2. Regeneration of haploid plantlets from anther-derived embryos from *Solanum sisiymbriifolium* Lam.

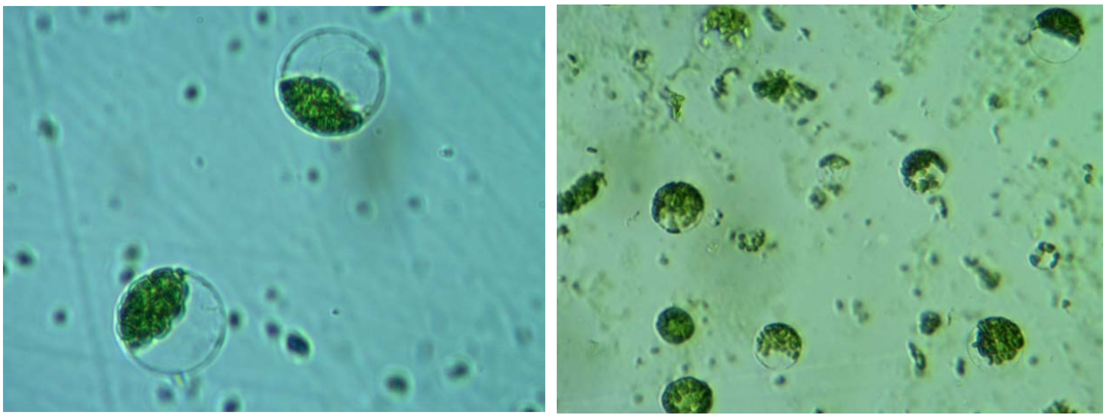

Figure 3. Freshly isolated protoplasts from haploid leaves of *Solanum sisymbriifolium* Lam.

STUDY ON SOME QUALITY AND MORPHO-PHYSIOLOGICAL TRAITS OF DURUM WHEAT (*Triticum durum* L. Desf.) GENOTYPES

Balkan, A.[1], Bilgin, O.[1], Başer, İ.[1] Göçmen, B. D.[1] and Özcan, K.[2]

[1]Tekirdağ Namık Kemal University, Agricultural Faculty, Department of Field Crops, Turkey
[2]Tekirdağ Namık Kemal University, Thrace Seed Valley Appl. and Research Center, Turkey
Corresponding author: ibaser@nku.edu.tr

ABSTRACT

The study was carried out in the experimental field of the Department of Field Crops, Faculty of Agriculture, Tekirdağ Namık Kemal University in 2020-2021. In the study, totally 25 durum wheat genotypes (6 cultivars, 12 advanced lines, and 7 landraces) were used as experimental material. The experiment was conducted in a randomized complete block design with 3 replications. In the study, the grain quality and morpho-physiological traits such as canopy temperature, chlorophyll content, leaf area index, and plant height were investigated in some durum wheat genotypes.

The canopy temperature ranged from 23.333-20.433 ^{O}C, chlorophyll content 52.533-43.167 SPAD, leaf area index 3.633-1.767, thousand-grain weight 34.667-41.833, protein content 14.233-16.333, test weight 78.933-87.033, semolina colour 14.880-15.627 and plant height 99.00-75.33 cm in investigated durum wheat genotypes. Genotypes Hacımestan and Sorgül for canopy temperature, genotypes Atkı 2, NZFM 1 and NZFM 7 for chlorophyll content, genotypes Atkı 2, NZFM 4 and NZFM 1 for leaf area index, genotypes Kıbrıs 2 and Ionia 3 for plant height, genotypes NZFM 1, NZFM 7 and Devedişi 2 for thousand-grain weight, genotypes Atkı 2 and Hacımestan 2 for protein rate, genotypes Japiga and Boğacak 2 for test weight and genotypes Japiga, Boğacak, Kızıltan 91 and NZFM 7 for semolina colour were determined as promising genotypes.

Keywords: Durum wheat, genotype, chlorophyll content, semolina colour, canopy temperature

1. INDRODUCTION

Durum wheat (*Triticum turgidum* L. ssp. *durum*, genome AABB, $2n = 4 \times = 28$) is the 10th most important and commonly cultivated cereal worldwide, representing 5% of total wheat production with a planting area of about 16 million hectares (Anonymous, 2020). It is also used in the production of different food products such as pasta, couscous, bulgur, etc., in different regions of the world.

Durum wheat is one of the important agricultural products in Turkey. It is cultivated 1.2 million ha with an average production of 3.2 million tons in 2021 (Anonymous, 2021). Durum wheat is grown in regions where there is sufficient rainfall and the temperature is not too low, since it is extremely affected by abiotic stresses, especially low temperatures.

Although it is possible to slightly increase the planted areas in order to meet the required demand in durum wheat production, it is possible to increase the irrigated area planted in the field, but providing an increase in yield under rain fed conditions emerges as the most important alternative (Laaboudi and Mouhouche, 2012; Haddad et al., 2016; Belagrouz et al., 2018). Yield increase in durum wheat production compared to bread wheat has not been reached to the desired levels yet. This is due to the low number of varieties in durum wheat breeding and the inadequacy of variation sources used in breeding. For this reason, it is important to use new genetic resources that have the desired characteristics in the breeding of durum wheat and are well compatible with each other in crossing (Alp, 2005). One of the easiest and most effective ways to enrich genetic diversity as a source of variation in variety breeding is to use landraces (Çoşkun et al., 2019; Demirel et al., 2019).

Landraces are considered to be important genetic sources in increasing genetic diversity for the varieties to be developed by showing better adaptation in regions where abiotic and biotic stress factors are located (Soriano and Royo, 2015; Maccaferri et al., 2019). In variety breeding studies, revealing the potential in landraces, varieties and lines is important in terms of the effectiveness of the studies that have been done and will be done. In wheat breeding, one of the most important breeding purposes along with yield and quality is resistance to abiotic stresses. Thus, it is very important to know the physiological traits that plants have and use against abiotic stress factors.

The aim of the study is to investigate the status of the durum wheat landraces, varieties, and promising advanced lines for quality and tolerance/resistance to abiotic stresses, and also to reveal the status of the advanced lines according to the varieties and landraces in terms of morpho-physiological traits.

2. MATERIALS AND METHODS

This study was carried out with 25 durum wheat genotypes (6 cultivars, 12 advanced lines, and 7 landraces) based on randomized complete block design with 3 replications at the experimental area of the Field Crops Department, Agricultural Faculty, Tekirdağ Namık Kemal University, Turkey, in 2020-2021 wheat growing season. Geographically, Tekirdağ district locates at latitude 40^{o} 36’-40^{o} 31’ and longitude 26^{o} 43’-28^{o} 08’.

According to soil analysis results, the experimental area’s soil was clay-loam, slightly acidic (pH 6.5), limeless, and poor (1.08%) in organic matter. The temperature and the rainfall from sowing to harvest are presented in Table 1.

Table 1. Rainfall (mm) and mean temperature (°C) of Tekirdağ from sowing to harvest (2020 to 2021).

Months	Nov.	Dec.	Jan.	Feb.	March	April	May	June	July	Total/Mean
Rainfall (mm)	1.2	37.7	127.8	53.5	45.3	43.6	57.6	54.7	3.4	424.8
Temperature (°C)	11.6	10.1	7.8	7.3	7.0	10.7	17.5	20.8	25.8	13.2

Seeds of each genotype were sown in 6 rows 5 m long with 0,17 m of inter-row spacing. The seeding rate used in sown was 500 seeds per m^2. The cultivation techniques recommended for the region were followed to raise a good crop. Twenty kg/da 20.20.0 fertilizer was applied just before sowing, and then 15 kg/da urea (46% N) and 15 kg/da ammonium nitrate (26% N) were broadcasted at the tillering and the pre-heading stages. Weeds were controlled chemically. In the study, plant height (cm), canopy temperature (°C), leaf area index, chlorophyll content (SPAD), thousand-grain weight (g), test weight kg/hl), protein content (%) and semolina colour were investigated. Canopy temperature was measured with a portable infrared thermometer (Extech Mini IR Thermometer Modell 42500) as ^{o}C (Reynolds et al. 2001). It was taken as two measurements per plot during the day between (11:00h to 14:00h). Chlorophyll content was measured with "Konica Minolta SPAD-502 Plus" portable chlorophyll meter in the fully-developed flag leaves and determined as "SPAD value". It was taken three averages of five leaves per plot, and were done from 11:00h to 14:00h. Leaf area index was measured with a portable leaf area meter at the heading stage (Pask et al. 2012).

The data obtained from the advanced lines, varieties and landraces used as material in the study were analyzed separately by using the JUMP statistical package program. Mean values were compared using Duncan's Multiple Range Test ($p \leq 0.01$).

3. RESULTS AND DISCUSSION

Data concerning canopy temperature, plant height, leaf area index, chlorophyll content, thousand grain weight, protein content, test weight and semolina colour are given in Table 2 and 3.

Canopy temperature: The effect of genotype on canopy temperature was statistically significant ($p \leq 0.01$) (Table 2). Canopy temperatures varied between 20.43-23.33 °C in the landraces, 20.73-22.43 °C in varieties, and 21.20-22.70 °C in advanced lines (Table 2). This result is also in agreement with the findings of Gautam et al. (2015), who found that canopy temperatures of durum wheat genotypes ranged from 20.20-24.90 °C. The highest variation for canopy temperatures was determined in the landraces. Similar to our findings, Bahar et al. (2008) and Ray and Ahmad (2015) revealed that the canopy temperatures of durum wheat genotypes were significantly different. Among the landraces, the lowest canopy temperature was found in the Sorgül with 20.43 °C and a lower canopy temperature could not be obtained from the advanced lines and varieties. Tunca 79, Kızıltan 91, Japiga and Zenit cultivars with 20.73, 21.20, 21.67 and 21.70 °C canopy temperature values, Hacımestan 2, Adana 2, and NZFM 8 advanced lines with 21.20, 21.33, 21.53 °C canopy temperature values were identified as genotypes to be considered. Canopy temperature has been used as a selection criteria for tolerance to drought and high-temperature stress in wheat breeding (Bahar et al. 2008). When the average of the landraces, varieties, and advanced lines are examined, it is seen that the landraces show the lowest canopy temperature, this value increases slightly in the cultivars, and this value is the highest in the lines on average. It is understood that the effect of global climate change is felt more and the canopy temperature, which is one of the most important selection criteria for drought resistance in plants grown in arid areas, is not at the desired level in varieties and lines.

Plant height: According to variance analysis results, plant height was significantly affected by genotype (Table 2). Mean values of plant height in durum wheat genotypes varied between 78.33-99.00 cm in landraces, 79.67-91.33 cm in varieties, and 75.67-96.00 cm in advanced lines. In a study with landraces and modern varieties of durum wheat, it was determined that the plant height ranged from 94.00 to 126.00 cm (Royo et al., 2020). When landraces, varieties, and advanced lines were compared in terms of plant height, the mean plant height of varieties was shorter than the landraces. This result was similar to the finding of Royo et al. (2020). Also, Baykara et al. (2022) stated that the plant height of durum wheat varieties (103.9 cm) was significantly taller than modern varieties (94.7 cm). Considering the variation between 80-100 cm in terms of plant height in wheat. Plant height values of varieties and advanced lines are within the desired limits.

Table 2. Mean values and significance groups of canopy temperature, plant height, leaf area index, and chlorophyll content in durum wheat genotypes.

Genotypes	Canopy temperature (^{o}C)		Plant height (cm)		Leaf area index (LAI)		Chlorophyll content (SPAD)	
Landraces								
Kurtalan 24	21.333	bc	99.000	a	3.200	ab	47.733	ab
Devedişi	21.867	ab	79.000	cd	2.767	bc	45.333	bcd
Karakılçık	23.333	a	90.333	ab	3.633	a	43.867	cd
Atkı	21.400	bc	86.000	bc	2.433	cde	50.433	a
Hacımestan	20.800	cd	83.000	bcd	1.967	e	44.200	bcd
Sorgül	20.433	d	78.333	d	2.067	de	46.967	abc
Boğacak	21.067	cd	90.000	ab	2.500	cd	42.700	d
Mean	***21.46***		***86.52***		***2.65***		***45.89***	
Varieties								
Tunca-79	20.733	b	79.667	c	2.600	b	43.167	c
Zenit	21.700	ab	85.000	ab	2.900	ab	49.400	ab
Svevo	22.367	a	90.333	a	2.533	b	50.300	a
Ç-1252	22.433	a	91.333	a	3.633	a	50.100	ab
Japiga	21.667	ab	84.333	bc	2.867	ab	46.567	bc
Kızıltan-91	21.200	ab	80.667	bc	2.333	b	47.567	ab
Mean	***21.68***		***85.22***		***2.81***		***47.85***	
Advanced lines								
NZFM-13	21.833	b-e	84.000	d	2.900	bcd	46.700	cde
Hacımestan-2	21.200	f	88.000	bcd	2.500	def	43.667	e
Boğacak-2	21.667	c-f	96.000	a	2.633	cde	45.467	de
Atkı-2	21.467	def	92.333	ab	3.333	ab	52.533	a
NZFM-4	22.000	bcd	86.333	cd	3.533	a	47.833	bcd
NZFM-1	22.100	abc	94.333	a	3.033	abc	50.267	abc
NZFM-7	22.200	abc	93.000	ab	2.433	def	51.133	ab
Devedişi-2	22.333	ab	88.000	bcd	2.333	ef	46.500	cde
Ionia-3	22.700	a	75.333	e	2.167	fg	48.233	a-d
NZFM-8	21.533	def	90.333	abc	2.200	efg	47.433	b-e
Cyprus-2	22.000	bcd	75.667	e	2.433	def	47.200	b-e
Adana-2	21.333	ef	85.000	d	1.767	g	47.967	a-d
Mean	***21.86***		***87.36***		***2.61***		***47.91***	

Leaf area index: The number of leaves in the plant is an important factor in determining the amount of light absorbed by the canopy, which controls the photosynthetic rate. So, the leaf area index may be good tool to screen wheat genotypes under terminal heat stress conditions (Dhyani et al., 2017). In our study, the effect of genotype on leaf area index was statistically significant (Table 2). While durum wheat varieties gave higher values with an average leaf area index of 2.81, landraces and advanced lines gave lower and similar values with leaf area index values of 2.65 and 2.61. In the landraces, the highest area index was 3.63 in the Karakılçık, while the landraces of Hacımestan showed a low value of 1.97. In durum wheat varieties, Ç-1252 variety gave the highest leaf area index (3.63). Similar findings were reported that Bavec et al. (2008), who indicated that leaf area index varied between 2.5-6.5 in wheat. When the advanced lines are examined, there is no advanced line that exceeds the leaf area index of the landrace of Karakılçık and variety of Ç 1252. Among the advanced lines, Atkı-2, NZFM-4, NZFM-1 are genotypes with leaf area index values above 3.0. Adana-2 advanced line gave a very low value with 1.77 leaf area index. Dhyani et al. (2017) reported that the leaf area index in wheat changed from 2.96 to 5.82.

Chlorophyll content: Chlorophyll and carotenoid are two pigments related to the physiological functions of leaves that absorb light energy during photosynthesis. Chlorophyll provides photosynthesis in the plant and its amount is one of the main factors used in the evaluation of environmental and growing conditions for wheat. In our study, while the chlorophyll content was the lowest with 45.89 (SPAD) in landraces, it was determined as 47.85 and 47.91 (SPAD) values by increasing in varieties and lines. Among the genotypes examined, the highest chlorophyll content was found in Atkı 2 and NZFM 7 durum wheat lines with 52.53 and 51.13 (SPAD) values. Atkı landraces, Svevo variety, NZFM 1 forward line and Ç 1252 durum wheat cultivar followed these lines with values of 50.43, 50.3, 50.27 and 50.1 (SPAD). The lowest chlorophyll content value was obtained in Boğacak landraces with 42.70. While the chlorophyll content in landraces was 45.89 on average, the chlorophyll content in cultivars and lines showed a remarkable increase, reaching 47.85 and 47.91 values. Similar to our results, Talebi (2011) stated that genotypes differ chlorophyll content values in durum wheat. Our results also show that the chlorophyll content in genotypes has increased significantly as a result of breeding studies.

Thousand-grain weight: The weight of one thousand grains of wheat, which is the weight in grams, is important in terms of giving an idea about the grain's size, fullness, thinness and flour yield. Results of our study show that according to the landraces and varieties of durum wheat, significant increases were achieved in terms of thousand grain weight in the forward lines. While the mean of thousand-grain weight was 35.57 g in landraces, it was determined as 36.60 g in the varieties and 38.74 g in advanced lines. Our findings are in agreement with the findings of Akan et al. (2021), who determined that the thousand grain weight in durum wheat genotypes varied between 26.52-37.96 g. It is seen that these obtained values show a significant increase in varieties and especially in lines according to the landraces. While there was no genotype with a grain weight over 40.00 g in landraces, Svevo with 41.93 g thousand grain weight in cultivars, NZFM 7 line 43.83 g, NZFM 1 line 43.00 g and Devedisi 2 line 41.80 g were the genotypes with high thousand-grain weight.

Protein Content: It is known that protein content and composition are the most important factors determining the quality of wheat, protein content varies depending on genetic and environmental factors, but protein composition is not affected by environmental factors (Autran and Bourdet, 1979). In the study, the mean of protein content was 14.99% in the landraces, while it was found to be 15.31% in varieties and lines. These obtained data show that an increase in protein content in varieties and lines is provided to landraces. Akan et al. (2021) determined that the protein content in durum wheat varieties varies between 15.85-19.40%. Among the landraces, the highest protein content was in the Hacımestan genotype with 15.40%, while the varieties Tunca 79, Zenit, Svevo, Ç-1252 gave a higher value than the landraces of Hacımestan. Eight of the advanced lines gave higher protein content than the landraces

Hacımestan genotype that gave the highest protein content. The obtained data reveal that the protein content increased in durum wheat lines and varieties.

Table 3. Mean values and of significance groups of thousand-grain weight, protein content, test weight and semolina colour in durum wheat genotypes.

Genotypes	Thousand-grain weight (g)		Protein content (%)		Test weight (kg/hl)		Semolina colour	
Landraces								
Kurtalan 24	39,800	a	14,433	c	86,333	a	14,890	d
Devedişi	36,867	abc	14,833	bc	84,233	ab	15,007	cd
Karakılçık	33,600	c	15,833	a	82,467	bc	15,413	ab
Atkı	35,867	bc	15,267	ab	81,400	c	15,247	bc
Hacımestan	39,267	ab	15,433	ab	83,067	bc	15,310	ab
Sorgül	39,633	a	14,567	c	84,667	ab	15,487	ab
Boğacak	37,967	ab	14,533	c	86,100	a	15,567	a
Mean	***37.57***		***14.99***		***84.04***		***15.27***	
Varieties								
Tunca-79	32,967	c	15,500	ab	82,133	bc	15,380	a
Zenit	36,300	bc	15,567	ab	84,267	ab	15,423	a
Svevo	41,933	a	15,733	a	84,467	ab	14,890	b
Ç-1252	35,867	bc	15,200	bc	83,100	bc	15,433	a
Japiga	37,867	ab	14,967	c	87,033	a	15,603	a
Kızıltan-91	34,667	bc	14,900	c	80,367	c	15,627	a
Mean	***36.60***		***15.31***		***83.56***		***15.39***	
Advanced lines								
NZFM-13	37,833	c	15,567	bcd	84,767	ab	14,880	
Hacımestan-2	37,100	c	16,067	ab	83,033	b	15,093	
Boğacak-2	38,367	bc	15,167	de	86,900	a	15,133	
Atkı-2	35,433	c	16,333	a	78,933	c	15,240	
NZFM-4	38,267	bc	15,467	bcd	82,733	b	15,350	
NZFM-1	43,000	a	15,467	cd	83,967	ab	15,050	
NZFM-7	43,833	a	14,933	ef	84,733	ab	15,547	
Devedişi-2	41,800	ab	14,233	g	85,600	ab	15,047	
Ionia-3	37,933	c	14,467	fg	85,333	ab	14,663	
NZFM-8	37,867	c	15,733	abc	84,567	ab	14,923	
Cyprus-2	36,500	c	14,800	ef	85,600	ab	15,103	
Adana-2	36,900	c	15,467	cd	85,633	ab	15,343	
Mean	***38.74***		***15.31***		***84.32***		***15.11***	

Test Weight: Test weight is expressed in kg of 100 litres of wheat. Test weight varies depending on the species, variety, sowing time, growing period and ecological conditions. In wheat, the shape and size of the grain, whether the shell is thin or thick, whether the abdomen is deep or flat, whether the shell is polished or not, affects the test weight. The test weight values of durum wheat genotypes are close to each other on average in landraces, cultivars and lines in this study. Among the landraces, Kurtalan 24 and Boğacak ranked first with a higher test weight of 86.00 kg/hl, and the Japiga variety with a test weight of 87.03 outperformed them.

Among the forward lines, the Boğacak 2 genotype is the one that draws attention with a test weight of 86.9. While weft 2 gave a lower value of 78.93 kg/hl from the forward lines, a significant part of the lines showed a test weight of 84-85 kg/hl.

Semolina Colour: Bright yellow colour in pasta or semolina is one of the most important quality parameters. Therefore, breeding of durum wheat varieties with high pigment content is an important breeding goal. It has been reported by different researchers that the content of yellow colour in durum wheat varies according to varieties (Şahin et al. 2006, Coşkun et al. 2010). In our study, the highest values for semolina colour were in varieties and the lowest values were obtained in advanced lines. There was no statistical difference between the advanced lines for semolina colour. All local varieties except Kurtalan 24 and all varieties had semolina colour over 15.0 in the study. While among the advanced lines, 9 lines gave semolina colour over 15.00, the highest semolina value colour was in NZFM 7, NZFM 4 and Adana 2 genotypes. The data obtained reveal that a significant part of the varieties and lines show similar characteristics with the landraces in terms of semolina colour.

4. CONCLUSION

In the study carried out with durum wheat landraces, varieties and lines, canopy temperature, plant height, leaf area index, chlorophyll content, thousand-grain weight, protein content, test weight, and semolina colour characteristics were investigated. While landraces have a lower value for canopy temperature, it is seen that the canopy temperature has increased slightly in varieties and lines. The advanced lines and cultivars have slightly longer plant heights than landraces. Leaf area index values were the highest in cultivars and showed similar values in landraces and lines. In terms of chlorophyll content, significant increases were achieved in varieties and lines compared to landraces. Advanced lines gave higher thousand grain weight than landraces and varieties. The protein content of varieties and advanced lines showed a significant increase compared to landraces. Test weight was lower in cultivars, and similar in landraces and advanced lines. The semolina colour was slightly higher in varieties compared to the landraces and advanced lines.

The obtained results showed a significant increase in chlorophyll content, leaf area index, protein content and thousand grain weight in varieties and advanced lines. In the canopy temperature, which is desired to be low, there was an increase in varieties and advanced lines. Test and semolina colour did not change significantly in breeding material and landraces.

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EFFECT OF DROUGHT STRESS ON SEEDLING GROWTH IN BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES

Başer, İ., Akseki, S. A., Göçmen B.D., Bilgin O. and A. Balkan,
Tekirdağ Namık Kemal University, Agricultural Faculty, Department of Field Crops -Turkey
Author for correspondence: ibaser@nku.edu.tr

ABSTRACT

The study was carried out in different drought/osmotic stresses (0.00 MPa-control, 0.25 MPa, 0.50 MPa, 0.75 MPa and 1.00 MPa applications) created by using PEG-6000 with 43 genotypes under laboratory, with 5 replications according to a split-plot experiment design. The genotypes constituted the main plots, and the drought/osmotic stress applications constituted the sub-plots.

In the study, seedling weight, root number, root length, root weight, shoot length, and shoot weight characters were determined. It was determined that drought stress applications caused statistically significant decreases in root and shoot characters. In the study carried out with forty-three genotypes, 1.00 MPa and 0.75 MPa applications of PEG 6000 caused statistically significant reductions in root and shoot characters.

The results indicate that early and mid-early varieties were more tolerance to drought than the late varieties. Although Aglica, Anapo, Enola and Hamza varieties stand out for their root properties, while Maden, NKÜ Ergene and Bezostaya 1 cultivars showed more appropriate shoot characteristics than other cultivars. Enola, Aglika, Bezostoja 1, NKÜ Ergene, Anapo, Hamza and Maden bread wheat varieties showed the well growth characteristics under drought stress conditions in the study.

1. INTRODUCTION

Wheat production in the world in 2020 was 780 million tons, and in our country it was 20.5 million tons (FAO, 2021). Along with the increasing population around the world, it is necessary to consider the quality and yield factors as well as the varieties that have adapted to abiotic and biotic stresses in the regions where the food demand is cultivated (Güngör and Dumlupınar, 2019). Drought which is one of the most common abiotic stress factors is the most important factor limiting crop production in most agricultural areas. Wheat production is generally carried out in dry agricultural areas and drought often causes serious problems in wheat production in these areas.

The decrease in productivity under drought stress conditions is one of the most important factors threatening global food production (Fahad et al. 2017). High temperatures occurring in global climate change increase the drying rate of agricultural soils and cause higher drought stress to occur (Fischer and Knutti, 2015). Therefore, it is important for plants to withstand long-term water deficiencies, adapt to these environments, and improve the plants' ability to recover from water deficiencies. Stress tolerance of plants and the ability of plants to maintain productivity during stress periods is a complex phenotypic trait (Ngumbi and Kloepper, 2016). Plants have numerous mechanisms to tolerate drought stress down to cellular levels, such as root structure, above-ground growth, osmotic adjustment, water use optimization, and management of reactive oxygen species (Meena et al., 2017). With regard to plant growth and development, changes in root system architecture, especially the proliferation of high-grade roots, are known to be beneficial in short-term adaptation to water deficiency (Xu et al. 2015).

Drought is one of the most important environmental stress factors limiting crop production in many countries of the world. Insufficient/irregular precipitation and high temperature during the year are the main factors causing drought. One of the most important research studies to minimize the effects of drought is the breeding of drought-resistant varieties. However, it is difficult to develop studies on this subject unless the mechanism of drought resistance and the parameters that indicate it are well understood. In arid conditions, plants reduce all enzyme activity, slow down their growth, cause the closure of stomata, causing a decrease in CO2 assimilation (Baranyiova et al., 2014). More than 50% of wheat growing areas are affected by periodic drought. Although drought affects wheat development in all phenological periods, its greatest negative effect occurs during pollination and grain filling periods. While mild drought after pollination reduces wheat yield by 1-30%, mild drought during flowering and grain filling period reduces grain yield up to 58-92% (Farooq et al., 2014). Grain yield is affected by the interaction of genetic and environmental factors. Soil type, sowing time, sowing method, sowing frequency, fertilization and irrigation time, spacing between rows have an important role in obtaining high yields. Water stress significantly affects yield components such as the number of grains per spike and the number of spikes per plant (Aghanejad et al., 2015).

The study was carried out to identify drought resistant genotypes, which is one of the most important problems in cereal production in our country. In the study, a total of 43 genotypes, including 39 bread wheat, 1 rye, 1 emmer and 2 einkorn wheat genotypes with different growth characteristics, were used as material. Seedling and root development characteristics of these genotypes were investigated in a drought environment created with PEG in the laboratory.

2. MATERIALS AND METHODS

In the study, 39 bread wheat, 1 rye, 1 emmer and 2 einkorn varieties were used as material. The research was carried out according to a randomized plot design in 5 different drought conditions (0.00 MPa, 0.25 MPa, 0.50 MPa, 0.75 MPa and 1.00 MPa applications) created with PEG 6000 in laboratory conditions. The seeds used as material were kept in 80% alcohol for 1 minute, then put into a mixture of 2% sodium hypochlorite with 2-3 drops of tween, shaken for 20 minutes and then washed 4-5 times in autoclaved sterile water. Sterile filter paper was placed in the petri dish sterilized in autoclave under a sterile cabinet and 10 ml of PEG solution was applied to the filter paper. 15 sterilized seeds were placed on the filter papers to which PEG solution was added. After the seeds were placed in the petri dishes, filter paper was placed on the seeds and the lid of the petri dish was closed. Petri dishes with closed lids were wrapped with cling film. Then the petri dishes were placed in the climate chamber. After waiting for 3 weeks for the germination of the seeds treated with PEG solution, the seedling weight, root number, root length, root weight, shoot length and shoot weight values were determined in the germinated plants in each petri dish.

3. RESULTS AND DISCUSSION

Seedling weight, root number, root length, root weight, shoot length and shoot weight values were measured in plants growing in 5 different drought conditions created with PEG 6000 in forty-three genotypes. Differences between genotypes were determined by performing analysis of variance and significance testing on the values obtained. As a result of the analysis of variance, the effect of PEG application on the examined characters was found to be statistically significant.

3.1. Seedling weight, root number and root length

As a result of the analysis of variance, the effects of genotype and PEG application on seedling weight, root number and root length were found to be statistically significant. The results of the significance test (Tukey) performed to reveal the differences between the applications are given in Table 1 below.

As a result of the significance test (Table 1), the highest value for seedling weight was found in Enola cultivar with 0.343 g. Aglika, NKÜ Ergene, Bezostoja 1, Falado, Anopa, Maden, NKÜ Lider, Ambrogio, Hamza, Bora, Anica and Selimiye varieties were the same statistical significance group as Enola. Pannonia, Quality, Hakan, Mihelca, Refikbey and Adelaide varieties were listed later. The lowest value for seedling weight was obtained from Siyez-1 with 0.161 g. Siyez-2, Maya, Rebelde, Emmer colour, Esperia, Golia and Başkan varieties were in the same statistical group as Siyez-1.

According to the significance test ; when the number of roots was examined, the highest value was found in Aglika genotypes with 5.4 unit and Quality genotypes with 5.3 unit, followed by Esperia and NKÜ Lider. Aglika and Quality genotypes. The lowest value for root number was seen in the Başkan variety with 3.0 unit. Emmer colour, NKU Ergene, Misiia Odes'ka, Rumeli, Masaccio, Adelaide, Dukato, Krasunia Odes'ka, Genesi varieties were in the same statistical group with the Başkan.

Table 1. Average values and importance groups for seedling weight, root number and root length

	Seedling weight (gram)			Root number (unit)			Root length (cm)	
Genotypes	Ave.	Sig.	Genotypes	Ave.	Sig.	Genotypes	Ave.	Sig.
Enola	0,343	a	Aglika	5,400	a	Hakan	24,800	a
Aglika	0,306	ab	Quality	5,333	a	Falado	21,533	ab
NKÜ Ergene	0,296	abc	Esperia	5,200	ab	Kaan	21,067	abc
Bezostoja 1	0,293	a-d	NKÜ Lider	5,133	abc	Mihelca	20,667	a-d
Falado	0,284	a-e	Bora	5,067	a-d	Adelaide	18,267	b-e
Anopa	0,282	a-e	Anopa	5,067	a-d	Refikbey	18,233	b-e
Maden	0,282	a-e	Rebelde	5,000	a-e	Misiia Odes.	18,100	b-f
NKÜ Lider	0,280	a-e	TT-601	4,867	a-f	Golia	17,833	b-g
Ambrogio	0,278	a-e	Enola	4,867	a-f	Krasunia Odes.	17,567	b-h
Hamza	0,277	a-e	Hamza	4,667	a-g	Enola	17,133	b-ı
Bora	0,277	a-e	Almeria	4,667	a-g	Pannonia	17,033	b-ı

Anica	0,276	a-f	Golia	4,667	a-g	Rumeli	17,000	b-ı
Selimiye	0,274	a-f	Anica	4,667	a-g	Maden	16,900	c-ı
Pannonia	0,271	b-f	Bezostoja 1	4,600	a-h	Rebelde	16,900	c-ı
Quality	0,268	b-f	Prima	4,600	a-h	Quality	16,800	c-ı
Hakan	0,266	b-f	Selimiye	4,467	a-ı	Sarı Mustafa	16,700	c-j
Mihelca	0,266	b-f	Siyez-1	4,467	a-ı	NKÜ Asiya	16,533	c-j
Refikbey	0,265	b-f	İveta	4,400	a-j	Prima	16,333	d-k
Adelaide	0,262	b-f	LG59	4,400	a-j	İveta	16,067	e-l
TT-601	0,258	b-f	NKÜ Asiya	4,267	b-j	Selimiye	15,667	e-l
LG59	0,256	b-f	Maya	4,267	b-j	Başkan	15,467	e-m
İveta	0,253	b-f	Aldane	4,200	b-j	Hamza	15,067	e-m
Dukato	0,253	b-f	Refikbey	4,200	b-j	Bezostaja	14,800	e-m
Aldane	0,250	b-f	Ambrogio	4,200	b-j	Almeria	14,633	e-n
Misiia Odes.	0,246	b-f	Siyez-2	4,133	c-k	Bora	14,433	e-n
Masaccio	0,246	b-f	Energo	4,067	d-k	Aglika	14,200	e-n
Prima	0,245	b-f	Pannonia	4,000	e-l	LG59	13,933	e-n
NKÜ Asiya	0,244	b-f	Falado	3,933	f-l	Genesi	13,867	e-n
Energo	0,240	b-f	Kaan	3,800	g-l	Anica	13,700	e-n
Sarı Mustafa	0,238	b-f	Mihelca	3,800	g-l	Anopa	13,633	f-n
Almeria	0,236	b-g	Sarı Mustafa	3,800	g-l	Maya	13,467	g-n
Genesi	0,234	c-g	Maden	3,733	g-l	TT601	13,233	h-n
Kaan	0,233	c-g	Hakan	3,600	h-l	Ambrogio	12,733	ı-n
Rumeli	0,233	c-g	Genesi	3,600	h-l	Dukato	12,700	ı-n
Krasunia Odes.	0,232	c-g	Krasnia Odes.	3,600	h-l	Masaccio	12,600	ı-o
Başkan	0,227	c-h	Dukato	3,533	ı-l	Esperia	12,200	j-o
Golia	0,225	c-h	Adelaide	3,533	ı-l	Energo	11,833	k-o
Esperia	0,223	d-h	Masaccio	3,467	ı-l	NKÜ Lider	11,667	l-o
Emmer c.	0,213	e-h	Rumeli	3,467	ı-l	Aldane	10,967	mno
Rebelde	0,205	fgh	Misiia Odes.	3,400	jkl	Siyez-1	10,067	nop
Maya	0,205	fgh	NKÜ Ergene	3,400	jkl	Siyez-2	8,033	op
Siyez-2	0,165	gh	Emmer c.	3,133	kl	Emmer c.	5,867	p
Siyez-1	0,161	h	Başkan	3,000	l			

According to the results of the significance test, the genotype with the longest root with a root length of 24.80 cm was NKU Ergene. Hakan, Falado and Kaan varieties were ranked later for root length. While the genotype with the lowest value for root length was Emmer colour with 5,867 cm. Siyez-2, Siyez-1 and Aldane followed this variety.

Average values and importance groups for seedling weight, root number and root length obtained in PEG dose applications were given in Table 2.

When the effects of different PEG applications on the seedling weight were examined, the seedling weight varied between 0.280 - 0.230 g. The highest seedling weight was obtained in the control application with 0.280 g, followed by 0.25 MPa PEG application. The lowest seedling weight value of 0.230 g was obtained in the highest PEG application. This was followed by seedling weight obtained in 0.75 MPa PEG application. The results obtained, PEG application slowed down the water uptake of the plants and caused significant reductions in plant weight.

Table 2. Average values and importance groups of seedling weight, root number and root length

	Seedling weight (gram)			Root number (unit)			Root length (cm)	
PEG doses	Mean	Sig.	PEG doses	Mean	Sig.	PEG doses	Mean	Sig.
0,00 MPa	0,280	a	0,75 MPa	4,473	a	0,25 MPa	16,620	a
0,25 MPa	0,265	ab	0,50 MPa	4,302	a	0,00 MPa	16,031	a
0,50 MPa	0,252	bc	1,00 MPa	4,271	ab	0,50 MPa	15,895	a
0,75 MPa	0,237	cd	0,00 MPa	4,054	bc	1,00 MPa	14,109	b
1,00 MPa	0,230	d	0,25 MPa	4,023	c	0,75 MPa	13,589	b

When the effect of different PEG doses on the root length of the genotypes was examined, it was observed that the root length varied between 16.62 and 13.59 cm. The maximum root length was seen in the 0.25 MPa dose application with 16.62 cm. The control application with 16,031 cm and the 0.50 MPa dose application with 15,895 cm were in the same importance group with the 0.25 MPa dose application. The lowest root lengths were obtained with 13.59 cm and 14.11 cm in 0.75 and 1.0 MPa applications.

It was observed that there was a change between 0.0710 g and 0.0516 g for root weight in different doses of PEG applications. The highest value was obtained in the control application with 0.071 g. The data obtained on root weight in different PEG applications reveal that there is a decrease in root weight as the PEG dose increases, but the differences are statistically insignificant.

3.2. Root weight, shoot weight and shoot length

According to the variance analysis results, the effects of genotype and PEG applications on root weight, shoot length and shoot weight were statistically significant. Tukey test results, which were performed to see the significance between applications are given in Table 3.

Table 3. Average values and importance groups of root weight, shoot length and weight in genotypes

	Root weight (gram)			Shoot length (cm)			Shoot weight (gram)	
Genotypes	Ave.	Sig.	Genotypes	Ave.	Sig.	Genotypes	Ave.	Sig.
Enola	0,0862	a	Maden	20,067	a	Selimiye	0,1554	a
Bora	0,0799	ab	Bezostoja 1	18,833	ab	Maden	0,1538	ab
Anopa	0,0771	abc	NKÜ Ergene	18,633	abc	Enola	0,1531	ac
Ambrogio	0,0765	abc	Hakan	18,100	a-d	Bezostoja 1	0,1511	a-d
İveta	0,0762	abc	Selimiye	17,800	a-e	NKÜ Ergene	0,1507	a-d
Pannonia	0,0716	a-d	Sarı Mustafa	17,333	a-f	Prima	0,1433	a-e
Aglika	0,0714	a-d	Energo	16,667	a-g	TT601	0,1423	a-e
Hamza	0,0699	a-e	Prima	16,600	a-h	Refikbey	0,1351	a-f
Mihelca	0,0691	a-f	Falado	16,233	b-ı	Aglika	0,1345	a-f

NKÜ Asiya	0,0691	a-f	Kaan	16,167	b-ı	Hakan	0,1331	a-f
Falado	0,0689	a-f	Anica	15,733	b-j	Falado	0,1329	a-f
Adelaide	0,0672	a-g	Rumeli	15,733	b-j	Energo	0,1309	a-f
Quality	0,0669	a-g	Aglika	15,667	b-j	Anopa	0,1305	a-f
LG59	0,0668	a-h	Refikbey	15,600	b-k	Hamza	0,1292	a-f
Bezostoja 1	0,0647	a-h	Enola	15,600	b-k	Golia	0,1274	a-f
Misiia O.	0,0637	a-h	Hamza	15,233	c-k	Aldane	0,1271	a-f
NKÜ Lider	0,0634	a-h	TT601	14,867	d-l	Mihelca	0,1263	a-f
Masaccio	0,0631	a-h	Misiia Odes’ka	14,767	d-l	Sarı Mustafa	0,1258	a-f
Hakan	0,0628	a-h	Esperia	14,667	d-l	Bora	0,1256	a-f
Kaan	0,0614	a-h	Masaccio	14,433	e-l	NKÜ Lider	0,1247	a-f
Kras. O.	0,0607	a-h	Golia	14,400	e-l	Quality	0,1229	a-f
NKÜ Ergene	0,0603	b-h	Krasun.Odes’ka	14,267	f-l	Anica	0,1225	a-f
Anica	0,0601	b-h	Almeria	14,167	f-l	Ambrogio	0,1218	a-f
TT601	0,0596	b-h	Quality	14,167	f-l	Pannonia	0,1197	a-f
Refikbey	0,0579	b-h	NKÜ Lider	14,067	f-l	Adelaide	0,1170	a-g
Esperia	0,0575	b-h	Pannonia	13,900	f-l	LG59	0,1170	a-g
Rumeli	0,0575	b-h	Anopa	13,767	g-l	Dukato	0,1169	a-g
Almeria	0,0571	b-h	Aldane	13,700	g-l	Misiia Odes’ka	0,1154	a-g
Rebelde	0,0539	c-ı	Rebelde	13,633	g-l	Kaan	0,1146	a-g
Başkan	0,0520	c-ı	Genesi	13,467	g-l	Genesi	0,1139	a-g
Aldane	0,0487	d-j	Bora	13,433	g-l	Krasun.Odes’ka	0,1135	a-g
Golia	0,0475	d-j	Mihelca	13,400	g-l	Rumeli	0,1117	b-g
Genesi	0,0472	d-j	Siyez-1	13,300	g-l	İveta	0,1097	c-h
Prima	0,0451	e-k	Adelaide	13,300	g-l	Esperia	0,1085	d-h
Selimiye	0,0447	e-k	Başkan	13,267	g-l	Masaccio	0,1060	e-h
Maden	0,0443	e-k	Maya	13,133	h-l	Almeria	0,1044	e-h
Sarı Must.	0,0441	f-k	LG59	12,967	ı-l	Başkan	0,1040	e-h
Maya	0,0429	g-k	Dukato	12,933	ı-l	NKÜ Asiya	0,1034	e-h
Energo	0,0421	g-k	Siyez-2	12,600	jkl	Rebelde	0,1031	e-h
Dukato	0,0411	h-k	İveta	12,467	jkl	Maya	0,1009	e-h
Siyez-2	0,0307	ıjk	NKÜ Asiya	12,267	jkl	Emmer c.	0,0949	fgh
Siyez-1	0,0246	jk	Ambrogio	12,167	kl	Siyez-1	0,0749	gh
Emmer c.	0,0210	k	Emmer c.	11,400	l	Siyez-2	0,0665	h

According to the significance test, the highest root weight was from Enola genotype with 0.0862 g. Bora, Anopa, Ambrogio and Iveta varieties were found in the same statistical group as Enola. While the lowest root weight was 0.0210 g in Emmer colour genotype, Siyez-1, Siyez-2, Dukato, Energo and Maya genotypes was followed this genotype. In the significance test, it was determined that the highest shoot length was from Maden variety with 20,067 cm. Bezostoja 1, NKU Ergene, Hakan, Selimiye, Sarı Mustafa, Energo and Prima varieties were in the same statistical group with this genotype. The lowest shoot length was found in Emmer colored genotype with 11,400 cm. Ambrogio, NKÜ Asiya, İveta and Siyez-2 genotypes were ranked after Emmer colored genotype.

In the significance test, the highest value in terms of shoot weight was in Selimiye variety with 0.1554 g, Maden, Enola Bezostoja 1, NKÜ Ergene, Prima and TT601 genotypes were calculated in the same statistical group with Selimiye genotype. The lowest value for shoot weight was determined in Siyez-2 with 0.0665 g. Siyez-1, Emmer colored, Maya, Rebelde, NKÜ Asian, President, Almeria and Masaccio genotypes were in the same statistical group as Siyez-2. Average values of root weight, shoot length and shoot weight and importance groups in PEG dose applications were given in Table 4.

Table 4. Average values and significance groups of root weight, shoot length and weight

	Shoot weight (gram)			Shoot length (cm)			Shoot weight (gram)	
PEG doses	Mean	Sig.	PEG doses	Mean	Sig.	PEG dose	Mean	Sig.
0,00 MPa	0,0710	a	0,25 MPa	15,632	a	0,25 MPa	0,1358	a
0,25 MPa	0,0574	b	0,00 MPa	15,392	ab	0,00 MPa	0,1334	a
0,50 MPa	0,0569	b	0,50 MPa	14,802	bc	0,50 MPa	0,1222	b
0,75 MPa	0,0534	b	1,00 MPa	14,240	cd	0,75 MPa	0,1079	c
1,00 MPa	0,0516	b	0,75 MPa	13,760	d	1,00 MPa	0,1072	c

When the effects of different PEG applications on root weight are examined, it is seen that root weights vary between 0.0710-0.0516 g. The highest root weight was obtained with 0.0710 in 0.00 MPa PEG application. The lowest root weight was obtained with 0.534 g and 0.0516 g in the highest applications, 0.75 and 1.0 MPa PEG applications. Obtained results show that root weight decreases with increasing PEG dose.

It is seen that shoot length varies between 15,632 cm and 13,760 cm in different PEG applications. The highest shoot length was obtained with 15,632 cm in 0.25 MPa PEG application and 15,392 cm in plants without PEG application. The lowest shoot length was obtained with 13,760 cm from 0.75 MPa PEG application, followed by the highest dose of 1.00 MPA PEG application with 14.240 cm. The results obtained show that the shoot length decreases as the PEG dose increases.

When the data on shoot weight of different PEG applications were examined, the highest values were 0.1358 g in 0.25 MPa PEG application and 0.1334 g in 0.00 MPa PEG application. The lowest shoot weight was 0.1072 g and 0.1079 g in 0.75 and 1.00 MPa PEG applications were obtained.

4. CONCLUSION

In the study, plant weight, root number, root length, root weight, shoot length and shoot weight characters were determined in the drought stress created with different PEG doses. In the study carried out with forty-three genotypes, 1.00 MPa and 0.75 MPa applications of PEG 6000 caused statistically significant reductions in root and shoot characters. The results indicate that early and mid-early varieties were more tolerance to drought than the late varieties. Although Aglica, Anapo, Enola and Hamza varieties stand out for their root properties, while Maden, NKÜ Ergene and Bezostaya 1 cultivars showed more appropriate shoot characteristics than other cultivars. Enola, Aglika, Bezostoja 1, NKÜ Ergene, Anapo, Hamza and Maden bread wheat varieties showed the well growth characteristics under drought stress conditions in the study.

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Accelerated Pepper Breeding Studies with MAS and Androgenesis Techniques

Mesut NAR[1*] Hande Nur ALBEZİRGAN[1] Burcu DEMİRKAYA[1] Hakan FİDAN[2] Hakan AKTAŞ[3] Ş. Şebnem ELLİALTIOĞLU[4]

[1] AG Seed Industry Trade Inc., Antalya, Turkey
[2] Akdeniz University, Faculty of Agriculture, Plant Protection Department, Antalya, Turkey
[3] Isparta University of Applied Science, Faculty of Agriculture, Horticulture Department, Isparta, Turkey
[4] Ankara University, Technocity Doqutech Academy Ltd. Şti. Ankara, Turkey

*Corresponding Author: m.nar@agtohum.com.tr

By using molecular techniques and tissue culture studies together in plant breeding, it can produce superior with desired characteristics plants in a short time. By applying molecular markers in gene pools with relevant traits in the early period, new individual plants with desired genetic structure can be produced with reduced labor, time and costs. Determining the presence of the relevant resistance gene in plants at the seedling stage is easier within molecular markers than traditional methods such as artificial inoculations which requires time, labor and space. For determination of whether the resistance gene is either homozygous or heterozygous provides great knowledge to the breeder.

Another area for accelerating breeding studies in plant tissue cultures in biotechnology where double haploidy technology reduced time at least 5-8 times to obtain pure lines. Combinations of MAS and androgenesis techiniques have resulted in F1 hybrids and all relevant tests have also been conducted in 3 years.

According to statistics, the importance of pepper cultivation in Turkey is increasing day by day, and interest local varieties are gaining more interest due to their agronomic richness. The local varieties for instance, Hatay (Samandağ) pepper, are preferred in terms of quality characteristics e.g. hot, fresh and suitable for dried consumption, but it does not contain any disease resistance genes. Within the scope, we established the project is aiming to develop resistant hybrid varieties to Tomato Spotted Wilt Virus (TSWV) is causing high yield and quality losses in pepper production areas. For this purpose, studies are carried out to obtain pure resistant lines in a short time, a *Tsw* gene found in *Capsicum chinence*, which provides resistance to TSWV, was combined with Hatay pepper lines by crossbreeding. First of all, 20 of the Hatay pepper lines from the gene pool were selected according to weighted grading criteria, then the number was reduced to 4. In *C. chinense* lines, molecular screening was performed with SCAC568 primers (Moury et al., 2000) and individuals with *Tsw* gene were determined from donor parents and crosses. After then, backcrosses to Hatay peppers were conducted and GM1F1 was generated. Their seed samples were sown from them and brought until the first true leaves during the transition from seed to seedling stage. Meanwhile, molecular analyses were applied to find resistant individuals with *Tsw* gene. The homozygous and heterozygous plants were planted in a greenhouse and used in anther culture study.

In anther culture, haploid plants were developed using the protocol described Alremi et al. (2014). Whole study takes 22 months from the initiation of hybridization to the emergence of androgenic embryos and acclimatization to external conditions and development of DH seeds. Here, these findings are presented as a case study in biotechnology and the combined teqhniques are an indispensable part of accelerated breeding processes.

Keywords: Anther culture, Capsicum spp., Tsw, Hatay pepper, Molecular marker

1. Introductıon

Annual pepper production in the world is around 37 million tons (FAOSTAT 2020). Pepper, which is in the same family as tomato and eggplant, ranks second after tomato in terms of production value among Solanaceae vegetables in our country and has a total production amount of 2.6 million tons in an area of 792,617 ha (Anonymous 2020). Pepper is one of the vegetables with a wide distribution of types. Blocky bell peppers, Cubanella, Long sweet/hot, Poblano types of peppers are widely grown in our country. Pepper originated in South America (de Candolle 1886) and entered Anatolia in the 16th century and is cultivated. Anatolia, which has different ecologies and is on migration routes, has had a very rich diversity in terms of genetic resources in pepper over the years. One of them is our local variety, which is grown in and around Hatay, also known as Hatay pepper or Samandağ pepper, which is preferred in its smooth pointed form, and which is also consumed as fresh and dried chili peppers. However, crop losses have been experienced in recent years due to Tomato Spotted Wilt Virus (TSWV), which is one of the leading viral diseases that negatively affect yield and quality in open pepper cultivation. It is estimated that the TSWV, which infects more than thirty plant families, except the Solanaceae family in which pepper is found, causes more than 1 billion dollars of damage to agricultural products every year (Griep et al. 2000). TSWV; causes diseases and losses in important agricultural products such as tomatoes, peppers, eggplant, lettuce, beans, artichokes, celery and tobacco (Şevik 2014). TSWV viral infection causes yield losses of 30-100% (German et al. 1992). The use of resistant cultivars against the disease factor has become mandatory. Resistance is not available in the current native cultivars. Commercial foreign hybrid varieties have this resistance. Although the producer does not want to give up traditional pepper varieties, he necessarily turns to foreign varieties from which he can buy products. If resistance to TSWV factor is not transferred to our native material, it does not seem possible to maintain our genetic resources and existing native varieties in the market. It takes many years to develop varieties with traditional breeding methods, and although the cost is high, its effectiveness remains low. The inclusion of folded haploid techniques and molecular marker technologies in breeding programs is a basic need in today's conditions. In this study, the determination of the TSWV resistance gene (Tsw) with a molecular marker and its transfer to selected Hatay pepper breeding lines constituted the first stage of the study. The development of haploid pepper pure lines folded by the androgenesis technique, which is one of the genotypes with resistance in the first backcross generation, is the subject that is aimed to be done in the second stage.

2. Materials and Methods

In this project, which is aimed at breeding Hatay pepper varieties resistant to TSWV; Two basic biotechnological methods were used to accelerate the classical breeding methods: a. Determining the presence of disease resistance gene with a molecular marker, b. Obtaining homozygous pure lines using the folded haploid technique by androgenesis. To create a pepper gene pool, foreign hybrid cultivars, genitors, and local populations were collected from all over our country, some of which were interbred and some of them were inbred up to the F4-F7 stage. Thus, a rich genetic diversity has been achieved. In this project, hot Hatay-type peppers were studied.

In the first stage, morphological characterization (according to the selected UPOV criteria) and observation of agronomic traits were performed during a growing period in 20 local Hatay pepper breeding lines from the gene pool. Hatay pepper has different fruit shapes (Öntürk and Çürük 2019), 20 lines used in our study have more or less different characteristics from each other. Following the recording of the observations obtained from this stage, the selection was made with the weighted grading method to determine the 4 lines that our company would prefer to market primarily (Sönmez et al. 2015).

2.1. Determination of main (repetitive) parent lines by weighted grading method:

Determination of the main (repetitive) parent lines by weighted grading method: In 20 local Hatay pepper breeding lines selected from the gene pool of our company, plants were grown in the spring of 2021 and morphological and agronomic analyzes were carried out according to the selected UPOV criteria and market preferences. Weighed grading criteria (Table 1) such as plant structure, plant vigor, yield per plant, leaf cover, bitterness, fruit color and brightness were determined from Hatay type pepper populations, which is one of our local gene resources, and 4 different pepper lines with the highest scores were selected accordingly.

Morphological and agronomic analyzes were carried out according to the selected UPOV criteria and market preferences by growing plants in the spring of 2021 in 20 local Hatay pepper breeding lines selected from the gene pool of our company. Weighed grading criteria (Table 1) such as plant structure, plant vigor, yield per plant, leaf cover, bitterness, fruit color and brightness were determined from Hatay-type pepper (Cayenne type) populations, which is one of our local gene resources, and 4 different pepper lines with the highest scores were selected accordingly.

Table 1. Weighed grading observation criteria

Observation Criteria	%
Bitterness	30
Yield per plant	20
Plant Power	10
Plant Habitus (Closed)	10
Fruit shape	10
Fruit color (dark green)	10
Brilliance in fruit	10

2.2. Seeds from selected Hatay pepper and TSWV resistant lines in the nursery

Sowing seeds from selected Hatay pepper and TSWV resistant lines in the nursery Main parent (Hatay pepper lines) and paternal parent (lines carrying the resistance gene) plants and seeds were planted in seedling trays filled with a mixture of peat perlite (3:1) and in a fully controlled seedling greenhouse. They are grown until they have 5 true leaves. Figure 1 shows the seedlings of Hatay pepper and Chile pepper grown in the spring of 2021 and grown for the parent determination stage.

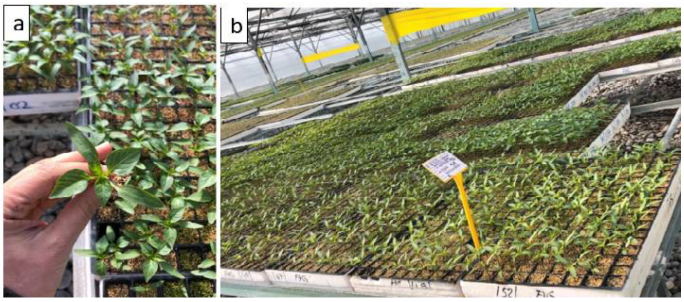

Figure 1. Images of the seedlings of the project breeding material grown in the seedling growing greenhouse in the spring of 2021 (a and b).

2.3. Planting the seedlings in the greenhouse and growing the plants in a healthy way

Greenhouses are arranged with materials suitable for growing plants and ventilation system in a way that will not cause disease and insect damage. To grow the plants in an environment free from diseases and thrips, aphid whitefly pests, applications such as 40 mesh insect netting, yellow and blue sticky traps, chemical control etc. were applied to the greenhouse ventilation openings. When the seedlings reach the stage with 4-5 true leaves, they were transferred to 1000 m^2 polyethylene covered greenhouses with 50x50 row spacing. In Figure 2, there are images of the stage of planting the pepper seedlings in the greenhouse.

Figure 2. Planting of seedlings of breeding material in the greenhouse in the spring of 2021

2.4. Making hybrids, taking seeds, planting seeds, growing seedlings

When the plants of 4 lines selected from Hatay peppers and 3-4 paternal parents that would give the resistance gene reached the flowering stage, hybridization was performed. For hybridization, pollen was first collected from fully opened paternal flowers into tubes, petri dishes or other suitable material with the help of a vibrator. Then, the fully developed but not opened buds in the main parent, and the anthers that have not yet burst, were selected and the petals and anthers were removed. The stigmas of the emasculated buds were pollinated by dipping into previously collected pollen, and the process was completed by attaching a label to the flower stem. Seeds from the fruits developed as a result of hybridization were harvested during the red maturity period, dried and replanted. In the second half of 2021, at this stage in the fall, backcrossing was done to Hatay pepper types and their seeds were taken in a healthy way.

In crosses made in 4 different Hatay pepper lines, pollen taken from 4 paternal parents was mixed and used in the pollination process with the mixed pollen technique. This method has a positive effect on obtaining hybrids with high adaptability and seed set rate. When the fruits formed were reddened, the seeds were removed, cleaned and dried. Using these seeds, replanting was done for the fall of 2021. It was planted in AG seed greenhouses on August 16, 2021. Hybridizations were started in the budding period. Thus, backcrossings were started in F1 plants and each line was crossed with its parent and GM1F1 A, B, C and D seeds were reached during the harvest period of the fruits. Seeds of these fruits were used as donor plants in anther culture studies in the 2022/1 development period

2.5. TSWV resistant analyses with molecular markers

Our lines developed from Chile peppers were tested for the presence of the Tsw gene. At this stage, 4 different pepper materials were selected as the father-parent. The pollen of these fathers was mixed and used in crosses with 4 Hatay pepper lines. The lines formed as a result of hybridizations were tested with the help of molecular markers in the molecular genetics laboratory established within the company. During the seedling period, 100 mg of leaves were taken from the true leaf samples of the pepper plant, and the CTAB protocol (Doyle and Doyle 1987) was applied and DNA was isolated (Figure 3). DNA samples were run on agarose gel and after quality control and concentration equalization, Moury et al.

(2000) PCR reaction was carried out using the CAPS marker (SCAC568). The protocol used for this is as follows: SCAC568 primers specific to the Tsw gene were used forward (5'GTGCCAGAGGAGGATTTAT 3') and reverse (5'GCGAGGTGACACTGATACT 3'). The PCR reaction is completed to a final volume of 50 µl with EcoTaq 2x PCR Master Mix 25 µl, Forward primer 10 µM 2 µl, Reverse primer 10 µM 2 µl, genomic DNA 10 pg-500 µg and ddH_2O. Cycle conditions 98 °C for 1 minute; 94 °C for 30 seconds, 57 °C for 30 seconds, 72 °C for 30 seconds 36 cycles and final elongation at 72 °C for 1 minute. The mixture prepared as 10 µl of the obtained PCR products, 1 µl of Thermo Scientific FastDigest XbaI enzyme, 2 µl of buffer and 17 µl of ddH_2O was cut at 37 ºC for 5 minutes and incubated at 65 ºC for 15 minutes.

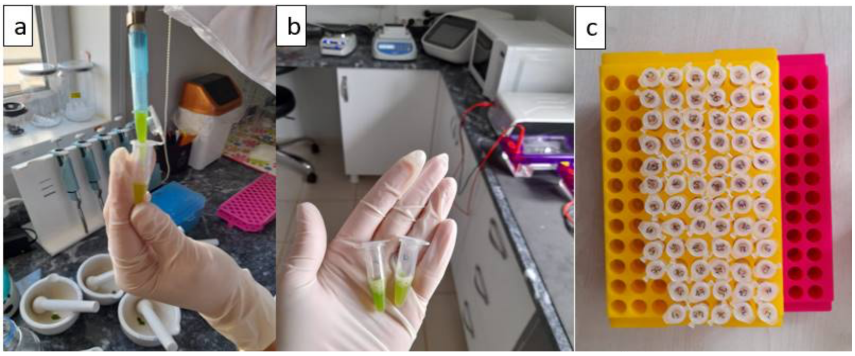

Figure 3. Examples of DNA isolation steps. a. Crushing the leaf samples with ctab solution in a mortar, b. Transferring the crushed samples to 1.5 microtubes, c. Arrangement of the crushed samples.

2.6. Collection and sterilization of buds in the appropriate period

In anther cultures, buds in the morphological development stage must be collected, subjected to surface sterilization in the laboratory and then cultured. It has been determined in previous studies that the buds in the suitable microspore period in pepper are the period when the petals and sepals reach the same level or pass 1-2 mm (Çömlekçioğlu and Ellialtıoğlu 2018). The blue-purple color transformation at the tips of the anthers is the key feature.

Process flow in anther cultures Bat et al. (2020) according to the method described (Figure 4). MS medium containing 4 mg/L NAA, 1.0 mg/L BAP, 0.25% activated charcoal, 30 g/L sucrose, 7 g/L agar and 15 mg/L silver nitrate was used as nutrient medium (Keleş et al. 2015). After the prepared nutrient media were adjusted to pH 5.8, they were sterilized in an autoclave at 121 ˚C for 20 minutes . The media removed from the autoclave was poured into petri dishes with a diameter of 60 mm in a sterile cabinet in equal amounts and left to solidify.

The cultures were incubated in a growth cabinet at a temperature of 25±1°C, with 16 hours of light and 8 hours of darkness (Vural et al. 2019). After the anthers were cultured, embryo emergence was observed in the 30-70 days of the incubation period in the climate chamber and the emergence was determined. A few days after the embryos were seen, they were first arranged in contact with the same environment, then germinated in hormone-free MS medium.

Plantlets that formed fringe roots and 4-6 true leaves were planted in mini pots filled with autoclaved ½ perlite + ½ peat mixture, giving life water. Developed plants were transferred to the greenhouse.

Figure 4. Anther culture stages. a. Disinfection of buds in 15% sodium hypochlorite for 12 minutes, b.Planting of anthers in nutrient media.

3. FINDINGS AND DISCUSSION

3.1. Identification of suitable lines from the gene pool

Weighed grading has been used for many years as a statistical and consistent selection method used in the selection of starting material suitable for breeding purposes from the gene pool or in highlighting the candidate variety among the variants obtained after the breeding program (Sönmez et al., 2015). It was also used effectively in the selection of breeding material for our project. Figure 5 shows the 4 Hatay pepper genotypes selected to be used as replicates in the study.

Figure 5. Plant habitus and fruit appearance of selected Hatay type peppers (a-b Hatay 1, c-d Hatay 2, d-e Hatay 3, f-g Hatay 4).

To transfer the Tsw gene to the sensitive Hatay peppers, the chile peppers at the F1-F3 stage found in our gene pool were tested with the molecular marker technique, and the genitors whose Tsw gene presence was confirmed and similar to the structure of the Hatay type pepper were selected.

3.2. Crossbreeding, generation advancement

Crosses were made with 4 selected Hatay-type pepper lines and Tsw-resistant chile peppers with mixed pollen technique. When the plants of 4 lines selected from Hatay peppers and 3-4 paternal plants that would give the resistance gene reached the flowering stage, hybridization was carried out using the mixed pollen technique. Harvesting and seed extraction of fruits that are at the stage of red ripening in the greenhouse was performed (Figure 6). Backcrossing was done on the plants grown from the seeds obtained. Backcrossings in the fall were made towards Hatay pepper types and their seeds were taken in a healthy way. Obtained individuals were subjected to molecular marker testing and it was examined whether they contain the Tsw gene. Those containing the resistance gene were used as donor plants for androgenesis studies.

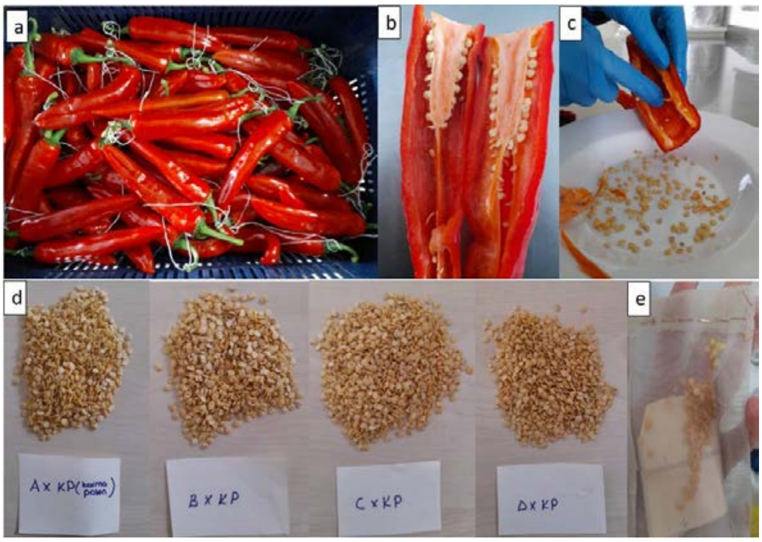

Figure 6. Cleaning and packaging of the fruits and seeds obtained as a result of the hybridization of Hatay pepper lines with Tsw-resistant peppers.

After the backcrossing, molecular marker tests were carried out in GM1F1 individuals of 4 different Hatay lines using SCAC568 primers specific to the Tsw gene and XBAI enzyme. In this context, the lines whose seeds were taken as a result of crosses in the previous season were grown and samples were taken from the real leaves while they were still in the seedling stage, and PCR tests were carried out after total nucleic acid isolation. Approximately 376 plants were tested during the season (Table 2). As a result, individuals with homozygous or heterozygous resistance were separated from individuals with homozygous recessive disease susceptibility characteristics in both alleles. For the anther culture, the buds were genotypes homozygous or heterozygous, containing the Tsw resistance gene, that is, the resistance gene and once backcrossed in the direction of Hatay pepper. Plants found to contain the resistance gene were transferred to the donor plant growing greenhouse to be used in the process of obtaining pure lines by androgenesis method, and anther culture was made from them at the stage of flower bud formation.

Table 2. Molecular marker (Tsw) test results

Number of plants tested	Homozygous (RR)	Heterozygous (Rr)	Susceptible (rr)	No tape
94	17	67	6	4
94	13	52	19	10
94	6	70	14	4
94	13	56	17	8
376	49	245	56	26

From androgenesis studies, approximately 2% haploid embryo formation was obtained as an average of genotype (Figure 7). The process of obtaining haploid plants, chromosome doubling and obtaining DH seeds are still in progress. DH seeds have started to be taken.

In Table 3, anther planting was made in the spring of 2022 and the embryo and plant numbers taken from them are given. Embryo emergence is continuing. Embryo formation frequencies close to each other were obtained from anthers taken from backcross donor plants in lines A, B, C and D, which have genetically similar characteristics. An average embryo formation frequency of 2.05 % was obtained. This number is within the embryo formation frequency range compatible with many previous studies (Çömlekçioğlu and Ellialtıoğlu, 2018; Atasoy et al., 2021). With the increase in the performance of the working system and personnel over time in the laboratory, it can be predicted that this ratio will also improve somewhat. However, since the embryo formation frequency is a genetic feature, the average success will still be in the same slice.

Figure 7. Development of pepper embryos from anthers and their transformation into plants (above), Growing haploid plantlets in vitro, Transferring to soil and acclimatization to external conditions (below).

Table 3. Anther numbers from plants from four different backcross combinations, their ratios with the number of embryos and plantlets obtained from them

Genotype	**Number of anthers cultured**	**Formed embryo number**	**The number of plantlets obtained**	**Embryo formation rate (%)**	**Plant formation rate (%)**
GM1F1 A	4000	82	73	2.05	1.83
GM1F1 B	3500	71	50	2.02	1.42
GM1F1 C	3500	96	81	2.40	2.31
GM1F1 D	3000	52	38	1.73	1.26
Total	13 500	301	242	2.05	1.71

4. Conclusion and Evaluation

In order to develop hybrid varieties in pepper, obtaining parent lines requires 6 generations of breeding, and breeding takes a long time. Pepper androgenesis, which was first initiated in the 1980s in our country, can be used successfully (Çömlekçioğlu and Ellialtıoğlu 2018). Until recently, almost all of the F1 hybrid varieties grown in our country were imported from abroad. In recent years, domestic hybrid varieties have started to take place in the market in some of the vegetable species, thanks to the establishment of their R&D enterprises by local seed companies, projects and incentives received with from government facilities. With the subject of trade in pepper and pepper products, an economic activity of approximately 1 billion dollars occurs in our country. In 2016, around 40,000 kg of open-pollinated and 350 kg of hybrid pepper seeds were produced, and some of the hybrid pepper seeds, all of which were purchased from abroad, could be met by domestic companies. The number of hybrids is less because Turkish consumer habits have peculiar characteristics in pepper, these demands cannot be met with varieties produced abroad, and most of the varieties grown in the open are local populations. Significant developments are expected in the seed sector in Turkey as well. Firms need to constantly increase their competitiveness

Since tissue culture and MAS technological infrastructure will contribute to product development in new areas, it will bring important innovations in the breeding process and shorten the development period of the variety. Obtaining pure lines in a short time, dihaploidization technique and anther culture can be practically integrated into breeding studies. When MAS technology is combined with selection and backcrossing programs, both faster and more reliable and easy results are obtained.

With the use of both techniques, it is possible to complete a 10-12 year breeding program in a short period of 3 years. Short-term breeding efforts and the rapid introduction of new varieties will generally improve the seed potential of Turkey.

With this ongoing study, pure lines in which the TSWV disease resistance gene is transferred to Hatay-type peppers, which is one of the genetic resources of our country, are successfully obtained. This material will be used as a parent in hybrid cultivar breeding and thus disease resistant local pepper varieties will be developed.

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Selection of Advanced Bread Wheat (*Triticum aestivum* L.) Lines in terms of Yellow Rust (*Puccinia striiformis* f. sp. *tritici*) and Grain Yield in Sakarya Conditions

Lutfu DEMIR[1*], Sinasi ORHAN[1], Sinan BAYRAM[1]

[1] Maize Research Institute, Sakarya, Türkiye

[*] Author for correspondence (lutfu.demir@tarimorman.gov.tr)

Abstract

Yellow rust (*Puccinia striiformis* f. sp. *tritici*) is one of the most important fungal diseases of wheat in our country. Fungus threats wheat production of Turkey and causes serious yield losses in suitable years via epidemics. Advanced bread wheat lines were evaluated in terms of yellow rust disease under natural epidemic and grain yield in this research, which was carried out in an augmented experimental design in the 2021-2022 growing season, in Sakarya rainfall-based conditions. In the research were used as material 125 bread wheat lines and 5 control varieties (Tahirova-2000, Mirsa, Kaynarca, Nusrat, Halis) in the preliminary yield trial carried out within the scope of the "South Marmara Region Bread Wheat Breeding Research" project carried out by Sakarya Maize Research Institute. Five of the 125 bread wheat lines tested in this study were in the "Resistance" group in terms of yellow rust. Six of the lines are grouped as “Sensitive”. It was determined that 82 lines used in the study were in the “Immune” group. Infection coefficient in bread wheat lines ranged from 2 to 100. The highest infection coefficient was determined as 100 in the 33 numbered bread wheat line. This line was followed by 6 and 22 bread wheat lines with an infection coefficient of 80. The lowest infection coefficient was determined as 2 in wheat lines 1 and 42. The grain yields of the bread wheat lines used in the research varied between 253.5-703.2 kg da^{-1}. The lowest grain yield was determined in line 25, and the highest yield was determined in line 66. As a result of this study, 68 promising lines among 125 advanced bread wheat lines evaluated in terms of yellow rust and grain yield were selected to be taken to the next stage.

Keywords: Bread wheat, yellow rust, grain yield

Introduction

Biotic stress factors are the most important factors limiting the production of bread wheat in our region, and rust diseases (especially yellow and leaf rust) come first. While leaf rust was the most common and effective rust disease in the region until the last few years, yellow rust has also started to be effective in recent years. Leaf rust is effective every year in Eastern Marmara and Thrace, although it may come late in some years. However, the effect of yellow rust has been increasing in recent years. New races developing in diseases can sensitize wheat genotypes known to be resistant to existing races. As a matter of fact, the "Warrior" race of yellow rust (Hovmøller et al., 2016), which was identified in England in 2011 and spreading rapidly in North Africa and many European countries, had a negative impact on wheat fields in Thrace and the Marmara Region in 2014.

Tahirova-2000 bread wheat variety, which is intensively cultivated in Eastern Marmara and resistant to yellow rust was severely affected by the new race of yellow rust and lost yields up to 80% (Demir et. al., 2017).

Chemical drugs used in the struggle against yellow rust are both costly and have negative effects on the environment and human health. A healthier way to prevent yield losses caused by yellow rust disease is possible by developing new varieties resistant to this disease.

This study was carried out to test the material in the preliminary yield trial established with 125 bread wheat lines and 5 control varieties within the scope of the "South Marmara Region Bread Wheat Improvement Research" project in terms of yellow rust disease and grain yield under natural epidemic in Sakarya rainfall-based conditions. Based on the data obtained as a result of the research, the lines showing superiority in terms of resistance to the disease and yield were determined and selected for use in the next stage of the breeding study.

Material and Method

This research was carried out at the Sakarya central experiment area of the Maize Research Institute in the 2021-2022 production season, under rainfall-based conditions. In the research were used as material 125 bread wheat lines and 5 control varieties (Tahirova-2000, Mirsa, Kaynarca, Nusrat, Halis) in the preliminary yield trial established within the scope of the "South Marmara Region Bread Wheat Breeding Research" project carried out by Sakarya Maize Research Institute.

Soil analysis was made by taking samples from 0-20 cm depth of the experiment area and some physical and chemical properties of the soil were determined. The results of the analysis showed that the texture class was clayey, the organic matter and phosphorus ratio was low, the reaction was slightly alkaline, the salt ratio was low, moderately calcareous and rich in potassium of the trial soils (Table 1).

Table 1. Some physical and chemical properties of experiment area soils*

Texture	K_2O (kg da^{-1})	P_2O_5 (kg da^{-1})	Calcareous (%)	Organic matter (%)	Total salt (%)	pH
Clayey	91.76	3.43	12.83	1.79	0.028	7.85

*Analysis was carried out in the Soil Analysis Laboratory of Ministry of Agriculture and Forestry.

Average temperatures (15.1 °C) in the 2021-2022 production season in Sakarya were above the long-term average (13.2 °C), especially the temperatures during the germination-emergence period of wheat affected growth and development positively. The total precipitation (825.4 mm) in the 2021-2022 production season was also higher than the total precipitation amount of long term average (727.8 mm) (Table 2).

Table 2. Climatic data of the experimental area for the 2021-2022 wheat production season*

Months	**Average temperature (°C)**		**Total precipitation (mm)**	
	2021-2022	**L.T.A.****	**2021-2022**	**L.T.A.**
October	21.4	15.4	68.4	78.5
November	13.0	11.5	35.3	78.7
December	12.9	8.4	56.9	101.9
January	10.2	6.1	139.0	91.1
February	8.1	6.8	79.8	76.2
March	7.9	8.7	101.4	71.2
April	12.6	12.7	80.6	58.9
May	19.0	17.5	74.4	52.3
June	21.0	21.5	88.1	67.8
July	25.2	23.4	101.5	51.2
Average	15.1	13.2		
Total			825.4	727.8

* It is taken from the annual climate data of Sakarya Meteorology Regional Directorate.
**L.T.A.: Long term average

The experiment was carried out in the form of 5 blocks, each consisting of 30 plots, according to the augmented experimental design. While the control types based on the calculation of the trial error were repeated in each block, the bread wheat lines in the trial were distributed sequentially to the blocks without replication (Petersen, 1994).

Sowing was carried out with a plot of 500 seeds/m^2 with a plot seeder, on 6.25 m^2 plots on November 12, 2022. With sowing, 7.5 kg da^{-1} pure N and 7.5 kg da^{-1} P_2O_5 were applied, and 7.5 kg da^{-1} pure N was applied during the jointing stage. In addition, herbicide application was made against broadleaf weeds. Grain yields were determined by harvesting with a parcel harvester when the plants reached maturity. Then, the grain yield was calculated as kg da^{-1}.

Yellow rust assessments were made according to the Modified Cobb Scale (Peterson et al., 1948). Reaction evaluations were made three times when the sensitive variety reached the 80-90 S level. Rust severity and reaction type were determined for the evaluation of the disease. The highest disease score of the variety was taken into account in the evaluation. The Infection Coefficient was calculated by multiplying the rust severity (the area covered by the disease on the leaf in %) with the coefficients determined for the type of infection (R=0.2; MR=0.4; MR-MS=0.6; MS=0.8; S=1). Evaluations were made according to this coefficient. In the evaluation, the Infection Coefficient was grouped as 0= Immune, 1-5= Resistant, 6-20= Medium Resistant, 21-40= Medium Sensitive, 41-100=Sensitive. In the selection of the material, according to the infection coefficient of the genotypes, those between 0-20 were considered the resistant group, and those with a value between 21-100 were considered the sensitive group.

Results and Discussion

When the 5 cultivars used as control varieties in the study were evaluated among themselves in terms of average values, it was seen that Nusrat variety was "immune" and Tahirova-2000 cultivar was "sensitive". Halis and Kaynarca varieties were determined as "medium resistant", and Mirsa variety was determined as "medium sensitive". The infection coefficient of the cultivars ranged from 7 to 44. The highest infection coefficient was determined in Tahirova-2000 cultivar, which is in the “sensitive” group (Table 3).

When the grain yields are examined, Kaynarca variety has the highest yield with 557.5 kg da^{-1}. This cultivar was followed by Tahirova-2000 (490.8 kg da^{-1}), Halis (454.2 kg da^{-1}) and Mirsa (426.7 kg da^{-1}) varieties, respectively. Nusrat, on the other hand, had the lowest value with a grain yield of 358.8 kg da^{-1} (Table 3).

Table 3. Yellow rust state and grain yields of control cultivars used in the research

Cultivars	Yellow rust					Grain yield (kg da^{-1})
	Rust severity	Reaction type	Infection Coefficient		Group	
Halis	10	S	1	10	Medium resistant	454.2
Kaynarca	7	S	1	7	Medium resistant	557.5
Mirsa	30	S	1	30	Medium sensitive	426.7
Nusrat	0	-	-	-	Immune	358.8
Tahirova-2000	44	S	1	44	Sensitive	490.8

When 125 bread wheat lines tested in the study were evaluated in terms of resistance to yellow rust, it was seen that 5 bread wheat lines were in the "resistant" group. 6 of the lines are grouped as “sensitive”. The fact that 82 lines used in the study are included in the "Immune" group shows that the selection made in the past years was successful. 23 of the lines are in the "medium resistant" and 9 of the lines are in the "medium sensitive" group (Table 4).

In advanced bread wheat lines, the infection coefficient varied between 2 and 100, excluding the immune ones. The highest infection coefficient was determined as 100 in line 33, followed by lines 6 and 22 with an infection coefficient of 80. The lowest infection coefficient was determined as 2 in lines 1 and 42 (Table 4).

Grain yields of bread wheat lines varied between 253.5-703.2 kg da^{-1}. Line 25 had the lowest grain yield, while line 66 had the highest yield (Table 4).

Table 4. Yellow rust state and grain yields of advanced bread wheat lines used in the research

No	Pedigree	Selection history	Yellow rust					Grain yield (kg da^{-1})
			Rust severity	Reaction type	Infection Coefficient		Group	
1	ADMIS//MILAN/DUCULA/4/CHEN/AE.SQ//2*WEAVER/3/OASIS/5*BORL95	SM-8705 0P 99P 99P 1P	5	MR	0.4	2	Resistant	551.4
2	ADMIS//MILAN/DUCULA/3/OPATA*2//WULP /CEYHAN99	SM-8714 0P 99P 99P 1P	0	-	-	-	Immune	501.4
3	ADMIS//MILAN/DUCULA/3/PRL/2*PASTOR//N566/OK94P597	SM-8716 0P 99P 99P 1P	0	-	-	-	Immune	603.5
4	CATBIRD//CHIL/CHUM18/3/Momtchil/4/Mudurnu-7 (2014)	SM-8723 0P 99P 99P 1P	10	S	1	10	Medium resistant	693.1
5	CATBIRD//CHIL/CHUM18/3/Momtchil/6/ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2	SM-8728 0P 99P 99P 1P	40	S	1	40	Medium sensitive	445.2
6	CATBIRD//CHIL/CHUM18/3/Momtchil/6/ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2	SM-8728 0P 99P 99P 1P	80	S	1	80	Sensitive	334.7
7	CATBIRD//CHIL/CHUM18/3/Momtchil/6/ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2	SM-8728 0P 99P 99P 1P	10	S	1	10	Medium resistant	268.1
8	CATBIRD//CHIL/CHUM18/3/Momtchil/4/NUSRAT	SM-8729 0P 99P 99P 1P	0	-	-	-	Immune	416.0
9	CATBIRD//CHIL/CHUM18/3/Momtchil/4/NUSRAT	SM-8729 0P 99P 99P 1P	0	-	-	-	Immune	436.8
10	CATBIRD//CHIL/CHUM18/3/Momtchil/4/NUSRAT	SM-8729 0P 99P 99P 1P	0	-	-	-	Immune	501.4
11	CATBIRD//CHIL/CHUM18/3/Momtchil/4/NUSRAT	SM-8729 0P 99P 99P 1P	0	-	-	-	Immune	382.7
12	FRTL/PIFED//KS970274/3/NAI80/HN7//BUC/3/F59/4/PRL/2*PASTOR//N566/OK94P597	SM-8734 0P 99P 99P 1P	0	-	-	-	Immune	478.5
13	FRTL/PIFED//KS970274/3/NAI80/HN7//BUC/3/F59/4/PRL/2*PASTOR//N566/OK94P597	SM-8734 0P 99P 99P 1P	0	-	-	-	Immune	391.0
14	BEREKET/5/BOW/URES//TRAP1*2/CARC/3/ATT/4 /RASSARINKO	SM-8736 0P 99P 99P 1P	40	S	1	40	Medium sensitive	395.2
15	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	0	-	-	-	Immune	509.7
16	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	0	-	-	-	Immune	316.0
17	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	0	-	-	-	Immune	343.1
18	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	0	-	-	-	Immune	301.4
19	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	0	-	-	-	Immune	257.1
20	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	10	S	1	10	Medium resistant	453.5
21	ALDANE/4/CHEN/AE.SQ//2*WEAVER/3/OASIS/5*BORL95	SM-8742 0P 99P 99P 1P	10	S	1	10	Medium resistant	403.5
22	ALDANE/4/CHEN/AE.SQ//2*WEAVER/3/OASIS/5*BORL95	SM-8742 0P 99P 99P 1P	80	S	1	80	Sensitive	320.2
23	ALDANE/4/CHEN/AE.SQ//2*WEAVER/3/OASIS/5*BORL95	SM-8742 0P 99P 99P 1P	0	-	-	-	Immune	526.4
24	ALDANE/3/OASIS/5*BORL 95//2*MARTAR	SM-8753 0P 99P 99P 1P	10	S	1	10	Medium resistant	399.3
25	NUSRAT/3/OPATA*2//WULP /CEYHAN99	SM-8764 0P 99P 99P 1P	0	-	-	-	Immune	253.5
26	OPATA*2/WULP //CEYHAN99/3/ALDANE	SM-8772 0P 99P 99P 1P	0	-	-	-	Immune	318.9
27	WUH1/VEE#5//MILAN/ SERI-82//VEE “S”/NAC/3/KATE A-1*2//CHIL/CHUM18	SM-8781 0P 99P 99P 1P	0	-	-	-	Immune	493.9
28	WUH1/VEE#5//MILAN/ SERI-82//VEE “S”/NAC/3/KATE A-1*2//CHIL/CHUM18	SM-8781 0P 99P 99P 1P	0	-	-	-	Immune	504.4
29	WUH1/VEE#5//MILAN/ SERI-82//VEE “S”/NAC/3/KATE A-1*2//CHIL/CHUM18	SM-8781 0P 99P 99P 1P	30	S	1	30	Medium sensitive	458.5
30	WUH1/VEE#5//MILAN/ SERI-82//VEE “S”/NAC/3/KARATOPAK	SM-8783 0P 99P 99P 1P	40	S	1	40	Medium sensitive	412.7
31	PRL/2*PASTOR//N566/OK94P597/3/ADANA-99	SM-8790 0P 99P 99P 1P	60	S	1	60	Sensitive	483.5
32	PASTOR/ HAHN"S"/MSİ//LİRA"S"/3/ADANA-99	SM-8793 0P 99P 99P 1P	10	S	1	10	Medium resistant	439.8
33	PASTOR/ HAHN"S"/MSİ//LİRA"S"/3/ADANA-99	SM-8793 0P 99P 99P 1P	100	S	1	100	Sensitive	337.7
34	PASTOR/ HAHN"S"/MSİ//LİRA"S"/3/NUSRAT	SM-8795 0P 99P 99P 1P	10	MS	0.8	8	Medium resistant	343.9
35	SAGETTARİO/FLORKWA-2/3/OASIS/5*BORL 95//2*MARTAR	SM-8803 0P 99P 99P 1P	10	S	1	10	Medium resistant	458.5
36	SAGETTARİO/FLORKWA-2/3/OASIS/5*BORL 95//2*MARTAR	SM-8803 0P 99P 99P 1P	0	-	-	-	Immune	543.9
37	SAGETTARİO/FLORKWA-2/3/OASIS/5*BORL 95//2*MARTAR	SM-8803 0P 99P 99P 1P	0	-	-	-	Immune	446.0
38	PAMUKOVA 97/TOWPE//ADANA-99/3/OASIS/5*BORL 95//2*MARTAR	SM-8806 0P 99P 99P 1P	0	-	-	-	Immune	473.1
39	OSMANİYEM//ERYTHROSPERMUM270/AVINT	SM-8811 0P 99P 99P 1P	5	MS	0.8	4	Resistant	514.8
40	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/CATBIRD/KARATOPAK	SM-8818 0P 99P 99P 1P	0	-	-	-	Immune	360.6
41	ADANA-99//BEZOSTAYA1/CITARI-9	SM-8840 0P 99P 99P 1P	5	MS	0.8	4	Resistant	381.4
42	OASIS/5*BORL 95//2*MARTAR/3/ALDANE	SM-8934 0P 99P 99P 1P	5	MR	0.4	2	Resistant	543.9
43	OASIS/5*BORL 95//2*MARTAR/3/ALDANE	SM-8934 0P 99P 99P 1P	0	-	-	-	Immune	389.8
44	FLAMURA85/BJY"S"/COC	SM-8953 0P 99P 99P 1P	10	S	1	10	Medium resistant	502.3
45	FLAMURA85/DOGANKENT-1	SM-8954 0P 99P 99P 1P	0	-	-	-	Immune	614.8
46	OPATA*2/WULP //CEYHAN99/3/KATE A-1*2//CHIL/CHUM18	SM-8768 0P 99P 99P 1P	0	-	-	-	Immune	677.3
47	OPATA*2/WULP //CEYHAN99/3/KATE A-1*2//CHIL/CHUM18	SM-8768 0P 99P 99P 1P	0	-	-	-	Immune	354.4
48	ADELAIDE/ADANA-99	SM-8963 0P 99P 99P 1P	0	-	-	-	Immune	425.2
49	YUNUS/NUSRAT	SM-8978 0P 99P 99P 1P	0	-	-	-	Immune	683.5
50	YUNUS/NUSRAT	SM-8978 0P 99P 99P 1P	0	-	-	-	Immune	648.1
51	NUSRAT/4/SNI/PBW65/3/KAUZ*2/TRAP//KAUZ	SM-8987 0P 99P 99P 1P	0	-	-	-	Immune	557.3
52	Adana99*4/70711//2*NUSRAT	SM-9019 F 0P 99P 99P 1P	0	-	-	-	Immune	509.4
53	Adana99*4/70711//2*NUSRAT	SM-9019 F 0P 99P 99P 1P	30	S	1	30	Medium sensitive	501.1
54	Adana99*4/70711//2*NUSRAT	SM-9019 F 0P 99P 99P 1P	0	-	-	-	Immune	613.6
55	Adana99*4/70711//2*NUSRAT	SM-9019 F 0P 99P 99P 1P	20	S	1	20	Medium resistant	453.2
56	NUSRAT*2/ADANA-99	SM-9030 F 0P 99P 99P 1P	10	MS	0.8	8	Medium resistant	613.6
57	NUSRAT*2/3/PAMUKOVA 97/TOWPE//ADANA-99	SM-9037 F 0P 99P 99P 1P	0	-	-	-	Immune	561.5
58	PAPULA/3/BEZOSTAJA-1//MV-17/UNK/4/SADOVO//Adana99*2/70711/5/STAR/3/Vratsa/Kate (8)*2//WU GENG8025/4/TODORA/MURGA	SM-9092 F 0P 99P 99P 1P	0	-	-	-	Immune	580.2
59	AISBERG/AE.SQUARROSA(369)//MURGA	SM-9103 0P 99P 99P 1P	40	S	1	40	Medium sensitive	578.2
60	AISBERG/AE.SQUARROSA(369)//OSMANİYEM	SM-9105 0P 99P 99P 1P	0	-	-	-	Immune	442.7
61	AISBERG/AE.SQUARROSA(369)//OSMANİYEM	SM-9105 0P 99P 99P 1P	0	-	-	-	Immune	515.7

62	ADANA 99/YAKAMOZ	SA 1600032-0SA-0SA-99P 1P	10	MS	0.8	8	Medium resistant	509.4
63	ADANA 99/YAKAMOZ	SA 1600032-0SA-0SA-99P 1P	10	S	1	10	Medium resistant	649.0
64	BURI/3/BECARD//ND643/2*WBLL1	SA 1600082-0SA-0SA-99P 1P	0	-	-	-	Immune	513.6
65	MILAN/KAUZ//PRINIA/3/BAV92/4/PASTOR*2/BAV92/5/ROLF07/6/GÖKKAN	SA 1600155-0SA-0SA-99P 1P	0	-	-	-	Immune	563.6
66	MILAN/KAUZ//PRINIA/3/BAV92/4/PASTOR*2/BAV92/5/ROLF07/6/GÖKKAN	SA 1600155-0SA-0SA-99P 1P	0	-	-	-	Immune	703.2
67	WAXWING/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/KARATOPAK	SA 1600164-0SA-0SA-99P 1P	10	S	1	10	Medium resistant	442.7
68	WAXWING/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/KARATOPAK	SA 1600164-0SA-0SA-99P 1P	0	-	-	-	Immune	471.9
69	FRNCLN*2/TECUE #1//DOĞANKENT	SA 1600218-0SA-0SA-99P 1P	0	-	-	-	Immune	526.1
70	FRET2*2/BRAMBLING/3/FRET2/WBLL1//TACUPETO F2001/4/WBLL1*2/BRAMBLING/5/KACHU*2/KISKADEE #1/6/KARATOPAK	SA 1600260-0SA-0SA-99P 1P	0	-	-	-	Immune	476.1
71	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/KAUZ//PRINIA/3/BAV92 /7/FRET2/KUKUNA//FRET2/3/YANAC/4/FRET2/KIRITATI/8/ YAKAMOZ	SA 1600274-0SA-0SA-99P 1P	10	MS	0.8	8	Medium resistant	688.6
72	GÖNEN 98/4/CROC-1/AE.SQUARROSA (224)//OPATA/3/FLAG-7	SEE16015-0S-0S 99P 1P	20	S	1	20	Medium resistant	524.0
73	GÖNEN 98/4/CROC-1/AE.SQUARROSA (224)//OPATA/3/FLAG-7	SEE16015-0S-0S 99P 1P	20	S	1	20	Medium resistant	488.6
74	SAGETTARİO/3/WBLL1*2/KURUKU//HEILO	SEE16033-0S-0S 99P 1P	0	-	-	-	Immune	559.4
75	CMH79A.1384/4/AGA/3/SN64/CNO67//INIA66/5/CMH82A.678/6/LUCO-M/7/SW89-5124*2/FASAN/8/ÖZCAN	SEE16100-0S-0S 99P 1P	0	-	-	-	Immune	391.9
76	CMH82A.1294/NEIXIANG 184//ELVIRA/3/BURI	SEE16112-0S-0S 99P 1P	0	-	-	-	Immune	303.0
77	CMH82A.1294/NEIXIANG 184//ELVIRA/3/BURI	SEE16112-0S-0S 99P 1P	0	-	-	-	Immune	361.3
78	CMH83.2578/ELVIRA//CATBIRD	SEE16117-0S-0S 99P 1P	0	-	-	-	Immune	313.4
79	CMH83.2578/ELVIRA//CATBIRD	SEE16117-0S-0S 99P 1P	20	S	1	20	Medium resistant	398.8
80	KAŞİFBEY95/4/TRAP#1/YACO/3/KAUZ*2/TRAP//KAUZ/5/CHEWINK/6/CROC_1/AE.SQUARROSA (205)//KAUZ/3/FINSI	SEE16128-0S-0S 99P 1P	0	-	-	-	Immune	353.0
81	İZMİR 85*3//BOBWHITE#1/FRENGKANG 15/4/QT8343/3/URES/PRL//BAV92	SEE16153-0S-0S 99P 1P	0	-	-	-	Immune	434.2
82	-		10	S	1	10	Medium resistant	498.8
83	Adana99*4/70711/3/ADMIS//MILAN/DUCULA	SM-8288 0P 99P 99P 1P 1P	0	-	-	-	Immune	407.2
84	Adana99*4/70711/3/ADMIS//MILAN/DUCULA	SM-8288 0P 99P 99P 1P 1P	0	-	-	-	Immune	384.2
85	Adana99*4/70711//NUSRAT	SM-8293 0P 99P 99P 1P 1P	0	-	-	-	Immune	367.6
86	D6301/HN VII//ERA/3/BUC/4/OPATA*2/WULP //CEYHAN99	SM-8344 0P 99P 99P 1P 1P	0	-	-	-	Immune	528.0
87	MARMARA 86/3/ADMIS//MILAN/DUCULA	SM-8397 0P 99P 99P 1P 1P	0	-	-	-	Immune	378.0
88	NUSRAT/ADANA-99	SM-8416 0P 99P 99P 1P 1P	0	-	-	-	Immune	401.7
89	NOGAL//JAGGER/ALLIANCE	TCI161249-0SE-050TE-050SBGH-050SBGH-2SBGH-0SE	0	-	-	-	Immune	355.1
90	53/3/ABL/1113//K92/4/JAG/5/KS89180B//VICTORY A//NE13515	x1621128-1B -1YM -0E	0	-	-	-	Immune	346.7
91	WIT910555/3/VPM/MOS83-11-4-8//PEW/4/KAPKA-I.P./BILINMIYEN96.55	TCI161256-0SE-36TE-1SE-0E	0	-	-	-	Immune	346.7
92	HBK0935-29-15/KS90W077-2-2/VBF0589-1/5/LCR/SERI/3/MEX-DW/BACA//VONA/4/TAM200/JI5418	TCI151151-0SE-050TE-1DYR-0E	0	-	-	-	Immune	473.8
93	ADMIS//MILAN/DUCULA/3/ROLF07/YANAC//TACUPETO F2001/BRAMBLING	SM-8706 0P 99P 99P 1P	0	-	-	-	Immune	661.3
94	ADMIS//MILAN/DUCULA/3/ATTILA*2/PBW65*2//MURGA	SM-8708 0P 99P 99P 1P	0	-	-	-	Immune	628.0
95	ADMIS//MILAN/DUCULA//FINSI/WBLL1	SM-8711 0P 99P 99P 1P	0	-	-	-	Immune	307.2
96	ADMIS//MILAN/DUCULA/3/KATE A-1*2//CHIL/CHUM18	SM-8712 0P 99P 99P 1P	10	MS	0.8	8	Medium resistant	550.9
97	ADMIS//MILAN/DUCULA/6/ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2	SM-8719 0P 99P 99P 1P	0	-	-	-	Immune	592.6
98	FRTL/PIFED//KS970274/3/NAI80/HN7//BUC/3/F59/4/NUSRAT	SM-8735 0P 99P 99P 1P	10	S	1	10	Medium resistant	486.3
99	OASIS/5*BORL 95//2*MARTAR/3/NUSRAT	SM-8741 0P 99P 99P 1P	0	-	-	-	Immune	528.0
100	ALDANE/4/CHEN/AE.SQ//2*WEAVER/3/OASIS/5*BORL95	SM-8742 0P 99P 99P 1P	60	S	1	60	Sensitive	436.3
101	NUSRAT/3/WUH1/VEE#5//MILAN/ SERI-82//VEE “S”/NAC	SM-8761 0P 99P 99P 1P	10	MS	0.8	8	Medium resistant	544.3
102	OSMANİYEM//ERYTHROSPERMUM270/AVINT	SM-8811 0P 99P 99P 1P	0	-	-	-	Immune	654.7
103	FLAMURA85/TNMU/MILAN	SM-8955 0P 99P 99P 1P	0	-	-	-	Immune	675.5
104	TAHİROVA-2000/KARATOPAK//NUSRAT	SM-8997 F 0P 99P 99P 1P	0	-	-	-	Immune	569.3
105	KAŞİFBEY/OSMANİYEM//NUSRAT	SM-8998 F 0P 99P 99P 1P	0	-	-	-	Immune	538.0
106	KAŞİFBEY/OSMANİYEM//NUSRAT	SM-8998 F 0P 99P 99P 1P	5	MS	0.8	4	Resistant	490.1
107	CEYHAN 99*2/3/ADMIS//MILAN/DUCULA	SM-9039 F 0P 99P 99P 1P	30	S	1	30	Medium sensitive	485.9
108	CEYHAN 99*2/3/ADMIS//MILAN/DUCULA	SM-9039 F 0P 99P 99P 1P	0	-	-	-	Immune	552.6
109	BEŞKÖPRÜ/3/SAUAL/YANAC//SAUAL	SA 1600061-0SA-0SA-99P 1P	0	-	-	-	Immune	275.5
110	SUNCO/2*PASTOR//ALTINÖZ	SA 1600094-0SA-0SA-99P 1P	0	-	-	-	Immune	402.6
111	MILAN/KAUZ//PRINIA/3/BAV92/4/PASTOR*2/BAV92/5/ROLF07/6/GÖKKAN	SA 1600155-0SA-0SA-99P 1P	0	-	-	-	Immune	542.2
112	MILAN/KAUZ//PRINIA/3/BAV92/4/PASTOR*2/BAV92/5/ROLF07/6/GÖKKAN	SA 1600155-0SA-0SA-99P 1P	0	-	-	-	Immune	546.3
113	ZEYBEK/GÖKKAN	SA 1600244-0SA-0SA-99P 1P	0	-	-	-	Immune	344.3
114	ZEYBEK/GÖKKAN	SA 1600244-0SA-0SA-99P 1P	0	-	-	-	Immune	352.6
115	TURACO/CHIL//SKAUZ/3/PASTOR /5/KIRITATI//HUW234/PRINIA/3/CHONTE/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI/6/YAKAMOZ	SA 1600271-0SA-0SA-99P 1P	0	-	-	-	Immune	410.9
116	META 2002/MISR-1	SEE16035-0S-0S 99P 1P	0	-	-	-	Immune	463.0
117	MUFITBEY/4/C-75-5/3/AGRI/NAC//KAUZ	TCI161277-0SE-050TE-050SBGH-19SBGH-0SE	0	-	-	-	Immune	619.3
118	DB/A 458/3/JI5418/MARAS//SHARK/F4105W2.1/7/BUL 2477-2/5/COL//093-44/AU/3/BEZ1//BEZ1/TVR/4/SAD1/6/GKKLS/BEUB	TCI162037-0SE-050TE-050SBGH-050SBGH-21SBGH-0SE	20	S	1	20	Medium resistant	398.4
119	MRS/CI14482//YMH/HYS/3/RONDEZVOUS/4/ABI 86*3414/X84W063-9939-2//KARL92/5/CMH83.2578/CHOIX//TEG	TCI161115-0SE-050TE-050SBGH-050SBGH-17SBGH-0SE	30	S	1	30	Medium sensitive	415.1
120	KS980511-3-~5/TX02U2510//KS06O3A~57/4/MNCH/ATTILA//TAM 400/3/N87V106/2180(OK97401)	TCI161425 -0SE-1TE -1E -0E	40	S	1	40	Medium sensitive	375.5
121	PANTHEON/BLUEGIL-2//KUYALNIK	TCI161195C24-1B -2YM -0E	60	S	1	60	Sensitive	365.1
122	06579G1-1/4/WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI	TCI131052-0SE-0100TE-2DYR-0E-2YM-0YM	0	-	-	-	Immune	377.6
123	TRCH/SRTU//KACHU/7/VEE#8//JUP/BJY/3/F3.71/TRM/4/BCN/5/KAUZ/6/163	TCI121038-0SE-0100TE-1DYR-3E-0E-3TE-0YM	0	-	-	-	Immune	319.6
124	MILAN/S87230//BABAX/3/HATCHER	TCI121125-0SE-0100TE-6DYR-0E-8YM-0YM	0	-	-	-	Immune	323.4
125	ATILA/3*BCN*2//BAV92/3/MV-18-2000	TCI151007-0SE-050TE-10DYR-0E	0	-	-	-	Immune	342.2

Conclusion

As a result of this study, 68 promising lines (1, 2, 3, 4, 8, 9, 10, 12, 13, 17, 20, 21, 23, 24, 26, 27, 28, 32, 35, 36, 37, 39, 41, 42, 45, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 61, 63, 65, 66, 70, 71, 72, 74, 77, 79, 80, 83, 84, 85, 86, 87, 88, 93, 94, 95, 96, 97, 99, 101, 102, 103, 104, 108, 111, 117, 123, 124) among 125 advanced bread wheat lines evaluated in terms of yellow rust and grain yield were selected to be used in the next stage. In addition, it can be said that the lines in the "resistant" group can be used as parents in yellow rust resistance breeding.

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e-mail: intpbc2022@figur.net

Secretariat

bisab

Fidanlık Mahallesi Adakale Sokak No:22/12
Kızılay / Ankara - Türkiye
Phone: 0312 433 30 65 – 66 / **Fax:** 0312 433 30 06
e-mail: secretary@intpbc2022.org

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